

Genetic diversity and population structure of three tree species across an urban to remnant landscape gradient

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Abstract

Trees in urban areas offer ecosystem services like carbon sequestration, storm water attenuation, reduction of energy used in buildings and wildlife habitat. Cities invest substantial funds and resources to maintain a healthy urban forest, and much research has been done to improve its resiliency and sustainability. Studies have been done to determine the quantity, density and variety of tree species in urban areas, but little is known about their genetic diversity. In this study the genetic diversity and population structure of three tree species (*Quercus rubra* (red oak), *Acer saccharum* (sugar maple) and *Fraxinus pennsylvanica* (green ash)) were compared on an urban to remnant gradient in the Chicago area. Microsatellites were used to compare neutral diversity. Genetic diversity did not differ significantly among land use types for any of the three species as measured by numbers of alleles, private alleles and heterozygosity. There was no genetic structure based on land use type among red oaks. However, genetic structure among sugar maple and green ash is evident with significant genetic differentiation between urban and remnant sites. The variance in genetic structure is due to the variable cultivation history of the three tree species. There are few red oak cultivars, and this species has remained genetically indistinguishable from remnant forests. Sugar maple and green ash have been cultivated over the last 50 years, leading to these species becoming genetically differentiated from remnant populations. Careful sourcing practices will be necessary to ensure the future genetic diversity of the urban forest.

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Introduction

The urban forest is defined as all of the trees that grow in urban areas (e.g. street and park trees, spontaneous trees in brown fields or in parking lots, those that grow in managed and unmanaged forests, and trees planted in private yards) (Nowak et al. 2010), and it provides a myriad of ecosystem services. In the face of climate change trees are championed for their ability to remove and store carbon dioxide and other pollutants, which is especially important in urban areas where both are produced in large quantities (Akbari and Pomerantz 2001; Nowak et al. 2010). The urban tree canopy can also offset the heat island effect in several ways. It cools urban areas through evapotranspiration and altering air flow (Sawka et al. 2013). Trees also shade buildings, reducing the amount of solar radiation stored in impermeable surfaces, which would otherwise be redirected as heat (Sawka et al. 2013). This shading also reduces the energy necessary to cool buildings (Akbari and Pomerantz 2001). The urban forest absorbs water runoff, which can prevent it from reaching the sewage system or polluting nearby bodies of water (Walsh et al. 2012). Finally, trees increase land value, improve aesthetics, reduce erosion, interrupt wind gusts and provide habitat for wildlife (Donovan et al. 2010, Nowak et al. 2010).

The urban forest is valuable, but it is also expensive to maintain and can be susceptible to pests that cause tremendous damage (Roman and Scatena 2011). Large cities budget millions of dollars annually to prune and maintain trees (Nowak et al. 2002). On top of this regular maintenance cities occasionally contend with massive tree failures: when a pest, disease or environmental condition (such as drought or severe weather) kills a large number of individuals in a brief time period (Jim et al. 1997). One of the most devastating occurrences of massive tree failure in the urban forest was caused by Dutch elm disease. The American elm (*Ulmus americana* L.) was once the most commonly planted street and shade tree in eastern North

America (Biggerstaff et al. 1999). Beginning in the 1920's the exotic disease swept through the American elms, eventually killing close to 95% of the population (Biggerstaff et al. 1999). Because American elm was planted so heavily, the death of these trees left many cities with a large percentage of trees needing removal; in some cases entire blocks were denuded of shade trees (Biggerstaff et al. 1999). Today, emerald ash borer (*Agrilus planipennis*, Fairmaire) is wreaking similar havoc on ash trees (*Fraxinus sp.*). By 2019 the emerald ash borer is expected to destroy 38 million trees in the Midwestern United States; 17 million of which are street and park trees and will need to be removed lest they cause a safety hazard, and in many cases replaced, at an estimated cost of \$10.7 billion (Kovacs et al. 2010). Additionally, the health of other species may be adversely affected by other stresses such as climate change, the gypsy moth or the Asian longhorn beetle; any one of which will cost cities millions of dollars (Ball et al. 2007; Nowak et al. 2010).

In the aftermath of Dutch elm disease, urban foresters have learned the importance of planting a variety of tree species (Raup et al. 2006; Ball et al. 2007). By planting many different species, genera and families the city can help ensure that a single pest will not destroy a large percentage of its trees (Schoene et al. 2011; Lacan et al. 2008). Much attention and research has gone into ensuring that the urban forest is species rich, and many urban forests strive to contain no more than 10% of a given species, 20% of a genus and 30% of a family (Santamour 1990). However, little is known about the genetic diversity within species of the urban forest. It is assumed that the urban forest is not genetically diverse (Fissore et al. 2012). Most trees that are planted by the city are sourced from a handful of growers, and these growers obtain their seed stock from a limited number of trees (Worfolk, interview 2012). Additionally, many of the trees that are planted in urban areas are cultivars, some of which are grafted clones (Santamour 1990).

Foresters seek out uniformity within species: individuals with the same origin will have similar survivorship, adaptability, morphological characteristics and performance (Santamour 1990). In short, these trees are predictable. However, morphological uniformity often comes at the expense of genetic uniformity, and a lack of genetic diversity may prove to be deleterious (Raupp et al. 2006, Sork et al. 2013, Reed and Frankham 2003).

Genetic diversity, and in particular levels of heterozygosity, have been found to be related to population health in a variety of studies (see Reed and Frankham (2003) and Leimu et al. (2006) for reviews). Correlations between genetic diversity and fitness show that low genetic diversity will result in increased homozygosity as closely related individuals interbreed through generations. This inextricably leads to the expression of deleterious alleles and inbreeding depression (Reed and Frankham 2003). However, many trees in the urban forest do not breed naturally. All trees that are intentionally planted in urban areas are sourced from nurseries. Lack of genetic diversity in these instances may be caused by the excessive planting of a single cultivar or related individuals, but because new individuals are created in nurseries and not from the existing population this does not lead to inbreeding depression among intentionally planted trees. There are trees, however, that grow spontaneously in the urban forest. Unmanaged properties and city forests have a host of trees that reproduce naturally (Nowak 2012). Many of these trees are remnants from historic forests, but when they are enveloped by urbanization the trees may be influenced by planted trees. In these areas cultivars may interbreed with the autochthonous trees and cause genetic swamping (Lesica and Allendorf 1999). Over generations the spontaneous trees in the urban forest may experience deleterious inbreeding effects.

Even in forests where natural breeding does not occur (and the threat of inbreeding depression is nonexistent), genetic diversity is an important predictor of forest sustainability. If,

for example, all of the maples in a city are genetic clones of one another, a single pest or disease could rapidly damage or kill them all, whereas, if they are genetically diverse some individuals may be resistant to that pest or disease, limiting overall losses (Sork et al. 2013). American elms that are resistant to Dutch elm disease have recently been discovered (Whittemore, 2011). Ashes have proven to be variably tolerant of the emerald ash borer, with some trees still surviving after many years of infection (Marshall et al. 2013). Trees have long generation times, meaning that they are poor at rapidly adapting to new pests, disease or changing climatic conditions (Aitken et al. 2008; Sork et al. 2013). Current genetic diversity may be one of the best predictors of a tree population's ability to survive disasters (Sork et al. 2013). Even in the case of catastrophic disease a few individuals in a diverse forest may persist. Knowledge about the genetic diversity of trees in the urban forest will foster a more advanced understanding of how the trees may react to massive tree failures and help guide city planning.

Research objectives

The objective of the study was to compare neutral genetic diversity and structure in three tree species across a land use gradient: planted trees in urban areas, trees that occur spontaneously in urban areas, and remnant forests. While neutral genetic diversity does not necessarily correlate with genetic fitness, it can be used to identify where there is a dearth of diversity (Holderegger et al. 2006). The study species were: red oak (*Quercus rubra* L.), sugar maple (*Acer saccharum* Marsh.), and green ash (*Fraxinus pennsylvanica* Marsh.). These species were chosen because they are easily found in both remnant and urban settings and are native to the Chicago region. Sugar maple and red oak are currently planted by the City of Chicago and although green ash is no longer planted, it is currently one of the most abundant street trees

(Nowak et al. 2010). Using microsatellite markers, the following hypotheses were tested: 1) There will be a decrease in genetic diversity across a land use gradient from remnant to spontaneous to planted land use for all three species, 2) There will be distinct genetic structure between the planted trees and the remnant forest, while spontaneous trees will have genetic structure that is a mix of the other two land use types.

Methods

Study site

This study focuses on the trees in and around the City of Chicago, a city that has made urban greening a priority in recent years. In the past 20 years canopy cover has increased from 11% to 17% largely through the planting of street and park trees (Nowak et al. 2010). However, this forest is under considerable stress right now. Emerald ash borer is predicted to affect 11% of the Chicago forest, around 3,000,000 trees (Nowak et al. 2010). Many of these trees will need to be removed and replaced. Chicago foresters are already planning on how best to replace these trees with the goal of making a sustainable urban forest. Developing an understanding of intraspecies genetic diversity could help achieve this goal.

Study species

Three species were analyzed in this study: red oak (*Quercus rubra* L.), sugar maple (*Acer saccharum* Marsh.), and green ash (*Fraxinus pennsylvanica* Marsh.) (henceforth all species will be referred to by their common names). All of these species are native and are common in the Chicago urban forest and in the surrounding remnant woodlands. Additionally, they are all planted intentionally and occur spontaneously in the City of Chicago (Nowak 2012). Pollination

strategies can affect the ability of a species to breed with distant populations. If the study species have varying pollination syndromes it could have an effect on the landscape genetics. These three genera were chosen because they are all wind pollinated and should have a similar capacity for gene flow through pollination (Dow and Ashley 1996; Fore et al. 1992; Heuertz 2003). All three species also have methods for seed dispersal. Green ash and sugar maples seeds are both dispersed by wind while red oak seeds are moved by squirrels. None of these methods tend to move seeds over great distances, but do allow for additional movement beyond what gravity alone would provide (Fore et al. 1992; Kennedy 1990; Sork 1984).

Field methods

For each individual tree included in the study, a leaf was taken for genetic analysis. This leaf was stored in a cooler immediately after collection, and then frozen at -20°C within three hours. Additional data taken included: the diameter at breast height (DBH) and GPS coordinates. This study endeavored to look at trees across an urban to remnant gradient. To do this, trees were sampled in three land use categories. The first category was trees that were intentionally planted in the city (hereafter known as planted). These trees were located along streets and in parks. Next, trees that had seeded spontaneously within the urban matrix were sampled (hereafter known as spontaneous). Planted and spontaneous trees were differentiated using strategies described by Nowak (2012). Remnant forests were found outside of the City of Chicago, and are areas that have been continuously forested since before European colonization. In the planted category, 59 red oak, 75 sugar maple and 69 green ash samples were collected; in the spontaneous category, 57 red oak, 42 sugar maple and 48 green ash samples were collected; and in the remnant category, 72 red oak, 80 sugar maple and 66 green ash samples were collected.

Planted trees were sampled differently from the other two land use types. Planted sites were selected using a grid system. Fifteen locations were chosen using a random number generator that corresponded with city blocks. Trees were sampled within a half mile by half mile square surrounding this point. Every sugar maple and red oak was sampled within these plots; while every fifth green ash was sampled, because ash trees were much more prevalent. Additionally, sugar maples and red oaks are generally less commonly planted as street trees, but are frequently found in city parks. For eight of the city blocks a nearby park was also identified and sampled (Figure 1).

Remnant and spontaneous areas were sampled in an identical manner to each other. First, an assessment of the forest composition was completed. In forests that had abundant maples and few oaks and ashes, every fifth maple encountered would be sampled and every other oak and ash. If oaks were encountered more frequently they were sampled less regularly and ashes and maples more regularly. Four urban forests were sampled: Catherine Chevalier Woods, Dan Ryan Woods, Labagh Woods, and the Montrose Point Bird Sanctuary. The remnant areas sampled were: Busse Woods, Morton Arboretum, and Somme Woods (Figure 1). These sites are all within the Chicago metropolitan area, are relatively pristine and have been wooded since before European colonization.

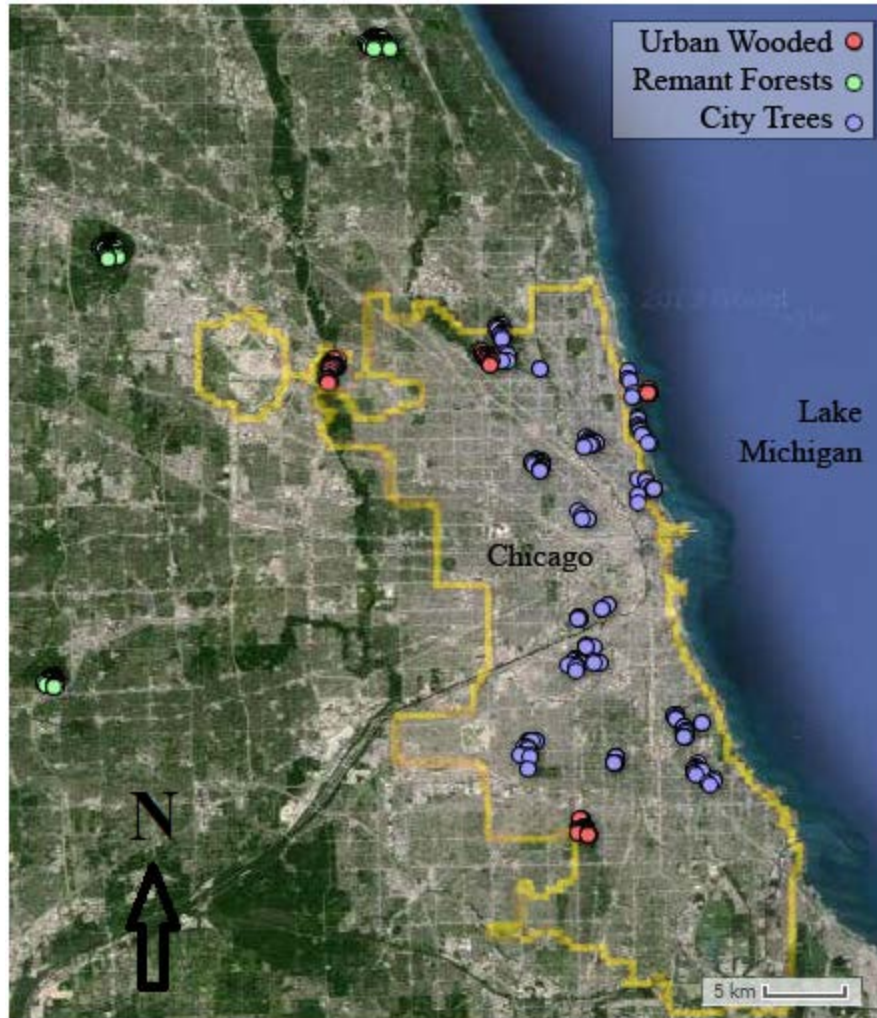


Figure 1: Sampling locations for study. Each point represents a single tree and the colors represent different land use types.

Molecular methods

A modified cetyltrimethyl ammonium bromide method was used to extract DNA (Doyle and Doyle 1987). Microsatellite primers measured neutral diversity in all species. DNA was amplified using the polymerase chain reaction (PCR) (methods for each species follow), and genotypes were obtained for nuclear microsatellite loci. All forward primers were modified with the addition of an M13 sequence to the 5' end (5'-CACGACGTTGTAAACGAC-3') and

labeled with Wellred Dye D2, D3 or D4 (Sigma-Proligo, St. Louis, Missouri, USA) for visualization (Schuelke 2000).

Primers and PCR conditions varied for each species. For red oak an initial 10 μ L reaction was conducted with 5 μ L of PCR MasterMix (Promega, Madison, Wisconsin, USA; final concentration of 0.025 μ g/ μ L Taq DNA polymerase in a proprietary reaction buffer [pH 8.5], 200 μ M of each dNTP, and 1.5 mM MgCl_2), along with 5 ng template DNA, and 0.25 μ M of both forward and reverse primers. The conditions for this PCR were: 1 min of denaturation at 94 $^{\circ}\text{C}$; then 15 cycles of 94 $^{\circ}\text{C}$ for 30 s, 45 $^{\circ}\text{C}$ for 45 s, and 72 $^{\circ}\text{C}$ for 30 s; and a final extension of 72 $^{\circ}\text{C}$ for 9 min. The product was labeled through a second 15- μ L PCR reaction containing 10 μ L of the original PCR product, with an additional 2.5 μ L MasterMix (Promega) and 0.25 μ M of M13 primer labeled with WellRed D2, D3, or D4 Dye. The conditions for this PCR were: 1 min of denaturation at 94 $^{\circ}\text{C}$; then 30 cycles of 94 $^{\circ}\text{C}$ for 30 s, 45 $^{\circ}\text{C}$ for 45 s, and 72 $^{\circ}\text{C}$ for 30 s; and a final extension of 72 $^{\circ}\text{C}$ for 9 min.

The same two-step reaction was used for both sugar maple and green ash. For the sugar maples the initial 10- μ L reaction contained 5 μ L PCR MasterMix (Promega), along with 5 ng template DNA, 0.5 ng/ μ L BSA, 0.25 ng/ μ L MgCl_2 and 0.25 μ M of both forward and reverse primers. The conditions of the PCR were: 15 min of denaturation at 95 $^{\circ}\text{C}$; then 15 cycles of 94 $^{\circ}\text{C}$ for 45 s, 56 $^{\circ}\text{C}$ for 1 min, and 72 $^{\circ}\text{C}$ for 45 sec; and a final extension of 72 $^{\circ}\text{C}$ for 10 min. The labeling 15- μ L PCR reaction contained 10 μ L of the original PCR product, with an additional 2.5 μ L of PCR MasterMix (Promega), 0.5 ng/ μ L BSA, 0.25 ng/ μ L MgCl_2 and 0.25 μ M of M13 primer labeled with the Wellred Dye. The conditions for this PCR were: 15 min of denaturation at 95 $^{\circ}\text{C}$; then 35 cycles of 94 $^{\circ}\text{C}$ for 45 s, 56 $^{\circ}\text{C}$ for 1 min, and 72 $^{\circ}\text{C}$ for 45 sec; and a final extension of 72 $^{\circ}\text{C}$ for 10 min.

The initial 10 µL reaction for green ash contained 5 µL PCR MasterMix (Promega), along with 5 ng template DNA, 0.5 ng/µL BSA, 0.25 ng/µL MgCl₂, and 0.25 µM of both forward and reverse primers. The conditions of the PCR were: 5 min at 96° C; then 15 cycles of 94 °C for 1 min, 52 °C for 1 min, and 72° C for 30 s; and a final extension of 72° C for 9 min. The labeling 15-µL PCR reaction contained 10 µL of the original PCR product, with an additional 2.5 µL of PCR 2× MasterMix (Promega), 0.5 ng/µL BSA, 0.25 ng/µL MgCl₂ and 0.25 µM of M13 primer labeled with Wellred Dye. The conditions for this PCR were: 5 min at 96° C; then 35 cycles of 94 °C for 1 min, 52 °C for 1 min, and 72° C for 30 s; and a final extension of 72° C for 9 min.

PCR products were analyzed and scored using a CEQ 8000 Genetic Analysis System version 9.0 (Beckman Coulter, Brea, California, USA). Each well included 30 µL of HiDi formamide (Azco Biotech., San Diego, CA), 3.3 µL of 400 bp ladder (Beckman Coulter, Brea, CA) and the following amounts of PCR product: 0.5 µL of Wellred Dye D4 labeled product, 1 µL of Wellred Dye D3 labeled product and 2.5 µL of Wellred D2 labeled product.

Primers used for each species are listed in Table 1. Primers used in the red oak analysis were originally described by Aldrich et al. (2002) and Aldrich and Jagtop (2003) Primers for green ash were originally developed for European ash (*Fraxinus excelsior* L.) and were described by Lefort and Frascaria-Lacoste (1999). Sugar maple primers were originally developed for sycamore leaf maple (*Acer pseudoplatinus* L.) by Pandey et al. (2004).

Table 1: Primers for red oak were developed by Aldrich et al. (2002) and Aldrich and Jagtop (2003). Primers used for sugar maple were developed by Pandey et al. (2004). Green ash primers were developed by Lefort and Frascaria-Lacoste (1999).

<i>Quercus rubra</i> (Red oak)				
Locus	Repeat	GenBank accession	Primer sequence	Size range (bp)
quru-GA-0A01	(GA) ₁₁	AF523851	F: CTCTCGCTCTGCACGTGACTCA R: TTTGATTGATATAATTGATCGCT	132-170
quru-GA-1G13	(GA) ₁₄	AF523862	F: AAAACTCACACAGCCGATTACTA R: GATTCCATTGTCAACTGCGAAGA	179-215
quru-GA-1C06	(GA) ₂₉	AF523858	F: CAAATAAATATTGTGGGGTTCA R: GGAGGGGATCCGGAAAA	247-305
quru-GA-0A03	(GA) ₁₇		F: ATTTTATATTAGCATAAGGGTG R: GGCTTCACATTGAGAACGTTG	187-245
quru-GA-1F02	(GA) ₁₅	AF523860	F: CCAATCCACCCTTCCAAGTTCC R: TGGTTGTTTTGCTTTATTCAGCC	165-215
quru-GA-0I21	(GA) ₁₆	AF523855	F: ATATGGTCCCGATTAATTC R: GGGCAACATTCAAATGTATCTA	173-213
quru-GA-2G07	(GA) ₂₃		F: GCCAACAAATTTAACTATCCAT R: TAACTGGGCTAGATAATCAG	218-258
quru-GA-1C08	(GA) ₂₉	AF523859	F: TCCCAATCGATGTTTGATAAGG R: GGGCTCTTGAGAGGATGTAGG	272-328
quru-GA-2H14	(GA) ₁₈		F: ATTACGCGAGCGTGCAGT R: GTGCTCCACGAATGCTCTAGCCA	281-347
quru-GA-0E09	(GA) ₁₆	AF523854	F: TGCCATCCCTATACACAACCA R: CCTCCATCACAAAGTTGCC	183-251
<i>Acer saccharum</i> (Sugar maple)				
Locus	Repeat	GenBank accession	Primer sequence	Size range (bp)
MAP2	(GT) ₂₃	AJ620722	F: CATTAAACACATTTAAGCAAAACAAG R: ATCGGTTTGACATTGAGTGG	152-186
MAP9	(GA) ₈	AJ620723	F: ACAATAAAAGAGCCCACATAGATAG R: TCTCTTCAATTGCAAGGCTTC	110-126
MAP33	(GT) ₁₈	AJ620726	F: GCAATGAACACATATACAAACAAGAG R: GCAACAAATGCCCTCTCAAG	132-168
MAP34	(CA) ₂₁	AJ620727	F: ACCATTCTCACCCTCCATC R: TAAGTGGGAACATGGCAAGG	142-186
MAP46	(GT) ₈ GAT	AJ620729	F: CATAATGTAGGGACACATATGAATG	169-177

(GT) ₈		R:GAGCGTCAAAGATTGACTTGG		
<i>Fraxinus pennsylvanica</i> (Green ash)				
Locus	Repeat	GenBank assession	Primer sequence	Size range (bp)
FEMSATL1	(TTAAAA) ₂ ... (GT) ₁₉	AF004829	F: AGCGCATTTTATGAATGTTC R: ATCAACTGAAGATGACGACG	179-201
FEMSATL4	(CA) ₂ (AG) ₂₄	AF006069	F: TTCATGCTTCTCCGTGTCTC R: GCTGTTTCAGGCGTAATGTG	208-226
FEMSATL16	(CA) ₃ (CG)(C A) ₁₀ (TA) ₂ (CA) ₃	AF029880	F: TTAAACAGTTAACTCCCTTC R:CAACATACAGCTACTAATCA	181-207
FEMSATL19	(CA) ₆ CGGC (CA) ₁₃	AF020400	F: CTGTTCAATCAAAGATCTCA R:TGCTCGCATATGTGCAGATA	161-199

Statistical methods

Each primer was tested for possible null alleles and deviations from Hardy Weinberg equilibrium using Microchecker (van Oosterhout et al. 2004). In order to determine if there was a decrease in genetic diversity from remnant to planted sites average number of alleles per loci (N_a), number of effective alleles (N_e), Shannon's information index (I), observed and expected heterozygosity (H_o and H_e) F statistics (inbreeding coefficient) and average number of private alleles per loci (P_a) were calculated using GenAlEx v.6.5 (Peakall and Smouse, 2012). F statistics used in this analysis are described by Hartl and Clark (1997). Significance of variation among across land use types and size classes was determined using ANOVA. If significant differences were found Tukey's honestly significant difference (HSD) test was used to determine the source of differences. Diversity was compared using two variables: land use and DBH. DBH has been shown to be a good predictor of tree age in these three species (Jones et al. 2006). DBH size classes are described in Table 2. It should, however, be noted that trees do increase in diameter much more quickly in urban areas than in natural forests. The correlation used in this

study was found in natural areas, and will overestimate the age of urban trees (Bowles, personal communication). DBH groupings were selected in such a way to create roughly equal numbers of individuals in each class.

Table 2: Tree size classes. Size classes using DBH and approximate tree age for each class is given for each species (calculated using data from M. Bowles (unpublished data)).

	Small	Medium	Large
Red oak	2.5-20 cm (10-60 years)	20-60 cm (60-165 years)	60+ cm (165+ years)
Sugar maple	2.5-15 cm (10-50 years)	15-30 cm (50-110 years)	30+ cm (110+ years)
Green Ash	2.5-20 cm (10-60 years)	20-35 cm (60-100 years)	35+ cm (100+ years)

A suite of analyses were used to detect structure and differentiation among land use types. First, AMOVA and pairwise F_{st} values were calculated using GenAlEx. Methods used to calculate F_{st} are described by Nei (1977). Isolation by distance can explain the origin of genetic differentiation. To determine if geographic distance could explain differentiation in these populations F_{st} was compared to the distance between sites using Genepop (Raymond and Rousset 1995; Rousset 2008). Distance between sites was determined by measuring the distance of the centroid of each site.

To identify population structure that may not be apparent with standard population genetic approaches, a Bayesian approach was taken using the program STRUCTURE (Pritchard et al. 2000). STRUCTURE identifies genetic clusters (K) that correspond to population structure. For each species, independent runs were carried out for each K. Twenty iterations were run using a 10,000 burn in period and data for 50,000 iterations were collected. The most likely K was selected from 1-25 theoretical populations using the procedure detailed in Evanno et al. (2005).

An unweighted pair group method for arithmetic mean (UPGMA) was also used to visualize relationships among individual trees. To do this, genetic distance was first determined using GenAlEx. This matrix was used to create a UPGMA tree with the program PHYLIP v. 3.6 (Felsenstein 2005). This tree was visualized using FigTree v. 1.4 (Rambaut 2012).

Results

Red oak

No diversity measures varied significantly for red oak across land use types. Table 3 shows the raw values for each diversity measure across all sites and land use types. Table 4 shows the results of an ANOVA that compared each variable across the land use types. Both of these tables show no variation among sites nor land use types. Diversity measures did vary significantly among DBH size classes, showing that diversity has changed over time (Tables 5 and 6). Post hoc Tukey's HSD on N_e , I and F (the three diversity values that showed significant variation) all showed that there was no significant difference between small and medium trees, but small and medium trees were both significantly different from large trees ($p < 0.01$).

Table 3: Summary of diversity data from all tree species in all sites and land use types. N is the number of individuals, Na the average number of alleles per loci, Ne the number of effective alleles per loci, I the Shannon information index, Ho the number of observed heterozygotes and He the expected, F is the difference of these two values ((He-Ho)/He) and Pa is the average number of private alleles in each population.

		Site	N	N _a	N _e	I	H _o	H _e	F	P _a
Red oak	Planted	Northwest	9	8.20	5.655	1.824	0.767	0.778	0.039	0.40
		Northeast	17	11.10	7.297	2.040	0.665	0.816	0.184	1.40
		Southwest	10	9.90	7.335	2.096	0.730	0.850	0.146	1.30
		Southeast	23	12.70	7.170	2.142	0.717	0.830	0.138	2.30
	Spon	Labagh	18	11.60	7.364	2.105	0.739	0.834	0.119	1.90
		Chavelier	26	13.20	8.118	2.165	0.735	0.823	0.103	2.90
		Dan Ryan	13	9.50	6.392	1.964	0.731	0.815	0.108	1.80
	Rem	Somme	32	15.20	8.101	2.251	0.720	0.840	0.151	3.40
		Morton	12	10.60	7.510	2.120	0.708	0.846	0.168	1.00
		Busse	28	13.10	7.686	2.090	0.718	0.794	0.111	1.60
Sugar maple	Planted	Northeast	18	4.80	2.855	1.020	0.411	0.492	0.193	0.80
		Northwest	21	5.20	2.521	0.963	0.360	0.468	0.487	1.40
		South central	20	4.80	2.741	0.936	0.488	0.443	-0.083	1.20
		South	16	4.00	2.477	0.823	0.343	0.413	0.302	0.80
	Spon	Montrose	12	4.40	2.799	0.984	0.374	0.474	0.361	1.20
		Chavelier	12	4.60	3.290	0.985	0.367	0.461	0.140	1.20
		Labagh	11	4.20	2.351	0.932	0.373	0.475	0.280	0.80
		Dan Ryan	7	2.80	1.826	0.575	0.286	0.292	-0.013	0.00
	Rem	Somme	27	5.60	2.218	0.944	0.322	0.451	0.474	1.60
		Morton	26	4.60	2.353	0.929	0.346	0.470	0.326	1.00
		Busse	27	5.00	2.378	0.962	0.320	0.485	0.395	1.20
Green ash	Planted	Northeast	15	6.50	3.325	1.415	0.517	0.671	0.220	0.25
		Northwest	20	6.75	3.059	1.247	0.500	0.596	0.179	0.25
		Southeast	18	6.00	3.094	1.249	0.520	0.614	0.170	0.50
		Southwest	16	5.00	2.732	1.118	0.484	0.574	0.213	0.25
	Spon	Montrose	9	5.25	3.519	1.333	0.594	0.668	0.118	0.25
		Chavelier	17	6.75	3.784	1.499	0.568	0.699	0.202	0.75
		Labagh	16	6.75	3.40	1.436	0.656	0.684	0.024	0.25
		Dan Ryan	24	7.25	2.754	1.325	0.536	0.631	0.140	0.50
	Rem	Somme	23	7.50	3.778	1.538	0.512	0.720	0.289	0.75
		Busse	25	7.25	3.722	1.539	0.617	0.723	0.151	0.25

Table 4: Comparison of diversity values from Table 3 using ANOVA across land use types. This table shows the p values of each ANOVA result. There are no significant variances in any measure for any species ($p > 0.05$). See Table 3 for definitions of terms.

	N _a	N _e	I	H _o	H _e	F	P _a
Red oak	0.327	0.321	0.404	0.674	0.065	0.289	0.460
Sugar maple	0.137	0.563	0.701	0.187	0.627	0.341	0.387
Green ash	0.209	0.110	0.158	0.857	0.181	0.184	0.588

Table 5: Summary of diversity data for each species in all land use types, divided by size classes. See Table 3 for definitions of terms.

		Size class	N	N _a	N _e	I	H _o	H _e	F	P _a
Red oak	Plant	Small	26	13.6	8.015	2.197	0.750	0.838	0.105	3.6
		Medium	17	10.9	7.447	2.056	0.706	0.814	0.133	1.3
		Large	13	9.5	6.363	1.954	0.746	0.810	0.084	1.6
	Spon	Small	24	12.8	7.766	2.143	0.696	0.823	0.163	2.4
		Medium	21	12.6	7.779	2.194	0.686	0.844	0.192	2.8
		Large	13	9.9	6.413	1.991	0.792	0.814	0.024	1.4
	Rem	Small	25	14.1	7.629	2.199	0.738	0.832	0.12	2.8
		Medium	32	14.7	8.560	2.259	0.688	0.840	0.192	2.7
		Large	15	9.9	6.672	1.936	0.748	0.788	0.074	0.5
Sugar maple	Plant	Small	23	5.2	2.895	1.034	0.383	0.505	0.381	0.8
		Medium	31	6.8	2.923	1.086	0.430	0.488	0.421	2.4
		Large	21	4.4	2.726	0.886	0.378	0.451	0.232	1.0
	Spon	Small	15	5.2	3.285	1.074	0.339	0.505	0.438	1.6
		Medium	16	4.6	2.581	0.917	0.383	0.462	0.073	1.2
		Large	11	4.2	2.364	0.902	0.345	0.460	0.309	0.8
	Rem	Small	45	6.2	2.250	0.960	0.326	0.454	0.483	2.6
		Medium	30	4.8	2.260	0.903	0.330	0.476	0.345	1.2
		Large	5	3.2	2.649	0.902	0.350	0.547	0.402	0.4
Green ash	Plant	Small	2	2.5	2.317	0.747	0.500	0.438	-0.156	0.0
		Medium	29	7.75	3.365	1.380	0.500	0.636	0.219	0.75
		Large	38	8.0	3.131	1.325	0.509	0.629	0.216	0.75
	Spon	Small	34	9.75	3.700	1.576	0.628	0.706	0.105	1.25
		Medium	13	5.5	3.552	1.426	0.545	0.704	0.220	0.0
		Large	19	6.0	2.679	1.255	0.518	0.620	0.166	0.5
	Rem	Small	31	8.5	3.649	1.571	0.549	0.720	0.233	1.0
		Medium	11	4.75	3.501	1.341	0.568	0.687	0.157	0.0
		Large	6	4.75	3.664	1.378	0.650	0.712	0.092	0.0

Table 6: Comparison of diversity values from Table 5 using ANOVA across size classes in each land use type. Only red oak values varied beyond the null expectation ($p < 0.05$). See Table 3 for definitions.

	N _a	N _e	I	H _o	H _e	F	P _a
Red oak	0.018*	0.005**	0.009**	0.358	0.064	0.015*	0.052
Sugar maple	0.114	0.708	0.409	0.554	0.899	0.325	0.25
Green ash	0.906	0.76	0.929	0.891	0.8	0.417	0.509

AMOVA gave little indication of differentiation among land use types: 99% of variation was within land use types and only 1% among. Comparison of pairwise F_{st} values for red oak also revealed little differentiation among sites, let alone among land use types (Table 7). Only a handful of the sites varied significantly from one another, and these differences were evenly

spread out among land use types. That is, planted sites were as varied from one another as they were from the remnant and spontaneous sites, and there is no evidence for variation among land use types.

Table 7: Pair wise comparison of F_{st} values for red oak. Each site is separated into its associated land use: planted, spontaneous and remnant.

	Planted				Spontaneous		Remnant		
	North-west	North-east	South-west	South-east	Labagh	Chavelier	Dan Ryan	Somme	Busse
Planted									
Northeast	0.030*						*	p < 0.05	
Southwest	0.021	0.018					**	0.05 < p < 0.001	
Southeast	0.029	0.024	0.018				***	p < 0.001	
Spontan.									
Labagh	0.024	0.021	0.016	0.021					
Chavelier	0.023	0.020	0.015	0.016	0.016				
Dan Ryan	0.042**	0.021	0.025	0.031*	0.029*	0.027**			
Remnant									
Somme	0.024*	0.014	0.012	0.017	0.016	0.013	0.020		
Busse	0.026*	0.012	0.013	0.016	0.019*	0.015	0.020	0.011	
Morton	0.026	0.019	0.018	0.024	0.020	0.019	0.031*	0.019	0.016

Often times genetic differences among sites is correlated with distance. However, this does not seem to be the case for red oaks. Comparison of genetic distance to geographic distance showed no significant correlation (Figure 2).

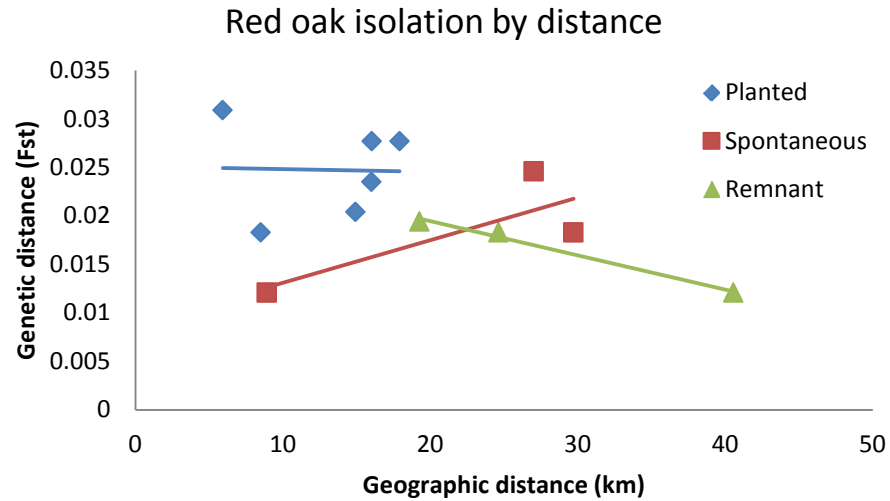


Figure 2: Isolation by distance for red oak. There is not significant relationship between F_{st} and geographic distance in any land use type ($p > 0.05$).

STRUCTURE analysis provided further evidence that the red oaks from different land use types have little to no genetic structure. No clear K value could be determined using the Evanno (2005) procedure. The best theoretical K value should be selected where the line plateaus when the theoretical K is plotted against average $L(K)$, however, no such point exists (Figure 3A). Additionally, a peak should be evident at the best K value when theoretical K is plotted against mean $L(K)$, again, no such peak is displayed (Figure 3B). This suggests that there is no genetic structure and that oaks across all land use types are essentially interbreeding.

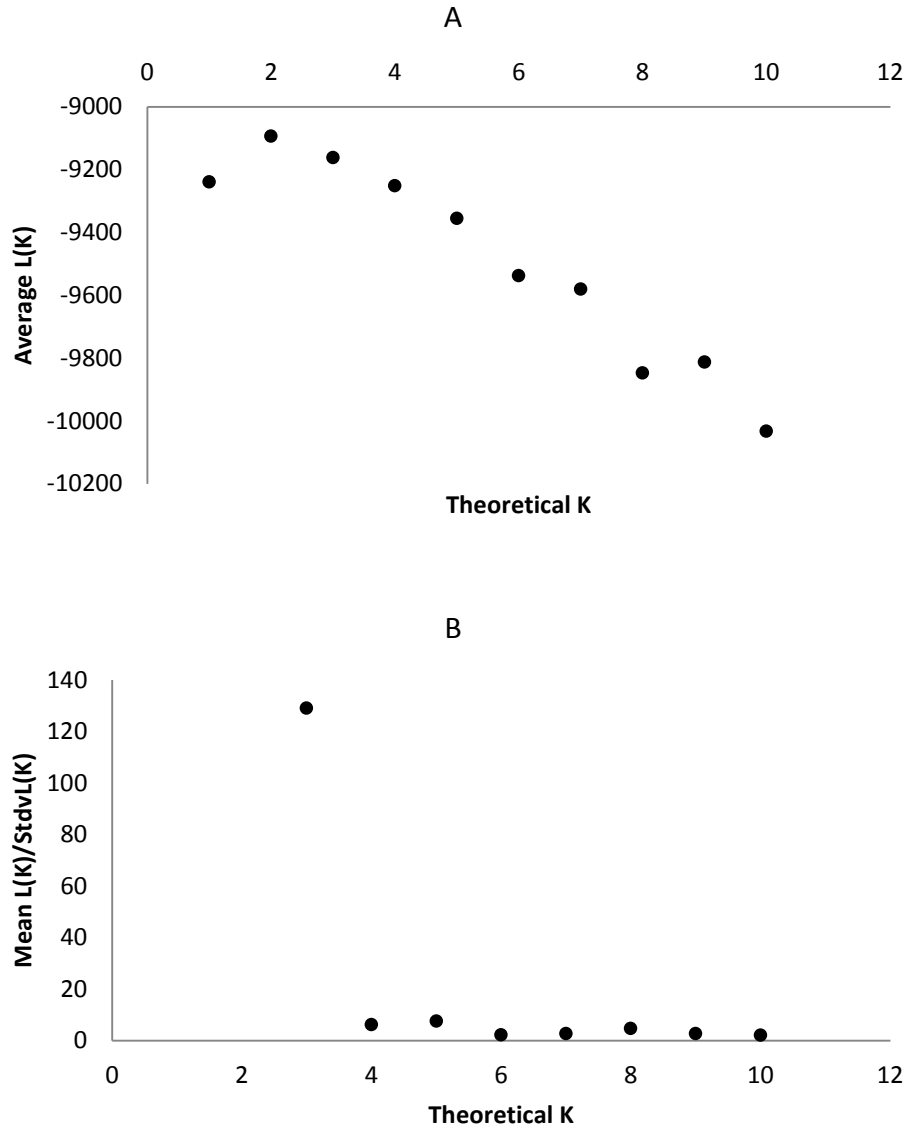


Figure 3: Determination of theoretical K for red oak using the Evanno method (2005). In Figure 2A a plateau should form at the correct value of K. In 2B a peak should form at the same value. Neither of these features is observed, indicating that the red oaks in the Chicago region are one interbreeding population with little genetic structure.

Because there is no genetic structure in red oaks an UPGMA was used to visualize relationships among individuals (Figure 4). Each individual is color coded to a specific site. If individuals from different sites or land use types clustered together on the dendrogram there

would be evidence for genetic boundaries in the landscape. However, red oak individuals from different sites and land use types appear evenly spread throughout the dendrogram, indicating no structure. There is one indication of differentiation in the UPGMA. In the lower right hand portion of the figure there are four individuals that are closely related both geographically and genetically (Planted049 – Planted053). These trees also have similar morphological qualities: all had a DBH of around 5 cm and identical leaf shape and branching structure.

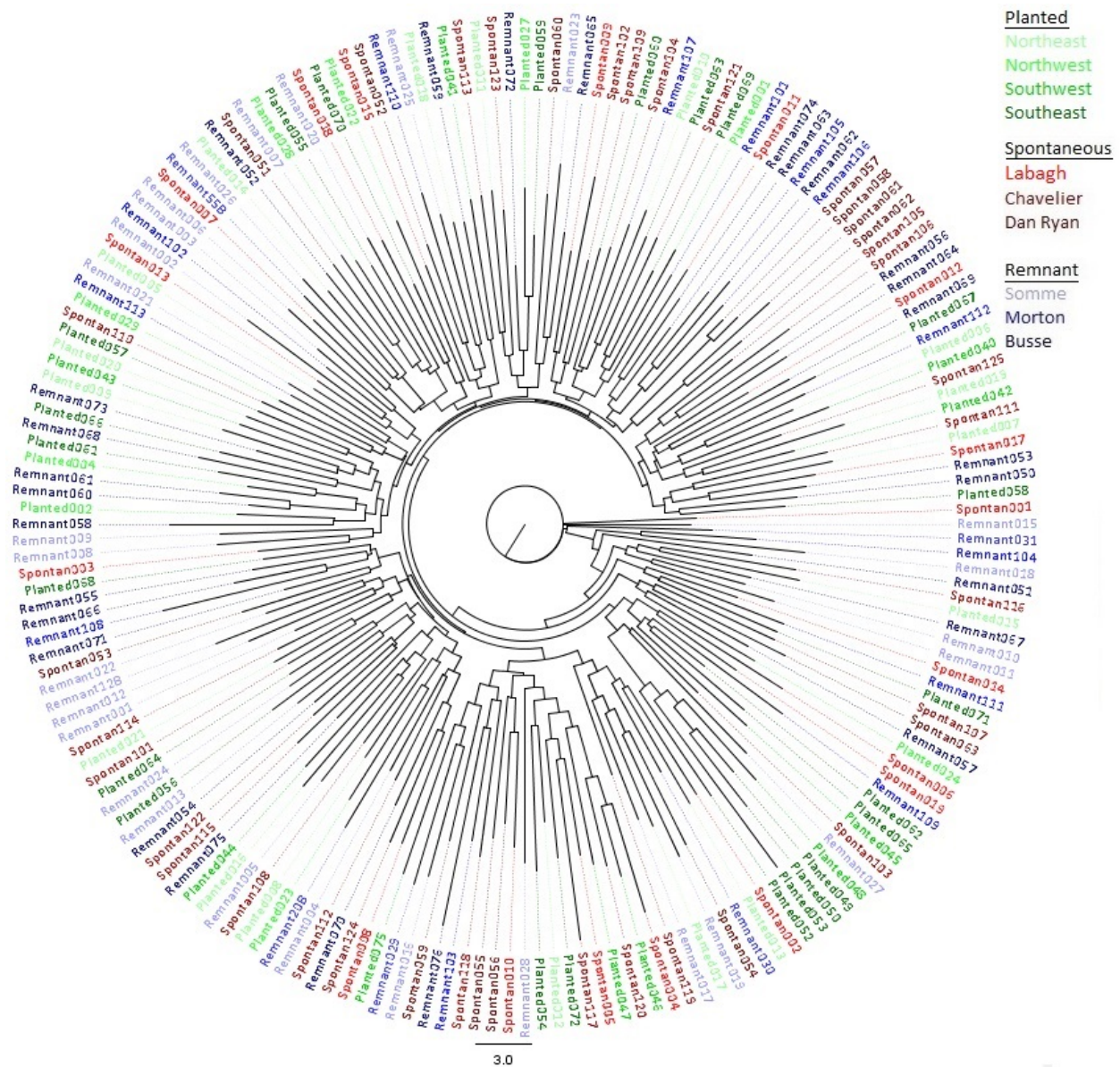


Figure 4: UPGMA tree for red oaks. The planted sites are all in green tones, the spontaneous sites are red tones and the remnant sites are in tones of blue. Further information including the size and geographic location of each individual can be found in the appendix.

Sugar maple

As with red oak, there was no significant variation of any diversity measure among land use types (Table 3 and 4). There was not, however, significant variation among DBH classes, indicating that diversity has not changed over time (Table 5 and 6). AMOVA for sugar maple shows a little evidence of differentiation of populations in sugar maple: 96% of variation occurred within sites and 4% among sites. Pairwise F_{st} did reveal differences in genetic distances among sites (Table 8). Nearly all of the planted sites varied from the spontaneous and remnant sites, and only one of the remnant and spontaneous site pairs did not vary significantly. However, these differences did not seem to be based on distances between the sites (Figure 5). Comparison of genetic and geographic distance showed no correlation.

Table 8: Pairwise comparison of F_{st} values for sugar maple.

	Planted					Spontaneous		Remnant		
	North-west	North-east	South-west	South-east	Montrose	Labagh	Chavelier	Dan Ryan	Somme	Busse
Planted										
Northeast	0.030*								*	p < 0.05
Southwest	0.028	0.021							**	0.05 < p < 0.001
Southeast	0.039*	0.041*	0.027						***	p < 0.001
Spontan.										
Montrose	0.057**	0.019	0.027	0.050*						
Labagh	0.043*	0.023	0.030	0.051*	0.028					
Chavelier	0.069**	0.070***	0.050*	0.019	0.069*	0.072*				
Dan Ryan	0.119***	0.086*	0.094**	0.144**	0.073	0.041	0.168**			
Remnant										
Somme	0.027*	0.040*	0.026	0.045**	0.043*	0.026	0.068***	0.075*		
Busse	0.028*	0.056***	0.041**	0.050***	0.079***	0.063***	0.073***	0.141***	0.020*	
Morton	0.023	0.042**	0.027*	0.037**	0.049**	0.043***	0.063***	0.121***	0.016	0.017

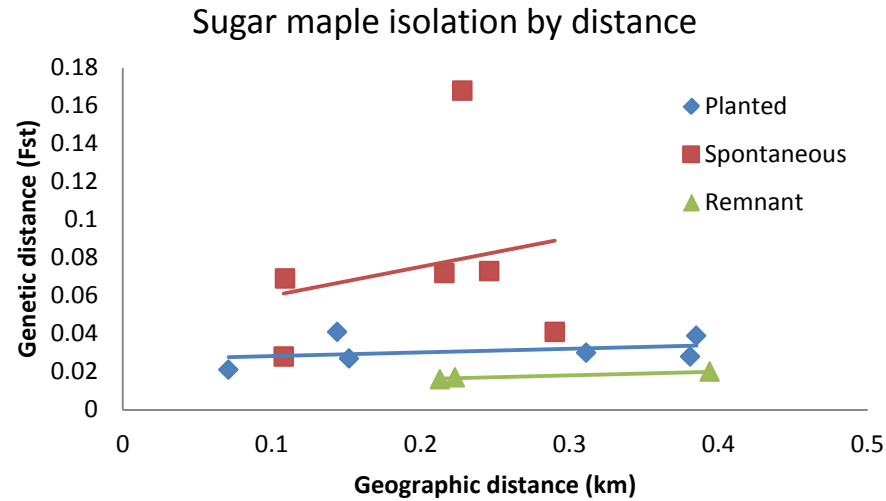


Figure 5: Isolation by distance for sugar maple. There is not significant relationship between F_{st} and distance for any land use type ($p > 0.05$).

Structure analysis confirmed that there was some variation among land use types. It was determined that there were five theoretical populations using the procedure described by Evanno (2005). The curve in Figure 6A levels out at K equals five, and in Figure 6B there is a small peak at the same value. There is some room for interpretation in these results, as the structure is fairly weak, but the visual readout for $K = 5$ does highlight some interesting features about the sugar maple population.

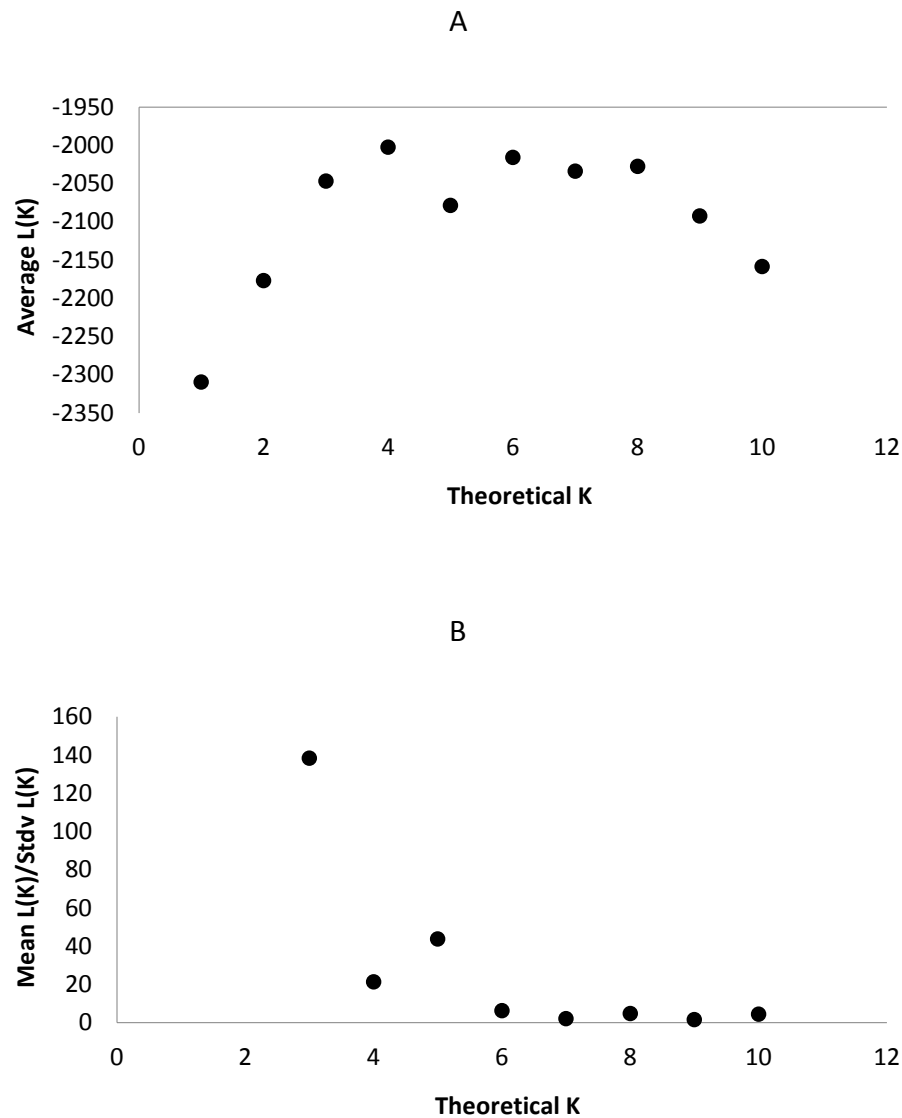


Figure 6: Determining theoretical K for sugar maple. Figure 6A shows a plateau at $K = 5$. This is further affirmed by Figure 6B, which shows a small peak at $K = 5$.

The structure analysis for $K = 5$ shows a large percentage of cluster three in the planted population while clusters one and two dominate the remnant population (Figure 7). Planted individuals are differentiated from remnant sites, and spontaneous individuals have intermediate characteristics (Figure 7B). The spontaneous sites have intermediate levels of clusters one two and three and these sites are dominated by clusters four and five. These clusters are less common

in the remnant and planted sites. It seems that the spontaneous sites do have some qualities that bridge between remnant and planted sites, but also have some unique characteristics (Figure 8). There is little indication that there is structure among sites. While there are many individuals in remnant land use types that are dominated by cluster one or two, these individuals are not separated by site.

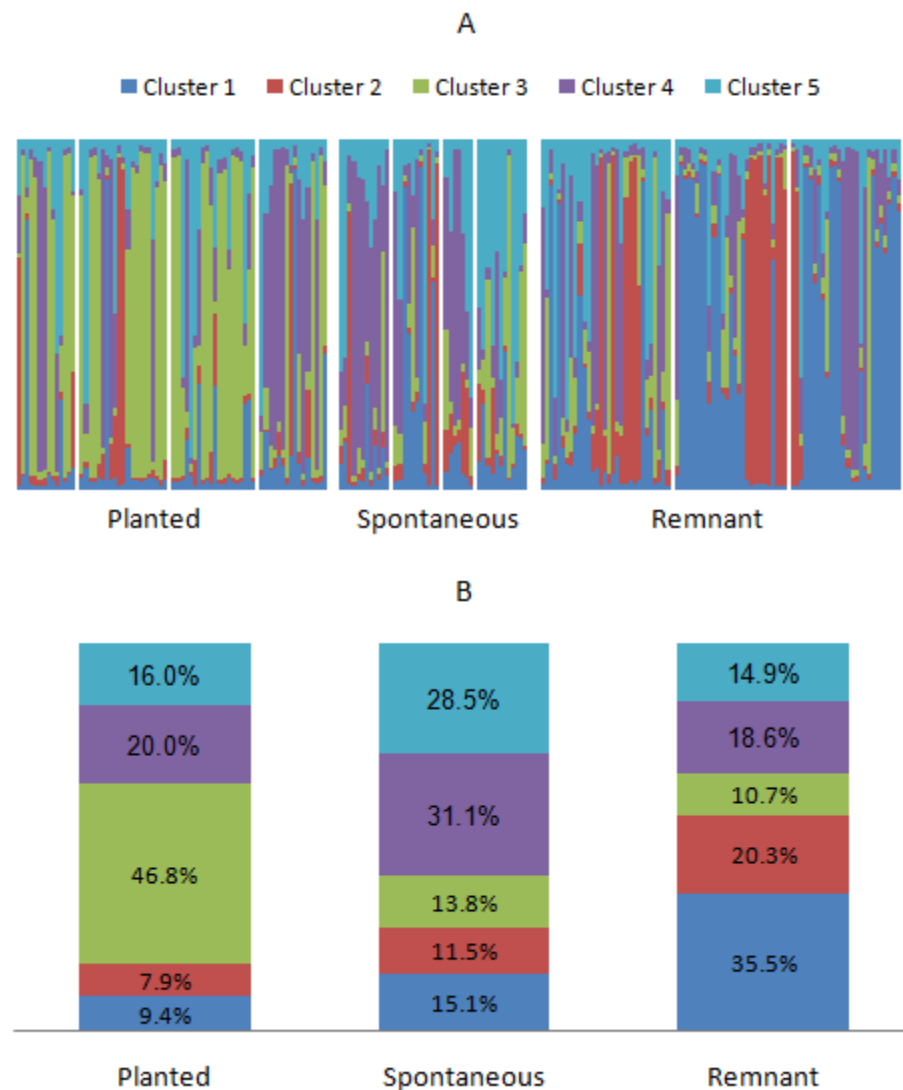


Figure 7: Sugar maple structure for $K = 5$. Figure 7A shows results for each individual, sorted by land use type and geographic proximity. Large gaps denote breaks in land use types and small gaps denote sites. 7B illustrates the average composition of each land use type. The planted trees have a large percentage of cluster three, showing that it is genetically distinct from the new and remnant populations.

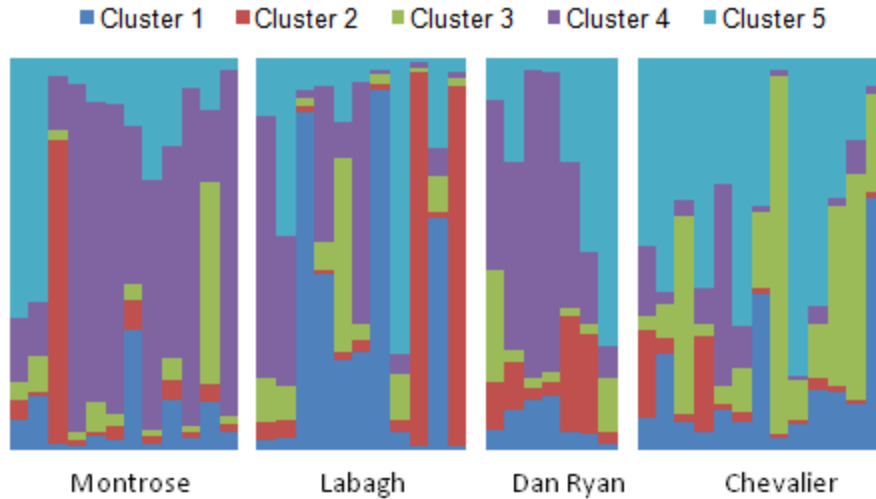


Figure 8: Detail of structure results for sugar maples spontaneous sites.

There is no indication of structure by DBH (Figure 9). This is especially interesting for the planted sites. I expected that smaller trees would be very similar to one another (because of an abundance of cultivars) than the older trees which might have more remnant individuals. There is not strong evidence that this is the case.

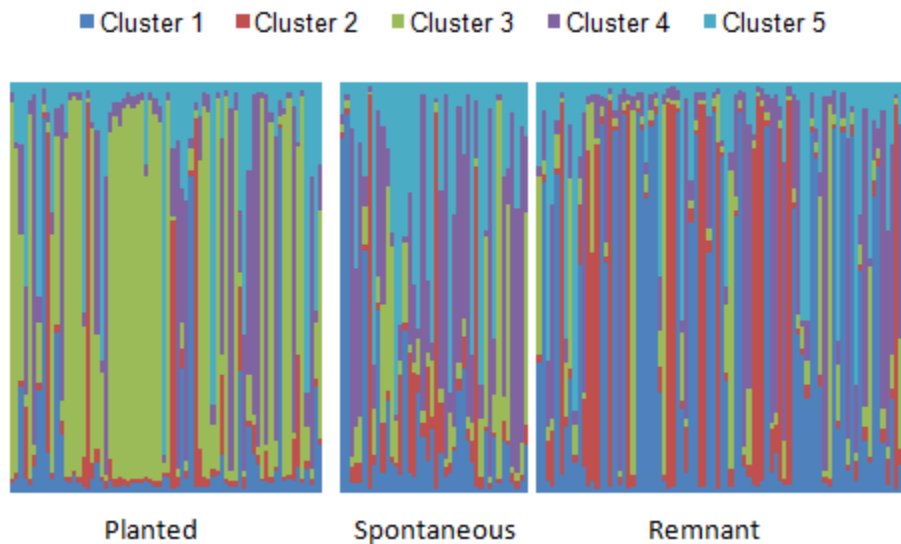


Figure 9: STRUCTURE results for sugar maple sorted by DBH across land use types. DBH is sorted by small to large, with smallest trees on the left.

An UPGMA further illustrates the structure in the sugar maple populations (Figure 10). Many of the planted individuals are clustered into two sections of the analysis. Remnant trees are also loosely clustered together in two sections. Spontaneous trees do not cluster out discretely, but are sprinkled throughout the dendogram and are often in between the remnant and planted clusters. Additionally, individuals are clustered more by land use types than by sites. The clusters of planted and remnant trees are composed of a mix of sites.

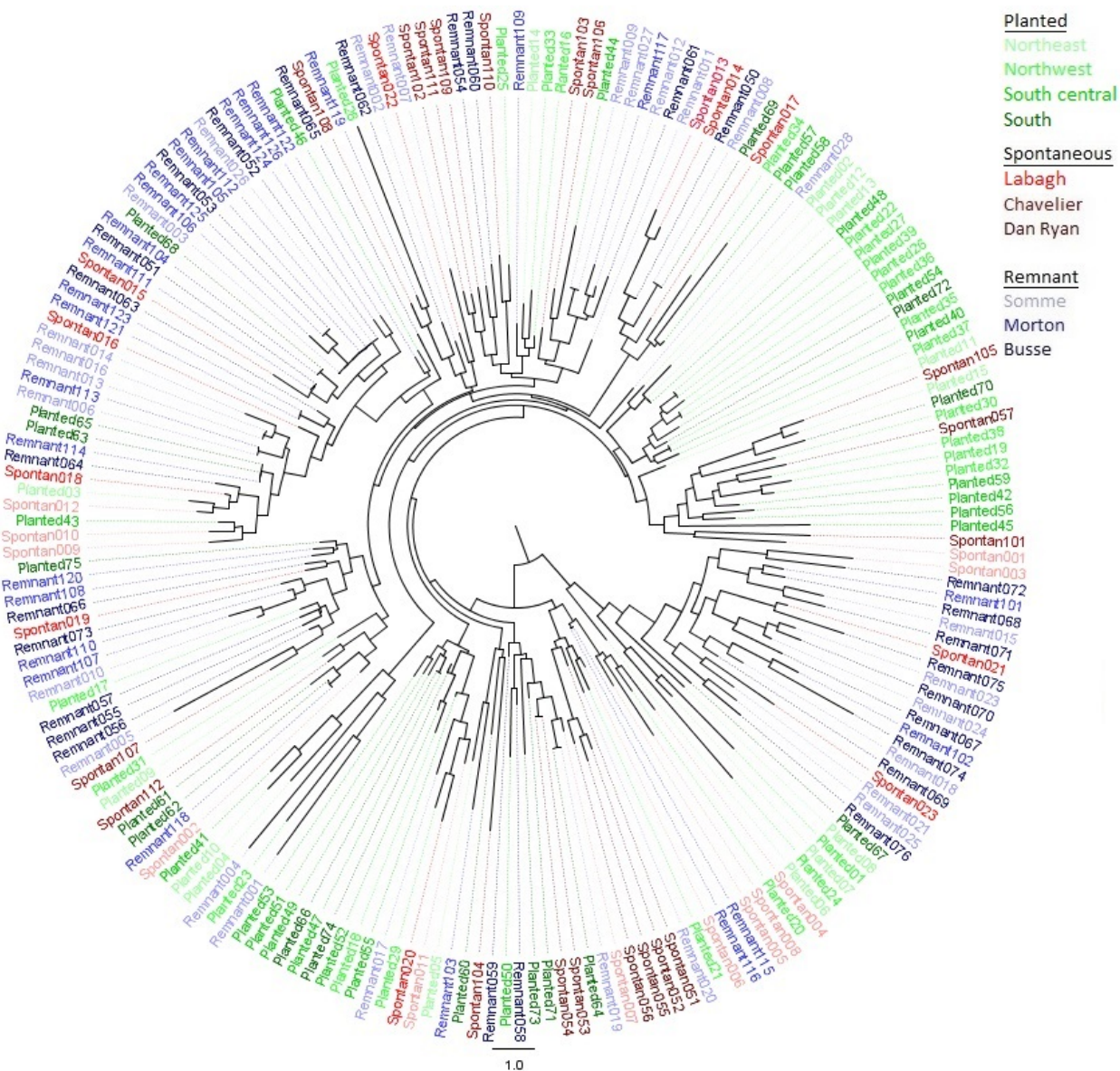


Figure 10: UPGMA for sugar maple. The planted sites are all in green tones, the spontaneous sites are red tones and the remnant sites are in tones of blue. Further information including the size and geographic location of each individual can be found in the appendix.

Green ash

Average number of alleles per locus did not vary significantly among land use types, nor did average number of private alleles, heterozygosity, F statistics, and Shannon's information

index. As with sugar maple and red oak, genetic diversity among all three land use types and DBH classes does not vary significantly (Table 3-5).

AMOVA for green ash was very similar to sugar maple: 95% of diversity existed within land use types and only 5% among land use types. Pairwise F_{st} shows little variation within land use types (Table 9). However, 62.5% of planted sites varied from spontaneous sites and 100% varied from remnant sites. Most spontaneous sites also varied from remnant sites.

Table 9: Pairwise comparison of F_{st} values for green ash.

	Planted				Spontaneous			Remnant	
	North-west	North-east	South-west	South-east	Montrose	Labagh	Chavelier	Dan Ryan	Somme
Planted									
Northeast	0.046**							* $p < 0.05$	
Southwest	0.025	0.026						** $0.05 < p < 0.001$	
Southeast	0.021	0.042*	0.024					*** $p < 0.001$	
Spontan.									
Montrose	0.043*	0.041	0.020	0.032					
Labagh	0.037**	0.024	0.013	0.041**	0.016				
Chavelier	0.035**	0.054***	0.022	0.040**	0.031	0.024			
Dan Ryan	0.051**	0.046**	0.036**	0.039**	0.034	0.050***	0.063***		
Remnant									
Somme	0.040**	0.036*	0.038*	0.036*	0.041*	0.050***	0.070***	0.013	
Busse	0.057***	0.045**	0.037**	0.037**	0.032	0.051***	0.065***	0.004	0.014

There is not a significant correlation between genetic distance and geographic distance for green ash (Figure 11). There is a positive correlation for spontaneous sites, but it is not significant ($p = 0.209$).

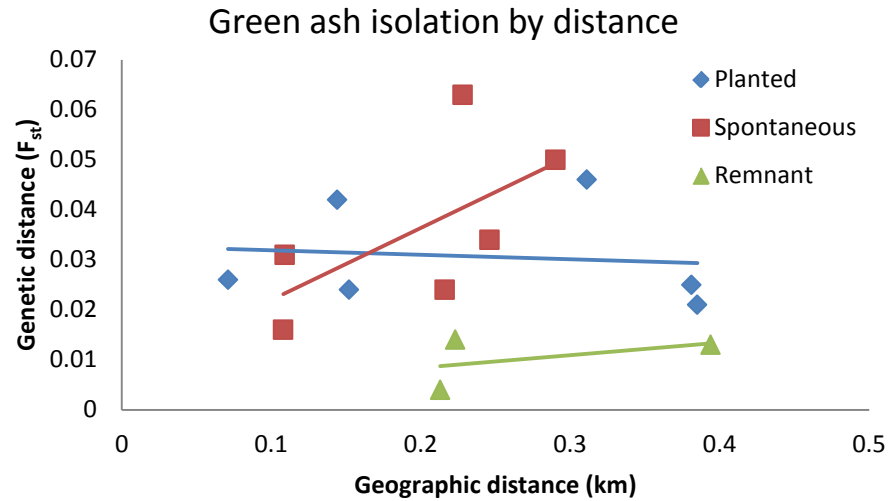


Figure 11: Isolation by distance for green ash. There is not a significant relationship between F_{st} and distance in any land use type ($p > 0.05$).

Structure analysis further illustrates that the city trees were differentiated from the remnant forests, although the differentiation was again weak. The determination of the number of theoretical populations is not clear, and there is room for interpretation. In Figure 12A the curve peak begins to level out at $K = 5$, but there is a small peak in Figure 12B at $K = 6$. For this analysis $K = 6$ was selected, but the structure results for $K = 5$ were very similar and the same conclusions would be made using that number of theoretical populations.

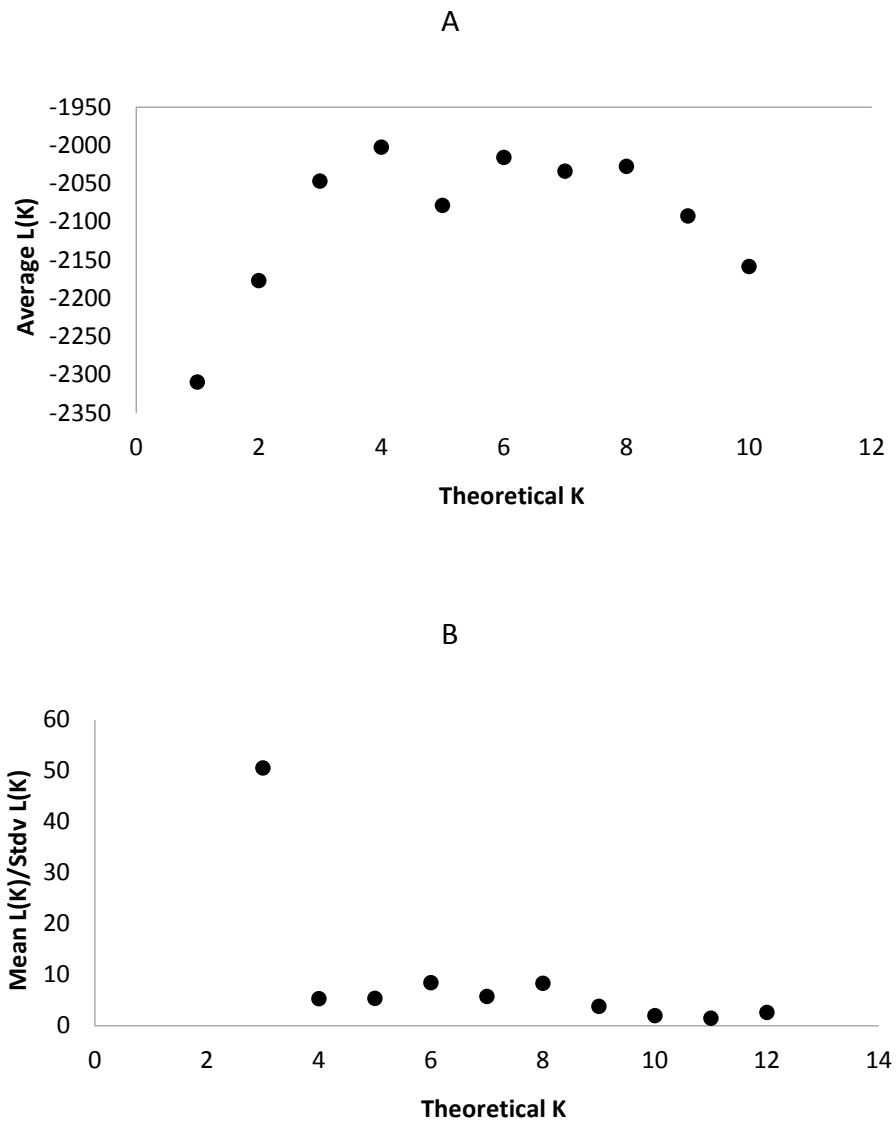


Figure 12: Determination of theoretical K for green ash. The correct K value is not readily apparent. The curve begins to level out at K = 5 in 6A, but there is a slight peak in K = 6 in 6B. K = 6 was selected for structure analysis.

Spontaneous and remnant forests appear to have nearly identical genetic structure to one another, but the planted trees look quite different from the forested areas (Figure 13A and B). The planted trees have a much higher percentage of clusters one and five and lower percentages of the other clusters. There is no indication of genetic structure among sites.

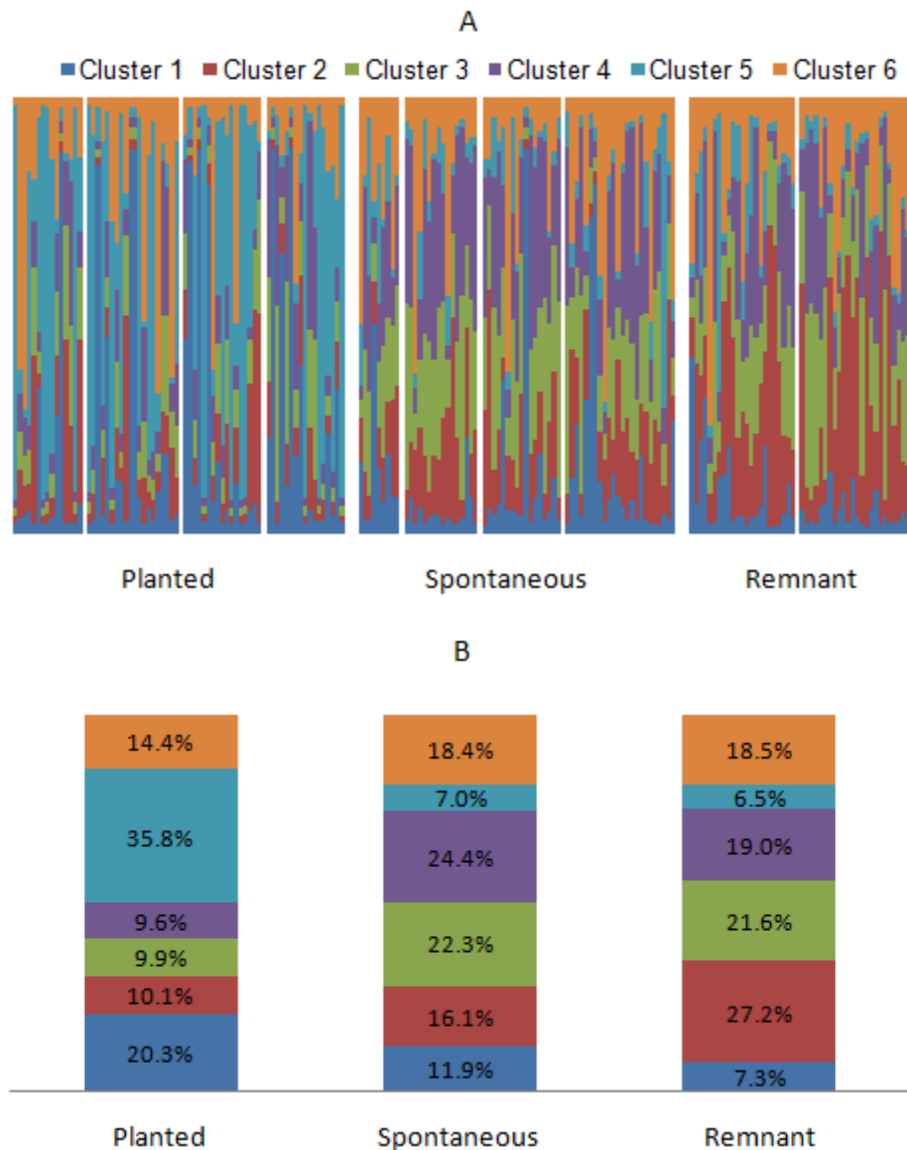


Figure 13: Green ash structure for $K = 6$. In 12A large gaps denote breaks in land use types and smaller gaps denote sites. There is little difference between spontaneous and remnant trees. However, the planted population has much more of clusters one and five. This is further illustrated by 12B.

Structure results that were sorted by DBH of individuals show an interesting pattern in the planted sites (Figure 14). Cluster five is has a much higher abundance in small planted trees than in larger ones. This indicates that genetically similar individuals (likely cultivars) are being planted more heavily in recent years. This was not shown to correlate with a drop in genetic

diversity (Table 5). However, DBH size classes for these analyses were chosen to create a roughly even distribution of individuals in each size class across all land use types. This resulted in the presence of only two small individuals in the planted sites. When size classes are redistributed in the planted sites a drop in all diversity measures in small trees is observed (Table 10). There are not enough individuals in this analysis to determine if the differences in diversity are significant.

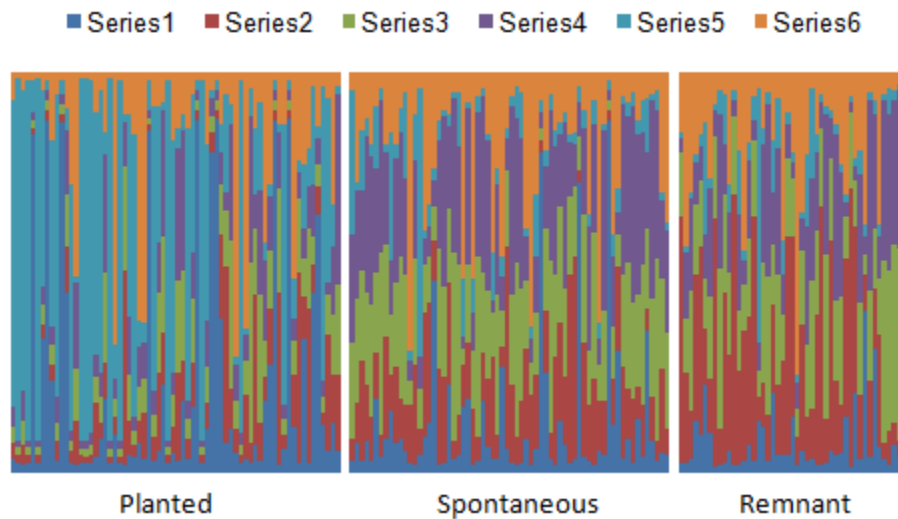


Figure 14: Green ash structure results sorted by DBH and land use type.

Table 10: Diversity measures for planted green ash across size classes. Size classes have been redefined from Table 5 in order to make roughly even numbers of individuals in each size class.

	N	N _a	N _e	I	H _o	H _e	F	P _a
Small	22	5.250	2.312	0.954	0.489	0.487	0.030	0.250
Medium	22	7.500	3.395	1.414	0.527	0.662	0.224	0.408
Large	24	8.500	3.577	1.498	0.500	0.678	0.263	0.500

The majority of planted individuals are again clustered into two sections in the UPGMA (Figure 15). Most of the trees that are in these planted clusters are small to medium individuals, again indicating that planting of genetically similar individuals has increased in recent years. However, unlike with the sugar maples the remnant individuals do not cluster at all. Instead, the remnant and spontaneous sections look more like red oak: entirely intermixed.

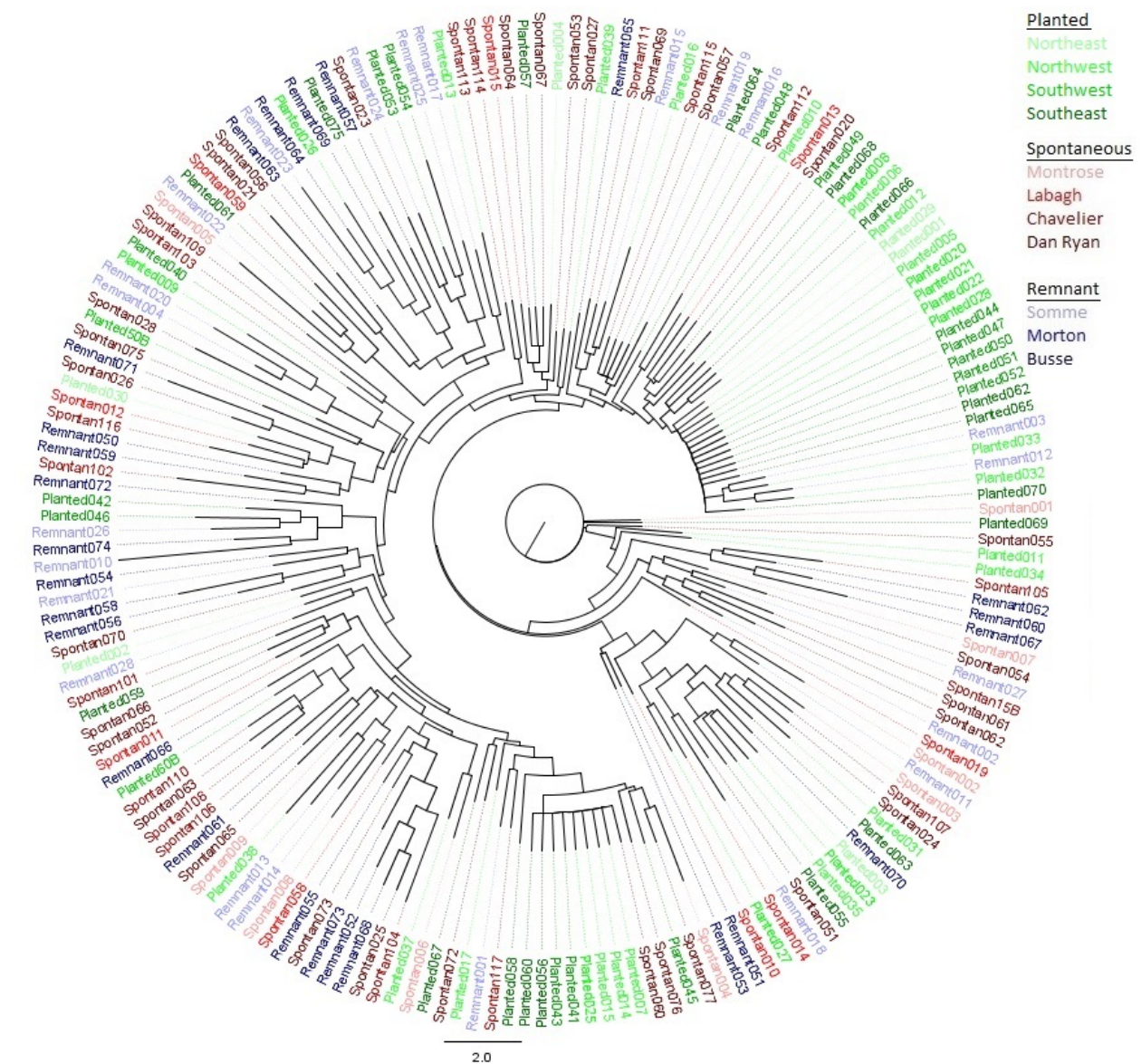


Figure 15: UPGMA for green ash. The planted sites are all in green tones, the spontaneous sites are red tones and the remnant sites are in tones of blue. Further information including the size and geographic location of each individual can be found in the appendix.

Discussion

Genetic diversity across all three species did not vary across the land use gradient. No diversity measure varied significantly. In short, planted trees were not less diverse than spontaneous trees nor than remnant forests. While red oaks had identical genetic structure across

all three land use types, sugar maple and green ash city trees were differentiated from the remnant forests. The differences in population structure among these three species can be explained by the history of cultivation of each species.

Red oak

The lack of genetic structure in red oak is likely due to two factors: a dearth of red oak cultivars and oak's ability to spread pollen over great distances. There are only two red oak cultivars currently in production, and both of them are uncommon (University of Connecticut Horticulture Website 2013). Red oaks are difficult to graft, and the majority of red oaks planted in urban areas are grown from seed. These seeds usually come from a small subset of parents that are known to produce reliable seedlings (Worfolk interview 2012). This practice could reduce genetic diversity in the city trees, except that oaks broadcast pollen over great distances, which allows for gene flow (Dow and Ashley 1996). There is sufficient gene flow into planted trees to not only maintain genetic diversity, but also to keep the red oak city trees from becoming genetically distinct.

There is one portion of the UPGMA results that indicates the potential for a decrease in red oak genetic diversity in the City of Chicago. Four planted oak trees were side by side along a city block (Figure 4). They had similar DBH (they were around 20 years old) and physical appearance (branching structure, bark, and tree health were identical). These four individuals were likely planted at the same time. These oaks were not clones of one another, but were very closely related. It is likely that they are full siblings or even the result of several generations of inbreeding. If these sorts of breeding practices become more widespread genetic diversity in the planted trees will decrease and its genetic structure will become distinct from remnant forests.

Even though there is potential for decreases in diversity with the planting of related individuals, it does not seem to be the current trend. Almost all of the measures of diversity in red oak showed significant variances across size classes (Table 6). Tukey's HSD indicated that small and medium trees were significantly varied from large trees, and Table 5 shows that smaller trees have higher diversity measures than larger ones. The UPGMA results showed that planted trees are overall not different from remnant sites, so it is not likely that the increase in diversity is coming from this source. The Chicago urban forest (like most developed areas) has become fragmented through urbanization. One would expect this to cause barriers to breeding among disparate populations, which would likely lead to decreased diversity in populations, and eventually lead to inbreeding and decreased population fitness. That does not seem to be the case with these red oaks, and very few other studies have documented a drop in diversity in fragmented populations of long lived, wind dispersed species (see Kramer et al. (2008) for a review). Some studies have even shown an increase in genetic diversity in fragmented forests (Fore et al. 1992; Muir et al. 2004; Young et al. 1993). The species in each of these studies were self incompatible, like red oak (Cottam et al. 1982). It is suspected that fragmentation encourages self incompatible species to accept pollen from other fragmented populations, leading to overall higher outcrossing rates than would be seen in a continuous forest (Kramer et al. 2008). This may be the case with the oaks in this study.

Sugar maple

Diversity measures among land use types for sugar maple were not significantly different, but AMOVA, F_{st} , STRUCTURE and UPGMA suggested differences among the three populations. The structure results did not indicate strong differentiation across land use types, but

there were some key difference between the sites. City trees have far more of the cluster three, while the remnant forest is dominated by clusters one and two (Figure 7). UPGMA also showed clustering of planted trees in two different sections (Figure 10). Sugar maple has been widely planted in urban areas for over a century (Worfolk interview 2012), and unlike red oak, there are a number of maple cultivars, some of which have been available since the 1960's (Flemer 1962). It is likely that heavy cultivation and wide planting of cultivars in the city has led to a genetic divergence from the sugar maples in remnant forests.

The presence of a large number of sugar maple cultivars (which are often clonal) in the city was expected to reduce the genetic diversity in city trees when compared to remnant trees. However, even though planted individuals are differentiated from other forests, there were no significant differences in diversity measures between these land use types (Tables 3 and 4). It is possible that a number of different cultivars are being planted in the Chicago region, and this serves to keep diversity comparable to remnant forests, even though the populations are differentiated. UPGMA results indicate that this is the case. There are two distinct clusters of sugar maples that are genetically similar to one another but distinct from the rest of the sampled individuals. These trees could be different sugar maple cultivars. Planted trees in the urban forest seem to be made up of several cultivars and a number of autochthonous or wild type trees. This combination keeps diversity as high as in remnant forests.

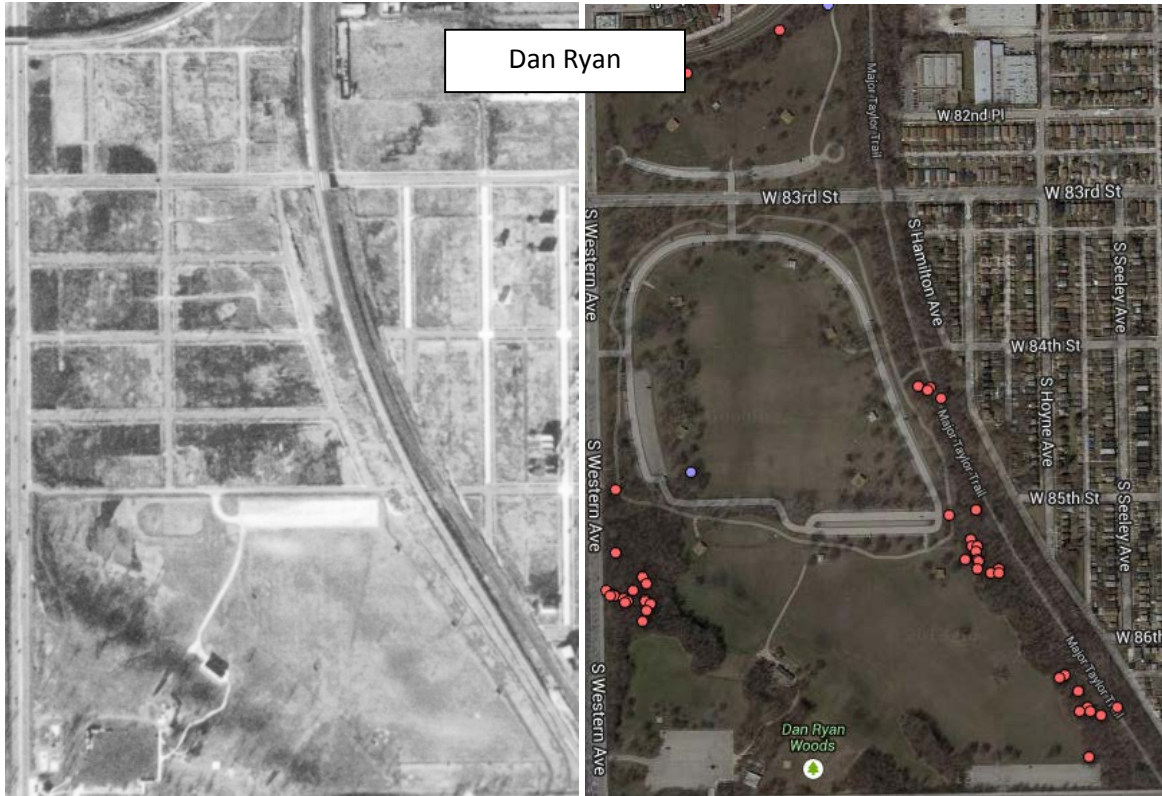
I predicted that spontaneous trees would have elements of genetic structure from both planted trees and remnant forests. Sugar maples have been shown to have high capacity for gene flow (Fore et al. 1992), allowing city trees to interact with nearby forests, which could alter their genetic identity. To some extent, the STRUCTURE results show that this may be the case (Figure 7). Clusters one and two dominated in the remnant forests, while cluster three (and to a

lesser four and five) were the most abundant in the city trees. Some of the spontaneous population did look similar to remnant forests, but other parts were more similar to the planted trees. UPGMA results further illustrate these relationships (Figure 10). There are two clusters of planted individuals and two clusters of remnant individuals in the sugar maple dendrogram. Spontaneous trees are not entirely intermixed with either land use type, but instead are scattered in the areas between with planted and remnant clusters: some spontaneous trees are more like planted trees and others are more like remnant forests. The reason for this differentiation is not immediately evident. It seemed likely that younger trees in spontaneous sites would have more in common genetically with planted trees than older trees. Over time more cultivars have been developed and planted and urbanization has continued to push closer to wild areas. It would stand to reason that these planted trees would have an increasing influence on spontaneous trees in more recent years. To see if this is the case I sorted STRUCTURE results by DBH (Figure 9). The clusters associated with city trees (cluster three and to a lesser extent four) were not more prevalent in the smaller trees in the spontaneous sites. Age of trees cannot explain the apparent influence of planted trees on the spontaneous sites.

Instead differences within the spontaneous trees fell by site (Figure 8). Clusters three and five were mostly present in Catherine Chevalier Woods, cluster four was largely found in Montrose Point Bird Sanctuary and Dan Ryan Forest Preserve, while Labagh Woods was dominated by clusters one and two (Figure 8). Aerial maps from 1939 show that Labagh Woods was largely unchanged from current forest cover. Chevalier Woods was forested in the early 20th century but much of the surrounding land was being farmed, while the areas sampled in Dan Ryan Preserve and Montrose Point were largely denuded of trees (Figure 16). Structure results show that the continuously forested Labagh Woods was not differentiated from remnant forests

(see Figure 7 for comparison). The disturbance and reforestation that has occurred in Chevalier Woods, Montrose Point and Dan Ryan Preserve caused a change in their genetic structure. These sites are now largely composed of clusters that are more associated with city trees than remnant forests. These results indicate that while sugar maple is able to interbreed among land use types, the city trees do not seem to influence the spontaneous trees unless disturbance of some sort has occurred.





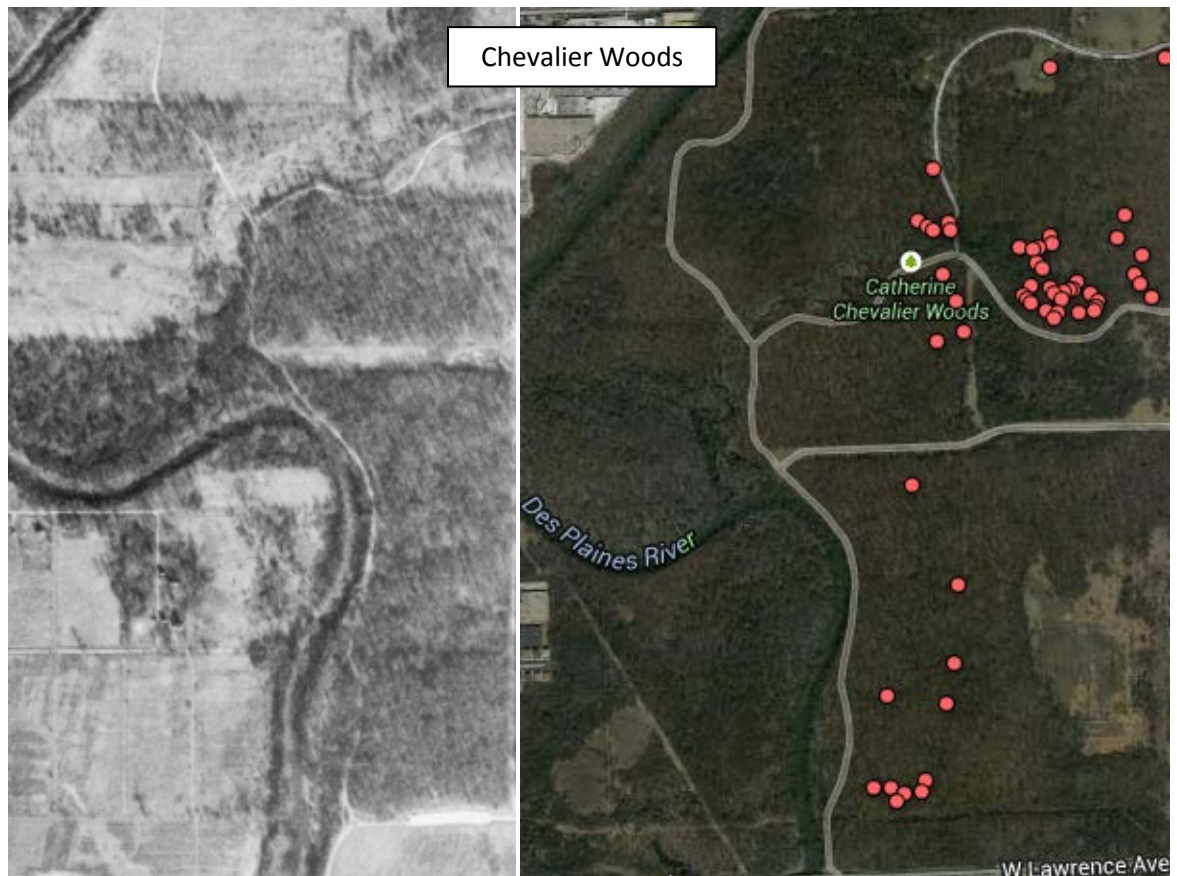


Figure 16: Comparison of 1939 aerial maps to satellite images from 2010-2013 of trees sampled in spontaneous sites. The black and white images are from 1939 and the colored ones are current. The dots on the current maps note locations of samples trees.

Green ash

Green ash and sugar maple results were very similar, as are the species' cultivation histories. Genetic diversity did not vary among land use types for green ash, but AMOVA, pairwise F_{st} , STRUCTURE analysis and UPGMA suggest weak population differentiation among land use types. In the city trees there were two dominant clusters: one and five (Figure 13). There are also two groupings of planted individuals in the UPGMA (Figure 15). These results could indicate that there are two different cultivars that are prevalent in the city, neither of which is present in the other land use types. Genotyping of known cultivars would be necessary to confirm this hypothesis. Green ash cultivars have been developed since the 1970's (Klehm

and Klehm 1973), and a variety of them are currently planted in the City of Chicago (Scott unpublished data). Planted green ash in the City of Chicago seem to be composed of several different cultivars and a number of autochthonous trees, and this combination keeps genetic diversity in the urban forest on the same level as what exists in remnant areas.

There were several indications that green ash diversity is changing over time. STRUCTURE results sorted by the size of the trees showed large percentage of a single cluster in the smallest trees (Figure 14). These trees were genetically distinct from the older planted trees. Furthermore, the trees that clustered together in the UPGMA results had relatively small DBHs. I predicted that an abundance of cultivars would result in a decrease in genetic diversity. When size classes were redefined to have roughly equal numbers of individuals in each class it became apparent that this was the case (Table 10). An abundance of a few cultivars without a large number of autochthonous trees can result in reduced genetic diversity in the urban forest.

Unlike sugar maple, there was no structure between spontaneous and remnant sites. The STRUCTURE readout for green ash was nearly identical for spontaneous and remnant forests (Figure 13). In the UPGMA results individuals from spontaneous and remnant sites were completely intermixed (Figure 15). The spontaneous areas bore no similarity to the city trees, indicating that there is no gene flow between these land use types. This is even true at disturbed sites where the sugar maples were differentiated from the remnant forests. This is at first surprising, as green ash has nearly identical reproductive strategies as sugar maple. They are wind pollinated and have seeds that are wind dispersed. However, green ash pollen has been shown to spread less far than sugar maple pollen (Kennedy et al. 1990, Fore et al. 1992). This could reduce its ability to interact with spontaneous areas. Additionally, the majority of green ash cultivars that are intentionally planted in urban areas are either male or seedless varieties

(University of Connecticut Horticulture Website 2013). This means that green ash cultivars are only able to interact with spontaneous areas through pollen transfer, and because green ash has been shown to only move pollen from 60-80 m (Kennedy et al. 1990), its ability to breed with spontaneous trees is also reduced. Only green ash cultivars that are planted very close to spontaneous areas would have any ability to interbreed in these sites, and even then they may only be able to interact with trees on the perimeter of the spontaneous site.

Diversity results for green ash are especially interesting given that ash trees are under eminent threat from the emerald ash borer. It has been shown that some ash individuals are more able to cope with the borer than others. Marshall et al. (2013) showed that susceptibility to the borer varied with the roughness of the trunk, but more data is required to determine if these morphological variations have a genetic basis.

Comparisons of genetic diversity to other regions

None of these species had significant changes in diversity across an urban to remnant gradient. However, it is uncertain whether this is caused by urban areas having relatively high diversity or remnant areas having low diversity. To determine which is the case, this data set needs to be compared with data from other remnant forests. This is possible for red oaks. Aldrich et al. quantified red oak diversity in a large remnant forest in northern Indiana (2003). They found diversity levels that were very similar to those found in this study using nearly identical microsatellite primers. This shows that planted red oaks in the City of Chicago are not only as genetically diverse as trees in surrounding forests, but in healthy, large forests. There are no comparable studies for sugar maple or green ash. The levels of diversity found in this study are similar to what was reported in the primer notes (Pandey et al. 2004; Lefort and Frascaria-

Lacoste 1999). However, these measurements were for different species (*A. psuedoplatanus* and *F. excelsior*). We can make some inferences on the possible state of genetic diversity of these species in remnant forests based on the ecological history of the area. Both sugar maple and green ash were somewhat rare before mesophication of Illinois forests (Nowacki et al. 2008). The area surrounding the City of Chicago was historically fire prone, which selected for oak species and against more mesophytic species like ashes and maples. This could mean that all of the ash and maples in the region have come from a fairly small founder population, and could have comparatively low genetic diversity. To be certain if this is the case additional individuals should be sampled at the heart of green ash and sugar maple diversity.

Past and future changes in genetic diversity

Only red oaks had significant variation across size classes (Tables 5 and 6). Although smaller red oaks were found to have higher neutral diversity than larger ones, there are several indications that genetic diversity in the urban forest may decrease in coming years. STRUCTURE and UPGMA analyses showed that sugar maple and green ash city trees were genetically distinct from the remnant areas. City trees from these species are dominated by cultivars, and if a reduced number of cultivars are planted diversity could decrease and the city trees will become further differentiated. This already seems to be happening with green ash. The smallest green ashes in the planted trees are less diverse than larger trees and spontaneous and remnant sites (Table 10). This is also possible with red oaks. The current diversity in red oaks is high, and there is no differentiation from planted trees to remnant forests. However, UPGMA results show that some planted individuals are very closely related, and with the increased

planting of closely related individuals diversity in the city trees could plummet, causing this land use type to become genetically differentiated from remnant forests.

In order to maintain or increase genetic diversity in the urban forest managers need to plant trees from multiple sources. This could be achieved by planting a variety of cultivars and by planting trees from seed sources from multiple areas. Adding diversity to the urban forest can be done in a way to maximize sustainability. In the context of climate change it may be advantageous to start planting cultivars (or source trees from other regions) that are known to be better adapted to drier and warmer conditions. By making small changes in sourcing practices the urban forest could be made more robust and potentially better able to withstand diseases, pests and climate change.

Application for other species and sites

The results from this study can be applied to other tree species with caution. This study showed that the genetic diversity in city trees is dependent upon the trees cultivation history and its interactions with the surrounding forests. The species in this study were chosen because they are common in forests surrounding the City of Chicago. This is not the case for most trees in the urban forest. Many of the trees planted in Chicago are not native to North America (e.g. little leaf linden (*Tilia cordata* Mill.) and Norway maple (*Acer platanoides* L.)) while others are native but are not common (e.g. catalpa (*Catalpa speciosa* Englem), and Kentucky coffee tree (*Gymnocladus dioica* K. Koch)). These species would have no influence from the surrounding forest, and their diversity would be completely dependent upon what was planted anthropogenically. Their genetic diversity would, like the trees in this study, be influenced by the cultivation history of the species; cultivars could reduce diversity but with the presence of a

variety of cultivars high diversity can be achieved. Some trees like hackberry (*Celtis occidentalis* L.) and ironwood (*Ostrya virginiana* K. Koch) could have very similar results to the species in this study. They are native, common and have similar cultivation history. Species in other cities would likely have similar diversity results, given that the cultivation history and influences from surrounding forests were the same.

Conclusion

Red oak, sugar maple and green ash in the Chicago region do not appear to have reduced genetic diversity, as measured by standard diversity measures, across an urban to remnant gradient. However, the genetic structure of green ash and sugar maple from city streets and parks is distinct from remnant forests. This pattern was not observed in red oak, which had no genetic structure across land use types. Although the urban forest currently has comparable genetic diversity to remnant forests, there is indication that the diversity might change in the future. There was one cluster of red oak street trees that were nearly genetically identical to one another. Red oak cultivars are currently rare, but these trees indicate that the planting of full siblings or inbred individuals can reduce diversity. On the other hand, green ash and sugar maple cultivars are very common, and STRUCTURE and UPGMA results indicate that they are frequently planted. There are currently several different cultivars planted along with autochthonous, which maintains genetic diversity that is comparable to remnant forests. But if a single cultivar is planted in mass it could greatly reduce genetic diversity of a species in the urban forest.

The state of genetic diversity in the urban forest is dictated by decisions made by city foresters. Currently trees are sourced from nurseries with little concern for their genetic makeup, and although efforts are made to increase species diversity, little thought is put into intraspecies

diversity (Santamour1990). The genetic diversity in the urban forests could be one of the major predictors of the forests ability to withstand stressors (Sork et al. 2013). A sustainable, resilient forest will need to have a mixture of genotypes. To attain this, foresters should not only increase species diversity but intraspecies diversity by planting an increased number of cultivars and seedlings from a variety of parents.

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Appendix: List of all individuals sampled. Data includes identification number and species; the land use, site and geographic location of the individual; also the tree's DBH and health.

ID	Species	Landuse	Site	Lat	Long	DBH	Health
AM01	A. saccharum	Spontaneous	Montrose sanctuary	41.96249	-87.63448	29.5	good
AM02	A. saccharum	Spontaneous	Montrose sanctuary	41.96232	-87.63453	35.5	poor
AM03	A. saccharum	Spontaneous	Montrose sanctuary	41.96273	-87.63432	29.7	good
AM04	A. saccharum	Spontaneous	Montrose sanctuary	41.96257	-87.63433	34.9	good
AM05	A. saccharum	Spontaneous	Montrose sanctuary	41.96251	-87.63386	53.0	good
AM06	A. saccharum	Spontaneous	Montrose sanctuary	41.9625	-87.63408	2.7	fair
AM07	A. saccharum	Spontaneous	Montrose sanctuary	41.96251	-87.63411	23.8	fair
AM08	A. saccharum	Spontaneous	Montrose sanctuary	41.96235	-87.63366	51.7	good
AM09	A. saccharum	Spontaneous	Montrose sanctuary	41.96248	-87.63359	37.2	good
AM10	A. saccharum	Spontaneous	Montrose sanctuary	41.9625	-87.63357	40.6	good
AM101	A. saccharum	Spontaneous	Catherine Chevalier	41.97671	-87.84969	17.5	good
AM102	A. saccharum	Spontaneous	Catherine Chevalier	41.97605	-87.84944	16.5	good
AM103	A. saccharum	Spontaneous	Catherine Chevalier	41.97594	-87.84936	11.2	fair
AM104	A. saccharum	Spontaneous	Catherine Chevalier	41.97598	-87.84913	11.9	poor
AM105	A. saccharum	Spontaneous	Catherine Chevalier	41.97601	-87.84899	21.2	poor
AM106	A. saccharum	Spontaneous	Catherine Chevalier	41.97597	-87.84853	8.7	good
AM107	A. saccharum	Spontaneous	Catherine Chevalier	41.97582	-87.84836	12.2	good
AM109	A. saccharum	Spontaneous	Catherine Chevalier	41.97574	-87.84839	36.1	good
AM109	A. saccharum	Spontaneous	Catherine Chevalier	41.97585	-87.84916	11.3	fair
AM11	A. saccharum	Spontaneous	Montrose sanctuary	41.96247	-87.63351	63.5	good
AM110	A. saccharum	Spontaneous	Catherine Chevalier	41.97563	-87.84925	17.6	fair
AM111	A. saccharum	Spontaneous	Catherine Chevalier	41.97972	-87.84942	31.5	fair
AM112	A. saccharum	Spontaneous	Catherine Chevalier	41.97989	-87.84685	37.6	fair
AM12	A. saccharum	Spontaneous	Montrose sanctuary	41.96269	-87.63281	19.8	good
AM13	A. saccharum	Spontaneous	Labagh woods	41.97943	-87.74465	5.2	good
AM14	A. saccharum	Spontaneous	Labagh woods	41.97956	-87.74481	2.8	good
AM15	A. saccharum	Spontaneous	Labagh woods	41.97958	-87.74422	2.5	good
AM16	A. saccharum	Spontaneous	Labagh woods	41.97979	-87.74422	9.3	good
AM17	A. saccharum	Spontaneous	Labagh woods	41.98023	-87.74369	10.4	good
AM18	A. saccharum	Spontaneous	Labagh woods	41.98204	-87.7454	23.1	good
AM19	A. saccharum	Spontaneous	Labagh woods	41.98193	-87.74559	2.5	good
AM20	A. saccharum	Spontaneous	Labagh woods	41.9819	-87.74573	20.4	good
AM21	A. saccharum	Spontaneous	Labagh woods	41.98232	-87.74322	8.3	good
AM22	A. saccharum	Spontaneous	Labagh woods	41.98324	-87.743	7.4	fair
AM23	A. saccharum	Spontaneous	Labagh woods	41.98238	-87.74287	18.0	good
AM51	A. saccharum	Spontaneous	Dan Ryan Preserve	41.7387	-87.67645	10.1	good
AM52	A. saccharum	Spontaneous	Dan Ryan Preserve	41.7387	-87.67654	18.8	fair
AM53	A. saccharum	Spontaneous	Dan Ryan Preserve	41.73879	-87.67657	23.8	fair
AM54	A. saccharum	Spontaneous	Dan Ryan Preserve	41.73678	-87.67423	16.9	good
AM55	A. saccharum	Spontaneous	Dan Ryan Preserve	41.73668	-87.67449	15.5	good
AM56	A. saccharum	Spontaneous	Dan Ryan Preserve	41.73679	-87.67469	16.0	fair
AM57	A. saccharum	Spontaneous	Dan Ryan Preserve	41.73697	-87.67485	30.1	fair
AN01	A. saccharum	Remnant	Somme	42.13849	-87.82129	16.4	good
AN02	A. saccharum	Remnant	Somme	42.13851	-87.82137	26.3	good
AN03	A. saccharum	Remnant	Somme	42.13882	-87.82144	12.1	good

AN04	A. saccharum	Remnant	Somme	42.13953	-87.81117	25.2	good
AN05	A. saccharum	Remnant	Somme	42.14058	-87.8134	13.0	fair
AN06	A. saccharum	Remnant	Somme	42.14047	-87.81436	32.4	good
AN07	A. saccharum	Remnant	Somme	42.14069	-87.81599	6.2	fair
AN08	A. saccharum	Remnant	Somme	42.13978	-87.81801	66.5	good
AN09	A. saccharum	Remnant	Somme	42.13928	-87.81909	6.0	good
AN10	A. saccharum	Remnant	Somme	42.13921	-87.81917	6.2	good
AN101	A. saccharum	Remnant	Morton	41.81663	-88.04152	15.7	poor
AN102	A. saccharum	Remnant	Morton	41.81559	-88.04128	6.4	good
AN103	A. saccharum	Remnant	Morton	41.81633	-88.04162	4.3	good
AN104	A. saccharum	Remnant	Morton	41.81602	-88.04077	7.2	good
AN105	A. saccharum	Remnant	Morton	41.81532	-88.04066	21.4	fair
AN106	A. saccharum	Remnant	Morton	41.81527	-88.04089	12.3	fair
AN107	A. saccharum	Remnant	Morton	41.81432	-88.04031	24.4	good
AN108	A. saccharum	Remnant	Morton	41.81373	-88.04079	25.8	fair
AN109	A. saccharum	Remnant	Morton	41.81545	-88.04658	2.5	good
AN109	A. saccharum	Remnant	Morton	41.81359	-88.0406	22.2	good
AN11	A. saccharum	Remnant	Somme	42.13942	-87.81988	74.0	good
AN110	A. saccharum	Remnant	Morton	41.81311	-88.04043	8.8	good
AN111	A. saccharum	Remnant	Morton	41.81258	-88.04056	14.4	good
AN112	A. saccharum	Remnant	Morton	41.81272	-88.04158	19.8	good
AN113	A. saccharum	Remnant	Morton	41.81288	-88.0415	25.9	good
AN114	A. saccharum	Remnant	Morton	41.81284	-88.04189	15.1	good
AN115	A. saccharum	Remnant	Morton	41.81377	-88.0456	7.1	poor
AN116	A. saccharum	Remnant	Morton	41.81343	-88.04312	21.0	good
AN117	A. saccharum	Remnant	Morton	41.81351	-88.04454	18.5	fair
AN118	A. saccharum	Remnant	Morton	41.81341	-88.04707	24.0	good
AN119	A. saccharum	Remnant	Morton	41.8144	-88.04827	10.1	good
AN12	A. saccharum	Remnant	Somme	42.14078	-87.82669	11.3	fair
AN120	A. saccharum	Remnant	Morton	41.81467	-88.04798	6.4	fair
AN121	A. saccharum	Remnant	Morton	41.81522	-88.04723	17.4	good
AN122	A. saccharum	Remnant	Morton	41.81547	-88.04645	4.0	good
AN123	A. saccharum	Remnant	Morton	41.81573	-88.04644	14.3	good
AN124	A. saccharum	Remnant	Morton	41.81527	-88.04624	19.9	good
AN125	A. saccharum	Remnant	Morton	41.81618	-88.04552	8.4	fair
AN126	A. saccharum	Remnant	Morton	41.81778	-88.04269	29.0	good
AN127	A. saccharum	Remnant	Morton	41.81808	-88.04159	19.8	fair
AN128	A. saccharum	Remnant	Morton	41.81731	-88.04244	11.1	good
AN129	A. saccharum	Remnant	Morton	41.81715	-88.0434	14.3	fair
AN13	A. saccharum	Remnant	Somme	42.14264	-87.8243	11.5	poor
AN14	A. saccharum	Remnant	Somme	42.14265	-87.82423	6.3	fair
AN14b	A. saccharum	Remnant	Somme	42.1398	-87.81991	5.6	good
AN15	A. saccharum	Remnant	Somme	42.13988	-87.81982	55.0	fair
AN16	A. saccharum	Remnant	Somme	42.13982	-87.81991	16.2	good
AN17	A. saccharum	Remnant	Somme	42.14028	-87.8168	7.4	poor
AN18	A. saccharum	Remnant	Somme	42.14034	-87.81781	5.2	good
AN19	A. saccharum	Remnant	Somme	42.14038	-87.81764	16.2	good
AN20	A. saccharum	Remnant	Somme	42.14255	-87.81698	5.0	good
AN21	A. saccharum	Remnant	Somme	42.14259	-87.81746	6.3	fair

AN23	A. saccharum	Remnant	Somme	42.14414	-87.82191	15.9	good
AN24	A. saccharum	Remnant	Somme	42.14392	-87.82186	11.0	good
AN25	A. saccharum	Remnant	Somme	42.14391	-87.82172	6.3	good
AN26	A. saccharum	Remnant	Somme	42.14382	-87.82161	23.8	good
AN27	A. saccharum	Remnant	Somme	42.14101	-87.82134	21.8	good
AN28	A. saccharum	Remnant	Somme	42.1408	-87.82123	19.3	good
AN50	A. saccharum	Remnant	Busse	42.0383	-88.00255	15.3	good
AN50	A. saccharum	Remnant	Busse	42.03795	-88.00245	83.0	fair
AN51	A. saccharum	Remnant	Busse	42.03621	-88.00266	11.1	good
AN52	A. saccharum	Remnant	Busse	42.03916	-88.00269	7.6	good
AN53	A. saccharum	Remnant	Busse	42.03941	-88.00274	16.0	good
AN54	A. saccharum	Remnant	Busse	42.03967	-88.00292	7.1	good
AN55	A. saccharum	Remnant	Busse	42.03971	-88.00396	5.0	good
AN56	A. saccharum	Remnant	Busse	42.0397	-88.00404	12.4	good
AN57	A. saccharum	Remnant	Busse	42.03966	-88.00411	7.5	good
AN58	A. saccharum	Remnant	Busse	42.03934	-88.00505	9.3	fair
AN59	A. saccharum	Remnant	Busse	42.03801	-88.00518	29.0	good
AN60	A. saccharum	Remnant	Busse	42.038	-88.00543	77.3	good
AN61	A. saccharum	Remnant	Busse	42.03812	-88.00619	13.7	good
AN62	A. saccharum	Remnant	Busse	42.03816	-88.00634	20.5	fair
AN63	A. saccharum	Remnant	Busse	42.03741	-88.00644	6.6	good
AN64	A. saccharum	Remnant	Busse	42.03706	-88.00718	17.8	good
AN65	A. saccharum	Remnant	Busse	42.03642	-88.00922	6.1	good
AN66	A. saccharum	Remnant	Busse	42.03601	-88.00803	8.1	good
AN67	A. saccharum	Remnant	Busse	42.037	-88.006	16.3	fair
AN68	A. saccharum	Remnant	Busse	42.03543	-88.0046	12.1	good
AN69	A. saccharum	Remnant	Busse	42.03512	-88.00434	12.1	good
AN70	A. saccharum	Remnant	Busse	42.03508	-88.00405	16.8	good
AN71	A. saccharum	Remnant	Busse	42.03495	-88.00393	15.7	good
AN72	A. saccharum	Remnant	Busse	42.03526	-88.00331	6.6	good
AN74	A. saccharum	Remnant	Busse	42.03553	-88.00291	7.3	good
AN75	A. saccharum	Remnant	Busse	42.03561	-88.00299	10.5	good
AN76	A. saccharum	Remnant	Busse	42.03536	-88.00322	12.7	good
AN76	A. saccharum	Remnant	Busse	42.03452	-87.99978	11.5	good
AU01	A. saccharum	Planted	Northeast	41.93965	-87.67651	21.2	fair
AU02	A. saccharum	Planted	Northwest	41.99043	-87.73347	14.1	good
AU03	A. saccharum	Planted	Northwest	41.99566	-87.73827	34.7	fair
AU04	A. saccharum	Planted	Northwest	41.99578	-87.73823	36.2	poor
AU05	A. saccharum	Planted	Northwest	41.99573	-87.73499	44.5	poor
AU06	A. saccharum	Planted	Northwest	41.99253	-87.73508	8.3	good
AU07	A. saccharum	Planted	Northwest	41.99218	-87.73487	13.7	good
AU08	A. saccharum	Planted	Northwest	41.99085	-87.73377	22.2	good
AU09	A. saccharum	Planted	Northwest	41.99312	-87.73381	67.2	good
AU10	A. saccharum	Planted	Northwest	41.99325	-87.73388	38.8	good
AU11	A. saccharum	Planted	Northwest	41.99333	-87.73254	34.9	good
AU12	A. saccharum	Planted	Northwest	41.99245	-87.73256	48.2	good
AU13	A. saccharum	Planted	Northwest	41.99294	-87.73256	34.6	poor
AU14	A. saccharum	Planted	Northwest	41.99221	-87.73355	43.6	fair
AU15	A. saccharum	Planted	Northwest	41.97511	-87.70739	21.8	fair

AU16	A. saccharum	Planted	Northeast	41.91325	-87.62966	21.0	good
AU17	A. saccharum	Planted	Northeast	41.91322	-87.62961	22.0	good
AU18	A. saccharum	Planted	Northeast	41.9132	-87.62949	22.4	good
AU19	A. saccharum	Planted	Northeast	41.91381	-87.63058	16.2	good
AU20	A. saccharum	Planted	Northeast	41.91846	-87.64054	27.2	poor
AU21	A. saccharum	Planted	Northeast	41.91057	-87.64092	21.2	poor
AU22	A. saccharum	Planted	Northeast	41.89834	-87.67469	11.7	good
AU23	A. saccharum	Planted	Northeast	41.89816	-87.67961	18.0	good
AU24	A. saccharum	Planted	Northeast	41.96984	-87.64729	32.0	poor
AU25	A. saccharum	Planted	Northeast	41.96254	-87.64323	59.6	fair
AU26	A. saccharum	Planted	Northeast	41.96871	-87.64686	6.2	good
AU27	A. saccharum	Planted	Northeast	41.93783	-87.67568	25.1	good
AU28	A. saccharum	Planted	Northeast	41.93507	-87.67801	44.5	fair
AU29	A. saccharum	Planted	Northeast	41.93881	-87.67309	21.1	good
AU30	A. saccharum	Planted	Northeast	41.9369	-87.66959	39.6	fair
AU31	A. saccharum	Planted	Northeast	41.93686	-87.6698	43.5	poor
AU32	A. saccharum	Planted	Northeast	41.93581	-87.67426	14.3	good
AU33	A. saccharum	Planted	Northwest	41.92717	-87.71218	7.5	good
AU34	A. saccharum	Planted	Northwest	41.92641	-87.71337	52.6	good
AU35	A. saccharum	Planted	Northwest	41.92842	-87.71089	7.1	poor
AU36	A. saccharum	Planted	Northwest	41.9254	-87.70702	18.5	good
AU37	A. saccharum	Planted	Northwest	41.92499	-87.70697	11.2	poor
AU38	A. saccharum	Planted	Northwest	41.92273	-87.70747	19.5	good
AU39	A. saccharum	Planted	Northwest	41.92417	-87.70747	15.4	good
AU40	A. saccharum	Planted	South Central	41.85385	-87.66144	17.2	fair
AU41	A. saccharum	Planted	South Central	41.85389	-87.66142	12.2	fair
AU42	A. saccharum	Planted	South Central	41.85245	-87.66506	14.9	fair
AU43	A. saccharum	Planted	South Central	41.85244	-87.66526	10.6	poor
AU44	A. saccharum	Planted	South Central	41.85246	-87.66552	20.3	good
AU45	A. saccharum	Planted	South Central	41.82513	-87.67024	12.2	good
AU46	A. saccharum	Planted	South Central	41.82501	-87.66661	21.4	good
AU47	A. saccharum	Planted	South Central	41.82468	-87.68023	27.5	good
AU48	A. saccharum	Planted	South Central	41.82461	-87.68025	26.7	good
AU49	A. saccharum	Planted	South Central	41.82455	-87.68025	22.2	good
AU50	A. saccharum	Planted	South Central	41.82258	-87.6831	30.9	poor
AU51	A. saccharum	Planted	South Central	41.82319	-87.68333	19.8	good
AU52	A. saccharum	Planted	South Central	41.82315	-87.68356	15.9	good
AU53	A. saccharum	Planted	South Central	41.82325	-87.68353	10.1	good
AU54	A. saccharum	Planted	South Central	41.82325	-87.68365	17.3	good
AU55	A. saccharum	Planted	South Central	41.82318	-87.68363	16.5	good
AU56	A. saccharum	Planted	South Central	41.82645	-87.68331	16.5	good
AU57	A. saccharum	Planted	South Central	41.82618	-87.68295	9.1	good
AU58	A. saccharum	Planted	South Central	41.82622	-87.68264	7.9	good
AU59	A. saccharum	Planted	South Central	41.82623	-87.68268	8.4	good
AU59	A. saccharum	Planted	South	41.78436	-87.71088	23.3	poor
AU60	A. saccharum	Planted	South	41.78432	-87.71102	24.5	fair
AU61	A. saccharum	Planted	South	41.78419	-87.71444	34.2	good
AU62	A. saccharum	Planted	South	41.78065	-87.71627	35.3	good
AU63	A. saccharum	Planted	South	41.77782	-87.72003	9.0	good

AU64	A. saccharum	Planted	South	41.77693	-87.71515	34.2	good
AU65	A. saccharum	Planted	South	41.77772	-87.71529	34.5	fair
AU66	A. saccharum	Planted	South	41.77302	-87.65757	23.7	good
AU67	A. saccharum	Planted	South	41.77312	-87.6568	9.4	good
AU68	A. saccharum	Planted	South	41.77312	-87.65654	9.1	good
AU69	A. saccharum	Planted	South	41.77328	-87.65611	14.5	fair
AU70	A. saccharum	Planted	South	41.77325	-87.65696	15.2	fair
AU71	A. saccharum	Planted	South	41.77634	-87.65594	25.5	good
AU72	A. saccharum	Planted	South	41.76239	-87.59135	16.3	good
AU73	A. saccharum	Planted	South	41.76929	-87.60109	53.5	good
AU74	A. saccharum	Planted	South	41.79342	-87.59644	11.2	good
AU75	A. saccharum	Planted	South	41.79338	-87.59643	10.1	good
FM01	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96231	-87.63399	16.6	fair
FM02	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96247	-87.6346	5.0	good
FM03	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96249	-87.63489	2.5	good
FM04	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96241	-87.63414	12.2	poor
FM05	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96241	-87.63414	8.4	fair
FM06	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96235	-87.63417	3.7	poor
FM07	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96243	-87.63379	5.3	fair
FM08	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96257	-87.63375	24.3	fair
FM09	F. pennsylvanica	Spontaneous	Montrose sanctuary	41.96262	-87.63304	6.8	fair
FM10	F. pennsylvanica	Spontaneous	Labagh woods	41.97637	-87.74253	27.0	fair
FM101	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97659	-87.84737	54.8	fair
FM102	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.9767	-87.84982	24.4	poor
FM103	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97645	-87.84974	24.6	poor
FM104	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97672	-87.85013	23.6	fair
FM105	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97608	-87.84987	18.4	fair
FM106	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97602	-87.8489	42.3	fair
FM107	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97615	-87.84883	65.2	poor
FM108	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.9758	-87.84985	11.1	poor
FM109	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97593	-87.85001	18.2	poor
FM11	F. pennsylvanica	Spontaneous	Labagh woods	41.97704	-87.74193	33.7	fair
FM110	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.9675	-87.85288	19.2	fair
FM111	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.96773	-87.853	15.1	poor
FM112	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.96764	-87.85268	14.3	fair
FM113	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.977	-87.85164	9.7	good
FM114	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97715	-87.85171	13.7	fair
FM115	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97702	-87.85203	27.6	poor
FM116	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97706	-87.85217	18.8	poor
FM117	F. pennsylvanica	Spontaneous	Catherine Chevalier	41.97716	-87.8524	16.2	fair
FM12	F. pennsylvanica	Spontaneous	Labagh woods	41.97752	-87.7417	32.5	fair
FM13	F. pennsylvanica	Spontaneous	Labagh woods	41.97839	-87.74155	71.1	good
FM14	F. pennsylvanica	Spontaneous	Labagh woods	41.97856	-87.74411	41.4	fair
FM15	F. pennsylvanica	Spontaneous	Labagh woods	41.97955	-87.74467	9.8	fair
FM16	F. pennsylvanica	Spontaneous	Labagh woods	41.98027	-87.74363	36.2	good
FM19	F. pennsylvanica	Spontaneous	Labagh woods	41.98057	-87.74355	46.1	poor
FM20	F. pennsylvanica	Spontaneous	Labagh woods	41.98169	-87.74302	57.3	fair
FM21	F. pennsylvanica	Spontaneous	Labagh woods	41.98151	-87.74323	4.5	good
FM22	F. pennsylvanica	Spontaneous	Labagh woods	41.98188	-87.74391	38.2	fair

FM23	F. pennsylvanica	Spontaneous	Labagh woods	41.98209	-87.74557	9.7	poor
FM24	F. pennsylvanica	Spontaneous	Labagh woods	41.98218	-87.74724	16.9	poor
FM25	F. pennsylvanica	Spontaneous	Labagh woods	41.98206	-87.74624	17.5	good
FM26	F. pennsylvanica	Spontaneous	Labagh woods	41.98231	-87.7419	81.9	poor
FM27	F. pennsylvanica	Spontaneous	Labagh woods	41.98182	-87.7412	30.1	poor
FM28	F. pennsylvanica	Spontaneous	Labagh woods	41.98161	-87.74053	74.1	poor
FM51	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73938	-87.68222	21.4	poor
FM52	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73863	-87.68223	11.8	fair
FM53	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73817	-87.68194	26.0	fair
FM54	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73807	-87.68176	6.5	fair
FM55	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73805	-87.68203	52.3	good
FM56	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73812	-87.68225	35.0	fair
FM57	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73813	-87.68228	24.7	poor
FM58	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73804	-87.68208	47.6	fair
FM58	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73811	-87.68232	55.2	fair
FM59	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73808	-87.68211	10.2	poor
FM60	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73907	-87.6769	9.0	poor
FM61	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73864	-87.67648	63.5	poor
FM62	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73844	-87.67612	11.3	fair
FM63	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73839	-87.67625	17.8	poor
FM64	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73853	-87.67644	54.5	poor
FM65	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73854	-87.67645	72.5	fair
FM66	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73854	-87.67664	37.7	poor
FM67	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73844	-87.67645	17.7	fair
FM69	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.74047	-87.67703	4.2	good
FM70	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.74485	-87.67961	17.0	fair
FM71	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.74435	-87.68119	13.1	poor
FM72	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.74434	-87.6811	13.0	poor
FM73	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73674	-87.67466	39.9	poor
FM74	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73716	-87.67507	18.8	fair
FM75	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73714	-87.67515	11.2	fair
FM76	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73673	-87.67482	34.5	fair
FM77	F. pennsylvanica	Spontaneous	Dan Ryan Preserve	41.73619	-87.67468	18.7	fair
FN01	F. pennsylvanica	Remnant	Somme	42.1392	-87.82268	28.4	poor
FN02	F. pennsylvanica	Remnant	Somme	42.13835	-87.81044	9.2	poor
FN03	F. pennsylvanica	Remnant	Somme	42.13883	-87.81091	6.2	poor
FN04	F. pennsylvanica	Remnant	Somme	42.13909	-87.81105	31.5	poor
FN10	F. pennsylvanica	Remnant	Somme	42.13893	-87.82443	15.4	poor
FN11	F. pennsylvanica	Remnant	Somme	42.14061	-87.82683	13.5	poor
FN12	F. pennsylvanica	Remnant	Somme	42.14062	-87.82592	9.7	poor
FN13	F. pennsylvanica	Remnant	Somme	42.14044	-87.82566	23.0	fair
FN14	F. pennsylvanica	Remnant	Somme	42.14036	-87.82553	25.6	fair
FN15	F. pennsylvanica	Remnant	Somme	42.14214	-87.82514	7.4	good
FN16	F. pennsylvanica	Remnant	Somme	42.14202	-87.82512	14.0	good
FN17	F. pennsylvanica	Remnant	Somme	42.14265	-87.82414	14.6	fair
FN18	F. pennsylvanica	Remnant	Somme	42.14262	-87.82414	8.0	fair
FN19	F. pennsylvanica	Remnant	Somme	42.13976	-87.81985	17.0	fair
FN20	F. pennsylvanica	Remnant	Somme	42.13988	-87.8193	31.1	good
FN21	F. pennsylvanica	Remnant	Somme	42.13988	-87.81981	33.7	good

FN22	F. pennsylvanica	Remnant	Somme	42.14385	-87.81929	13.7	poor
FN23	F. pennsylvanica	Remnant	Somme	42.14253	-87.82223	24.3	poor
FN24	F. pennsylvanica	Remnant	Somme	42.142	-87.82254	17.9	poor
FN25	F. pennsylvanica	Remnant	Somme	42.14193	-87.82272	17.1	poor
FN26	F. pennsylvanica	Remnant	Somme	42.14182	-87.82292	21.7	poor
FN27	F. pennsylvanica	Remnant	Somme	42.14098	-87.82143	12.7	good
FN28	F. pennsylvanica	Remnant	Somme	42.14101	-87.82142	28.0	fair
FN50	F. pennsylvanica	Remnant	Busse	42.04023	-88.00277	21.6	poor
FN51	F. pennsylvanica	Remnant	Busse	42.04021	-88.00289	37.6	poor
FN52	F. pennsylvanica	Remnant	Busse	42.03964	-88.00433	37.0	fair
FN53	F. pennsylvanica	Remnant	Busse	42.03951	-88.00486	7.1	poor
FN54	F. pennsylvanica	Remnant	Busse	42.03798	-88.00586	54.3	poor
FN55	F. pennsylvanica	Remnant	Busse	42.03805	-88.00604	38.3	fair
FN56	F. pennsylvanica	Remnant	Busse	42.03764	-88.00659	15.0	poor
FN57	F. pennsylvanica	Remnant	Busse	42.03648	-88.00875	43.7	poor
FN58	F. pennsylvanica	Remnant	Busse	42.03626	-88.00705	15.7	poor
FN59	F. pennsylvanica	Remnant	Busse	42.0368	-88.0064	5.5	poor
FN60	F. pennsylvanica	Remnant	Busse	42.03751	-88.00338	9.2	poor
FN61	F. pennsylvanica	Remnant	Busse	42.03748	-88.00333	5.3	fair
FN62	F. pennsylvanica	Remnant	Busse	42.03752	-88.00319	14.9	fair
FN63	F. pennsylvanica	Remnant	Busse	42.03738	-88.00312	18.6	fair
FN64	F. pennsylvanica	Remnant	Busse	42.03243	-88.00655	6.9	fair
FN65	F. pennsylvanica	Remnant	Busse	42.03234	-88.00638	7.4	fair
FN66	F. pennsylvanica	Remnant	Busse	42.03274	-88.00555	6.2	good
FN67	F. pennsylvanica	Remnant	Busse	42.03291	-88.0049	7.8	fair
FN68	F. pennsylvanica	Remnant	Busse	42.03404	-88.0057	39.6	good
FN69	F. pennsylvanica	Remnant	Busse	42.03326	-87.99877	2.5	good
FN70	F. pennsylvanica	Remnant	Busse	42.03288	-87.9979	2.5	poor
FN71	F. pennsylvanica	Remnant	Busse	42.03261	-87.99786	8.5	poor
FN72	F. pennsylvanica	Remnant	Busse	42.03256	-87.99799	21.9	good
FN73	F. pennsylvanica	Remnant	Busse	42.03255	-87.99806	2.5	fair
FN74	F. pennsylvanica	Remnant	Busse	42.03236	-87.99805	15.7	poor
FU01	F. pennsylvanica	Planted	Northeast	41.93687	-87.67456	30.6	good
FU02	F. pennsylvanica	Planted	Northeast	41.93687	-87.67456	33	good
FU03	F. pennsylvanica	Planted	Northeast	41.93568	-87.67415	48.5	fair
FU04	F. pennsylvanica	Planted	Northeast	41.93577	-87.67411	36.1	fair
FU05	F. pennsylvanica	Planted	Northwest	41.99473	-87.73732	28.9	good
FU06	F. pennsylvanica	Planted	Northwest	41.99691	-87.73745	33.8	good
FU07	F. pennsylvanica	Planted	Northwest	41.99662	-87.73754	22.2	good
FU08	F. pennsylvanica	Planted	Northwest	41.99655	-87.73747	29.8	good
FU09	F. pennsylvanica	Planted	Northwest	41.99684	-87.73375	77.5	poor
FU10	F. pennsylvanica	Planted	Northwest	41.99492	-87.73261	27.2	good
FU11	F. pennsylvanica	Planted	Northwest	41.97879	-87.73045	89.1	poor
FU12	F. pennsylvanica	Planted	Northwest	41.97886	-87.73099	80.8	fair
FU13	F. pennsylvanica	Planted	Northwest	41.97907	-87.73304	65.4	poor
FU14	F. pennsylvanica	Planted	Northwest	41.9787	-87.73369	64.2	fair
FU15	F. pennsylvanica	Planted	Northwest	41.97521	-87.70732	56.5	fair
FU16	F. pennsylvanica	Planted	Northeast	41.91843	-87.63473	76.8	fair
FU17	F. pennsylvanica	Planted	Northeast	41.89831	-87.67464	23.8	poor

FU18	F. pennsylvanica	Planted	Northeast	41.89841	-87.67967	51.0	fair
FU19	F. pennsylvanica	Planted	Northeast	41.90008	-87.67972	55.5	fair
FU20	F. pennsylvanica	Planted	Northeast	41.90227	-87.68121	28.3	good
FU23	F. pennsylvanica	Planted	Northeast	41.9698	-87.64732	52.6	fair
FU24	F. pennsylvanica	Planted	Northeast	41.96988	-87.64768	37.8	fair
FU25	F. pennsylvanica	Planted	Northeast	41.93715	-87.63344	26.0	poor
FU26	F. pennsylvanica	Planted	Northeast	41.94585	-87.64029	57.5	fair
FU27	F. pennsylvanica	Planted	Northeast	41.9375	-87.63225	36.4	fair
FU28	F. pennsylvanica	Planted	Northeast	41.93787	-87.6707	49.4	good
FU29	F. pennsylvanica	Planted	Northwest	41.926	-87.71212	30.1	good
FU30	F. pennsylvanica	Planted	Northeast	41.93691	-87.67008	51.7	fair
FU31	F. pennsylvanica	Planted	Northwest	41.92712	-87.71345	27.3	good
FU32	F. pennsylvanica	Planted	Northwest	41.92767	-87.71334	59.3	good
FU33	F. pennsylvanica	Planted	Northwest	41.92651	-87.70717	25.0	poor
FU34	F. pennsylvanica	Planted	Northwest	41.92522	-87.70723	30.5	fair
FU35	F. pennsylvanica	Planted	Northwest	41.92312	-87.70741	37.3	poor
FU36	F. pennsylvanica	Planted	Northwest	41.92411	-87.70748	66.9	poor
FU37	F. pennsylvanica	Planted	Northwest	41.92423	-87.70755	30.3	poor
FU38	F. pennsylvanica	Planted	Northwest	41.92683	-87.70765	50.4	good
FU39	F. pennsylvanica	Planted	Northwest	41.9269	-87.70929	31.4	fair
FU40	F. pennsylvanica	Planted	Southwest	41.84787	-87.68123	26.1	fair
FU41	F. pennsylvanica	Planted	Southwest	41.84746	-87.68117	33.0	good
FU42	F. pennsylvanica	Planted	Southwest	41.83239	-87.67658	39.7	fair
FU43	F. pennsylvanica	Planted	Southwest	41.8337	-87.67654	24.3	fair
FU44	F. pennsylvanica	Planted	Southwest	41.83272	-87.67043	35.6	good
FU45	F. pennsylvanica	Planted	Southwest	41.82452	-87.67035	40.3	fair
FU46	F. pennsylvanica	Planted	Southwest	41.82503	-87.66666	32.9	poor
FU47	F. pennsylvanica	Planted	Southwest	41.82458	-87.67995	38.1	fair
FU48	F. pennsylvanica	Planted	Southwest	41.82457	-87.68032	21.0	fair
FU49	F. pennsylvanica	Planted	Southwest	41.82313	-87.68841	34.2	good
FU50	F. pennsylvanica	Planted	Southwest	41.82594	-87.68404	30.3	good
FU50B	F. pennsylvanica	Planted	Southwest	41.78416	-87.7134	64.8	good
FU51	F. pennsylvanica	Planted	Southwest	41.78434	-87.71545	28.7	good
FU52	F. pennsylvanica	Planted	Southwest	41.78458	-87.71566	23.0	good
FU53	F. pennsylvanica	Planted	Southwest	41.78142	-87.71602	80.8	fair
FU54	F. pennsylvanica	Planted	Southwest	41.78064	-87.71641	44.4	fair
FU55	F. pennsylvanica	Planted	Southeast	41.77292	-87.65758	35.5	good
FU56	F. pennsylvanica	Planted	Southeast	41.77305	-87.6562	39.1	fair
FU57	F. pennsylvanica	Planted	Southeast	41.77347	-87.65584	50.5	poor
FU58	F. pennsylvanica	Planted	Southeast	41.77346	-87.65595	79.4	fair
FU59	F. pennsylvanica	Planted	Southeast	41.77628	-87.65605	45.0	good
FU60	F. pennsylvanica	Planted	Southeast	41.77625	-87.65604	42.5	good
FU60B	F. pennsylvanica	Planted	Southeast	41.76333	-87.59317	52.5	poor
FU61	F. pennsylvanica	Planted	Southeast	41.77624	-87.65602	42.8	fair
FU62	F. pennsylvanica	Planted	Southeast	41.76413	-87.58836	22.1	good
FU63	F. pennsylvanica	Planted	Southeast	41.7689	-87.5965	107.0	good
FU64	F. pennsylvanica	Planted	Southeast	41.76777	-87.60218	51.7	good
FU65	F. pennsylvanica	Planted	Southeast	41.78648	-87.60856	16.0	good
FU66	F. pennsylvanica	Planted	Southeast	41.78645	-87.60851	13.9	good

FU67	F. pennsylvanica	Planted	Southeast	41.78651	-87.60841	24.5	good
FU68	F. pennsylvanica	Planted	Southeast	41.78662	-87.60849	31.8	good
FU69	F. pennsylvanica	Planted	Southeast	41.78975	-87.60821	74.6	good
FU70	F. pennsylvanica	Planted	Southeast	41.79833	-87.61502	39.2	good
FU75	F. pennsylvanica	Planted	Southeast	41.74516	-87.67883	31.1	poor
QM01	Q. rubra	Spontaneous	Labagh woods	41.97851	-87.74407	97.6	fair
QM02	Q. rubra	Spontaneous	Labagh woods	41.97968	-87.74446	16.8	good
QM03	Q. rubra	Spontaneous	Labagh woods	41.97981	-87.74416	6.6	good
QM04	Q. rubra	Spontaneous	Labagh woods	41.9805	-87.74307	62.4	fair
QM05	Q. rubra	Spontaneous	Labagh woods	41.98071	-87.74304	62.7	fair
QM06	Q. rubra	Spontaneous	Labagh woods	41.98157	-87.74422	11.3	good
QM07	Q. rubra	Spontaneous	Labagh woods	41.98159	-87.74396	4.7	fair
QM08	Q. rubra	Spontaneous	Labagh woods	41.98206	-87.74557	2.5	fair
QM09	Q. rubra	Spontaneous	Labagh woods	41.98185	-87.74633	11.3	fair
QM10	Q. rubra	Spontaneous	Labagh woods	41.98403	-87.74789	23.8	fair
QM101	Q. rubra	Spontaneous	Catherine Chevalier	41.9759	-87.84716	30.0	good
QM102	Q. rubra	Spontaneous	Catherine Chevalier	41.97612	-87.8474	8.4	fair
QM103	Q. rubra	Spontaneous	Catherine Chevalier	41.97626	-87.84754	21.4	fair
QM104	Q. rubra	Spontaneous	Catherine Chevalier	41.97689	-87.84794	19.5	good
QM105	Q. rubra	Spontaneous	Catherine Chevalier	41.97725	-87.84775	4.2	poor
QM106	Q. rubra	Spontaneous	Catherine Chevalier	41.97692	-87.84942	39.8	good
QM107	Q. rubra	Spontaneous	Catherine Chevalier	41.97677	-87.84939	74.1	fair
QM108	Q. rubra	Spontaneous	Catherine Chevalier	41.97637	-87.8496	81.2	good
QM109	Q. rubra	Spontaneous	Catherine Chevalier	41.97563	-87.84878	66.3	good
QM11	Q. rubra	Spontaneous	Labagh woods	41.98204	-87.74202	50.0	fair
QM110	Q. rubra	Spontaneous	Catherine Chevalier	41.97555	-87.84936	62.8	fair
QM111	Q. rubra	Spontaneous	Catherine Chevalier	41.97567	-87.84951	27.0	good
QM112	Q. rubra	Spontaneous	Catherine Chevalier	41.97586	-87.84993	46.5	poor
QM113	Q. rubra	Spontaneous	Catherine Chevalier	41.97532	-87.85135	17.8	good
QM114	Q. rubra	Spontaneous	Catherine Chevalier	41.97515	-87.85194	57.5	fair
QM115	Q. rubra	Spontaneous	Catherine Chevalier	41.97278	-87.85252	7.8	poor
QM116	Q. rubra	Spontaneous	Catherine Chevalier	41.97109	-87.85149	125.7	fair
QM117	Q. rubra	Spontaneous	Catherine Chevalier	41.96981	-87.85159	21.0	good
QM118	Q. rubra	Spontaneous	Catherine Chevalier	41.96914	-87.85175	80.3	fair
QM119	Q. rubra	Spontaneous	Catherine Chevalier	41.96786	-87.8522	10.8	fair
QM12	Q. rubra	Spontaneous	Labagh woods	41.98182	-87.78124	32.9	fair
QM120	Q. rubra	Spontaneous	Catherine Chevalier	41.96767	-87.85231	4.5	poor
QM121	Q. rubra	Spontaneous	Catherine Chevalier	41.96773	-87.85336	10.9	fair
QM122	Q. rubra	Spontaneous	Catherine Chevalier	41.96924	-87.85308	87.3	good
QM123	Q. rubra	Spontaneous	Catherine Chevalier	41.97583	-87.85154	7.6	good
QM124	Q. rubra	Spontaneous	Catherine Chevalier	41.97626	-87.85181	13.9	good
QM125	Q. rubra	Spontaneous	Catherine Chevalier	41.97802	-87.85205	8.4	fair
QM13	Q. rubra	Spontaneous	Labagh woods	41.98177	-87.74109	3.6	fair
QM14	Q. rubra	Spontaneous	Labagh woods	41.98197	-87.74092	20.5	good
QM15	Q. rubra	Spontaneous	Labagh woods	41.98205	-87.7408	60.3	good
QM17	Q. rubra	Spontaneous	Labagh woods	41.98212	-87.74085	11.7	good
QM18	Q. rubra	Spontaneous	Labagh woods	41.98217	-87.74073	5.4	fair
QM19	Q. rubra	Spontaneous	Labagh woods	41.98168	-87.74063	87.6	fair
QM51	Q. rubra	Spontaneous	Dan Ryan Preserve	41.7378	-87.68179	35.3	fair

QM52	Q. rubra	Spontaneous	Dan Ryan Preserve	41.73834	-87.6818	54.0	poor
QM53	Q. rubra	Spontaneous	Dan Ryan Preserve	41.73825	-87.68173	65.0	good
QM54	Q. rubra	Spontaneous	Dan Ryan Preserve	41.73794	-87.68173	19.6	poor
QM55	Q. rubra	Spontaneous	Dan Ryan Preserve	41.73805	-87.68176	19.0	poor
QM56	Q. rubra	Spontaneous	Dan Ryan Preserve	41.73802	-87.68168	4.0	good
QM57	Q. rubra	Spontaneous	Dan Ryan Preserve	41.73818	-87.68237	14.3	good
QM59	Q. rubra	Spontaneous	Dan Ryan Preserve	41.73839	-87.67612	29.2	good
QM60	Q. rubra	Spontaneous	Dan Ryan Preserve	41.73913	-87.67648	63.9	good
QM61	Q. rubra	Spontaneous	Dan Ryan Preserve	41.7406	-87.67721	28.7	fair
QM62	Q. rubra	Spontaneous	Dan Ryan Preserve	41.74061	-87.67741	29.8	poor
QM63	Q. rubra	Spontaneous	Dan Ryan Preserve	41.74056	-87.67724	9.4	fair
QN01	Q. rubra	Remnant	Somme	42.1391	-87.82277	23.2	poor
QN02	Q. rubra	Remnant	Somme	42.13838	-87.82136	31.5	fair
QN03	Q. rubra	Remnant	Somme	42.13882	-87.82135	34.0	fair
QN04	Q. rubra	Remnant	Somme	42.13945	-87.81111	43.3	fair
QN05	Q. rubra	Remnant	Somme	42.13986	-87.81223	40.4	fair
QN06	Q. rubra	Remnant	Somme	42.14082	-87.81312	10.7	fair
QN07	Q. rubra	Remnant	Somme	42.14056	-87.8156	43.5	good
QN08	Q. rubra	Remnant	Somme	42.14069	-87.81609	54.5	poor
QN09	Q. rubra	Remnant	Somme	42.13972	-87.81818	21.3	fair
QN10	Q. rubra	Remnant	Somme	42.13929	-87.81911	65.4	poor
QN101	Q. rubra	Remnant	Morton	41.81482	-88.0408	10.3	good
QN102	Q. rubra	Remnant	Morton	41.8139	-88.04067	19.5	good
QN103	Q. rubra	Remnant	Morton	41.81311	-88.04001	33.6	fair
QN104	Q. rubra	Remnant	Morton	41.81305	-88.0398	48.1	fair
QN105	Q. rubra	Remnant	Morton	41.813	-88.04023	43.5	good
QN106	Q. rubra	Remnant	Morton	41.81292	-88.04013	28.2	good
QN107	Q. rubra	Remnant	Morton	41.81346	-88.04254	27.0	fair
QN108	Q. rubra	Remnant	Morton	41.81544	-88.04699	47.2	good
QN11	Q. rubra	Remnant	Somme	42.13952	-87.81981	59.2	poor
QN110	Q. rubra	Remnant	Morton	41.81768	-88.04153	71.2	fair
QN111	Q. rubra	Remnant	Morton	41.81696	-88.04173	2.5	good
QN112	Q. rubra	Remnant	Morton	41.81222	-88.04227	2.5	good
QN113	Q. rubra	Remnant	Morton	41.81737	-88.04401	3.7	fair
QN12	Q. rubra	Remnant	Somme	42.14022	-87.82058	70.0	fair
QN12b	Q. rubra	Remnant	Somme	42.13897	-87.82424	26.4	poor
QN13	Q. rubra	Remnant	Somme	42.13896	-87.82429	27.8	fair
QN14	Q. rubra	Remnant	Somme	42.14046	-87.82561	10.4	fair
QN15	Q. rubra	Remnant	Somme	42.14246	-87.82544	17.7	good
QN16	Q. rubra	Remnant	Somme	42.14264	-87.82309	6.8	fair
QN17	Q. rubra	Remnant	Somme	42.14273	-87.82302	8.0	fair
QN18	Q. rubra	Remnant	Somme	42.14274	-87.8229	11.3	good
QN19	Q. rubra	Remnant	Somme	42.14284	-87.82293	12.4	good
QN20	Q. rubra	Remnant	Somme	42.1403	-87.81776	51.0	good
QN20B	Q. rubra	Remnant	Somme	42.14266	-87.81704	12.5	fair
QN21	Q. rubra	Remnant	Somme	42.14262	-87.81719	7.0	fair
QN22	Q. rubra	Remnant	Somme	42.14357	-87.81894	5.1	fair
QN23	Q. rubra	Remnant	Somme	42.14413	-87.81823	29.2	fair
QN24	Q. rubra	Remnant	Somme	42.14438	-87.81925	36.3	fair

QN25	Q. rubra	Remnant	Somme	42.14432	-87.81944	25.3	good
QN26	Q. rubra	Remnant	Somme	42.14248	-87.82097	25.9	good
QN27	Q. rubra	Remnant	Somme	42.14243	-87.82126	5.2	fair
QN28	Q. rubra	Remnant	Somme	42.14255	-87.8221	15.7	fair
QN29	Q. rubra	Remnant	Somme	42.14258	-87.82215	26.6	fair
QN30	Q. rubra	Remnant	Somme	42.14255	-87.82225	6.5	good
QN31	Q. rubra	Remnant	Somme	42.14244	-87.82237	20.8	good
QN50	Q. rubra	Remnant	Busse	42.0385	-88.00249	37.7	fair
QN51	Q. rubra	Remnant	Busse	42.03629	-88.00863	15.0	good
QN52	Q. rubra	Remnant	Busse	42.03646	-88.00284	16.2	fair
QN53	Q. rubra	Remnant	Busse	42.03987	-88.00375	17.3	fair
QN54	Q. rubra	Remnant	Busse	42.03829	-88.00653	71.0	good
QN54	Q. rubra	Remnant	Busse	42.03997	-88.00362	9.7	poor
QN55	Q. rubra	Remnant	Busse	42.03707	-88.00889	59.4	poor
QN56	Q. rubra	Remnant	Busse	42.03676	-88.00942	115.5	fair
QN57	Q. rubra	Remnant	Busse	42.03675	-88.00952	92.5	fair
QN58	Q. rubra	Remnant	Busse	42.0364	-88.00962	90.2	fair
QN60	Q. rubra	Remnant	Busse	42.03703	-88.00619	64.3	fair
QN61	Q. rubra	Remnant	Busse	42.0373	-88.0064	91.5	fair
QN62	Q. rubra	Remnant	Busse	42.03792	-88.00374	13.8	fair
QN63	Q. rubra	Remnant	Busse	42.03735	-88.00391	50.7	fair
QN64	Q. rubra	Remnant	Busse	42.03731	-88.00406	4.1	poor
QN65	Q. rubra	Remnant	Busse	42.03284	-88.00515	41.0	fair
QN66	Q. rubra	Remnant	Busse	42.03207	-88.00496	49.6	good
QN67	Q. rubra	Remnant	Busse	42.03322	-88.0048	87.0	fair
QN68	Q. rubra	Remnant	Busse	42.0305	-88.00482	63.6	good
QN69	Q. rubra	Remnant	Busse	42.03395	-88.00486	64.2	good
QN70	Q. rubra	Remnant	Busse	42.03412	-88.00488	67.5	fair
QN71	Q. rubra	Remnant	Busse	42.03426	-88.00461	65.0	fair
QN72	Q. rubra	Remnant	Busse	42.03475	-88.00487	49.6	fair
QN73	Q. rubra	Remnant	Busse	42.03529	-88.00499	20.2	good
QN74	Q. rubra	Remnant	Busse	42.03505	-88.00422	76.1	fair
QN75	Q. rubra	Remnant	Busse	42.03505	-88.00423	25.0	good
QN76	Q. rubra	Remnant	Busse	42.03739	-87.99883	16.5	fair
QU01	Q. rubra	Planted	Northwest	41.99512	-87.73506	57.7	poor
QU02	Q. rubra	Planted	Northwest	41.99402	-87.73257	54.3	good
QU03	Q. rubra	Planted	Northwest	41.98151	-87.73003	49.5	good
QU04	Q. rubra	Planted	Northwest	41.98247	-87.73119	45.1	good
QU05	Q. rubra	Planted	Northeast	41.91464	-87.63383	50.2	good
QU06	Q. rubra	Planted	Northeast	41.91808	-87.63475	84.9	poor
QU07	Q. rubra	Planted	Northeast	41.90683	-87.64101	12.3	fair
QU08	Q. rubra	Planted	Northeast	41.97397	-87.64818	76.4	poor
QU09	Q. rubra	Planted	Northeast	41.9434	-87.6407	9.2	poor
QU10	Q. rubra	Planted	Northeast	41.94528	-87.64071	13.0	poor
QU11	Q. rubra	Planted	Northeast	41.9437	-87.63982	18.4	poor
QU12	Q. rubra	Planted	Northeast	41.94156	-87.63848	5.8	good
QU13	Q. rubra	Planted	Northeast	41.94158	-87.63859	7.2	good
QU14	Q. rubra	Planted	Northeast	41.94151	-87.63855	6.0	good
QU15	Q. rubra	Planted	Northeast	41.94318	-87.63905	6.8	good

QU16	Q. rubra	Planted	Northeast	41.94955	-87.64103	13.6	fair
QU17	Q. rubra	Planted	Northeast	41.94966	-87.64056	17.1	fair
QU18	Q. rubra	Planted	Northeast	41.95	-87.64074	63.3	good
QU19	Q. rubra	Planted	Northeast	41.96094	-87.64502	16.9	fair
QU20	Q. rubra	Planted	Northeast	41.93576	-87.67248	16.6	good
QU21	Q. rubra	Planted	Northeast	41.93592	-87.67237	15.1	fair
QU22	Q. rubra	Planted	Northwest	41.92824	-87.70762	21.4	fair
QU23	Q. rubra	Planted	Northwest	41.92742	-87.70707	10.0	good
QU24	Q. rubra	Planted	Northwest	41.92666	-87.70711	12.8	fair
QU25	Q. rubra	Planted	Northwest	41.92519	-87.70708	12.2	fair
QU26	Q. rubra	Planted	Northwest	41.92263	-87.7073	21.4	good
QU27	Q. rubra	Planted	Northwest	41.92655	-87.70779	20.7	fair
QU28	Q. rubra	Planted	Northwest	41.9267	-87.7077	15.9	fair
QU40	Q. rubra	Planted	Southwest	41.84722	-87.6816	13.1	poor
QU41	Q. rubra	Planted	Southwest	41.84726	-87.68169	11.3	poor
QU42	Q. rubra	Planted	Southwest	41.84753	-87.68099	14.0	poor
QU43	Q. rubra	Planted	Southwest	41.84758	-87.68086	13.8	poor
QU44	Q. rubra	Planted	Southwest	41.83233	-87.67659	32.8	fair
QU45	Q. rubra	Planted	Southwest	41.78148	-87.71867	70.4	good
QU46	Q. rubra	Planted	Southwest	41.77771	-87.72155	52.0	fair
QU47	Q. rubra	Planted	Southwest	41.77321	-87.65676	10.2	good
QU48	Q. rubra	Planted	Southwest	41.76503	-87.58888	39.0	fair
QU49	Q. rubra	Planted	Southeast	41.82608	-87.68309	5.2	good
QU50	Q. rubra	Planted	Southeast	41.82609	-87.68323	5.0	fair
QU51	Q. rubra	Planted	Southeast	41.82609	-87.68309	5.5	fair
QU53	Q. rubra	Planted	Southeast	41.82612	-87.68291	5.2	good
QU54	Q. rubra	Planted	Southeast	41.76696	-87.60112	74.7	fair
QU55	Q. rubra	Planted	Southeast	41.77104	-87.60126	57.1	poor
QU56	Q. rubra	Planted	Southeast	41.77111	-87.60132	45.7	good
QU57	Q. rubra	Planted	Southeast	41.76956	-87.60134	85.2	fair
QU58	Q. rubra	Planted	Southeast	41.76981	-87.60198	65.5	fair
QU59	Q. rubra	Planted	Southeast	41.77013	-87.60142	81.3	fair
QU60	Q. rubra	Planted	Southeast	41.78641	-87.60856	49.2	fair
QU61	Q. rubra	Planted	Southeast	41.78642	-87.60833	36.3	good
QU62	Q. rubra	Planted	Southeast	41.78882	-87.60816	57.5	fair
QU63	Q. rubra	Planted	Southeast	41.78929	-87.60822	60.8	good
QU64	Q. rubra	Planted	Southeast	41.78953	-87.60803	56.4	fair
QU65	Q. rubra	Planted	Southeast	41.79167	-87.60861	79.0	fair
QU66	Q. rubra	Planted	Southeast	41.79189	-87.60881	62.9	fair
QU67	Q. rubra	Planted	Southeast	41.79193	-87.60886	53.0	fair
QU68	Q. rubra	Planted	Southeast	41.79571	-87.61503	49.1	good
QU69	Q. rubra	Planted	Southeast	41.79631	-87.61509	51.8	good
QU70	Q. rubra	Planted	Southeast	41.79731	-87.61535	41.0	fair
QU71	Q. rubra	Planted	Southeast	41.79773	-87.61553	59.4	fair
QU72	Q. rubra	Planted	Southeast	41.79842	-87.61437	70.5	good
QU75	Q. rubra	Planted	Southwest	41.73958	-87.68102	73.4	fair