Propagating native Salicaceae for afforestation and restoration in New York City's five boroughs

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ABSTRACT

Identifying superior Salicaceae genotypes for afforestation and restoration activities in urban areas can greatly increase the provision of ecosystem services for long-term ecological sustainability. To address this opportunity, we collected native *Populus* L. (Salicaceae) and *Salix* L. (Salicaceae) scions from 3 sites on Staten Island, New York, and conducted a propagation study followed by greenhouse and nursery scale-up activities. Our objectives were to: 1) identify hormone treatments that enhanced root initiation and early growth of the native genotypes; 2) incorporate Salicaceae propagation methodology into phyto-recurrent selection; and 3) establish a population of genotypes that can be used for afforestation and restoration efforts throughout New York City. For Objective 1, we tested the response of 112 native genotypes and 11 common clones to 3 root hormone treatments (36-h water soak plus 12-h soak in 1% IBA + 0.5% NAA; 48-h water soak plus powder dip in 0.3% IBA; 48-h water soak plus 5-s dip soak in 20% IBA) and a water soak control. After 75 d of growth, the control treatment was more effective than the 0.3% IBA powder dip and as effective as the other treatments. Given broad clonal variation, there is a high probability of selecting genotypes for both afforestation and restoration. Although *Salix* exhibited greater relative propagation success than *Populus*, both genera should be used to increase overall genetic diversity. From a practical standpoint, scale-up activities led to establishment of a nursery population that will be used for ongoing afforestation and restoration activities in New York City.

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CONVERSIONS
1 cm = 0.4 in
1 km = 0.62 mi
(°C x 1.8) + 32 = °F
1 l = 0.26 gal

KEY WORDS

plant selection, cottonwood, *Populus deltoides*, *Populus grandidentata*, root hormone, *Salix eriocephala*, *Salix nigra*, willow

NOMENCLATURE

USDA NRCS (2014)

The global need for green space within urban areas has prompted an advancement of tree planting efforts in major cities such as New York City. For example, the MillionTreesNYC program is underway with the goal of planting one million new trees across the city's 5 boroughs during the course of a decade (2007 to 2017). Similar "Million Trees" programs have been initiated in Los Angeles, London, and Shanghai. While the potential social and ecological benefits are great with such programs, one challenge has been the availability of sites for such afforestation along with the associated need for proper plant material. Furthermore, little data exist to support the long-term success of native afforestation efforts in urban areas (Oldfield and others 2013). Looking at the situation from a crop-development context, focusing efforts on matching specific native genotypes to soil and climate conditions has the potential to greatly increase the success of such efforts. In addition, identifying favorable genotype × environment interactions will help to achieve quicker canopy closure, thereby helping to gain relatively quick control of the site by shading out exotic invasive plant species. The end goal of such efforts is to identify and establish workhorse pioneer genotypes on the site, followed by a transition to later successional species that will ultimately make up mature urban forests (Zalesny and others 2012).

Identifying superior Salicaceae genotypes for afforestation and restoration activities in urban and rural areas can greatly increase the provision of ecosystem services for long-term ecological sustainability (Hoag and Landis 2001). More specifically, cottonwoods, poplars, and aspens (*Populus* L. [Salicaceae]) and willows (*Salix* L. [Salicaceae]) have a rich history of successful utilization in such systems (Isebrands and Karnosky 2001; Schultz and others 2004), especially given their broad genetic variability (Eckenwalder 1984; Aravanopoulos and others 1999) and traits such as ease of propagation, fast growth, and extensive root systems (Zalesny and others 2011).

Phyto-recurrent selection (PRS), a crop development methodology developed for phytotechnologies (Zalesny and Bauer 2007a; Zalesny and others 2007), involves the use of multiple testing cycles to evaluate, identify, and select favorable genotypes based on their response to variable site conditions. Applying PRS to MillionTreesNYC and similar programs is one way to achieve the aforementioned selection of workhorse species and genotypes. More specifically, early cycles are relatively short and data collection is relatively easy (typically done in the greenhouse or growth chamber), while later cycles require more time and resources to increase knowledge of advancing genotypes (typically done in the field). Fewer genotypes are tested as the complexity of the data increases. The ultimate goals of PRS are to deploy a combination of genotypes with improved potential over commonly used species and varieties, and with adequate genetic variation to maintain ecological sustainability and associated conservation objectives (Zalesny and Bauer 2007a; Zalesny and others 2007).

To address these goals, we collected native *Populus* and *Salix* scions from 3 sites on Staten Island, New York, and conducted a propagation study followed by greenhouse and nursery scale-up activities. Our specific objectives were to: 1) identify hormone treatments that enhanced root initiation and early growth of the native genotypes; 2) incorporate Salicaceae prop-

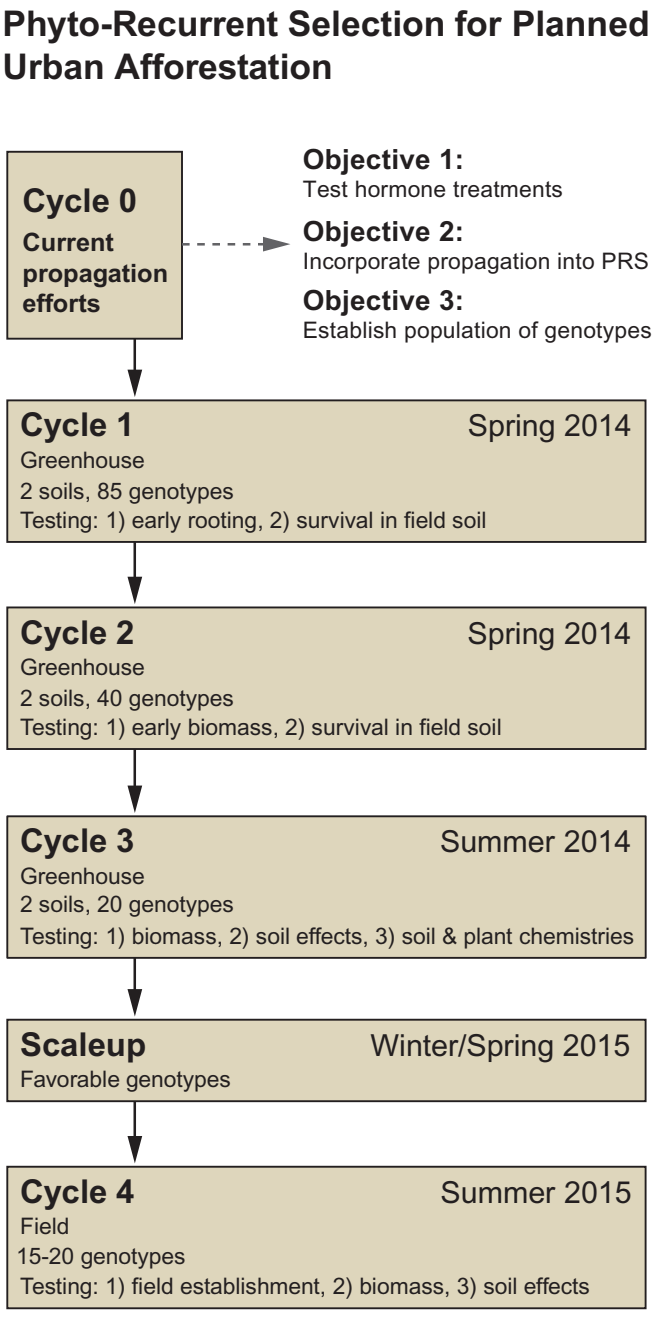


Figure 1. Phyto-recurrent selection for planned urban afforestation. Note the incorporation of the current propagation efforts in Cycle 0.

agation methodology into phyto-recurrent selection (Figure 1); and 3) establish a population of genotypes that can be used for afforestation and restoration efforts in New York City's 5 boroughs.

MATERIALS AND METHODS

Site Selection

Freshkills Park (formerly Fresh Kills Landfill), Mariner's Marsh Park, and Ocean Breeze Park on Staten Island were selected based on research priorities at Freshkills Park (Zalesny and others 2012) and a partnership with the Greenbelt Native Plant Center of the New York City Department of Parks and Recreation, located 2 km from Freshkills (Figure 2). In addition, collecting plant materials from a range of sites on Staten Island will ensure sufficient genetic diversity for afforestation and restoration activities in all other New York City boroughs, as well.

Scion Collection and Processing

Populus and *Salix* scion material was collected from the 3 sites on 29 February to 5 March 2012. The goal was to collect from 20 trees of each genus at each site, which was achieved at Mariner's Marsh and Ocean Breeze. The number of potential *Salix* parent trees was minimal at Freshkills, however; therefore, only 12 *Salix* genotypes were collected. In total, 112 genotypes were sampled across sites. The number of genotypes collected for each species at each site is listed in Table 1. The primary species collected were eastern cottonwood (*Populus deltoides* W. Bartram ex Marshall), black willow (*Salix nigra* Marshall), and Missouri River willow (*S. eriocephala* Michx.). Three bigtooth aspen (*P. grandidentata* Michx.) genotypes and several unknown *Salix* species were also sampled.

For collection, parent trees were selected based on a 3-tiered health rating system, whereby 1 = excellent health, 2 = good health (minor disease and form issues), and 3 = moderate health (moderate disease, prominent frost cracks, and other form issues). Trees with poor health issues were not considered as potential parent trees. Overall, 88% of the trees sampled exhibited excellent health, 6% good health, and 6% moderate health. Scions were cut from parent trees using an extendable pruning pole, processed in the field into lengths ranging from 7.6 to 35.6 cm (acceptable diameters ranged from 6.4 to 19.1 mm, placed into plastic drawstring bags, and temporarily stored at 3 °C at the Greenbelt Native Plant Center (Figure 3). Collected scions were immediately sent to the Institute for Applied Ecosystem Studies (IAES) (Rhinelander, Wisconsin) where material was stored at 3 °C until being processed for the propagation study and scale-up activities described below.

On 14 to 15 May 2012, all scion material was processed into 7.6-cm cuttings with at least one primary bud located not more than 1.3 cm from the top of each cutting. Two genotypes from Ocean Breeze (B17 and B18) were cut to 6.4-cm length due to limited scion material. For all genotypes, the cuttings were separated into 3 length categories and their number was recorded: 1) 7.6 cm (6.4 cm for B17 and B18); 2) 5.1 to 7.6 cm (5.1 to 6.4 cm for B17 and B18); and 3) <5.1 cm. The cuttings were then stored in plastic drawstring bags at 3 °C until being used for the propagation study.

Figure 2. Staten Island field sites (Freshkills Park, Mariner's Marsh Park, and Ocean Breeze Park) where scion material was collected.

TABLE 1

Number of genotypes and trees outplanted for Populus *L. (Salicaceae) and* Salix *L. (Salicaceae) collected from 3 sites on Staten Island, New York, as well as genomic groups associated with common clones tested as experimental controls.*

Staten Island collections				Common clones	
Site Species	Number of genotypes collected	Number of trees outplanted	Percent survival	Genus Genomic group	Clone(s)
Freshkills				***Populus***	
P. deltoides	19	256	80.5	*P. deltoides* × *P. maximowiczii*	NC14105
P. grandidentata	1	6	50.0	(*P. trichocarpa* × *P. deltoides*) × *P. deltoides*	NC13624
S. eriocephala	1	10	100.0	*P. nigra* × *P. maximowiczii*	NM6
S. nigra	7	337	95.9	*P. deltoides* × *P. nigra*	DN34
S. spp.	4	127	95.3	*P. deltoides* × *P. deltoides*	91.08.09
Total	32	736	90.1	*P. deltoides*	D105; D110
Ocean Breeze				***Salix***	
P. deltoides	19	221	81.0	*S. eriocephala*	9837-77; S25
P. grandidentata	1	8	75.0	*S. miyabeana*	SX64
S. eriocephala	10	239	95.0	*S. dasyclados*	S
S. nigra	7	401	96.3		
S. spp.	3	116	95.7		
Total	40	985	92.3		
Mariner's Marsh					
P. deltoides	19	256	85.6		
P. grandidentata	1	0	—		
S. eriocephala	13	358	99.4		
S. nigra	7	311	84.9		
Total	40	925	90.7		
Grand Total	112	2646	91.3		

Note: Percent survival is based on the number of trees alive at 106 d after outplanting.

Propagation Study (Objectives 1 and 2)

Treatment and Genotype Selection

Given the influence of hormones on the ability of *Populus* and *Salix* to develop adventitious roots (Haissig and Davis 1993; DesRochers and Thomas 2003), 3 synthetic root hormone treatments were selected: 1) SOAK = soaked cuttings in water for 36 h, then soaked in Dip'N Grow solution (Clackamas, Oregon) for 12 h (1% indole-3-butyric acid [IBA] + 0.5% 1-naphthaleneacetic acid [NAA]); 2) DRY DIP = soaked cuttings in water for 48 h, then dipped bottom of cuttings in Hormodin 2 powder (Mainland, Pennsylvania) (0.3% IBA); and 3) WET DIP = soaked cuttings in water for 48 h, then dipped bottom of cuttings in Rhizopon AA solution (New York, New York) for 5 s (20% IBA).

In total, 123 genotypes were selected (Table 1). The first group consisted of the 112 native genotypes collected from Staten Island. The second group consisted of 11 "common" clones (7 *Populus* + 4 *Salix*) representing research genotypes and commercial clones used for short-rotation woody crop production systems. Much is known about the propagation and rooting potential of these common clones (Zalesny and others 2005), and they were included to serve as experimental controls.

Experimental Design and Tree Establishment

Trees were arranged in a split-plot design with 7 blocks, 4 treatments (SOAK, DRY DIP, WET DIP, CONTROL = unfiltered well water), and 123 genotypes (112 Staten Island, 11 common). Treatments were considered whole plots and clones

Figure 3. Scion collection (*left*) and processing (*right*) in the field. Photos by Nancy Falxa-Raymond

split plots. All cuttings were soaked in unfiltered well water to a height of 5.1 cm (4.3 cm for B17 and B18) beginning at 1200 CDST on 16 May 2012. Cuttings of the SOAK treatment were transferred to their Rhizopon solution for the final 12 h of soaking. Cuttings of all other treatments remained in the water until planting.

All trees (n = 3,444 = 7 blocks × 4 treatments × 123 genotypes × 1 tree per block) were planted with one primary bud above the soil surface on 18 May 2012 into 72-cell speedling transplant trays (Peaceful Valley Farm and Garden Supply, Grass Valley, California) (Figure 4) containing Fafard 1P Mix (Agawam, Massachusetts), a lightweight growing medium consisting of 80% peat moss, perlite, wetting agent, dolomitic limestone, and starter nutrients. Each cell contained 206 cm^3 of growing medium. For the SOAK and CONTROL treatments, cuttings were planted directly out of plastic cups containing the Dip'N Grow solution and water, respectively. The WET DIP treatment required one extra step and the DRY DIP treatment required 2 additional steps. Specifically, cuttings of the WET DIP treatment were removed from the cup of water and the lower two-thirds of each cutting was dipped into the Rhizopon AA solution for 5 s and then immediately planted. For the DRY DIP treatment, cuttings were removed from their water cups and blotted dry, then the bottom half of each cutting was dipped into the Hormodin 2 powder (with excess powder shaken off) and immediately planted. All treatments took 75 min to plant; treatments were planted in the following order: SOAK, WET DIP, CONTROL, DRY DIP. Each cell (that is, tree) was individually labeled with a clear, return address label (Avery 5667, Brea, California) adhered to a 1.6- × 10.2-cm Pylon pot label (Joliet, Illinois), with color coding for specific treatments (Figure 4). After all trees were planted, the speedling trays were moved to a greenhouse at the IAES and put into custom-made metal planters (hereafter referred to as pans) that accommodated 6 speedling trays per pan (Figure 4). The sides of each pan were 15.2 cm high, and unfiltered well water was added to a height of 3.8 cm. The pans also included a wooden frame that prevented the long vertical sides of the pan from bowing out under water pressure. Last, 2.5-cm flexible tubing was installed as a frame above the pans to hold shade cloth that reduced the risk of sun scald to the trees. The greenhouse conditions included a 16-h photoperiod and constant temperature of 21 °C. Water levels were monitored daily and kept at the height of 3.8 cm.

Data Collection and Analysis

Monitoring was conducted for 27 d after planting (DAP) for: 1) presence of floral buds; 2) flushing; 3) root initiation; and 4) wilting or necrosis (Figure 5; Table 2). Binary responses were recorded for each dependent variable such that a value of one was given if a tree had floral buds, flushed, initiated roots, or wilted or died. A zero value indicated the converse of these responses. All monitoring data at 27 DAP were evaluated nonparametrically using a Chi-square (χ^2) test from frequency counts to analyze differences among treatments.

At 74 DAP, height was measured to the nearest 0.1 cm from the point of attachment between the stem and the original cutting to the tip of the apical bud. Trees belonging to 3 of the original 7 blocks were harvested, washed, and dissected at 75 DAP (Figure 6). Individual plant tissues were dried at 60 °C until constant mass, and stem, leaf, root, and cutting dry mass were recorded. Height and dry mass data were analyzed using

Figure 4. Trees growing in speedling trays (*left*) within pans (*right*). Photos by Ronald S Zalesny Jr

Figure 5. Monitoring conducted to assess the presence of floral buds (A), bud flushing (B), root initiation (C), and wilting or mortality (D). Photos by Ronald S Zalesny Jr

TABLE 2

Monitoring events for 1) presence of floral buds; 2) flushing; 3) root initiation; and 4) wilting or necrosis.

Date (2012)	Days after planting	Floral buds	Flushing	Rooting	Wilting/Necrosis
21 May	3	*****			
23 May	5	*****			
25 May	7	*****			
29 May	11	*****	*****		
5 June	18	*****	*****		
14 June	27	*****	*****	*****	*****

Note: Asterisks denote when monitoring occurred.

analyses of variance (PROC MIXED; SAS Institute 2004) according to the split-plot design of Model 1 described above (that is, treatment whole plots and clone split plots), as well as after pooling clones according to the 3 predominant Staten Island species tested (*P. deltoides*, *S. eriocephala*, *S. nigra*) and the experimental controls (that is, resulting in 4 species groups) (Model 2). For Model 2 analyses, the experimental design was a split-plot with the same blocks and treatments as Model 1 but substituting the 4 species groups as split plots in lieu of clones. For both analyses, treatments and clones were considered fixed in the analysis; therefore, we evaluated means rather than variances. Six of the original 123 clones exhibited 100% mortality and were not included in the analyses for either model. Twenty-three additional clones were excluded because of a lack of trees for one or more treatments, rendering the SAS analyses nonestimable. Thus, 94 clones were included in all final analyses. Cutting dry mass across all trees ranged from 0.2 to 6.0 g at 75 DAP. Therefore, analyses of covariance were conducted to test for the effect of cutting size on height and dry mass for both models. Cutting dry mass did have a significant effect ($P < 0.001$ for all traits); thus, adjusted means are reported. Fisher's protected least significant difference (LSD) was used to compare adjusted means for all traits.

A weighted summation index was used to prioritize genotypes within genera for greenhouse scale-up activities. Weighted allometric traits (sum of weights = 1) were used

Figure 6. Stem, leaf, root, and cutting material during harvest. Photos by Ronald S Zalesny Jr

based on their relative propagation success and perceived importance for early establishment and growth. The weights were multiplied by the adjusted means for individual traits, followed by summation of values. In general, roots contributed 60% and aboveground traits 40% to each index value. Favorable genotypes for scale-up were those that exhibited greater relative index values. Using the traits described above at 75 DAP (HT = height; SDM = stem dry mass; LDM = leaf dry mass; RDM = root dry mass), the following model was used in the analysis:

Index Value (IV) = 0.15*HT + 0.15*SDM + 0.10*LDM + 0.60*RDM.

Scale-up (Objective 3)

Greenhouse and nursery scale-up activities were conducted, which consisted of transplanting the 4 residual blocks from the propagation study into Accelerator pots (Chambersburg, Pennsylvania) and standard 3.8- and 7.6-l pots (Figure 7). After the speedling trays were empty, and using a combination of the selection index values and rooting hormone results presented below (that is, using the CONTROL as the soaking pretreatment rather than any of the hormones), a second round of speedling propagation was initiated during September 2012. From then until January 2013, approximately 3500 and 2000 trees were growing in speedling trays and Accelerator pots, respectively. Dead trees were removed from speedling trays on 22 January 2013, and new trees were planted, along with transplanting additional trees to standard pots. From September 2012 to June 2013, approximately 6000 trees were grown in the greenhouse under similar environmental conditions as those described above. On 12 to 13 June 2013, trees were sorted for health and quality, and 2646 trees were outplanted into long-term stool beds at Hugo Sauer Nursery, Rhinelander, Wisconsin. The number of trees for each combination of site and species is listed in Table 1.

RESULTS AND DISCUSSION

Early Monitoring

Collection of female and male scions is essential for maintaining long-term genetic diversity in certain restoration projects requiring sexual reproduction and natural afforestation (Dreesen 2003; Landis and others 2003). The overarching goal of afforestation and restoration activities in the current study is to utilize selected genotypes throughout the first decade and then transition to shade-tolerant, longer-lived species appropriate for the given site conditions (Zalesny and others 2012). Therefore, we did not purposefully sample trees to end up with a balance of genders. Given the dioecious nature of both genera and the elder age of most trees sampled, we anticipated that scions from both female and male trees would be collected (Farmer 1964). Recognizing this, monitoring for presence of

Figure 7. Trees growing in speedling trays (*above*) shortly before being transferred to Accelerators (*below*) at 75 d after planting. Photos by Ronald S Zalesny Jr

and excising floral buds began 3 DAP and was conducted 6 times in the first 27 d (Table 2).

The percentage of floral buds excised at 27 DAP differed among treatments ($P < 0.0065$), ranging from 13.7% for trees of the DRY DIP treatment to 19.7% for the CONTROL, and 15.7% for both remaining treatments (Table 3). Likewise, the percentage of trees flushed was determined 3 times in the first 27 d. Treatments differed at 27 DAP ($P = 0.0012$), where trees of the CONTROL (90.9%) had 6% (WET DIP), 4.6% (SOAK), and 4.5% (DRY DIP) more flushing than their root hormone counterparts (Table 3). Results for these aboveground traits agree with previous physiological studies of Salicaceae (Smith and Wareing 1972; DesRochers and Thomas 2003; Volk and others 2004), and are consistent with the general trend of leaf inhibition with the application of IBA and NAA (Davies and Hartmann 1988; Haissig and Davis 1994). Nevertheless, it was important to remove floral buds to maintain carbohydrates for root initiation and shoot growth (Okoro and Grace 1976), as well as to remove dead trees based on a lack of flushing.

Treatments differed for the percentage of wilted and (or) dead trees at 27 DAP ($P = 0.0439$), with the DRY DIP treatment causing 2.1% more impact than the WET DIP treatment and 1.3% more wilting and mortality than both of the remaining treatments (SOAK, CONTROL) (Table 3). Although treatment differences were negligible for the percentage of root initiation at 27 DAP ($P = 0.0697$), the rooting response to treatments mirrored that for wilting and mortality (Table 3). More specifically, the WET DIP and DRY DIP treatments were most and least favorable, respectively, while the SOAK and CONTROL had intermediate responses. Combining wilting or mortality with rooting, the treatments segregated into 4 response groups (listed in order of most to least favorable): 1) WET DIP, low mortality with high rooting; 2) SOAK, moderate mortality with moderate rooting; 3) CONTROL, moderate mortality with low rooting; and 4) DRY DIP, high mortality with low rooting.

Height and Dry Mass

Height and dry mass data are necessary allometric traits in early phyto-recurrent selection cycles (Zalesny and Bauer 2007a; Zalesny and others 2007). For the current study, decisions for propagation methods during scale-up were substantially based on these data. While significant clone and treatment × clone interactions were useful for assessing the range of variability in the population of genotypes selected (Table 4), interpretations of the results for both ANOVA models were focused on treatment main effects (that is, Objective 1 of this study). We believe this approach is valid given that our intention is to incorporate Salicaceae propagation methodology into phyto-recurrent selection (Objective 2) in order to build a population of genotypes that can be used for afforestation and restoration (Objective 3).

Height at 74 DAP was significantly influenced by treatment main effects ($P = 0.0347$) (Table 4). The CONTROL treatment exhibited the greatest height (16.4 ± 0.8 cm) that was not different from the WET DIP treatment (14.8 ± 0.8 cm), which itself had similar height as the SOAK treatment trees (14.0 ± 0.8 cm). Trees of the DRY DIP treatment had the least amount of height growth (12.6 ± 0.8 cm) that was not different from the SOAK treatment. Overall, these results corroborated the inhibition of aboveground traits (following root hormone treatments) shown in the monitoring activities described above, as well as general responses for Salicaceae (Haissig and Davis

TABLE 3

Percentage (%) and number (n) of Populus and Salix trees with buds flushed, floral buds removed, roots initiated, and leaves wilted or dead at 27 d after planting.

	Flushed		Buds removed		Rooted		Wilted/Dead	
Treatment	**%**	***n***	**%**	***n***	**%**	***n***	**%**	***n***
SOAK	86.3	743	15.7	135	69.3	597	2.3	20
DRY DIP	86.4	744	13.7	118	67.1	578	3.6	31
WET DIP	84.9	731	15.7	135	72.4	623	1.5	13
CONTROL	90.9	783	19.7	170	67.4	580	2.3	20
Overall ($n = 3444$)	87.1	3001	16.2	558	69.0	2378	2.4	84
Probability value	$P = 0.0012$		$P = 0.0065$		$P = 0.0697$		$P = 0.0439$	

Notes: Pre-planting treatments included soaking with water (CONTROL) or one of 3 root hormone treatments (SOAK = 36-h water soak plus 12-h soak in 1% IBA + 0.5% NAA; DRY DIP = 48-h water soak plus powder dip in 0.3% IBA; WET DIP = 48-h water soak plus 5-s dip soak in 20% IBA). For each treatment, $n = 861 = 7$ blocks × 123 genotypes. Probability values according to Chi-square (χ^2) tests from the frequency counts are listed. See Materials and Methods for detailed treatment descriptions.

TABLE 4

Probability values from analyses of variance comparing height and dry mass of Populus *and* Salix *genotypes propagated from scions collected on Staten Island, New York.*

		Dry mass			
Source of variation	**Height**	**Stem**	**Leaf**	**Root**	**Total**
Model 1					
Treatment	0.0132	<0.0001	0.0160	0.0654	<0.0001
Clone	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
Treatment × Clone	0.0347	<0.0001	0.0004	0.0061	0.0001
Model 2					
Treatment	0.0038	<0.0001	0.0073	0.0144	<0.0001
Species group	<0.0001	<0.0001	0.0007	<0.0001	<0.0001
Treatment × Species group	<0.0001	0.0011	0.5436	0.0073	0.1128

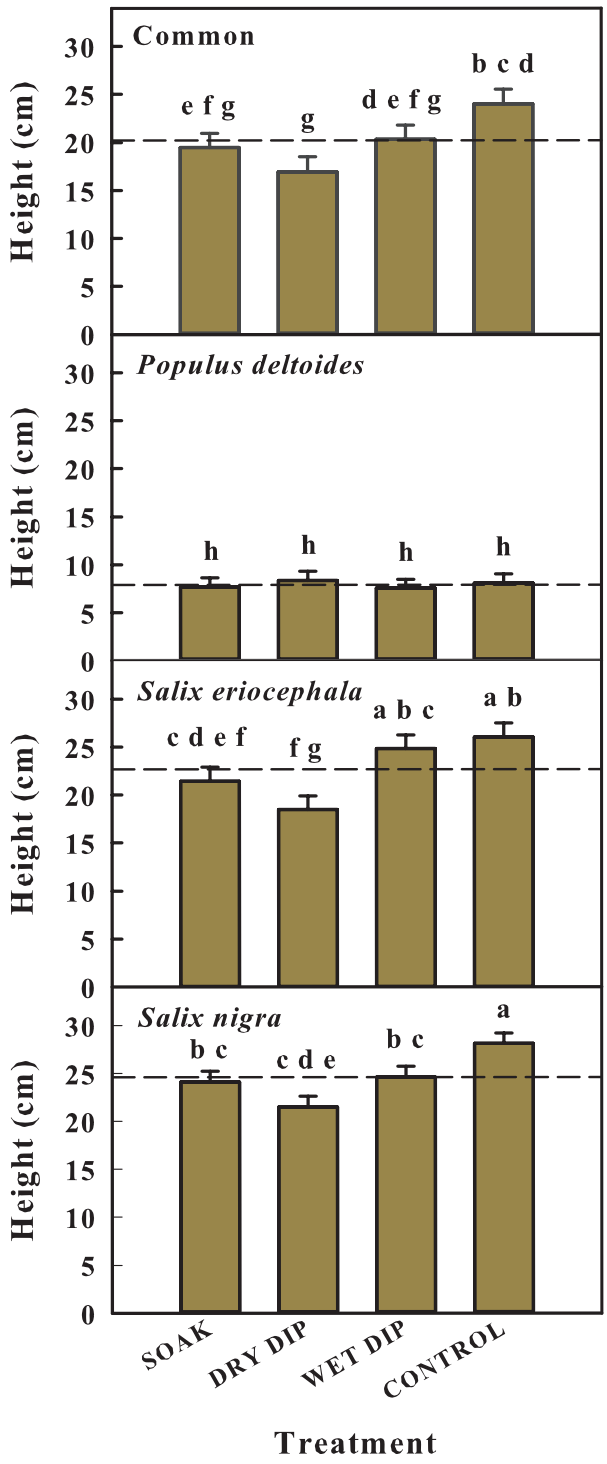
Notes: See Materials and Methods for descriptions of all fixed effects. Cutting dry mass was tested as a covariate and associated *P*-values for all traits were $P < 0.0001$.

1994). Another factor worth noting is that attention to root-to-shoot ratios (R:S) is important for scale-up activities. While these data were not tested in the current study, using root hormones at low IBA concentrations has been shown to result in optimal R:S for *Populus* (DesRochers and Thomas 2003). Furthermore, the treatment and species group main effects were significant for all traits of the species group ANOVA model, while their interaction was significant for height, stem dry mass, and root dry mass but not for leaf dry mass or total dry mass (Table 4). Treatment rankings for height were equal to those described above (that is, CONTROL > WET DIP > SOAK > DRY DIP) for all species groups except *P. deltoides*, which responded with DRY DIP > CONTROL > SOAK > WET DIP. Treatment differences for *P. deltoides* were, however, negligible (Figure 8). In addition, the 4 species groups were all different from one another and exhibited mean height of 24.6 ± 0.7 cm (*S. nigra*), 22.7 ± 0.9 cm (*S. eriocephala*), 20.2 ± 0.9 cm (common), and 7.9 ± 0.7 cm (*P. deltoides*) (Figure 8). Two general trends were worth noting. First, the superiority of the CONTROL treatment for the common species group is not surprising given selection of these genotypes using the common pre-planting protocol of soaking in water (Petersen and Phipps 1976; Volk and others 2004). Second, a height advantage the 2 Staten Island *Salix* species had relative to the lower performance of *P. deltoides* was likely due to the erratic rooting ability of the latter rather than treatment effects (Zalesny and others 2005). Overall, species group trends for dry mass variables were similar to those for height.

With the exception of root dry mass ($P = 0.0654$), treatments also significantly influenced dry mass of the trees (Figure 9; Table 4). The CONTROL treatment had 14% significantly greater stem dry mass than the next best treatment (WET DIP), which was 10% and 22% better than the SOAK and DRY DIP treatments, respectively. The magnitude and rank of treatment differences for leaf dry mass was similar to those for stems, while trends for root dry mass were nonexistent. Using Fisher's unprotected LSD, root dry mass of the DRY DIP treatment was 22% less than the other treatments, which were all equal to each other. Nevertheless, analysis of total dry mass resulted in the CONTROL treatment being 4% significantly heavier than the WET DIP treatment, which was 5 to 6% significantly greater than with the remaining rooting hormones. Once again, these data corroborated previous reports. For example, Petersen and Phipps (1976) reported that water soaking significantly increased root production and early establishment potential of 3 hybrid poplar clones, one of which contained *P. deltoides* parentage. More specifically, DesRochers and Thomas (2003) recommended 2 to 4 d of soaking to maximize the success of greenhouse production of 4 hybrid poplar clones, two of which had *P. deltoides* lineage.

Weighted Summation Index

Index values were used to prioritize genotypes for greenhouse and nursery scale-up activities. Overall, values ranged from 0.20 to 6.11, with a mean of 2.32. For all 123 genotypes assessed, *Salix* genotypes exhibited ranks 1 to 41 with 5 exceptions: the *Populus* experimental controls (NM6, D105, DN34, NC14105, 91.08.09; mean = 3.14). Of those *Salix* genotypes in



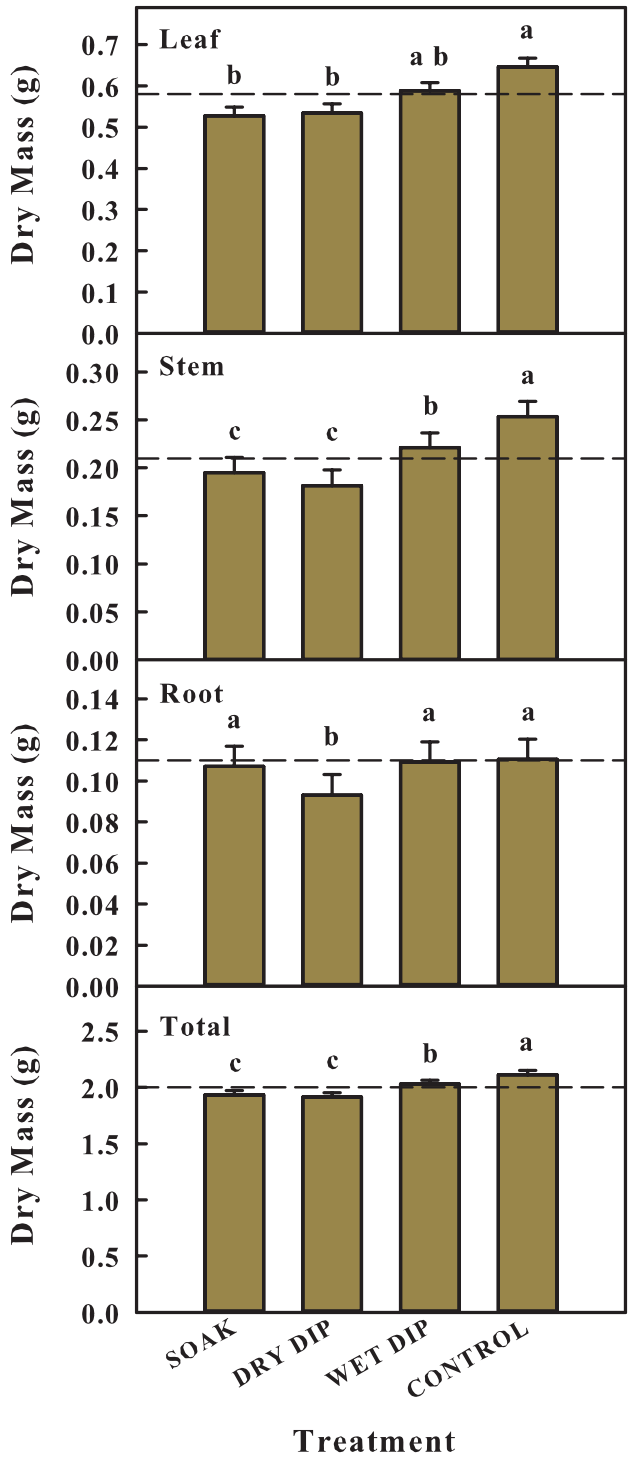


Figure 8. Height (0.1 cm) (adjusted for cutting dry mass) of 4 Salicaceae species groups at 74 d after planting. Trees were subjected to soaking with water (CONTROL) or one of 3 root hormone treatments (SOAK = 36-h water soak plus 12-h soak in 1% IBA + 0.5% NAA; DRY DIP = 48-h water soak plus powder dip in 0.3% IBA; WET DIP = 48-h water soak plus 5-s dip soak in 20% IBA). The common species group consisted of 7 *Populus* and 4 *Salix* clones commonly used for short rotation woody crop production systems. The dashed line represents the overall mean for each species group. Each bar represents the mean of 20 to 131 trees with one standard error. Bars labeled with different letters across treatments and species groups were different according to Fisher's protected LSD at $P < 0.05$.

Figure 9. Leaf, stem, root, and total (leaf + stem + root + cutting) dry mass (0.1 g) (adjusted for cutting dry mass) across 94 Salicaceae genotypes at 75 d after planting. Trees were subjected to soaking with water (CONTROL) or one of 3 root hormone treatments (SOAK = 36-h water soak plus 12-h soak in 1% IBA + 0.5% NAA; DRY DIP = 48-h water soak plus powder dip in 0.3% IBA; WET DIP = 48-h water soak plus 5-s dip soak in 20% IBA). The dashed line represents the overall mean for each plant tissue. Each bar represents the mean of 221 to 235 trees with one standard error. Bars labeled with different letters within plant tissues were different according to Fisher's protected LSD at $P < 0.05$.

the top 41, 4 were the *Salix* controls (S25, 9837.77, SV1, SX64; mean = 3.25). The range within *Salix* was 2.55 to 6.10, with a mean of 3.64. Genotypes ranking 42 to 94 were all *Populus* and ranged from 0.20 to 2.43, with a mean of 1.29. Site-related advantages were negligible for both genera, indicating a similar probability of successful propagation and scale-up with selection from multiple sites. The greater index scores for *Salix* relative to *Populus* were not surprising, as others have reported similar growth and biomass advantages during early stages of growth (Labrecque and Teodorescu 2005; Zalesny and Bauer 2007b). In addition, as with height above, the erratic rooting ability of *P. deltoides* from hardwood cuttings (Zalesny and others 2005) likely contributed to the lower potential for biomass accumulation relative to *S. eriocephala* and *S. nigra* in the current study.

Nevertheless, while *Salix* outperformed *Populus*, both genera had a broad range of index values, indicating great potential for selecting superior genotypes (that is, the probability for successful selection is proportional to variation). The elevated means of the experimental controls corroborated this assertion. The controls of the current study have been repeatedly selected for similar traits tested in multiple applications (Zalesny and others 2011), resulting in a minimal 4% advantage of *Salix* controls versus *Populus*. In contrast, the mean value of *Salix* genotypes from Staten Island was 2.8 times greater than for *Populus*. Ultimately, regardless of genera, selecting within the variability present among this population of genotypes has the potential to advance the success of phyto-recurrent selection for afforestation and restoration throughout New York City and surrounding urban areas.

CONCLUSIONS

Scion material from native *Populus* and *Salix* was collected from 3 sites on Staten Island, New York, for the purpose of propagating and selecting genotypes for afforestation and restoration activities throughout New York City. In addition to ensuring that an adequate amount of genetic diversity existed in the final population of potential genotypes, a substantial effort was placed on testing the rooting ability of the genotypes during early propagation and growth. For both genera, rooting is the first biological prerequisite for successful development and, therefore, is one of the most important traits for crop development. Therefore, 3 root hormone treatments were tested, and a broad amount of variability occurred among all genotypes with a relative advantage of *Salix* over *Populus*. In addition, root dry mass following soaking with water was as good as 2 of the root hormone treatments and better than the remaining treatment. Similar results were shown for height and other dry mass traits. Salicaceae propagation methodology was successfully completed, and planned efforts are underway to incorporate it into phyto-recurrent selection as Cycle 0 (Figure 1). From a practical standpoint, we scaled up propagation efforts and established a nursery population of *Populus* and *Salix* genotypes that can be used for ongoing afforestation and restoration activities in New York City. In addition, we developed a model for researchers and resource managers interested in similar efforts across the rural to urban interface, regardless of specific site and climate conditions.

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