Content

GREENWOOD
RESOURCES

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Introduction: GreenWood Resources

- Global Investment and Asset Management Company founded in 1998

- Focus on short rotation high yield tree farms

- Expertise in agronomy, forestry, harvest engineering, financial management, and varietal development

- Operations in U. S., China, Chile, Poland

- 80 employees

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Introduction: Poplar for Multiple Markets

Logs for sawn products, veneer, and engineered wood products
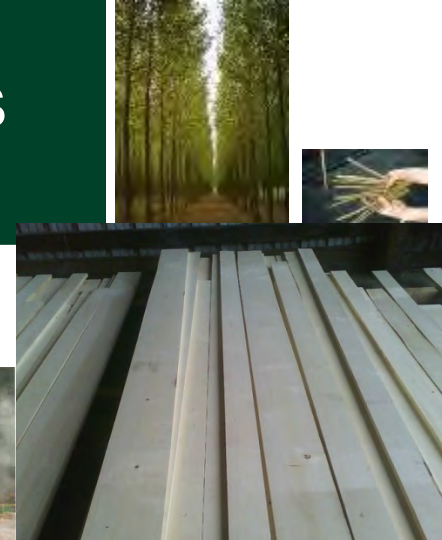
Chips:

- Pulp
- Biomass Energy

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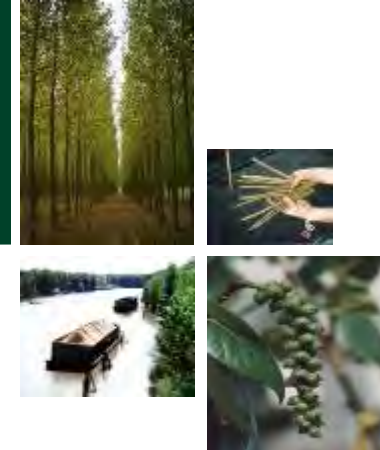# Introduction: Poplar Genetic Tree Improvement.

- Parental pure species improvement. Multiple populations.

- Varietal Development: hybridization, testing and selection.

- Traditionally, several stages of testing: nursery progeny, clonal, verification.

Year 1	Year 2	Year 3	Year 4	Year 5	Year 6	Year 7	Year 8	Year 9	Year 10	Year 11	Year 12	Year 13	Year 14
Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing		Scale-up	Verification						Commercial Deployment
	Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing		Scale-up	Verification					
		Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing		Scale-up	Verification				
			Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing		Scale-up	Verification			
				Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing		Scale-up	Verification		
					Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing		Scale-up	Verification	
						Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing		Scale-up	Verification
							Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing		Scale-up
								Parental Selection	Hybridization	Propagation Scale-up		Clonal Progeny Testing	

Introduction: Positive Results and in Poplar Tree Improvement.
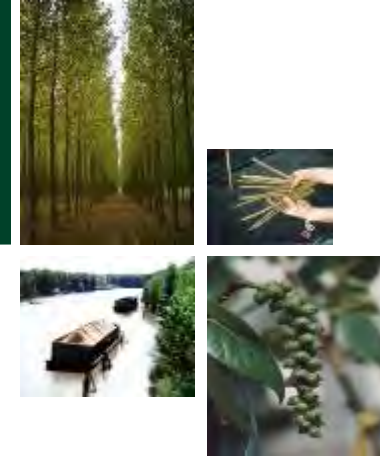
- **GreenWood Resources proprietary technology**
  - Hybrid development at LCTF:
    - 15 hybrid populations under testing and evaluation
    - 78 elite clones selected to date from 11 populations completing testing
  - Top selections show 25%-35% yield improvements above best available public domain clones.
  - Resistant to disease- leaf rust and shoot blight
  - 15%-25% improvement in specific gravity (strength, pulp yield)
  - Marked improvement in tree form – straightness, taper, branch angle
  - Continuous improvement into future owing to breeding of constituent parental species into their second generation; Creating 5 to 8 new elite clones per year
  - Work in biofuels area

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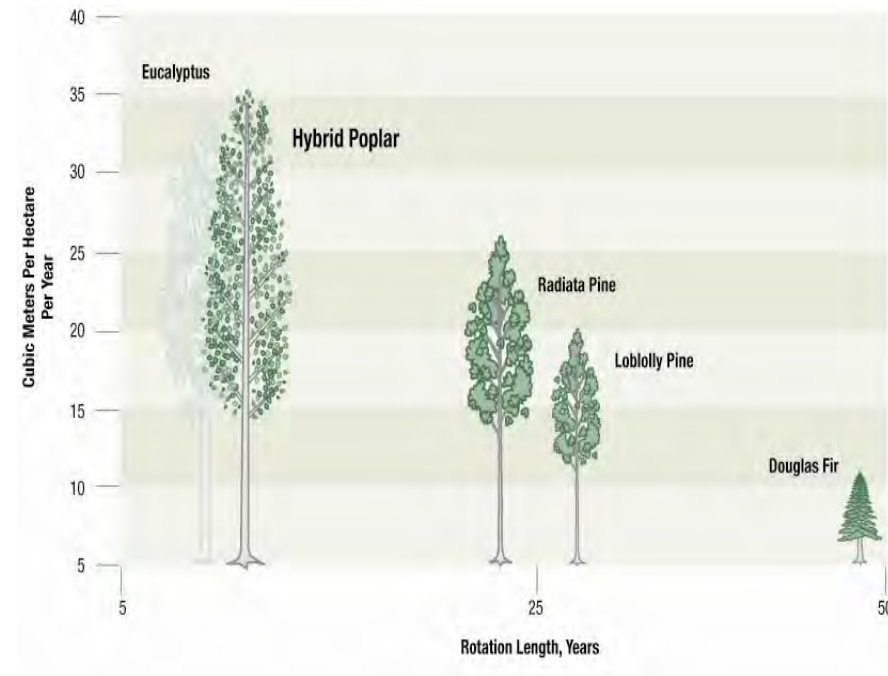
Objectives.

➤ Estimate genetic parameters from clonal trials planted and managed at biomass spacing.

➤ Use these genetic parameters to guide decision making in the tree improvement program for biomass production.

  ➤ Level of genetic control of several traits of economic importance.

  ➤ Detect changes in genetic control of these traits before and after coppice.

  ➤ Determine the magnitude of GxE interaction.

  ➤ Determine selection age for biomass traits.

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Material and Methods - Trials
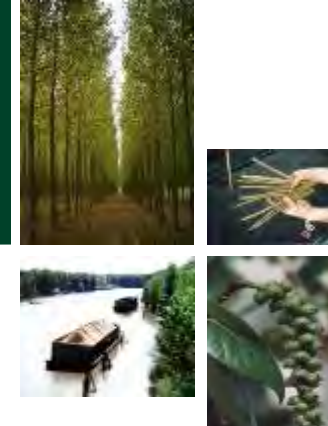
➤ Two series of trials established in 2009 and 2011.

2009 Trials:	2011 Trials:
➤ Design: RCBD, STP, 4 reps.	➤ Design: RCBD, 2 tree plots, 3 reps.
➤ Number of Sites: 2 - Westport (WPT)	➤ Number of Sites: 2 - Westport (WPT)
- Boardman (BRS)	- Boardman (BRS)
➤ Spacing: 3.05m x 0.91m => 3,597 sph.	➤ Spacing: 1.8m x 1.8m => 3,076 sph.
➤ Genetic material: 168 clones at WPT	➤ Genetic material: 41 clones at WPT
90 clones at BRS	60 clones at BRS
➤ Coppiced twice: age 2 and age 5.	➤ No coppice.

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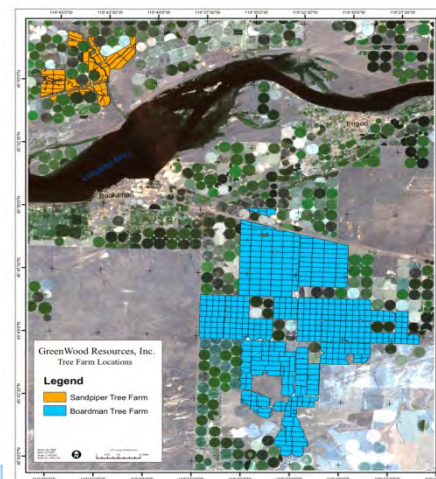
Material and Methods - Trials

Westport
- Alluvial Sites
- Network of levees and drainage canals
- Intensive weed control management
- Pruning – 3 annual lifts from age 2 to 4 years
- Rotation – 15 years for furniture, molding, veneer, pallets
- Productivity – 30 m3/ha/year

Boardman
- Sandy soils
- Desert environment
- Irrigation – River pumping station, drip irrigation.
- Intensive crop management (weed control, pruning age 2 to 4 years)
- Rotation – 12 - 14 years for furniture, molding, veneer, pallets, bioenergy residual.
- Productivity –40 m3/ha/year

GreenWood Resources, Inc.
Tree Farm Locations
Legend
Sandpiper Tree Farm
Boardman Tree Farm

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➢ Linear mixed models were used to estimate variance components.

➢ Genetic parameter were estimated to answer the following questions.

- What's the genetic control of commercially important traits?

- What happens with genetic parameters before and after coppice?

- What's the genetic correlation among traits before and after coppice?

- Is it possible to select clones as early as age one or two, before coppice?

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Results – Heritabilities, 2011 Trials.

Genetic Analysis WPT11SUNG

Trait	H^2	$SE(H^2)$
DBH2	0.6338	0.0712
HT2	0.6921	0.0622
WT2	0.6705	0.0619
BIO2	0.6303	0.0727

Genetic Analysis BRS11SUNG

Trait	H^2	$SE(H^2)$
DBH2	0.2981	0.0797
HT2	0.3669	0.0828
WT2	0.3494	0.0690
BIO2	0.3252	0.0796
DBH3	0.2225	0.0717
HT3	0.4077	0.0763
WT3	0.2116	0.0636
BIO3	0.2107	0.0701
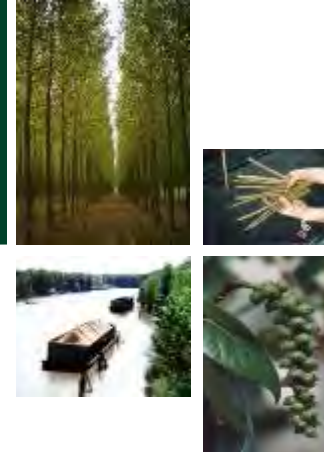
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Results – Genetic Correlations among Traits, 2011 Trials.

Genetic Analysis: 2011 Trial at BRS

Correlation of Genetic Values
DBH2 - DBH3

Type A gen. correlation, $Rg_A = 0.773$

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Genetic Analysis: 2011 Trial at BRS

Correlation of Genetic Values DBH2 - WT3

Type A gen. correlation, $Rg_A = 0.740$

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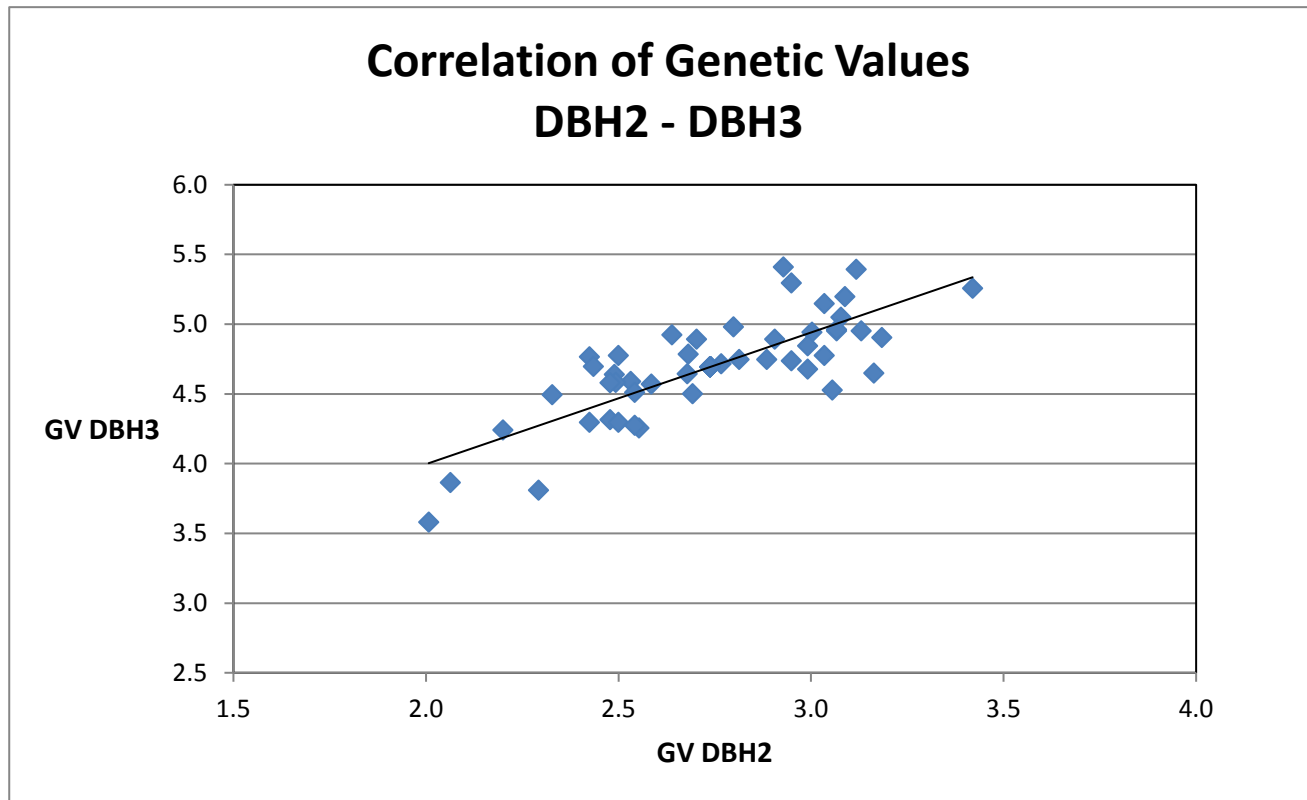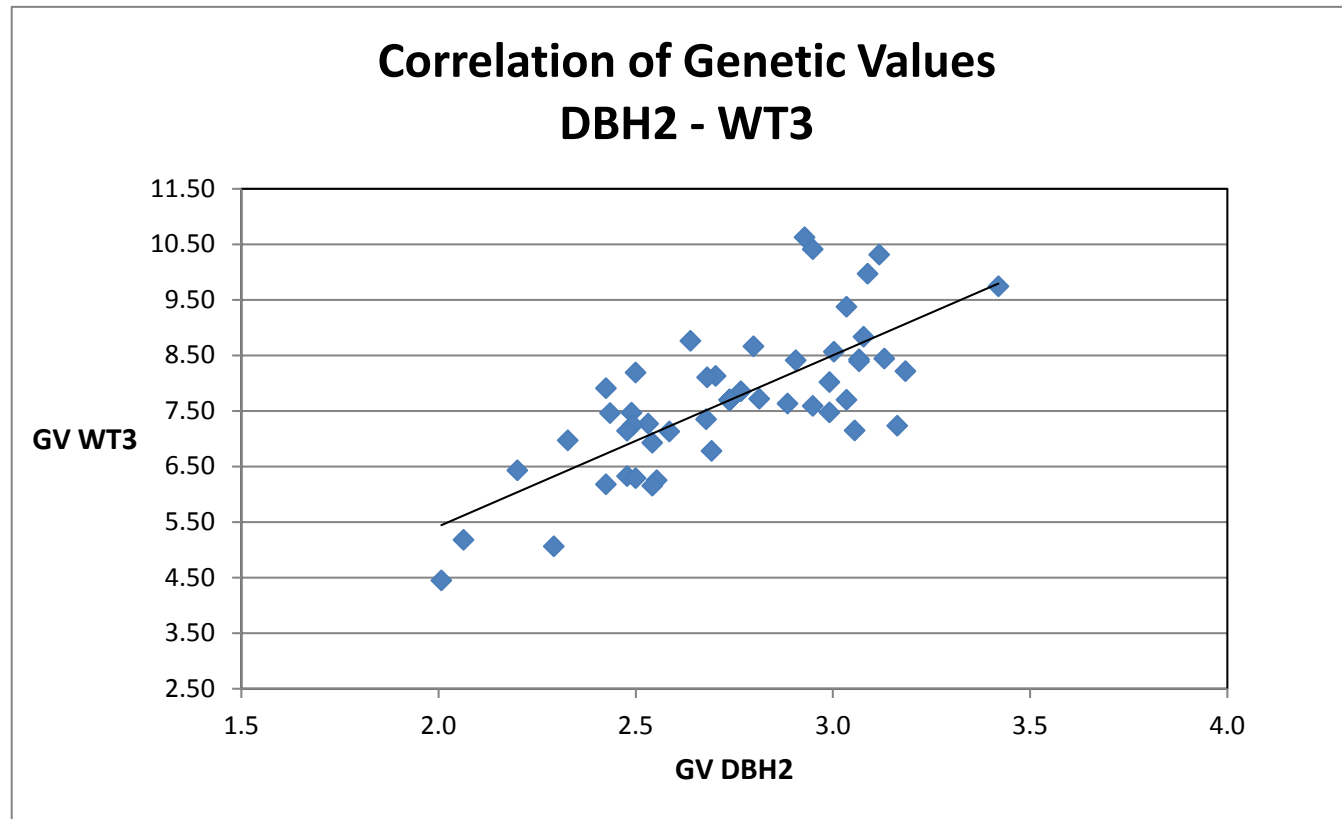
Results – Genetic Correlations among Traits, 2011 Trials.
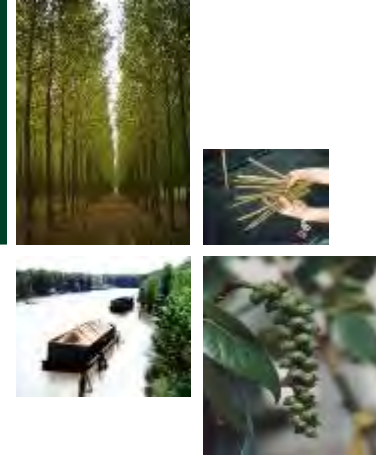
Genetic Analysis: 2011 Trial at BRS

Genetic Corelations (below the diagonal) and Standard error of the correlation (above the diagonal)

		Standard Error							
		DBH2	HT2	DBH3	HT3	WT2	WT3	BIO2	BIO3
Genetic Correl.	DBH2		0.027	0.083	0.096	0.002	0.100	0.008	0.092
	HT2	0.944		0.099	0.065	0.032	0.119	0.021	0.095
	DBH3	0.773	0.736		0.087	0.087	0.006	0.093	0.021
	HT3	0.696	0.821	0.748		0.097	0.100	0.086	0.052
	WT2	0.997	0.931	0.766	0.701		0.101	0.004	0.091
	WT3	0.740	0.695	0.994	0.727	0.737		0.107	0.019
	BIO2	0.990	0.956	0.755	0.753	0.993	0.721		0.089
	BIO3	0.759	0.778	0.954	0.888	0.764	0.955	0.778	

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Results – Genotype by Environment Interaction, 2011 Trials.
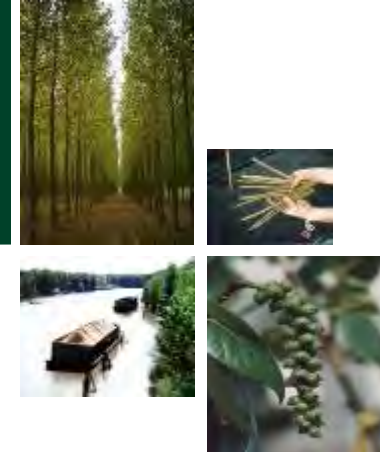
Rank	BRS 2011 Clone	WT2		WTP 2001 Clone	WT2
1	C105	4.047387		C105	5.04297
2	C104	3.251487		C107	3.83897
3	C103	3.176387		C108	3.80297
4	C130	3.107487		C104	3.30997
5	C131	3.055587		C106	2.88497
6	C106	3.054787		C101	2.05117
7	C111	3.053087		C100	2.02317
8	C113	3.040287		C131	1.76457
9	C100	2.914387		C130	1.67837
10	C107	2.907987		C110	1.61367
11	C121	2.883887		C103	1.35297
12	C127	2.844387		C118	1.33177
13	C123	2.769387		C119	1.20197
14	C108	2.705787		C102	1.15306
15	C102	2.690487		C125	1.08067
16	C109	2.625687		C111	1.07607
17	C128	2.404327		C117	0.91457
18	C132	2.375387		C128	0.74017
19	C120	2.209687		C109	0.65857
20	C110	2.204587		C129	0.60677
21	C116	2.186787		C121	0.53687
22	C129	2.158787		C124	0.52607
23	C118	1.967987		C122	0.44747
24	C124	1.926087		C127	0.41667
25	C114	1.852287		C112	0.40547
26	C125	1.846487		C113	0.38747
27	C101	1.845887		C126	0.36967
28	C117	1.831887		C123	0.33967
29	C126	1.820487		C132	0.30887
30	C122	1.691987		C115	0.28697
31	C112	1.665287		C120	0.20417
32	C115	1.398187		C116	0.08897
33	C119	1.200387		C114	-0.04903

Type B genetic correlation across sites (GxE), between clones in 2011 Trials at BRS and WPT.

	TypeB	SE
DBH2	0.836	0.1388
HT2	0.688	0.1489
WT2	0.817	0.1431
BIO2	0.785	0.1399

➢ 2009 Trials were coppiced.

**End of first growing season.
Measurements in yr. 1,
then Coppice.**

**Coppice again, in yr. 3 and yr. 5
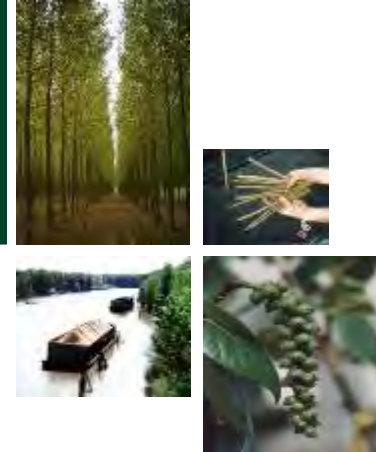Measurements before
each coppice.**

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Results – Heritabilities, 2009 Trials.

Genetic Analysis WPT09SUNG

Trait	H^2	$SE(H^2)$
HT1	0.5338	0.0384
DBHA2	0.3985	0.0420
DBHA3	0.4775	0.0403
DBHA5	0.1941	0.0411
HT5	0.2572	0.0429
BIO5	0.3663	0.0425
BIOA5	0.2895	0.0426
BACUM	0.5017	0.0396

Genetic Analysis BRS09SUNG

Trait	H^2	$SE(H^2)$
HT1	0.4730	0.0573
DBHA2	0.4379	0.0581
STCA2	0.2487	0.0600

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Genetic Analysis: 2009 Trial at WPT.

Correlation of Genetic Values
DBHA2 - DBHA3

GV DBHA3

GV DBHA2

Type A gen. correlation, $Rg_A = 0.965$

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Genetic Analysis: 2009 Trial at WPT.

Correlation of Genetic Values
DBHA2 - BIOA5

Type A gen. correlation, $Rg_A = 0.850$

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Results – Genetic Correlations among Traits, 2009 Trials.

Genetic Analysis: 2009 Trial at WPT.

Correlation of Genetic Values
DBHA2 - BACUM

Type A gen. correlation, $Rg_A = 0.945$

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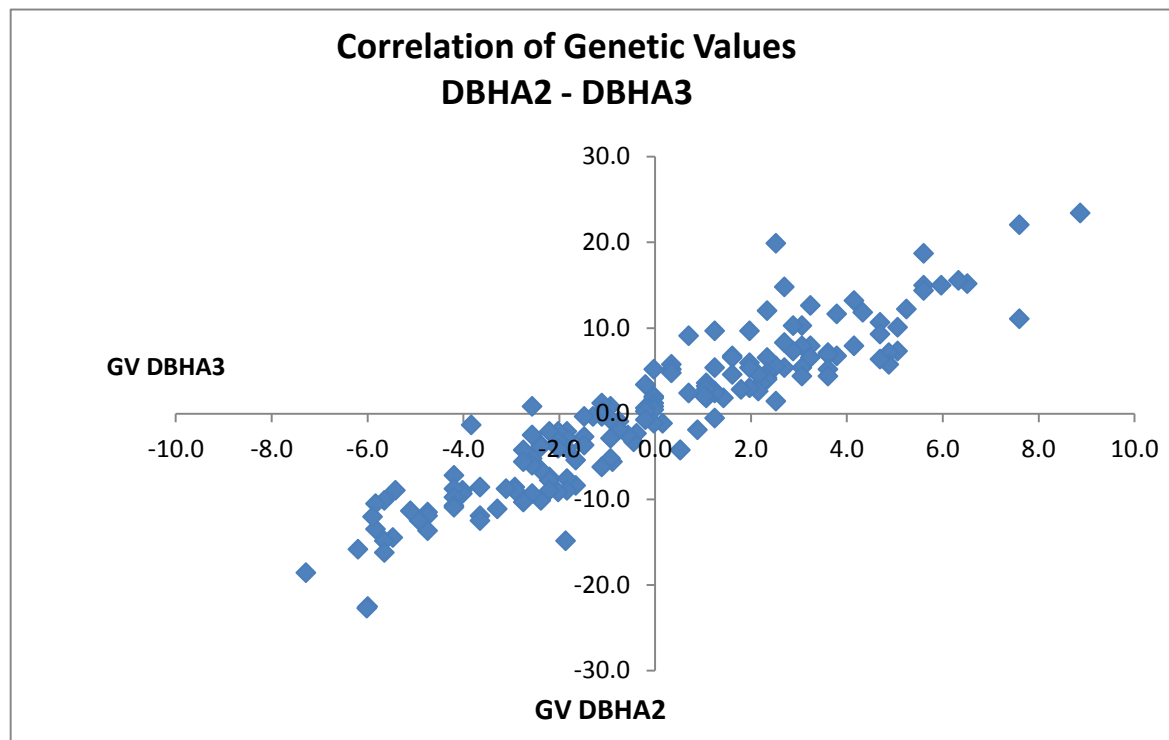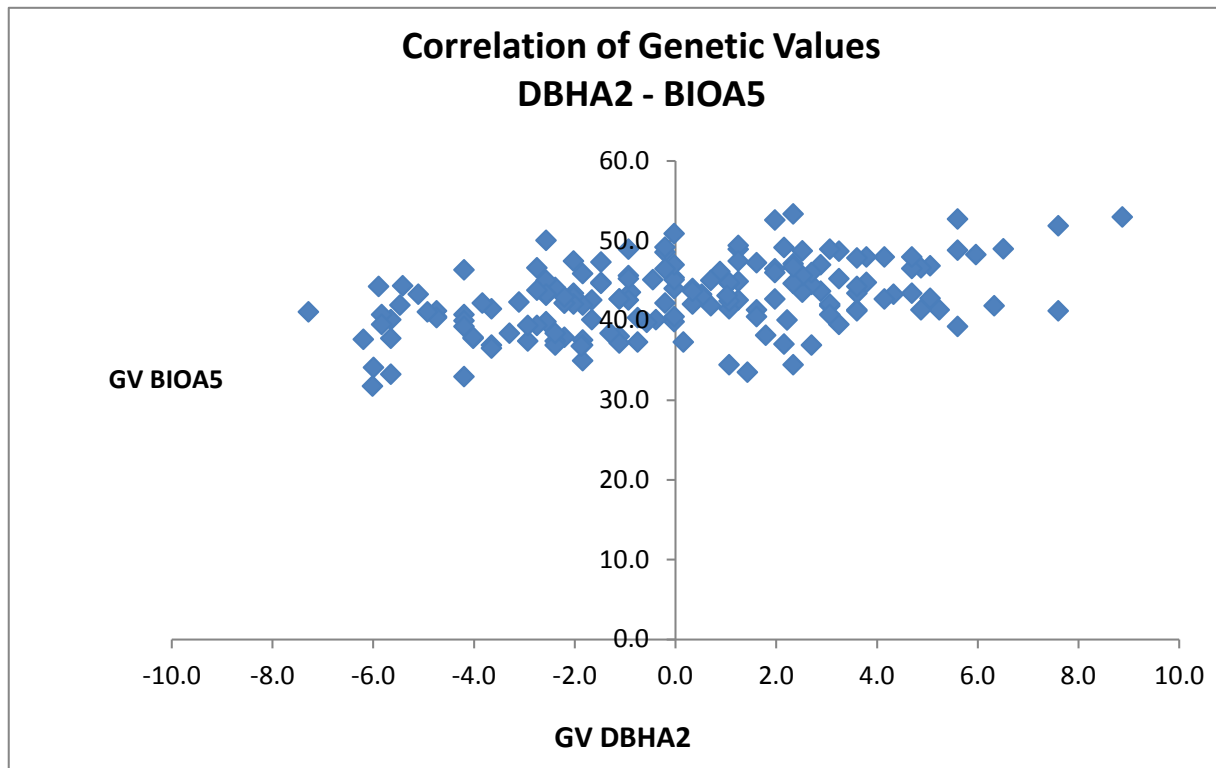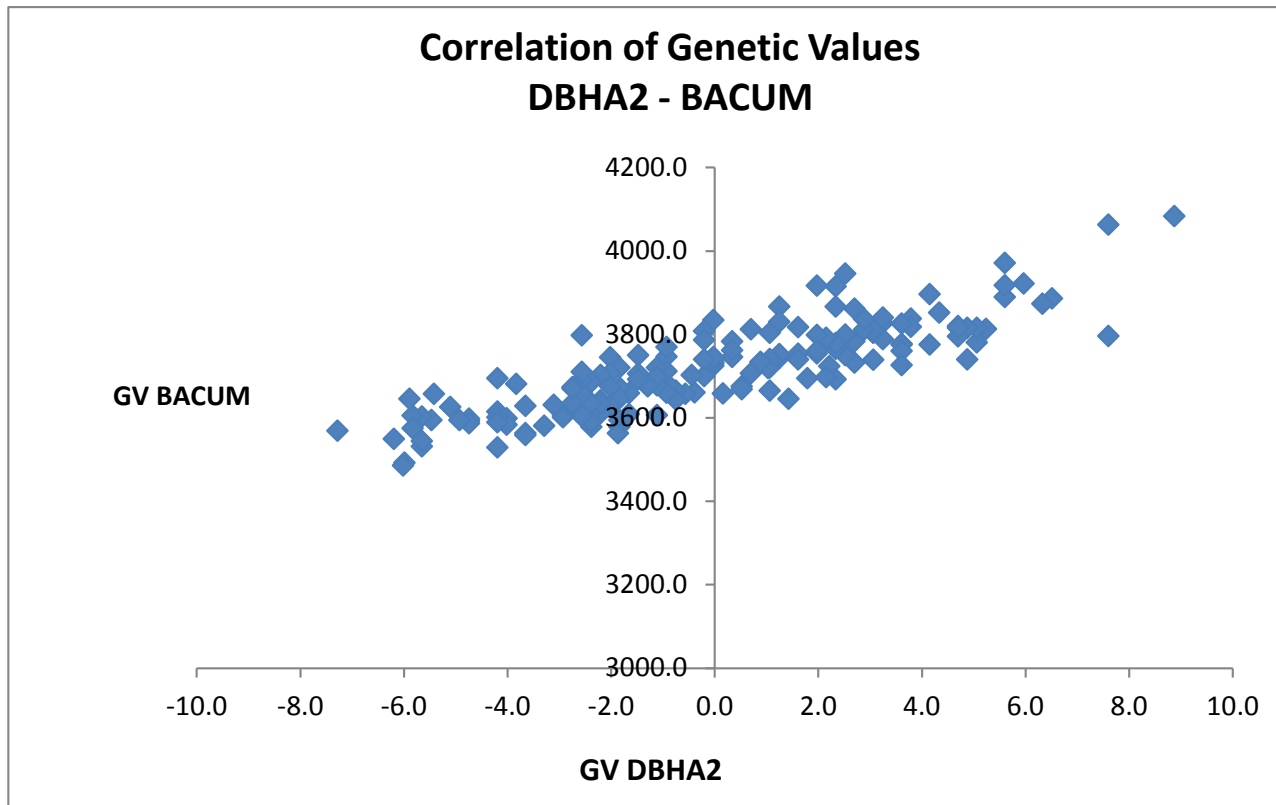
Results – Genetic Correlations among Traits, 2009 Trials.
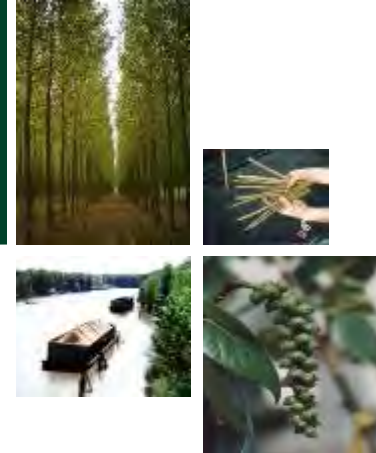
Genetic Analysis: 2009 Trial at WPT.

Genetic Corelations (below the diagonal) and
Standard error of the correlation (above the diagonal)

		Standard Error						
		HT5	DBHA5	BIO5	BIOA5	BACUM	DBHA3	DBHA2	HT1
Genetic Correlations	HT5		0.03416	0.05043	0.03543	0.06587	0.08903	0.10191	0.10827
	DBHA5	0.880		0.03615	0.01540	0.05071	0.09058	0.10404	0.11736
	BIO5	0.800	0.941		0.02671	0.04244	0.06623	0.07156	0.09228
	BIOA5	0.873	0.963	0.815		0.02748	0.06156	0.07390	0.09771
	BACUM	0.711	0.896	0.823	0.939		0.01005	0.02375	0.07855
	DBHA3	0.652	0.825	0.736	0.879	0.985		0.01143	0.07862
	DBHA2	0.581	0.792	0.766	0.850	0.945	0.965		0.07870
	HT1	0.315	0.359	0.386	0.425	0.467	0.465	0.514	

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Genetic Analysis: 2009 Trial at WPT.

Genetic Gain (%)

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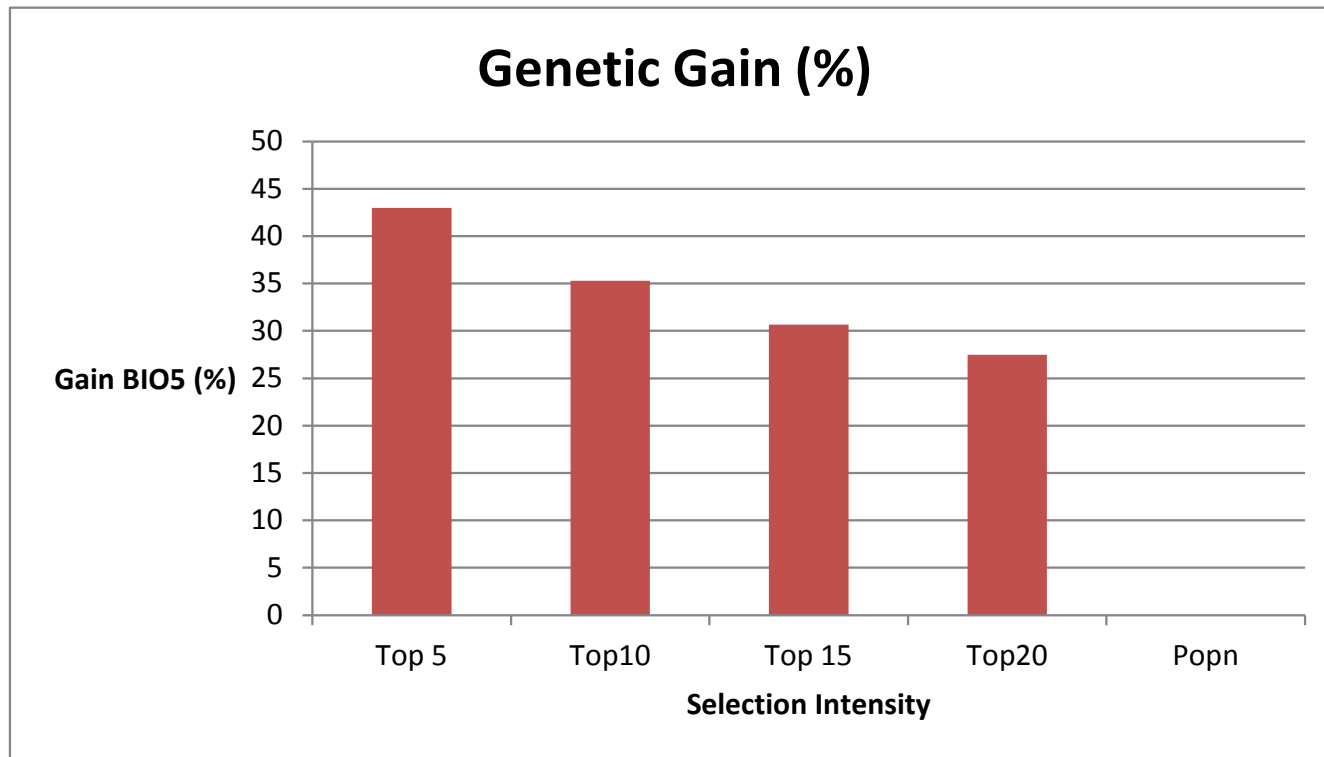
Conclusions.

1) Most of important trials for biomass production are under moderate to high genetic control (H^2 = 0.3 to 0.6).

2) Heritability values for DBH, total height, Biomass and weight are slightly lower after coppice but still high to ensure good results from selections.

3) The sum of Total Biomass produced after two harvesting cycles have the highest heritability (H^2 = 0.50.

4) The results of Type A genetic correlations, suggests that:

   a. DBH is a good predictors of biomass production.

   b. Age-Age genetic correlations suggest that clones for biomass could be selected as early as after the first growing season after the first coppice.

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