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# Selection for Both Growth and Wood Properties in Hybrid Poplar Clones

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**ABSTRACT.** To better understand the genetic control of growth and wood properties in the hybrid poplar (*Populus* spp.), genetic relationships of selected wood properties with growth traits were examined in a 3-yr-old clonal trial located in Windsor and St-Ours, southern Quebec, Canada. In total, 371 trees from 21 hybrid poplar clones were sampled at the two locations. Clone effects are stronger than growth traits effects on wood density and initial moisture content. The estimated clonal repeatability for wood density (0.92) and initial moisture content (0.80) across the two sites are thus considerably higher than for dbh (0.64) and tree height (0.72). Neither wood density nor mean fiber length were found to significantly correlate with growth traits. This suggests that in the hybrid poplar clones selection for growth traits will not result in a significant reduction in the wood quality traits. Selection for stem dry fiber weight appears to be an optimal selection strategy, as it will lead to the highest genetic gain in stem dry fiber yield, or maximum fiber production while wood density is improved. *FOR. SCI.* 49(6):00–00.

**Key Words:** Hybrid poplar clones, tree growth, wood properties, dry fiber weight, clonal repeatability, genetic gains

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**I**N RECENT YEARS, the forest industry has shown a particular interest in planting hybrid poplar clones for high-yield fiber production as the wood supply is emerging as a constraint, and an increasing amount of land base is becoming available. Thanks to high growth rate, the plantations of genetically improved hybrid poplar clones in eastern Canada could reach sawlog size in 15 yr with an annual yield of 8–15 m<sup>3</sup>/yr/ha (Vallée 1995a, 1995b). In fact, potentially high yields and short rotation ages make hybrid poplar clones the preferred tree species in most provinces. Several provinces (e.g., Quebec, Saskatchewan, Alberta) are developing a hybrid poplar agroforestry program. Recognizing the great potential of fast-growing and short-rotation hybrid poplar clones for high-yield fiber production a couple of decades ago, the Quebec Ministry of Natural Resources has set up an active poplar breeding program. Over the years, a number of poplar clonal and progeny trials have been established. The program has been focused on growth rate, form, adaptability,

and disease resistance (Vallée 1995a, 1995b). As forest products companies are interested in hybrid poplar clones for the manufacture of a variety of products (e.g., pulp, panels, veneer, solid products), the selected clones must meet the needs of the forest industry for diverse end uses. It is well known that different end uses require different wood characteristics (Zhang et al. 1997). Therefore, wood properties and end-use potential of hybrid poplar clones need to be evaluated and taken into account in the breeding program. To this end, it is critical to understand the genetics of wood properties and their relationships with growth traits.

Genetics of wood properties have been subjected to numerous studies (Zobel and van Buijtenen 1989). However, end-use potential in tree breeding programs and genetic selection for specific end uses have received little attention (Zobel and Jett 1995). A number of hybrid poplar trials established around the world have been evaluated for basic wood properties (Walters and Bruckmann 1965, Posry et al.

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1969; Murphey et al. 1979, Farm and Wilcox 1968, Farm 1970, Olson et al. 1985, Beaudoin et al. 1992, Koubaa et al. 1998, Geyer et al. 2000). However, most of these studies were either performed on a single site or included a limited number of samples or clones, whereas the present study used 21 clones at 2 sites. For tree improvement purposes, estimates of quantitative parameters require that more genotypes than used in the previous studies be tested, and that testing be done at different locations. In addition, it is important that the genetic correlation of major wood properties with growth traits be examined before wood quality traits can be incorporated into tree breeding programs to maximize the genetic gains.

In this study, we examined wood properties and growth of 21 hybrid poplar clones at two locations in southern Quebec, Canada. The objectives of this study are: (1) to evaluate inheritance of wood properties and growth traits; (2) to examine genetic relationships between wood properties and growth traits, and (3) to compare different selection scenarios and to examine the feasibility of incorporating wood quality traits into hybrid poplar breeding programs.

## Materials and Methods

### Materials

The materials for this study came from a hybrid poplar clonal trial established by the Forest Research Branch of the Quebec Ministry of Natural Resources in the spring of 1993. The trial is located in St-Ours (lat. 45°54' N, long. 73°09' W, alt. 50 m) and Windsor (lat. 45°42' N, long. 71°57' W, alt. 300 m), southern Quebec, Canada. The trial was composed of 198 clones at the Windsor site and 186 clones at the St-Ours site. In each site, 21 clones were sampled based on available growth rate and disease resistance data obtained from nursery and field experiments. We selected ten clones of *P. deltoides* × *P. nigra*, three clones of *P. trichocarpa* × *P. deltoides*, two clones of *P. deltoides* × *P. maximowiczii*, four clones of *P. maximowiczii* × *P. balsamifera*, one clone of *P. nigra* × *P. maximowiczii*, and one clone of *P. deltoides*. The origin of the materials can be traced back to the 1980s when a large number of hybrid poplar families were produced from crosses among these poplar species. Subsequently, these hybrids together with hybrid clones from Belgium, Ontario, France, and Germany were planted in nurseries, and their performance was evaluated based on some adaptive traits including growth, cold hardiness, and insect and disease resistance. Based on these evaluations, some 2000 clones were selected to establish clonal trials at different locations in Quebec. In this study, ten clones were selected from Quebec, six clones from Belgium, three clones from Ontario, one clone from France and one clone from Germany.

The two sites represent two soil types in which hybrid poplar clones are expected to be planted in southern Quebec. The St-Ours site is part of the Champlain marine deposit with rich salty-clay soil (40% clay), and the Windsor site belongs to the sandy loam soil type. The two sites were originally used for agriculture, but had been abandoned for several years before the hybrid poplar clones were planted. Each site was established in a complete randomized block design, with ten

blocks each. Clones were planted in row plots containing four trees at a 1.5 × 3.5 m spacing at the St-Ours site and a 1.2 × 3.5 m spacing at the Windsor site. One systematic thinning was carried out in the spring of 1996; the final spacing after the thinning was 2.5 × 3.0 m at the St-Ours site and 3.0 × 3.5 m at the Windsor site.

### Measurements of Tree Growth and Evaluation of Wood Properties

Each tree was measured for total tree height and diameter at breast height (dbh) by the Quebec Ministry of Natural Resources in October of 1995. Since the trees were young, a surrogate value for stem volume was arrived as height × dbh<sup>2</sup> (Causton 1985, Ceulemans 1992, Yu et al. 2001a). In spring 1996, 371 sample trees were collected from the two sites through thinning. The number of trees sampled from each clone varies from five to ten ramets at the St-Ours site and from seven to ten ramets at the Windsor site. The sample trees were transported to the Eastern Laboratory of Forintek Canada Corp. in Quebec City, Canada, for wood quality evaluation. A 5 cm thick disk was collected 15 cm above the stump level of each sample tree and sealed immediately in a plastic bag to prevent any moisture loss. Based on this disk, wood density, initial moisture content and fiber length were evaluated for each sample tree. A pie-shaped sample was collected from each disk and measured immediately for green weight. Each sample was then oven-dried at 103°C until a constant oven-dry weight was attained. Initial moisture content is expressed as the weight loss (the green weight minus the oven-dry weight) divided by the oven-dry weight. Basic wood density was calculated as oven-dry weight divided by the green volume. The green volume of the samples was determined by the water immersion method following the ASTM D 2395 (method B). Basic wood density multiplied by stem volume was calculated for each tree as an index of stem dry fiber yield (Zhang and Morgenstern 1995).

To reduce the cost, fiber length was not measured for each sample tree. Instead, the pie-shaped samples from the ramets of each clone at each site were combined as one sample for the measurement of fiber length. As a result, only an average fiber length was obtained for each clone at each site. For this reason, we only analyzed the phenotypic correlation between fiber length and other wood and growth traits. The combined pie-shaped samples were macerated together in a solution of 30% hydrogen peroxide (2 parts) and acetic acid (1 part). Arithmetic average fiber length was measured using the Fiber Quality Analyzer (FQA).

### Statistical Analysis

Data were analyzed for the two tested locations combined with an analysis of variance according to the following linear model:

$$X_{ijk} = \mu + C_i + L_j + C_iL_j + \varepsilon_{ijk}, \quad (1)$$

where  $X_{ijk}$  is an observation on the  $k$ th ramet from the  $i$ th clone in the  $j$ th location;  $\mu$  is the overall mean;  $C_i$  is the effect due to the  $i$ th clone;  $L_j$  is the effect due to the  $j$ th location;  $C_iL_j$  is the interaction between the  $i$ th clone and  $j$ th location; and  $\varepsilon_{ijk}$  is random error. All terms were considered random,

except for location considered as a fixed factor. Variance components were calculated using the appropriate mean square values and corresponding expected mean square coefficients generated from PROC GLM; RANDOM/TEST option (SAS Inc. 1990).

Repeatability of clone means was calculated using the following formula:

$$R_c^2 = \frac{\sigma_c^2}{\frac{k_2 \sigma_c^2}{k_2} + \frac{k_1 \sigma_{L \times C}^2}{k_2} + \frac{\sigma_e^2}{k_2}} \quad (2)$$

where  $k_1$  is the coefficient associated with the variance due to location by the clonal interaction term ( $\sigma_{L \times C}^2$ ); and  $k_2$  is the coefficient associated with the variance due to clonal variation ( $\sigma_c^2$ ). The standard error for repeatability estimates was calculated using the following formula (Becker 1992):

$$SW(R_c^2) = \sqrt{\frac{2(1 - R_c^2)^2 [1 + (k_2 - 1)R_c^2]^2}{k_2(k_2 - 1)(N - 1)}} \quad (3)$$

where  $N$  is the number of clones tested.

The intertrait clonal correlations were calculated as follows:

$$r_{A(X,Y)} = \frac{\sigma_{C(x,y)}}{\sqrt{\sigma_{C(x)}^2 \sigma_{C(y)}^2}} \quad (4)$$

where  $r_A$  is the intertrait clonal correlation between the traits  $x$  and  $y$ ;  $\sigma_{C(x,y)}^2$  is the estimated clonal covariance between  $x$  and  $y$ ; and  $\sigma_{C(x)}^2$  and  $\sigma_{C(y)}^2$  are the clonal components of variance estimated for  $x$  and  $y$ , respectively. The corresponding clonal components of variance were estimated from data collected from the same individual tree data, following the analysis of variance method described before.

The procedure adopted to derive the clonal covariances was the same as that applied to estimate the clonal variance. This means equating the observed mean cross products to their Type III expectations of mean cross products, and solving the equations as explained before. The MANOVA statement of the SAS PROC GLM provided the sum of cross products. The options HTYPE = 3 and ETYPE = 3 were used to give the matrices with the Type III sum of cross products for clone and error, respectively.

**Table 1. Mean values of tree growth and wood properties of the twenty-one 3-yr-old hybrid poplar clones at the two sites.**

	St-Ours			Windsor		
	Mean	Range	CV(%)	Mean	Range	CV(%)
Tree ht (cm)	629.6 ± 7.6	395–880	15.8	355.7 ± 5.1	120–530	18.4
Dbh (mm)	55.1 ± 0.9	27–92	21.9	24.3 ± 0.7	0–50	34.4
Stem vol. (dm <sup>3</sup> )	21.1 ± 0.9	3.0–66.0	54.5	2.7 ± 0.2	0.05–13.3	92.6
Initial moisture content (%)	147.6 ± 2.1	79.2–211.4	18.3	149.3 ± 1.5	89.4–200.8	11.5
Basic wood density (kg/m <sup>3</sup> )	351.4 ± 2.1	274–434	7.9	400.7 ± 1.9	343–480	3.7
Stem dry fiber wt (kg)	7.3 ± 0.3	1.1–22.4	54.4	1.1 ± 0.1	0.02–5.5	91.44
Arithmetic average fiber length (mm)*	0.381 ± 0.007	0.32–0.44	54.4	0.365 ± 0.009	0.23–0.45	11.6

\* Arithmetic average fiber length of ramets within a clone at one site.

The standard error of genetic correlations was computed using the following equation (Falconer 1981):

$$\sigma = \frac{1 - r^2}{\sqrt{2}} \sqrt{\frac{\sigma_{(R^2_x)} \sigma_{(R^2_y)}}{R^2_x R^2_y}} \quad (5)$$

where  $r$  is the genetic correlation estimate;  $R_x^2$  is the repeatability estimate of the character  $x$ ;  $R_y^2$  is the repeatability estimate of the character  $y$ ;  $\sigma_{(R_x^2)}$  is the standard error of  $R_x^2$ ;  $\sigma_{(R_y^2)}$  is standard error of  $R_y^2$ .

The clonal correlation coefficients between pairs of traits were based on measurements of different ramets from the same clone planted in different environments. Under such conditions the inter-site genetic correlation between two traits  $x$  and  $y$  can be estimated as follows:

$$r_{B(X,Y)} = \frac{r_{P(x1,y2)}}{R_{C(x1)} R_{C(y2)}} \quad (6)$$

where  $r_{p(x1,y2)}$  is the phenotypic correlation coefficient between the clone means estimated between  $x$  measured in site 1 and  $y$  measured in site 2;  $R_{c(x1)}$  and  $R_{c(y2)}$  are the square roots of their clonal mean repeatability estimated for  $x$  and  $y$  at site 1 and 2 respectively (Burdon 1977).

The SAS PROC CORR was applied to calculate the phenotypic correlation of least-squares clonal means for each pair of traits, measured on common clones at two sites.

In this study, the selection intensity is assumed to equal 1.244, which corresponds to the selection of 5 clones out of 21 (Becker 1992). The formula for expected genetic gain at trait  $y$  based on clonal selection at trait  $x$  can be written as follows (Falconer 1981):

$$\Delta G_y = \sqrt{R_x} \sigma_y r_{xy} \quad (7)$$

where  $i_x$  (intensity of selection) = 1.244;  $R_x$  = repeatability of clonal means for trait  $x$ ;  $\sigma_y$  = clonal standard deviation for trait  $y$ ;  $r_{xy}$  = genetic correlation between trait  $x$  and trait  $y$ .

## Results and Discussion

### Clonal Variations and Repeatability

A remarkable difference in tree height, dbh, stem volume, and stem dry fiber weight was found between the two sites (Table 1). On average, trees from the St-Ours site have a much higher growth rate and a much higher stem dry fiber weight than those from the Windsor site due to poor drainage

and geographical and site quality. With respect to wood properties, trees at the St-Ours site have a considerably lower basic wood density ( $351.4 \text{ kg/m}^3$ ) than at the Windsor site ( $400.7 \text{ kg/m}^3$ ), as expected. However, trees at the St-Ours site have longer fibers (0.381 mm) than at the Windsor site (0.365 mm) despite a much faster growth rate. In addition, trees at the St-Ours site have a slightly lower initial moisture content.

Beaudoin et al. (1992) reported an average wood density of  $349.5 \text{ kg/m}^3$  for ten 9-yr-old clones of hybrid poplar (*P. euramericana*) grown in Quebec. An average wood density of  $330 \text{ kg/m}^3$  was recorded by Olson et al. (1985) for 75 3-yr-old clones of *P. deltoides* grown along the Lower Mississippi River Valley. The difference in wood density of hybrid poplar clones between this study and previous reports may be due to the genotype of the clones, to differences in location and site quality, and or tree age. With respect to the radial variation in wood density in poplars, Hernandez et. al (1998) found that the wood density of *P. euramericana* decreased slightly from the pith to the first third of the diameter, and then increased outwards. Trembling aspen wood exhibited a similar pattern of radial variation (Yanchuk et al. 1983).

The mean fiber length of individual clones ranges from 0.32 to 0.44 mm at St-Ours, and from 0.23 to 0.45 mm at Windsor. Phelps et al. (1982) reported that fiber length of 4-yr-old *Populus deltoides* hybrids ranged from 0.58 to 0.70 mm. Geyer et al. (2000) found that average fiber length for 4-yr-old poplar hybrid clones was 0.84 mm. Arithmetic average fiber length of hybrid aspen clones measured by Kajaani FS-200 fiber length analyzer ranged from 0.43–0.70 mm (Yu et al. 2001b). Obviously, the fiber length of these hybrid poplar clones measured by the Fiber Quality Analyzer is much shorter than that of the other hybrids. The lower fiber length may be partly explained by the fact that the Fiber Quality Analyzer underestimates fiber length because of the inclusion of curled and broken fibers and vessel elements (Robertson et al. 1999).

Table 2 presents ANOVA results and repeatability for wood properties and growth traits at individual sites. A similar analysis was performed for the two sites combined, and the results are presented in Table 3. Significant differences in both wood properties and growth traits were found among the clones at two individual sites (Table 2). No significant differences in stem volume and stem dry

**Table 2. Analysis of variance and repeatabilities for tree growth and wood properties at each site.**

	Source	df	MS	F	P- value	$R_c^2$
St-Ours						
Tree ht (mm)	Clones	20	41789	7.3	0.001	0.85±0.04
	Error	152	5676			
Dbh (mm)	Clones	20	523	5.4	0.001	0.79±0.06
	Error	152	96			
Stem vol. (dm <sup>3</sup> )	Clones	20	470	5.31	0.001	0.78±0.05
	Error	152	88			
Initial moisture content (%)	Clones	20	3116	16.9	0.001	0.85±0.04
	Error	152	409			
Basic wood density (kg/m <sup>3</sup> )	Clones	20	4532	7.6	0.001	0.93±0.02
	Error	152	267			
Stem dry fiber wt (kg)	Clones	20	61	6.2	0.001	0.82±0.05
	Error	152	10			
Windsor						
Tree ht (mm)	Clones	20	13430	3.3	0.001	0.72±0.07
	Error	177	4116			
Dbh (mm)	Clones	20	240	3.4	0.001	0.74±0.07
	Error	177	70			
Stem vol. (dm <sup>3</sup> )	Clones	20	16.5	7.6	0.001	0.71±0.07
	Error	177	5.1			
Initial moisture content (%)	Clones	20	1539	5.3	0.001	0.83±0.05
	Error	177	292			
Basic wood density (kg/m <sup>3</sup> )	Clones	20	5078	23.2	0.001	0.96±0.01
	Error	177	219			
Stem dry fiber wt (kg)	Clones	20	2.69	7.6	0.001	0.74±0.07
	Error	152	0.75			

fiber weight were found among the clones at the sites combined (Table 3). Therefore, we did not estimate the repeatability of stem volume and stem dry fiber weight for the two traits. For all traits (except for wood density), variance due to error (namely differences among ramets within a clone) accounts for most of the variation in these traits, ranging from 60.2 to 71.3% of the total variation (Table 3). Most of the variance in wood density (61.9%), however, was due to clone. Therefore, wood density in the hybrid poplar clones has the highest repeatability (0.92).

In this study, clone  $\times$  site interaction is significant for all wood and growth traits studied (Table 3). Stem volume and stem dry fiber weight have a higher percentage of variance due to clone  $\times$  site interaction (28.1% and 29.9%, respectively) than other traits. The interactions were probably caused by different microclimates or edaphic conditions at the two sites, leading to the poor performance of all clones at the Windsor site.

Significant genotype  $\times$  environment interactions have been reported in young cottonwoods by Randall and Co-

per (1973) for growth traits, but not for wood density. Riemenschneider et al. (2001) found that clone  $\times$  location interaction was weak on an experiment-wide basis for year 1 height and basal calliper, but that it increased significantly by year 3 and remained high relative to the clone main effect through the life of the experiments. However, the genotype  $\times$  environment interactions for wood properties are generally uncommon and thus of little practical importance (Dinus et al. 2001). A study of four *Eucalyptus urophylla* progeny trials in Southeast China did not reveal any genotype  $\times$  environment interaction for wood density and other wood characteristics (Wei and Borralho 1997).

Numerous studies have reported a large genetic variation in wood density and a moderate to strong heritability for wood density (Zobel and Jett 1995). Of the various traits studied in the hybrid poplar clones, wood density has the highest repeatability, 0.92 (Table 3). This estimate is reasonably consistent with those presented in the literature despite the fact that studies were performed on populations of different ages. Individual-tree heritability for wood density was

**Table 3. Analysis of variance, variance components and repeatabilities for tree growth and wood properties at the two sites combined.**

	Source	df	MS	F	P value	%	$R_c^2$
Tree ht (mm)	Site	1	6,5721,89	560.2	0.0001		0.72 $\pm$ 0.07
	Clones	20	42,623	3.6	0.0031	23.9	
	Sites x Clone	20	11,833	2.5	0.0006	10.9	
	Error	327	4,837			65.2	
Dbh (mm)	Site	1	84,112	441.7	0.0001		0.64 $\pm$ 0.08
	Clones	20	545	2.8	0.0120	17.7	
	Sites x Clone	20	192	2.3	0.0011	11.0	
	Error	327	82			71.3	
Stem vol. (dm <sup>3</sup> )	Site	1	28,953	140.5	0.0001		—
	Clones	20	290	1.40	0.23	7.0	
	Sites x Clone	20	208	4.8	0.0001	28.1	
	Error	327	43.85			64.8	
Initial moisture content (%)	Site	1	250	0.4	0.5352		0.80 $\pm$ 0.05
	Clones	20	3,884	5.1	0.0003	31.2	
	Sites x Clone	20	771	2.2	0.0021	8.5	
	Error	327	346			60.2	
Basic wood density (kg/m <sup>3</sup> )	Site	1	228,884	325.0	0.0001		0.92 $\pm$ 0.02
	Clones	20	9,051	12.8	0.0001	61.9	
	Sites x Clone	20	707	2.9	0.0001	6.9	
	Error	327	241			31.1	
Stem dry fiber wt (kg)	Site	1	3,363	129.5	0.0001		—
	Clones	20	39	1.5	0.1817	9.4	
	Sites x Clone	20	26	5.7	0.0001	29.9	
	Error	327	5			60.7	

**Table 4. Intertrait genetic correlations (above the diagonal: standard error in parentheses) and phenotypic correlations (below the diagonal: *P* value in parentheses) between wood properties and growth traits across the two sites.**

	Tree ht	Dbh	Stem vol.	Initial moisture content	Basic wood density	Stem dry fiber wt
Tree ht		1.00	1.11	0.20 (0.05)	-0.07 (0.03)	1.04
Dbh	0.96 (0.001)		1.25	0.26 (0.06)	-0.20 (0.04)	1.12
Stem vol.	0.90 (0.0001)	0.96 (0.0001)		0.09 (0.09)	-0.03 (0.06)	0.98 (0.01)
Initial moisture content	0.20	0.20	0.14		-0.52 (0.02)	-0.05 (0.05)
Basic wood density	-0.08	-0.16	-0.05	-0.48 (0.03)		0.29 (0.18)
Stem dry fiber wt	0.90 (0.0001)	0.93(0.0001)	0.98 (0.0001)	0.05	0.12	
Arithmetic average fiber length	-0.05	-0.06	-0.15	-0.13	-0.11	-0.18

NOTE: Only significant *P* values for phenotypic correlations are given in parentheses.

estimated to be 0.62 (Olson et al. 1985) and 0.64 (Farmer 1970) in cottonwood clones, 0.69 (Farmer and Wilcox 1968) and 0.69 in *P. euramericana* clones (Beaudoin et al. 1992).

### Phenotypic and Genetic Correlations

Table 4 shows the phenotypic and genetic correlations between wood properties and growth traits. Wood density has a significant and negative correlation with initial moisture content. Wood density was not significantly correlated with growth traits both phenotypically and genetically. This indicates that selection for growth traits may not result in a significant reduction in wood density. However, there exists a weak and negative correlation between wood density and growth traits (especially dbh). This suggests that selection for dbh might lead to a minor reduction in wood density. Arithmetic average fiber length was not correlated with growth traits or wood traits. There are some autocorrelations among stem volume, tree height, and dbh because stem volume was derived from tree height and dbh. Similarly, stem dry fiber weight, stem volume, and wood density also have some autocorrelations as stem dry fiber weight was derived from wood density and stem volume.

According to the literature, correlations between wood density and growth traits are variable in nature (Dinus et al. 2001). To incorporate wood quality traits into tree breeding programs, tree breeders need information on the genetic correlations between growth and wood quality traits. Zhang (1995) found that growth rate generally had very little effect on wood density in *P. cathayana* and *P. tomentosa*. In aspen hybrids, Ilstedt and Gullberg (1993) did not note an association between fast growth and low wood density. In contrast, Beaudoin et al. (1992) noticed a significant negative correlation (-0.49) between wood density and growth rate in *P. euramericana* hybrid clones. Also, Olson et al. (1985) noted a strong negative correlation (-0.65) between wood density and growth in *Populus deltoides* clones, and assumed simultaneous improvement was impractical.

Wood density and initial moisture content show the highest intersite genetic correlation (0.86 and 0.73, respectively), whereas growth traits and stem dry fiber weight have the lowest intersite genetic correlations (Table 5). This indicates that wood properties are more similar across sites than growth traits. The strong intersite genetic correlations for the two wood properties suggest that wood quality traits are stable and could be selected for most

suitable sites. This result was expected, as Zobel and Jett (1995) showed a more stable genotype performance across environments for wood properties.

Less research has been done on fiber length than another traits in hardwoods. Yu et al. (2001) found that, genetically, the fiber length of hybrid aspen was positively correlated with growth traits. Dinus et al. (1990) suggested that fiber length had little or no association with wood density, but rather strong and positive relationships with growth in North American hardwoods. In the hybrid poplar clones studied, mean fiber length appears not to be phenotypically correlated with growth traits and other wood traits. The genetic correlation between this parameter and growth traits could not be analyzed because all trees from each clone at each site were combined to measure the mean fiber length of each clone.

### Implications for Tree Improvement

We could not show the expected genetic gains from different criteria at two sites combined because there was no repeatability for stem volume and stem dry fiber weight due to insignificant difference among clones. Table 6 presents expected genetic gains resulting from different selection criteria at each site. Although wood density had the highest repeatability among the traits, it appears that only small gains could be made due to its low clonal standard deviation. When selection is made for wood density alone, a 7.8% and 6.9% genetic gain in wood density is expected at St-Ours and Windsor, respectively. However, no gains in stem volume and little in stem dry fiber weight can be achieved. As expected, selection for growth traits will achieve a remarkable gain in both stem volume (35.7–41.0%) and in stem dry fiber weight (35.8–41.5). However, selection for growth traits will result at the same time in a minor decrease in wood density (-0.2 to

**Table 5. Inter-site genetic correlations for the wood properties and growth traits.**

Traits	Genetic correlation (SE)
Tree ht (cm)	0.63 ± 0.03
Dbh (mm)	0.56 ± 0.04
Stem vol. (dm <sup>3</sup> )	0.52 ± 0.04
Initial moisture content (%)	0.73 ± 0.02
Basic wood density (kg/m <sup>3</sup> )	0.86 ± 0.002
Stem dry fiber wt (kg)	0.52 ± 0.04

**Table 6. Expected response ( $\Delta G/\bar{X}$ ) in wood density, stem volume, and stem dry fiber wt at each site when different selection criteria are used.**

Selection criterion	Response (%)					
	St-Ours			Windsor		
	Basic wood density	Stem vol.	Stem dry fiber wt	Basic wood density	Stem vol.	Stem dry fiber wt
Basic wood density (kg/m <sup>3</sup> )	7.8	0.4	5.4	6.9	-1.4	3.4
Tree ht (cm)	-0.6	35.5	36.3	-0.3	40.5	40.8
Dbh (mm)	1.6	35.6	37.2	-0.6	41.5	40.9
Stem vol. (dm <sup>3</sup> )	-0.2	35.7	36.8	-0.2	41	41.3
Stem dry fiber wt (kg)	1.6	35.8	38.9	0.7	41.5	42.6

-0.6%), except diameter of tree at St-Ours. Selective breeding programs need to take into account the implications of adverse genetic correlation. When growth traits are selected, attention should be paid to the implications for wood quality traits. However, previous studies on two softwoods (Zhang and Morgenstern 1995, Zhang and Chui 1996) revealed that selection for dry fiber weight will not only achieve a higher genetic gain in stem dry fiber yield, but also minimize the adverse effect on wood density. Similar results were found in this study. As shown in Table 6, this selection criterion will lead to the highest genetic gain in stem dry fiber yield (38.9–42.6%) and stem volume (35.8–41.5%). In addition, this selection will not result in a reduction in wood density (1.6–0.7%). Therefore, this study also indicates that selection for stem dry fiber weight presents an optimal compromise between tree growth and wood quality traits and thus constitutes the best selection strategy.

Our study on expected genetic gains should be interpreted with caution and scope of inference. We might overestimate the expected genetic gains because we excluded the genotype  $\times$  environment interaction effects. Also, the intergenotype competition at the two sites would be expected. There exists a possibility that the yield of genotypes with high growth potential is overestimated, because the trees compete directly with genotypes of lower growth potential rather than with con-genotype trees.

This study was based on a 3-yr-old clonal trial at two testing sites. As the wood density may vary considerably with cambial age and location, further research on older materials at more locations is needed to better understand the genetic control of wood properties and growth in the hybrid poplar clones.

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## APPENDIX

**Table A.1. Expect mean square tables for combined field site combined site analysis, St-Ours, and Windsor.**

Source of variation	Expect mean squares
Combined site analysis	
Location (Loc)	$\sigma^2 (\text{Error}) + 8.5 \sigma^2 (\text{Loc} * \text{clone}) + Q(\text{Loc})$
Clone	$\sigma^2 (\text{Error}) + 8.6 \sigma^2 (\text{Loc} * \text{clone}) + 17.3 \sigma^2 (\text{clone})$
Loc*clone	$\sigma^2 (\text{Error}) + 8.6 \sigma^2 (\text{Loc} * \text{clone})$
Error	$\sigma^2$
St-Ours	
Clone	$\sigma^2 (\text{Error}) + 8.2 \sigma^2 (\text{clone})$
Error	$\sigma^2$
Windsor	
Clone	$\sigma^2 (\text{Error}) + 9.4 \sigma^2 (\text{clone})$
Error	$\sigma^2$