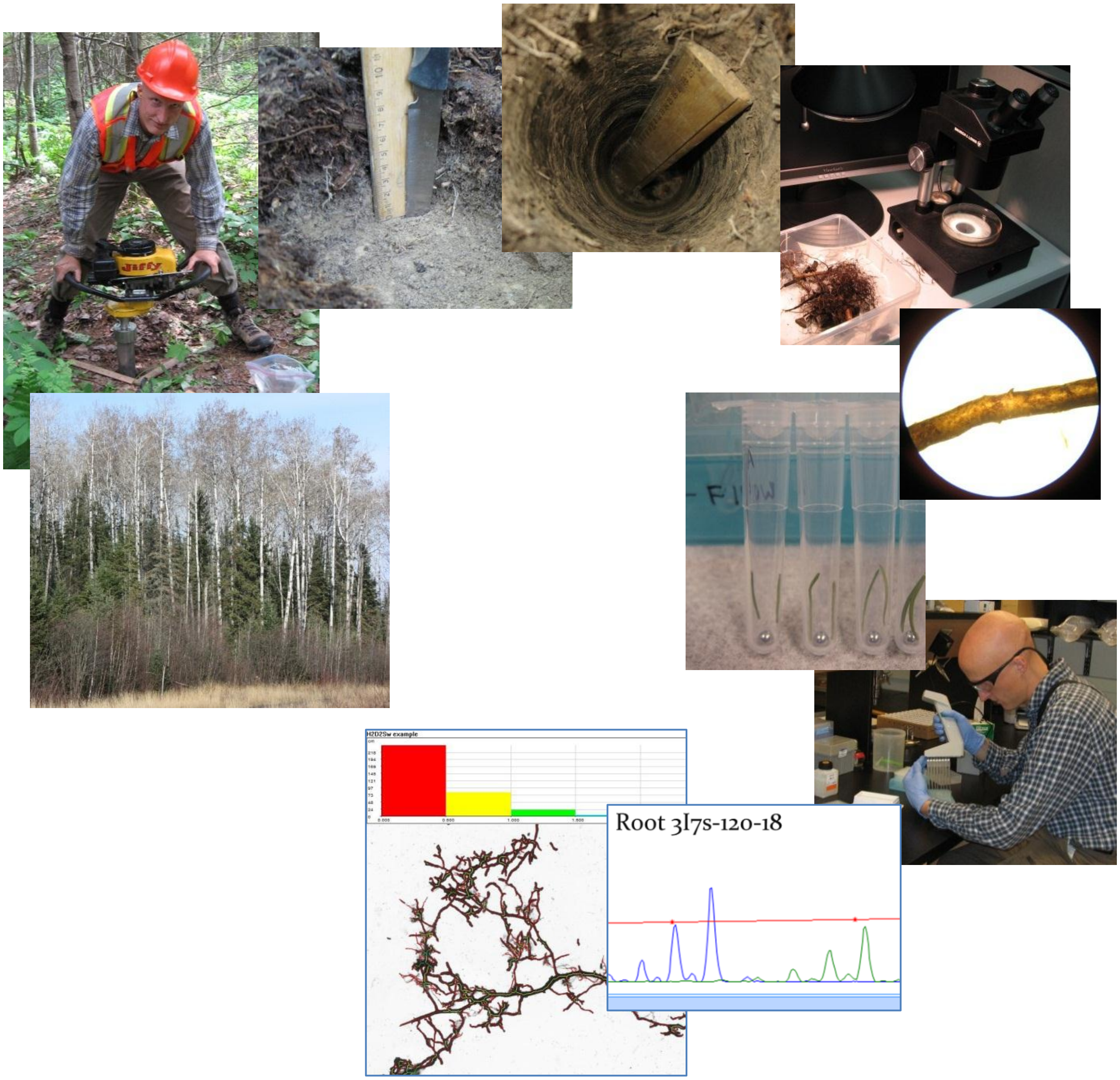
CHARACTERIZATION OF ROOTING PATTERNS IN MIXEDWOOD FORESTS OF WHITE SPRUCE AND TREMBLING ASPEN: IS COMPETITION REDUCED BELOWGROUND?

By

Derek J. Lawrence



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CHARACTERIZATION OF ROOTING PATTERNS IN MIXEDWOOD FORESTS OF WHITE SPRUCE AND TREMBLING ASPEN: IS COMPETITION REDUCED BELOWGROUND?

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ABSTRACT

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Keywords: facilitation, fine roots, image analysis, microsatellites, *Picea glauca*, *Populus tremuloides*, root length, root mass, simple sequence repeat, vertical and horizontal distribution

Mixedwood forests of white spruce (Sw, *Picea glauca* (Moench) Voss) and trembling aspen (Pt, *Populus tremuloides* Michx.) have been assumed to better utilize soil resources compared to monospecific forests. Reduction of competition might occur, wherein species occupy at least partially separate niches, possibly resulting in vertical stratification of fine roots (d ≤ 2mm), with Pt roots below Sw. This shift may also result in changes to specific root length (SRL). Facilitation of resource extraction may also occur, with Pt litter improving soil quality. These effects may provide incentive for Sw to preferentially exploit upper soil layers in mixedwood stands, resulting in wider Sw root systems. Direct evidence of these effects in Sw and Pt mixedwood forests is lacking; this research sought out such substantiation.

Research was conducted at the Fallingsnow Ecosystem Project site in northwestern Ontario, Canada. Twenty-six plots were selected across three blocks representing mixedwood (9), pure Sw (9) and pure Pt (8) stands. Tree positions, species, basal area and density were measured. Foliage samples were collected from each tree, and three root/soil core samples were collected per plot, up to a depth of 40 cm, separated into depth classes. Fine roots were separated into Sw, Pt and ―other” categories, scanned to determine length, dried and weighed. Simple sequence repeat DNA profiles were determined for all Sw foliage samples and for a subsample of Sw root fragments. Root fragment DNA profiles were matched to originating trees. Horizontal distributions of Sw roots were calculated. Vertical distributions of all roots were described.

The concept of reduced belowground competition in mixedwoods garnered only weak support. No significant vertical stratification of Sw and Pt roots was noted. Mass and length of ―other” fine roots in the organic layer was significantly greater in pure Pt plots. Specific root length of Pt was significantly greater in mixedwood plots. Organic soils in mixedwood and pure Pt plots were significantly less acidic than in Sw plots in one block. Eighty percent of Sw root fragments were < 3.2 m from originating tree stems. Root fragment prevalence decreased rapidly with distance from tree stems. A subtle significant trend towards wider Sw root distributions was noted in mixedwood plots.

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ACKNOWLEDGEMENTS and FOREWORD

This thesis is structured as two complete stand-alone papers, to be submitted to scientific journals (chapters 2 and 3). Chapter 1 presents an introduction overviewing both papers, and chapter 4 contains conclusions drawn from both papers. The research is divided into two papers by dimension: vertical root distribution and horizontal root distribution.

This study was greatly aided by the work done by others prior to the inception of this study. Research took place at the Fallingsnow Ecosystem Project site, established by the Vegetation Management Alternatives Program of the Ontario Forest Research Institute, a part of the Ontario Ministry of Natural Resources. Additionally, this study leveraged pre-existing work from a larger research project entitled ―Intensive silviculture and competition theory: linking practice and science”, Natural Sciences and Engineering Research Council of Canada Strategic Project Grant 350778-07.

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1 Introduction

This study examined the rooting patterns of white spruce (Sw, *Picea glauca* (Moench) Voss) and trembling aspen (Pt, *Populus tremuloides* Michx.), and the effect of stand type upon such patterns. Specifically, contrasts were drawn comparing patterns in monospecific stands of these species with mixedwood stands. General rooting patterns of other species, *i.e.*, shrubs, herbaceous plants, *etc.* were also contrasted. To begin, however, the question should be addressed: Why study mixedwood forests at all?

Interest in mixedwood forests is not new. As early as 1662, commentary exists suggesting the use of mixedwood forests for aesthetic and economic purposes:

> –[Mediterranean Cyprus (*Cupressus sempervirens* L.)] … is very proper to intermix with evergreens of a second size next to Pines, to form clumps ; in which class it will keep pace with the trees of the same line, and be very handsome: Besides, the wood of this tree is very valuable, when grown to a size fit for planks."(Evelyn 1662)

In modern times, interest in mixedwood forests continues. Mixedwood forests have been recognized as potentially more productive than forests comprised of just one tree species (Vandermeer 1989; Kelty *et al.* 1992). They have been identified as integral parts of the natural forested environment in Canada (Rowe & Halliday 1972), and potentially important to promote a biodiverse environment (Man & Lieffers 1999). For these reasons, and others, sound management of forest resources may include the promotion of mixedwood forests, which is consistent with the principles of the Crown Forest Sustainability Act, 1994, c. 25, s. 2 (3):

> —1Large, healthy, diverse and productive Crown forests and their associated ecological processes and biological diversity should be conserved.
>
> 2. The long term health and vigour of Crown forests should be provided for by using forest practices that, within the limits of silvicultural requirements, emulate natural disturbances and landscape patterns while minimizing adverse effects on plant life, animal life, water, soil, air and social and economic values, including recreational values and heritage values."

Although motives exist to support the promotion of mixedwood forests, major difficulties are present in the details of such an undertaking, since the theory supporting the purported advantages of mixedwood forests is complex, and much is unknown, particularly of belowground systems.

Ecological theory presents two concepts that are key to understanding potentially increased productivity in mixedwood forests, competitive reduction and facilitative production. Competitive reduction occurs when species in mixture make fuller use of site resources than either species may use alone (Vandermeer 1989). This occurs when the mixed species occupy at least partially separate ecological niches. Two types of niches are recognized: the *fundamental* niche describes where in the environment an organism *may* exist, and the realized niche, where it does *in fact* exist (Hutchinson 1957). The dimensions of the fundamental niche will be determined by the theoretical capabilities of the organism, whereas the dimensions of the realized niche will depend on population, developmental stage and competitive pressures. In a system where competitive reduction occurs, competition experienced by at least one species is less intense when the neighbour is of a different species, and the net realized niche is enlarged, thereby increasing potential resource extraction.

Ecological niches may differ in space, time, physiological requirements, *etc.* Roots of one species may be able to persist in soil layers unoccupied by another, due to favoured conditions or growth habit (Kimmins 1987). Leaves of one species may be able to use low levels of light unprofitable for another (Lambers *et al.* 2008). Leaves of one species can emerge prior to those of another, or persist later than another, thereby utilizing “unused” light. Species may have different temperature thresholds required for root growth and soil resource extraction (Landhausser *et al.* 2001). This is by no means an exhaustive list of the ways in which niches may differ, but these details are relevant to mixedwood forests of Pt and Sw. Trembling aspen has been noted to have a deeper rooting habit than Sw in at least one study (Strong & Laroi 1983), possibly enabling it to access resources unavailable to Sw. Conifers are known to be shade tolerant compared to Pt, enabling them to adapt to lower light conditions under a Pt canopy (Man & Lieffers 1997). White spruce leaves are always present (although not necessarily photosynthesizing), whereas Pt is deciduous, thus presenting the possibility of Sw growth while Pt is leafless (Kelty *et al.* 1992). Landhausser *et al.* (2001) noted that root growth and net assimilation were less affected by low temperatures in Sw trees compared to Pt trees. All of these observations, and others, suggest that mixtures of these species may result in competitive reduction, and potentially greater forest productivity (Man & Lieffers 1999).

Facilitative production is a process whereby one species aids the growth and development of another (Vandermeer 1989). In mixedwood forests of conifers and hardwoods, an important way this may occur is through improvements to nutrient cycling rates (Kelty *et al.* 1992). Conifer litter is not readily decomposable; in pure Sw stands this can lead to available nitrogen being tied up in the litter layer. However, litter from hardwoods decomposes more readily and is generally less acidic than conifer litter (Gordon 1983); the presence of Pt mixed with Sw may improve the growing environment for Sw, particularly in upper soil layers.

This study is integrated into a larger research project entitled “Intensive silviculture and competition theory: linking practice and science”, focussing upon Sw and Pt mixedwood forest competition and productivity. Within this particular M.Sc.F. study, the concepts of competitive reduction and facilitation were studied as they pertain to belowground systems. These mechanisms, if at play, may result in more productive forests. Whether or not greater productivity actually does occur in mixedwood forests of Pt and Sw was beyond the scope of this M.Sc.F. study. Because of this, the study was designed in such a way as to make the research plots as similar as possible in terms of stocking and occupation, with the key independent variable being stand composition.

This M.Sc.F. study was greatly empowered through pre-existing work at the Fallingsnow Ecosystem Project (FEP) site in Northwestern Ontario, Canada (Lautenschlager *et al.* 1997). The FEP project was established in 1993 to study conifer release alternatives. The area was harvested in 1986-1989 and planted with Sw. Trembling aspen regenerated naturally, and was suppressed with a variety of treatments, applied in a random fashion within each of four blocks. Because of this prior work on the site, it currently contains relatively even aged monospecific stands of Sw and Pt, with a spectrum of mixedwood forests also existing between these extremes. Since this pattern was for the most part brought about by the random application of varying Pt suppression methods early in stand development, and *not* by underlying differences in the locations of these stands, the FEP project site represents a unique opportunity. Here, we may study belowground systems of Sw and Pt as affected by one main factor – stand composition – with far fewer confounding factors than would exist when studying completely natural stands brought about by the devices of nature.

Root studies are not common in the literature. Studying roots is less convenient than studying aboveground portions of trees; leaves, stems and branches can be measured and sampled with relative ease, whereas sampling and measuring roots involves labour intensive excavations. Additionally, when studying aboveground parts of trees, the whole tree is usually observable, knowledge which may inform a suitable representative sampling regime. The same cannot be said for roots: sampling is generally performed —blind” with little foreknowledge regarding the general distribution and dimension of the system to be sampled. This fact, combined with the labour intensive nature of root sampling, can result in a great deal of variability, or —noise”, in measures of root systems.

This study was divided into two sections in the form of two separate papers to be submitted to academic journals. Rooting behaviour was examined separately in two dimensions: vertical and horizontal. This division was convenient since the methods employed in these two dimensions were very different. Studying vertical root distribution is relatively straightforward: root and soil samples are collected, either by coring or through more extensive excavations, divided by depth, then the roots are separated and quantified. Because of this, studies of vertical root distributions, as opposed to horizontal, are more common.

In the vertical distribution study, the concept of root stratification warranted special attention. In this theoretical concept, a species, such as Pt, with the capability to be deeper rooting, may shift to lower soil layers when a second species, such as Sw, competes to occupy shallow layers. Such partitioning of the soil resources under competition would provide strong evidence of competitive reduction, in that the belowground niches occupied by the two species do not completely overlap. This study sought evidence for such behaviour in mixedwood forests of Sw and Pt.

Studying horizontal distributions of roots presents a unique challenge. It is relatively straightforward to assess the horizontal homogeneity of roots by taking numerous horizontally distributed samples. However, characterizing root horizontal distribution of *individual* trees, or even of a *typical* individual, is considerably more difficult. Within a forest, tree roots are usually highly intermixed; roots from an excavation cannot be assumed to originate from the nearest tree. Complete excavation of a site would yield unequivocal horizontal distribution information, but obviously such an approach would require prohibitive amounts of time and money, and would result in total destruction of the site, preventing future work. The use of tracers is a good option for studying horizontal extent of roots. In this method, stable isotopes such as N-15, or nutrient analogs (*i.e.*, relatively less abundant chemical species absorbed by plants that have similar size and charge as nutrient ions) are injected into the ground and then uptake is measured in trees (Casper *et al.* 2003). Uptake in trees indicates the presence of absorbing roots at the location of ground injection. This method is powerful since it measures actual absorption versus absorption assumed by virtue of root presence. The method reveals which trees have absorbing roots at a particular location; however, information regarding the *intensity* of rooting per individual at the injection point is not as precise. In other words, tracer studies are very good at telling us how far roots may spread, but aren't as good at describing the horizontal *distribution* of roots. Tracer methods are also limited in that the number of injection sites at a given location is limited by the number of tracers available, and different tracers are not necessarily absorbed at the same rate.

Horizontal root distributions can also be determined using simple sequence repeat (SSR, microsatellite) DNA markers (Brunner *et al.* 2004; Saari *et al.* 2005). Simple sequence repeat markers are regions of non-coding DNA containing short base pair sequences (*i.e.*, 1-6 base pairs) that are repeated many times (Weising *et al.* 2005). Specific SSR markers are usually unique to a particular species. Since these regions are non-coding and do not have a well understood purpose, when mutations occur they persist in the population. Mutations typically consist of additions or deletions of the repeated sequence. By examining the length of a SSR region, it is possible to differentiate individuals, and to match tissue samples with individuals. More than one SSR region may be used for this purpose, depending on the variability of the marker used and the number of individuals to be compared. In criminal forensics involving human DNA, usually 13 regions are used to obtain a high probability of a correct match, since the human population numbers into the billions. In studies involving only a few dozen trees, far fewer SSR regions are required.

In this study, horizontal distribution of Sw roots was determined using two Sw-specific SSR markers. This approach had a number of advantages. It was minimally destructive, requiring relatively small root samples. It provided information regarding the maximum extent of roots, as in tracer studies, and it also enabled descriptions of where roots are most prevalent in relation to the tree stem. It was also possible to describe horizontal root distributions specific to soil layers. In this experiment, horizontal distributions were characterized for roots in the organic layer only, due to restrictions upon experiment size imposed by time and budget. However, with more resources, this technique could easily provide two dimensional root distributions, describing root prevalence with respect to horizontal *and* vertical distance from tree stems. The main disadvantage of this approach is that it simply describes the presence of roots; it does not directly measure absorption of nutrients. It relies on a diameter size-based definition of root physiological function; in the present study, the assumption was made that roots having a diameter less than 2 mm are responsible for absorbing nutrients and water. This is probably a crude approximation (Pregitzer *et al.* 2002).

Through the study of rooting patterns presented in these papers, understanding of Pt and Sw mixedwood dynamics may be improved. Insight may be gained regarding competitive interactions and facilitative effects in these forests. Such enhanced knowledge may provide a solid basis for future investigations and empower evidence based modelling of forests as influenced by belowground interactions.

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2 Vertical distribution paper

2.1 Title

Vertical rooting patterns in 20 year old mixedwood stands of white spruce (*Picea glauca* (Moench) Voss) and trembling aspen (*Populus tremuloides* Michx.) in northwestern Ontario: Does stratification occur?

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2.3 Abstract

Mixedwood forests of white spruce (Sw; *Picea glauca* (Moench) Voss) and trembling aspen (Pt; *Populus tremuloides* Michx.) have been assumed to better utilize soil resources compared to monospecific forests. Reduction of competition might occur, wherein species occupy at least partially separate niches, possibly resulting in vertical stratification of fine roots (d ≤ 2mm), with Pt roots below Sw. This shift may also result in changes to specific root length (SRL). Facilitation of resource extraction may also occur, with Pt litter improving soil quality. Direct evidence of these effects in Sw and Pt mixedwood forests is lacking, this study sought out such substantiation.

Research was conducted at the Fallingsnow Ecosystem Project site in northwestern Ontario, Canada. Twenty-six plots were selected representing mixedwood (9), pure Sw (9) and pure Pt (8) stands, spread across three blocks.

Site composition, basal area and density were measured. Three root/soil core samples were collected per plot, up to a depth of 40 cm, separated into depth classes. Fine roots were separated into Sw, Pt and “other” categories, scanned to determine length, dried and weighed.

The concept of reduced belowground competition in mixedwoods garnered only weak support. No significant vertical stratification of Sw and Pt roots was noted. Mass and length of “other” fine roots in the organic layer was significantly greater in pure Pt plots. Specific root length of Pt was significantly greater in mixedwood plots, suggesting that resource extraction strategies may be changing in the mixedwood plots. Organic layers (a combination of Ah and thin F horizons) in mixedwood and pure Pt plots were significantly less acidic than in Sw plots in one block, providing support for the existence of facilitation.

2.4 Keywords

belowground competition, competitive reduction, facilitation, fine roots, image analysis, niche, root length, root mass, vertical distribution, WinRHIZO

2.5 Introduction

Mixedwood forests of white spruce (Sw; *Picea glauca* (Moench) Voss) and trembling aspen (Pt; *Populus tremuloides* Michx.) may possess ecological advantages over monospecific stands of these species, particularly in the extraction of belowground resources. Although mixedwood forests of these species are common throughout the Boreal Forest Region of Ontario (Rowe & Halliday 1972), traditional silvicultural practices have attempted to create monocultures of historically more desirable conifers throughout this forest region. However, mixedwood forests may be more productive overall, in part, due to belowground partitioning of resources (Kelty *et al.* 1992; Man & Lieffers 1999; Kelty 2006).

Belowground interactions are important to understanding mixedwood forest dynamics, but information on this topic is limited (Jose *et al.* 2006). Reduction of belowground competition may occur in mixedwood forests, leading to a greater exploitation of soil resources. Competition may be reduced through vertical stratification of fine roots (diameter ≤ 2.0 mm, hereafter referred to as —roots”), brought about by roots following —avoidance” strategies (Novoplansky 2009), occupying at least partially separate niches.

It has been assumed that Sw and Pt, when grown together, will develop stratified roots with Sw roots occupying shallower soil layers than Pt (Man & Lieffers 1999). However, support for this concept is indirect and contradictory: Pt has been noted to have a deeper rooting ability than Sw, but both species are also known to preferentially exploit upper soil layers (Bannan 1940; Safford & Bell 1972; Kimmins & Hawkes 1978; Strong & Laroi 1983; Ruark & Bockheim 1987). To our knowledge, direct evidence of root stratification in Pt and Sw mixedwood stands does not exist.

The existence of differences in the typical vertical rooting profile of Sw and Pt does not necessarily mean that mixtures of these species will lead to competition reduction and increased soil resource exploitation. Two comparisons may be drawn: mixedwood stands versus each species in monospecific stands. Comparing pure Pt and mixedwood stands, if Sw roots in the mixedwood stand simply *replace* Pt roots that would have otherwise been present had the stand been pure Pt, it is not clear that soil exploitation has increased. In this case, the belowground niche realized by Sw might be entirely overlapping with the realized niche for Pt (Hutchinson 1957; Vandermeer 1989), and any resource that Sw may access might have been accessed anyways by Pt had the stand been pure Pt. If, however, stratification occurs, and Sw roots in upper soil layers actually *displace* Pt roots to deeper soils rather than simply replacing them, a greater case would be made for increased soil exploitation, since then Pt would be increasing exploitation of previously under-utilized deeper soil layers. In contrast, this argument is not as strong when comparing pure Sw stands with mixedwood stands. In this instance, even if roots are not stratified, total soil exploitation might be increased in mixedwood stands by the simple fact that Pt roots may be accessing resources at depths below which Sw typically exploits. These concepts are illustrated in Figure 2-1. In a), rooting profiles are unchanged from that observed in monospecific stands. Niche of Sw completely overlaps with Pt; soil exploitation advantage of mixedwood vs. pure Pt stand is unclear. In b), stratification occurs, the net realized niche is greater than in a), and a stronger case is made for mixedwood advantage over pure Pt.

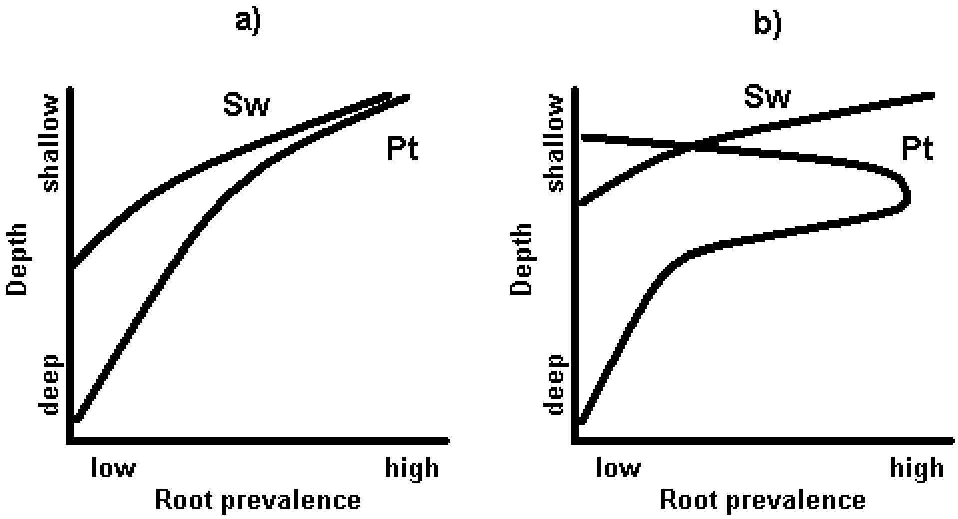

Figure 2-1. Hypothetical realized niches in mixedwood stands with respect to depth for fine roots of Sw and Pt. Root prevalence is intentionally lacking a specific definition and simply refers to relative presence of roots. Adapted from Bolte & Villanueva 2006.

This line of reasoning is an oversimplification that does not consider phenological differences, resource requirement differences, changes brought about to the environment by each species, for example, hydraulic redistribution (Burgess *et al.* 1998), ―nutrient pump" effects, facilitative benefits *etc.* It also does not take into account the greater dependency of conifers upon mycorrhizal associations (Bauhus & Messier 1999). Nevertheless, it does underscore the significance of stratified Sw and Pt root systems, if they exist. The observed or suspected importance of root stratification in other tree species pairs has been recognized by other authors (Kelty *et al.* 1992; Schmid & Kazda 2002; Legare *et al.* 2005a; Jose *et al.* 2006; Bolte & Villanueva 2006).

Additionally, the mechanism of facilitation may lead to greater exploitation of soil resources in mixedwood forests. Trembling aspen litterfall may facilitate resource capture for Sw roots in mixedwood forests. Litter from hardwood trees such as Pt is more readily decomposable (Gordon 1983) and less acidic than Sw litter; this may improve the growing environment for Sw, particularly in upper soil layers.

The purpose of this study was to contrast total root length and mass, as well as root vertical distribution for Sw, Pt and other species in three stand types: pure Sw, pure Pt and mixedwood stands. Basic root morphology, soil characteristics and relationships to aboveground tree statistics were also investigated. It was hypothesized that a) total root length and biomass would be greater in mixedwood stands than in either pure Sw or pure Pt stands; b) in mixedwood stands, Sw fine roots would shift to upper soil layers and Pt fine roots would shift to deeper soil layers, compared to distributions of fine roots observed for these species in pure stands; c) upper soil layers in mixedwood stands would be thinner, experience nutrient enrichment and less acidification compared to pure Sw stands; d) in mixedwood stands, Pt would have longer specific root length (SRL; describes the length of a root segment having a given mass) and Sw would have shorter SRL, compared to SRL observed in pure stands of these species. Roots of other species were assessed to determine trends associated with these different stand types.

In hypothesis a), root length and biomass were considered representative of exploitative capacity of root systems. Determining total exploitative capacity of root systems is a very difficult task. Attributes such as fine root mass and length have been used in the past as rough proxy measures for exploitative capacity; so too in this study these measures were used (Bauhus & Messier 1999; Atkinson 2000). Grouping fine root mass and length of all species together presents a crude approximation of total exploitative capacity: such an approach does not take into account physiological differences between species. Therefore, differences with these pooled statistics must be evaluated with caution.

In mixedwood stands, changes might be observed in SRL of Sw and Pt. Longer SRL may suggest rooting behaviour that is more explorative and foraging, especially in nutrient poor conditions (Fitter 1985; Atkinson 2000; Trubat *et al.* 2006; Lambers *et al.* 2008). Contradicting the former point, longer SRL has also been associated with increased nutrient conditions (Fitter 1976; Ryser 2006). However, in the case of stratification in mixedwood stands, increases in SRL have been associated with the species that explores deeper and less nutrient rich soil (Bolte & Villanueva 2006). If Pt fine roots begin to forage in less nutrient rich deeper soil, there may be incentive towards longer, thinner roots that enable exploration of greater volumes of soil. Conversely, if the growing environment experienced by Sw fine roots in upper soil layers is enriched, there may be decreased incentive for long narrow roots, leading to shorter SRL. Thicker roots (and thus shorter SRL) present a trade-off: they generally live longer leading to lower turnover costs, but they have a greater construction and maintenance cost and their nutrient extraction efficiency may decline, especially if the surrounding soil becomes depleted in nutrients (Fitter 2002; Eissenstat & Yanai 2002). Thicker roots might be favoured, presenting a worthwhile trade-off when soils are enriched, since there may be a pool of available nutrients that can sustain longer term extraction in one particular exploited soil zone.

2.6 Materials and Methods

2.6.1 Study Location

Research was conducted at the Fallingsnow Ecosystem Project (FEP) site in northwestern Ontario (48°10’N, 89°49’W), 60 km southwest of Thunder Bay, Ontario (Lautenschlager *et al.* 1997). The site location is depicted in Figure 2-2. This research site consists of four blocks ranging from 28 to 52 ha, established in 1993 to study ecological effects of conifer release alternatives. The FEP site is located in the transition zone between the Boreal and Great lakes-St. Lawrence forest zones (Rowe & Halliday 1972), at an elevation of approximately 400 m (Blocks 3 and 4) and 500 m (Block 2). Mean annual precipitation is 845 mm; mean annual temperature is 2.1 °C. Slope exposure is SE in Blocks 3 and 4, and NE in Block 2. The blocks were harvested in 1986-1989 and planted with Sw (Blocks 2, 3 and 4); Pt regenerated naturally. Block 1 was not used in this study since it was planted with black spruce (Sb, *Picea mariana* (Mill.) B. S. P.). Suppression of Pt occurred with varying degrees of success. Currently the site contains even aged monospecific stands of Sw and Pt, as well as mixedwood stands of these species in various proportions. Amongst plots used in this study, density ranges from 227 to 2901 stems ha^{-1} for Sw and 0 to 6301 stems ha^{-1} for Pt; basal area ranges from 0.8 to 23 m^2 ha^{-1} for Sw and 0 to 21 m^2 ha^{-1} for Pt. The presence of these even aged stands of varying species proportion makes this site ideal for the research presented in this paper. Blocks 2, 3 and 4 were used in this study.

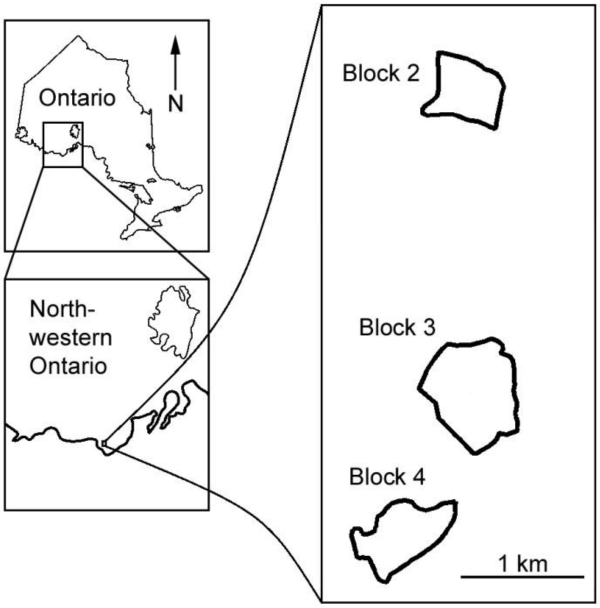

Figure 2-2. Fallingsnow Ecosystem Project site[1].

It is worth emphasizing that these stands are not of natural origin, and accordingly the dynamics between these two species will differ from natural mixedwood stands. In particular, forest succession did not occur in a normal manner with Sw coming up beneath a relatively established Pt canopy. Rather, Sw was often given a ~~h~~ead start" through the use of Pt suppression techniques, generally leading to a much smaller size difference between the two species than might otherwise be observed in nature.

2.6.2 Plot Selection

This study is integrated within a larger research project currently in progress. Within this larger project, 45 seven metre radius plots representing a spectrum of stand types ranging from pure Sw to pure Pt stands were randomly established in 2008. During the summer of 2009, species, diameter at breast

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[1] *Modified from:* Map of Ontario. St. Catharines, Ontario: Brock University Map Library. Available: Brock University Map Library Controlled Access http://www.brocku.ca/maplibrary/maps/outline/Ontario/ontario2.pdf (Accessed February 21, 2011).

height (dbh) and location within the plot were recorded for all trees having a dbh ≥ 6 cm; the same data were collected for smaller trees (2 cm to < 6cm dbh) within a radius of 3.5 m from plot center. Tree heights were measured for several representative trees per plot. Heights for remaining trees were calculated using a height-diameter equation (Sharma & Parton 2007). Plots were assigned names based on an alphanumeric grid system.

For this study, a subsample of 9 plots was identified in each block representing three stand types: pure Sw (3), pure Pt (3) and mixedwood (3). One pure Pt plot was eventually discarded. Plot categorization was based on the relative importance value (RIV; Curtis & McIntosh 1951) of conifer and hardwood trees having a dbh ≥ 2 cm. Relative importance value was calculated as the sum of density and basal area of the subject tree type, each expressed as a percentage of the total. The maximum RIV is 200. Pure Sw plots were defined as having RIV > 170 for conifers; pure Pt plots were defined as having RIV > 170 for hardwoods. Plots were dominated by Sw and Pt; other species were encountered occasionally, notably balsam fir (Bf, *Abies balsamea* (L.) Mill.) and white birch (*Betula papyrifera* Marsh.). Mixedwood plots were defined as having RIV between 30 and 170 for conifers, or, complementarily, between 30 and 170 for hardwoods.

All pure Sw plots identified were selected (3 per block), and 8 of 9 pure Pt plots identified were selected (3 each in Blocks 2 and 4, 2 in Block 3). Several mixedwood plots (9) were available per block. Mixedwood plots were selected based on criteria designed to minimize differences between plots in terms of total basal area and density of all trees. Large differences in site occupation were undesirable since this could potentially confound observation of stand composition effects. If mixedwood plots had considerably greater occupation, a type of –additive” design would be created, likely resulting in a confounding of stand density and composition effects (Harper 1977). Instead, a superior “substitutive” design was sought in order to minimize these problems. The experimental plots within the larger project were not established from the beginning with this goal in mind. Therefore, mixedwood plots were selected according to two criteria in order to create an experimental design as similar as possible to a substitutive design: they should have a density and a basal area per hectare in between the averages observed for the pure Sw and pure Pt plots, to the greatest extent possible. Plot attributes are summarized in Table 2-1. Layout of a typical plot is depicted in Figure 2-3.

Table 2-1. Selected mean plot attributes. Standard deviations are in parentheses.

Plot Attributes	block	Pure white spruce plots		Mixedwood plots		Pure trembling aspen plots	
		White spruce	Trembling aspen	White spruce	Trembling aspen	White spruce	Trembling aspen
Density (stems ha^{-1})	2	2901 (357)	-	2533 (1012)	1472 (487)	324 (361)	4135 (676)
	3	2251 (369)	194 (194)	1992 (1243)	4049 (1476)	227 (321)	3313 (551)
	4	1840 (228)	194 (234)	2641 (521)	2793 (2793)	259 (395)	6301 (2471)
Basal Area (m^2 ha^{-1})	2	20 (5)	-	17 (4)	3.6 (2.8)	1.1 (0.9)	20 (3)
	3	23 (1)	0.9 (0.9)	14 (6)	9.2 (5.1)	0.8 (1.2)	19 (2)
	4	15 (8)	0.7 (0.7)	14 (1)	7.9 (3.6)	1.2 (1.7)	21 (3)
Relative Importance Value (RIV)	2	184 (13) *	15 (13) *	133 (34) *	66 (34) *	13 (11) *	186 (11) *
	3	188 (10) *	11 (10) *	99 (34) *	100 (34) *	11 (10) *	188 (10) *
	4	189 (11) *	10 (11) *	127 (35) *	72 (35) *	22 (21) *	177 (21) *
Average Tree Height (m)	2	6 (0.5)	-	6.3 (0.3)	5.9 (1.3)	5.1 (0.6)	10 (0.9)
	3	7.7 (0.4)	7.7 (3.9) **	7.2 (0.9)	6.4 (1.3)	5.9 **	11.2 (2.6)
	4	6.2 (1.2)	5.5 (0.3) **	6.9 (0.1)	8.8 (1.3)	7.4 (0.9) **	9 (0.7)

* RIV values are for Conifers and Hardwoods, which includes species with a minimal presence such as balsam fir and white birch.

** Average heights for plots where species exist.

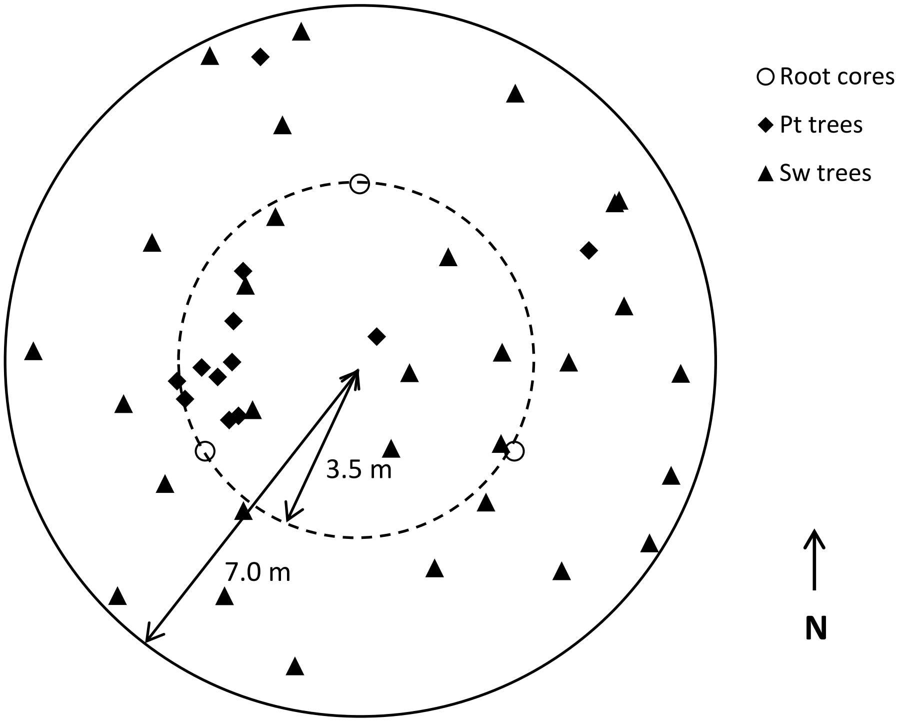

Figure 2-3. Typical plot layout, Plot 2D5 (mixedwood stand type), located in Block 2 near the junction of D and 5 gridlines.

2.6.3 Soil Characteristics

Soil samples for physical and chemical analyses were collected from the organic layer (F and/or Ah; Soil Classification Working Group 1998) and from the upper 40 cm of mineral soil (mainly Bm; Soil Classification Working Group 1998) from all 45 plots in Blocks 2, 3, and 4 during the summer of 2009. Soil types were assigned according to the northwestern Ontario forest ecosystem classification system (NWO-FEC) (Sims *et al.* 1997). Soil sample collection occurred only to a depth of approximately 40 cm; therefore soil types are approximate. All soils were assumed to be deep (> 100 cm, based on past exploratory soil pit excavations, Meyer 2011 personal communication) for purposes of keying by the NWO-FEC. Soil types range from S1 to S4 (three plots S1-2, twenty S3, two S4), with one plot being S6. Moisture regime ranged from dry to fresh. In the organic layer of Block 3, pH was significantly lower (p = 0.015) in pure Sw plots compared to mixedwood plots and pure Pt plots. Mineral soil pH levels were comparable between plot types and blocks. Within each block, textural class was similar between plot types. However, Block 4 had significantly higher levels of clay (p = 0.015) compared to Block 2. Available nitrogen (sum of nitrate and ammonium) did not vary with block or stand type within any soil layer. In organic layers, available phosphorus (available P, Bray P1 extractable) was similar between plot types within blocks, but was higher (p = 0.014) in Block 4 versus Block 3. Available P was similar in all ―A” mineral layers. In the “B” mineral layer, available P was similar between plot types within blocks, but was higher (p = 0.022) in Block 4 versus Block 2. In organic layers, available potassium (available K, ammonium acetate extractable) was similar between plot types within blocks. Available K was similar in all ―A” mineral layers. Available K in the ―B” mineral layer was similar between plot types within blocks, but was higher in Block 4 versus blocks 2 and 3. Soil texture and chemical attributes are summarized in Table 2-2.

Table 2-2. Soil texture and selected chemical attributes. Ranges in parentheses.

	Block 2			Block 3			Block 4		
	Pure Sw	Mixedwood	Pure Pt	Pure Sw	Mixedwood	Pure Pt	Pure Sw	Mixedwood	Pure Pt
Organic layer									
pH	5.3 (5-5.7)			4.9^{b} (4.7-5.1)	5.8^{a} (5.4-6.2)	6.3^{a} (6-6.5)	5.8 (5.5-6.4)		
N*	202 (82-680.4)			234.1 (143-417.6)			370.4 (185.7-729)		
P*	33.0^{xy} (16.1-75.7)			24.8^{y} (17.4-41.5)			42.0^{x} (19.6-65.6)		
K*	954 (504-1164)			797 (496-1085)			913 (524-1379)		
"A" mineral layer									
pH	4.8 (4-5.2)			5.0 (4.5-5.6)			4.9 (4.2-5.4)		
N*	24.7 (11-46.8)			30 (13.9-54.1)			31.2 (10.6-76.2)		
P*	9.7 (2.2-33.5)			10.8 (3.7-19)			26.0 (2.1-66.6)		
K*	184 (85.9-309.6)			177.8 (97.1-293.1)			250.3 (109.3-622.7)		
sand%	64 (49-80)			61.8 (47-74)			59.1 (43-72)		
silt%	32.2 (16-47)			32.7 (22.5-44)			32.4 (19-43)		
clay%	3.8^{y} (1-8)			5.6^{xy} (3-16)			8.4^{x} (3-14)		
"B" mineral layer									
pH	4.6 (4.3-4.9)			5.0 (4.5-5.9)			4.7 (4.3-5.5)		
N*	11.1 (6.8-16.5)			12.8 (7-17.9)			15.4 (5.1-31.9)		
P*	2.0^{y} (2.0-6.0)			4.0^{xy} (1.0-10)			14.0^{x} (2.0-52)		
K*	84^{y} (60-122)			84^{y} (47-127)			144^{x} (83-251)		
sand%	54.8 (43.5-77)			53.1 (34-75)			46.5 (29-77)		
silt%	38.1 (20-51)			35.2 (22-43)			37.1 (21-50.5)		
clay%	7.1 (3-15.5)			11.8 (3-23)			16.4 (2-41)		

* N, P, K values are plant available quantities in mg element/kg of soil.

Values are means with ranges in parentheses

Superscript letters signify differences within blocks (a,b,c) and between blocks (x,y) at the 0.05 level.

2.6.4 Root sample collection

Root samples were collected during June 2010. Plots were sampled in a random order. In each plot, three soil cores were collected at a distance of 3.5 m and azimuths of 0°, 120° and 240° from plot center. To ensure accurate delineation between organic and mineral layers, rectangular sections (~7.5 cm x 15 cm) of organic layers were extracted by hand using a knife (Figure 2-4). Mineral soil root samples were collected using a modified ice auger having a steel coring tube of inner diameter 67 mm. Root samples were divided by soil depth: organic, 0-5 cm, 5-15 cm and then 15-40 cm below the organic mineral interface. Coring continued until encumbered by rocks. Root samples were stored at -18°C. To aid root identification, at each sample point, a brief survey of the plant community was conducted noting relative abundance of each species within ~3 m.

Figure 2-4. Root sampling techniques.

2.6.5 Sample processing

Roots were separated from soil via the floatation method using a 1 mm sieve (Böem 1979). Roots were sorted using a stereomicroscope into three categories: conifer roots, Pt roots and ―other” roots. When possible, differentiation was made between species of conifer, mainly on the basis of aboveground species survey, but generally all conifer roots were assumed to be Sw, the predominant conifer species. Classification was based upon colour, morphology and through reference to aboveground species survey. Roots were then spread out and suspended in water in a shallow transparent tray and scanned to obtain estimates of root length using WinRHIZO software (Regent Instruments Inc., Quebec City, Quebec). Roots were then dried overnight at room temperature in small paper envelopes and were further dried for ~ 1 week in plastic re-sealable bags with silica gel. Oven drying was avoided to preserve DNA for other research. Fine roots ($d \leq 2$ mm) were separated and their mass recorded.

2.6.6 Analysis

Relative total exploitation of soil resources between plot types was estimated by analyzing total root length and mass. All root lengths were converted to root length per unit area of forest floor ($m\ m^{-2}$). Root masses were converted to root mass per unit area ($g\ m^{-2}$). Root length and mass per unit area was calculated for all species summed together to analyze relative exploitation between plot types. Root length and mass was also calculated separately per species class for descriptive purposes.

To investigate vertical distribution of roots, root measures were further subdivided into units of depth: organic layer and then mineral layers of depth 0-5 cm, 5-15 cm and 15-40 cm. In order to contrast vertical distribution patterns between Sw and Pt monospecific plots with mixedwood plots, it was necessary to account for differences in species abundance across plots. Otherwise, assessment of rooting behaviours arising on account of mixture type may be biased or highly confounded by between-plot differences in species abundance. Basal area (BA, m^2 of stem area per hectare) represents a reasonable measure of species abundance for this purpose. Across all plots, BA of Sw was positively and significantly correlated with total conifer root length and mass per unit area (Figure 2-5). A similar relationship existed between BA of Pt and Pt root length and mass per unit area. Other authors have also used BA as an adjustment factor for fine root attributes (Schmid & Kazda 2002; Bolte & Villanueva 2006). Total sapwood area might provide a better correlation since it transports the resource acquired by the fine roots (Shinozaki *et al.* 1964), however, such an analysis was beyond the scope of this study. Accordingly, root measures of mass and length per unit area for Sw and Pt were adjusted by dividing by the BA of that species present on the plot. The resulting measure, per depth unit, was root length (or mass) per unit area per unit of BA of that species present on the plot

((m or g) m^{-2} (m^2 ha^{-1})$^{-1}$). This calculation is summarized in Equation (2-1).

$$adjusted\ root\ attribute\ (length\ or\ mass) = \frac{quantity\ per\ area(species)}{plot\ basal\ area(species)} \qquad \textbf{(2-1)}$$

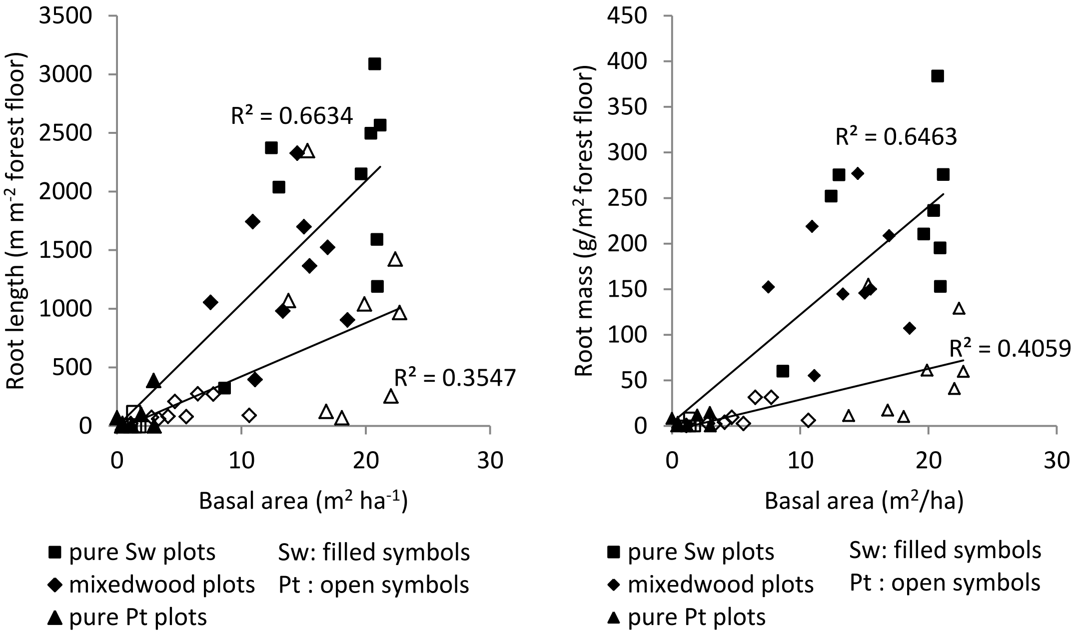

Figure 2-5. Basal area of Sw (n = 25) and Pt (n = 21) per plot is correlated with root length and mass of the respective species.

Adjusted root attributes were analyzed in two separate comparisons: to study Sw root behaviour, pure Sw plots were contrasted with mixedwood plots; to study Pt root behaviour, pure Pt plots were contrasted with mixedwood plots. One unified model was not used because generally minimal Sw roots existed in pure Pt plots and vice versa. Results were assessed through analysis of variance in a model having three factors: block (2,3,4), depth (organic, 0-5 cm, 5-15 cm, 15-40 cm) and plot type (mixedwood, monospecific plots).

Normality and homogeneity of variance were assessed numerically and visually. Residuals were normally distributed for Sw root length and mass ($p = 0.467$ and $p = 0.582$, Shapiro-Wilk test). Normality tests failed for Pt root length and mass ($p < 0.001$). Visual inspection revealed that the problem lies with a high level of kurtosis (for Pt length, 10.29; for Pt mass, 3.35)(Figure 2-6). This problem is being driven by observations from deep soil layers, where residuals are predictably quite small since the observed values are low or zero. Additionally, problems may exist due to a rather small sample size (n = 9 for mixedwood and pure Sw, n = 8 for pure Pt), and because the experiment was unbalanced with a missing pure Pt plot and several missing observations at deep soil depths due to coring being blocked by rocks. For similar reasons, variance of Sw and Pt root length and mass observations were not homogeneously distributed (Levene's test, Sw length $p = 0.008$ and mass $p = 0.013$; Pt length $p = 0.001$ and mass $p < 0.001$). Variances were greater at shallower depths where measured values are much larger, an expected issue with this type of study (see Figure 2-8). Square root transformations were attempted without success. However, F tests in ANOVA are robust to heterogeneity of variance; this homogeneity problem is not likely to strongly affect results (Glass *et al.* 1972).

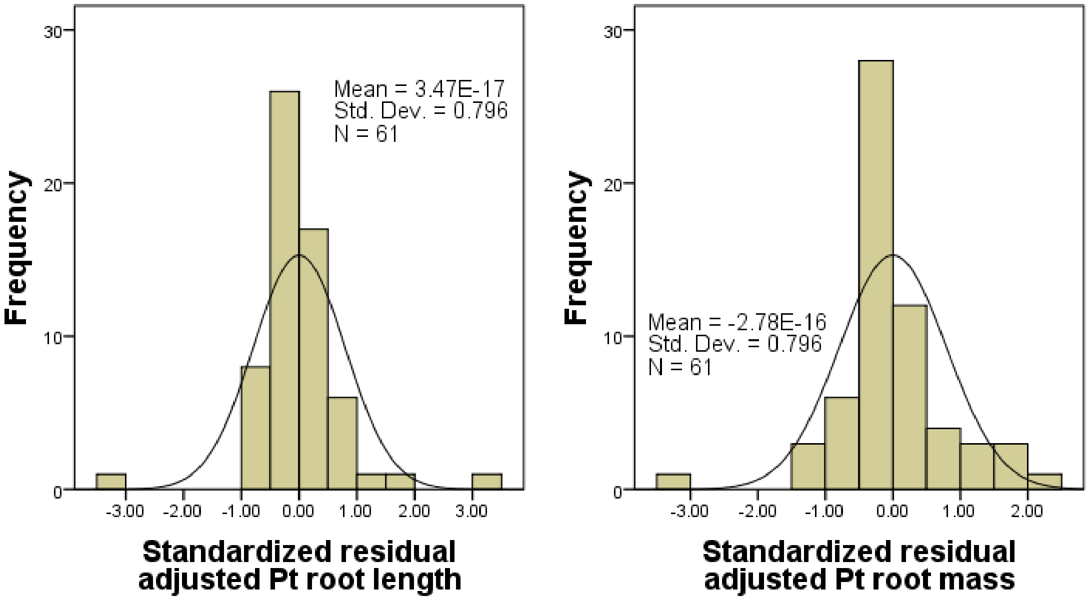

Figure 2-6. Histograms of standardized residuals for Pt adjusted root length and mass.

2.7 Results

2.7.1 Total root length and biomass

Total root length (all species summed together) did not vary significantly ($p > 0.05$) with plot type or block. Mean total root length was 3779, 3483 and 3334 m m^{-2} of forest floor in pure Pt, mixedwood and pure Sw stands, respectively (Figure 2-7). Root length of conifers (Sw with occasional Bf and Sb) was highest in pure Sw plots and lowest in pure Pt plots; root length of Pt followed a reverse trend. Root length in the —other” species category was highest in pure Pt plots and lowest in pure Sw plots. Total root mass (all species summed together) did not vary significantly ($p > 0.05$) with plot type or block. Mean total root mass was 265, 331 and 319 g m^{-2} of forest floor in pure Pt, mixedwood and pure Sw stands, respectively. Patterns of root mass by species class across plot types followed the same trends observed for root length. The mean number of species observed aboveground did not vary significantly with plot type or block ($p > 0.05$). The mean number of species in pure Sw stands was 9.3; in mixedwood stands, 10.5; and in pure Pt stands, 10.9.

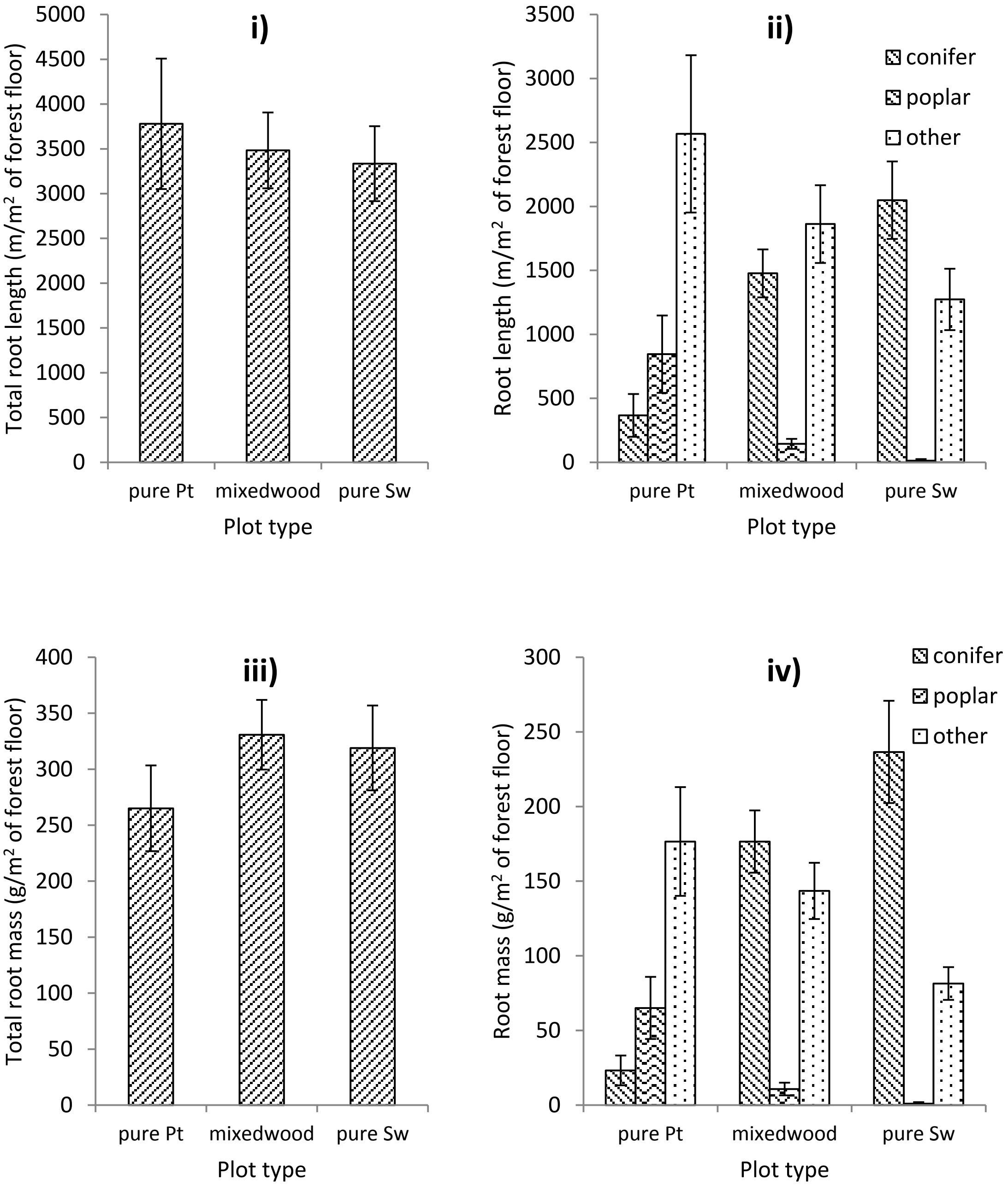

Figure 2-7. Root length and mass per unit area by plot type: all species summed together (i, iii) and subdivided by species (ii,iv). Error bars denote 1 SE.

2.7.2 Vertical distribution of root length and mass

Adjusted root length decreased significantly with depth for both Sw and Pt in all plot types. White spruce adjusted root length at depth 15-40 cm was significantly lower ($p < 0.001$) than that observed in organic and 0-5 cm soil depths. Trembling aspen adjusted root length at depths 15-40 and 5-15 cm was significantly lower ($p = 0.01$) than that observed in the organic layer. Adjusted root length of Sw and Pt at any particular depth was not affected by plot type.

Very similar trends were observed with root mass. Adjusted root mass decreased significantly with depth for both Sw and Pt in all plot types. White spruce adjusted root mass at depth 15-40 cm was significantly lower ($p < 0.001$) than root mass observed in organic and 0-5 cm soil depths. Trembling aspen adjusted root mass at depth 15-40 cm was significantly lower ($p = 0.022$) than root mass observed in the organic layer. Adjusted root mass of Sw and Pt at any particular depth was not affected by plot type. Adjusted root length and mass results are presented in Figure 2-8.

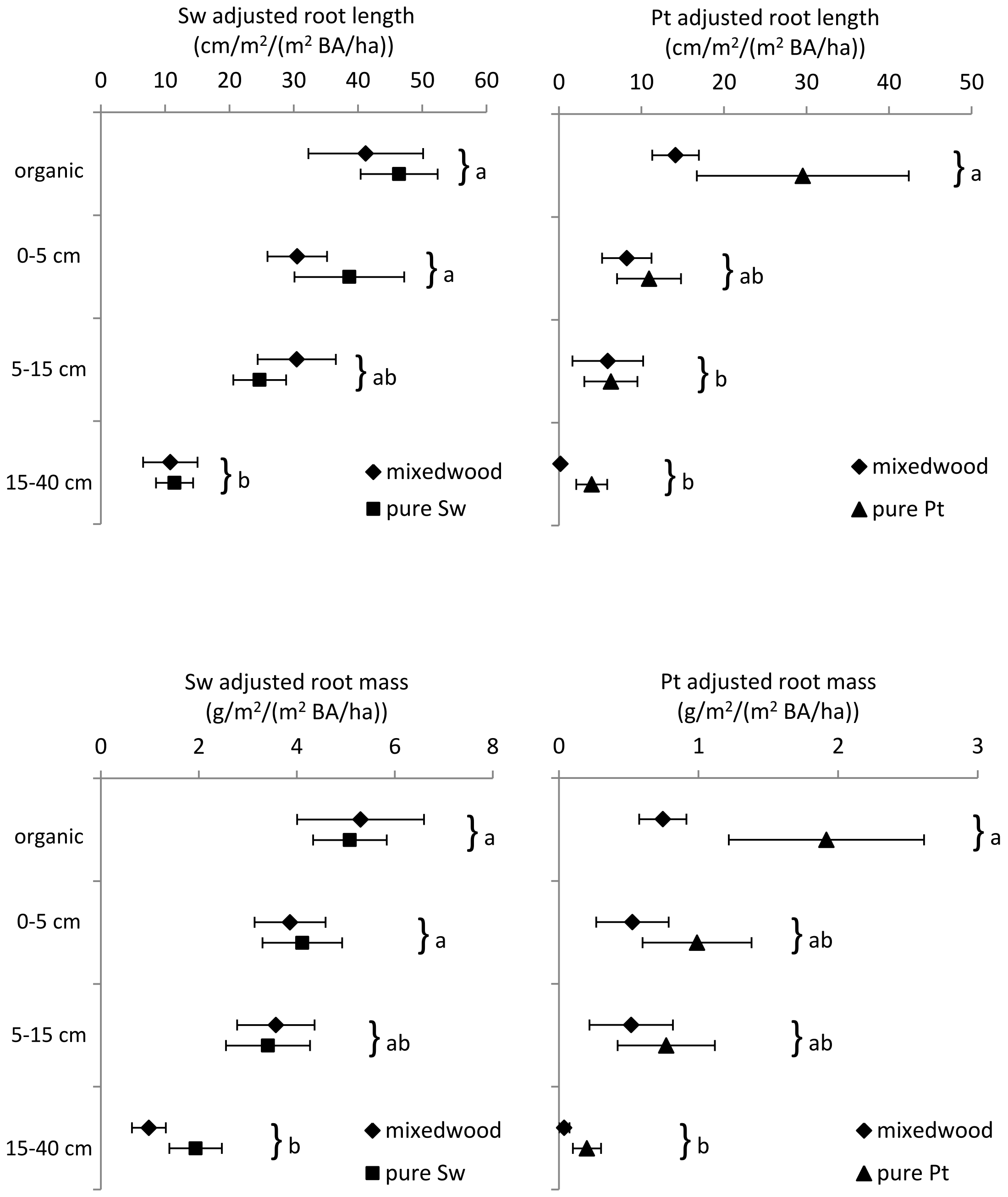

Figure 2-8. Adjusted root length and mass for Sw and Pt. For any particular depth, plot type was not significant. Letters indicate significant differences between depths, considering both plot types together. Error bars denote 1 SE.

Root length and mass of other species was contrasted across all three plot types. Root length of other species in the organic layer of pure Pt plots was significantly greater (p = 0.005) than in any other plot type at any depth. Root length of other species in mineral soil depth categories did not vary with plot type. Root mass of other species in the organic layer of pure Pt plots was significantly higher (p = 0.005) than that observed in the 15-40 cm depth of Pt plots and higher than in any depth category of mixedwood or pure Sw plots. Root mass of other species in mixedwood and pure Sw plots did not significantly differ by depth or plot type. Root length and mass of other species are presented in Figure 2-9.

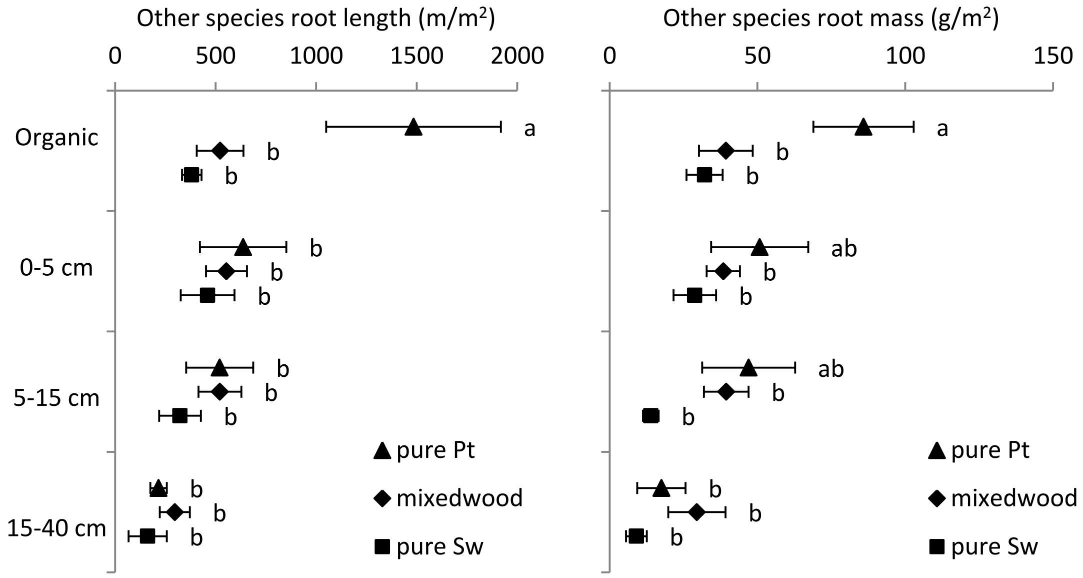

Figure 2-9. Root length and mass of "other" species. Letters indicate significant differences between levels of depth and plot type. Error bars denote 1 SE.

2.7.3 Facilitative effects – enrichment of upper soil layers

No significant differences were found between plot types in available N, P or K in organic soils or 0-5 cm mineral soils. In Block 3, pH was significantly higher in mixedwood and pure Pt plots compared to pure Sw plots (p = 0.015). See Table 2-2. No significant differences were found in the thickness of organic layers between plot types (p = 0.776). Mean organic soil thicknesses were 5.48 cm in pure Sw, 4.57 cm in mixedwood and 5.12 cm in pure Pt plots.

2.7.4 Specific root length

Specific root length of Sw and Pt was contrasted between mixedwood plots and pure plots of Sw and Pt, respectively. White spruce SRL did not differ significantly between mixedwood plots (mean 8.05 m/g) and pure Sw plots (mean 8.57 m/g). Trembling aspen SRL was significantly greater (p = 0.012) in mixedwood plots (mean 22.7 m/g) compared to pure Pt plots (mean 12.8 m/g).

2.8 Discussion

2.8.1 Total root length and mass

Total root length was greatest in Pt plots and lowest in pure Sw plots. Species diversity *i.e.*, the number of species observed aboveground, followed the same pattern. This result is consistent with the existence of complementary niches, since increased resource use, as measured through root length, was related to greater diversity (Kelty *et al.* 1992). Biomass belowground in the form of fine roots did not follow the same pattern; niche complementarity theory would predict increased biomass as well. However, inferences that many be drawn from these results regarding niche complementarity theory are limited, since differences in total root length and fine root biomass were not significant, and only fine root biomass was considered. Additionally, the number of species observed aboveground did not significantly vary.

2.8.2 Vertical distribution of roots

In virtually all cases, root prevalence decreased significantly with depth. This is in agreement with trends observed for Sw and Pt by other authors (Bannan 1940; Strong & Laroi 1983; Ruark & Bockheim 1987). The only exception was in the “other” species category; root length and mass did not vary significantly with depth in mixedwood and pure Sw plots. This may be an artefact of the calculation methodology; to facilitate efficient sampling, processing and sorting of roots, the sampling depth categories increased in size with depth on account of generally low root prevalence in deeper layers. This may also be a problem with insufficient sampling points per plot; the standard error is quite large relative to the observed values.

The stratification hypothesis was not supported. Neither Pt nor Sw had significantly different vertical rooting profiles between plots representing pure and mixedwood stands. However, there is a suggestion that a stratification process may be taking place, with Pt roots shifting away from upper soil layers. In organic layers, adjusted Pt root mass and length was dramatically lower in mixedwood plots, although these differences were not significant (root length, p = 0.41; mass, p = 0.15). Once again, the relative standard error was quite large; it is possible that significant differences might emerge with an increase in sampling points per plot, reducing variation observed between experimental units. It is also possible that these stands are simply too young for the development of significant root competition leading to stratified roots.

Comparing roots in the —other” species category, an interesting pattern was found between pure Pt and mixedwood plots. Within the organic layer, there is dramatically and significantly less —other” species root length and mass in mixedwood plots. However, within deeper layers, no significant difference for —other” species root length and mass was noted. This effect might be explained in two ways. In mixedwood stands, it could be that Sw outcompetes the —other” species, excluding them from the organic layer, or, perhaps the presence of Sw elicits certain changes in the organic layer *i.e.,* acidification, that renders it inhospitable to these “other” species. Either way, it seems that introducing Sw into the species mixture might have a greater negative impact on the resource capture capabilities of —other” species that are only shallowly rooted versus those that may root deeper. Put another way, in mixedwood compared to pure Pt plots, soil exploitation by Sw appears to occur at least in part at the expense of these —other” species that would otherwise be present in pure Pt plots. The addition of Sw seems to reduce the realized niche of these other species.

2.8.3 Facilitative effects – enrichment of upper soil layers

Less acidic organic soil pH in mixedwood plots of Block 3 versus pure Sw plots suggests the presence of a facilitative effect of Pt litter. This suggestion rests on the assumption that Pt litter is the cause of the lower organic layer pH. The influence of litter from *Populus* spp., and more generally, broadleaf species producing favourable pH conditions is supported by observations in the literature

(Sanborn 2001; Menyailo *et al.* 2002; Legare *et al.* 2005b; Sabau *et al.* 2010). This less acidic environment in organic soil layers may indicate increased nutrient availability and faster nutrient cycling (Kimmins 1987; Brady 1990). This observation provides further evidence of the potential for stratification of roots. If soil enrichment continues in shallow soils of mixedwood plots, Sw roots will have less and less incentive to compete in deeper soils since the availability of nutrients in upper soil layers will be improved.

This enrichment effect was only noted in Block 3. This might be due to differences in the relative proportion of conifers vs. hardwoods. Relative importance values of conifers versus hardwoods are matched more evenly for mixedwood plots of Block 3. Mean RIV values of conifers vs. hardwoods in mixedwood plots were 99 vs. 100 in Block 3. In contrast, for Blocks 2 and 4, RIV ratios were 133 vs. 66 and 127 vs. 72. At the very least, it can be said that at this stage in stand development at the FEP site, soil enrichment appears to be associated with mixedwood plots having RIV ratios of conifers vs. hardwoods of closer to 50:50, as opposed to ratios having more conifers.

It is likely that these stands are too young for dramatic effects of facilitation to become apparent in soil characteristics. Due to faster nutrient cycling encouraged by Pt litter, it would be reasonable to expect thinner organic layers in mixedwood and pure Pt plots. However, this was not observed at the FEP site.

2.8.4 Specific root length

The possibility of stratification beginning to take place is supported by observations of SRL. Trembling aspen SRL was 1.78 times greater (p = 0.012) in mixedwood plots, suggesting that Pt in mixedwood plots is adopting a more exploratory belowground strategy. A similar pattern of increased SRL was observed by Bolte & Villanueva (2006) in the deeper rooting European beech (*Fagus sylvatica* L.) when mixed with Norway spruce (*Picea abies* (L.) Karst.). Their study also revealed no change in SRL of Norway spruce between mixed and pure stands. Similarly, in our study, specific root length for Sw did not significantly vary with plot type.

Values for SRL were comparable to those reported in the literature. Mean SRL of Sw in this study was 8.31 m/g. Bauhaus & Messier (1999) found SRL for conifers (Sw and balsam fir) to be 10-13 m/g. Bolte & Villanueva (2006) observed SRL for Norway spruce to be 7.7-9.6 m/g. In a review by Ostonen *et al*. (2007), SRL of Norway spruce ranged from 4.5-26 m/g. Pregitzer *et al.* (2002) measured SRL for Sw around 20-40 m/g; however, their figures did not include any roots with diameters greater than ~0.5 mm.

Mean SRL of Pt in this study ranged from 12.8 - 22.7 m/g. Bauhaus & Messier (1999) found somewhat higher values for SRL in Pt, from 27.5 to 35.7 m/g. Records of Pt SRL are scarce in the literature, but several figures exist for other *Populus* spp. Heilman *et al.* (1994), reported SRL of ~30-50 m/g for *Populus deltoides* (Bartr. ex Marsh.), *Populus trichocarpa* (Torr. & Gray) and crosses of these species. Pregitzer *et al.* (2002) measured SRL in *Populus* *balsamifera* (L.) between ~50-100 m/g. Specific root lengths reported by these last two authors are a good deal higher than observed in this study; however, both of these authors only considered fine roots of diameter ~0.5mm or less. Consequently, it is expected that SRL values for Pt in this study, which includes thicker roots in the 0.5-2.0 mm category, will be lower. Additionally, it is possible that the washing and sieving process used in this study resulted in the loss of very fine Pt roots, thus depressing SRL values. In contrast, Pregitzer *et al.* (2002) used a more meticulous root extraction method, removing roots from soil in the field.

2.9 Conclusions

To the extent revealed by studying fine root length and mass at one point in time, evidence to support the concept of competitive reduction belowground in mixedwood plots ranged from weak to non-existent. In mixedwood plots, total root length and biomass were not greater, nor was there evidence of stratification of Sw and Pt roots. However, the results suggest that the rooting behaviour of Pt has changed in the mixedwood plots. Trembling aspen had greater SRL in mixedwood plots, suggesting a more exploratory, foraging strategy. Specific root length of Sw did not seem to be affected by plot type. Specific root length was not investigated separately by depth class due to insufficient samples; future work in this area might reveal more sophisticated patterns.

There was some evidence to suggest resource acquisition facilitation in upper soil layers of mixedwood plots; less acidification of organic soil was associated with the presence of Pt trees in mixedwood and pure Pt plots in one block. This less acidic organic soil may result in improved growing conditions for Sw and other species. The specific consequences of less acidic organic soil in these systems in terms of nutrient cycling and understory plant communities the soil may support was not investigated in this study. Large decreases of “other” species roots in organic soils of mixedwood and pure Sw plots *vs.* pure Pt plots could potentially be caused by pH differences, but such insight was beyond the scope of this study.

Relative standard errors in this study were quite large, a common problem in root studies. Greater insight may be gained in future work by focussing on a more specific definition of fine roots based upon linkages to actual physiological roles of size classes instead of arbitrary size limits, *i.e.*, < 2 mm. Subtle trends in root distribution would likely be better elucidated through increased sampling intensity per plot, perhaps resulting in reduced noise.

Several factors could not be considered due to the size of this study, but are likely to be very important. Physiological and temporal differences in resource requirements for these species could not be considered; study of these factors may reveal significant offsets in the timing and specificity of resource needs. Stand density and basal area per hectare were held relatively constant; increased competition from that present in this study might produce stronger support for the mechanisms of competitive reduction and facilitation. This study was conducted at a specific age in stand development *i.e.*, ~ 20 years old. This same study repeated at a later date, or in a different, older location might present divergent results.

2.10 Acknowledgements

Dave Morris, motorized soil auger
Numerous field and laboratory assistants

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3 Horizontal distribution paper

3.1 Title

Distribution of white spruce (*Picea glauca* (Moench) Voss) lateral fine roots as affected by the presence of trembling aspen (*Populus tremuloides* Michx.): root mapping using simple sequence repeat DNA profiling.

3.2 Authors

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3.3 Abstract

Mixedwood forests of white spruce (Sw, *Picea glauca* (Moench) Voss) and trembling aspen (Pt, *Populus tremuloides* Michx.) may possess ecological advantages over monospecific Sw stands. Belowground competition may be reduced via vertical stratification of roots; facilitation of resource acquisition in shallow soils may also occur through nutrient rich Pt litterfall. These effects may provide incentive for Sw to preferentially exploit upper soil layers in mixedwood stands, resulting in wider Sw root systems. The focus of this research was to characterize and contrast Sw fine root distributions in organic soils of Sw and mixedwood stands.

Research was conducted at the Fallingsnow Ecosystem Project site in northwestern Ontario, Canada. Eighteen plots were selected representing mixedwood (9) and pure Sw (9) stands. Tree positions were mapped and foliage samples collected. Three root/soil samples were collected per plot from the organic layer. Root fragments were separated by species and scanned to determine root length. Simple sequence repeat DNA profiles were determined for all Sw trees from foliage samples and for a subsample of 45 Sw root fragments per plot. Root fragment DNA profiles were matched to originating trees; corresponding distances were calculated. Root distributions were created, describing root prevalence with distance from Sw stems.

Most (80%) root fragments were within 3.2 m of originating tree stems. Root fragment prevalence decreased rapidly with distance from tree stems, following an inverse curve pattern. Organic soil pH was significantly less acidic in mixedwood plots, but only in one block. A subtle significant trend towards wider root fragment distributions was noted in mixedwood stands.

3.4 Keywords

belowground competition, facilitation, horizontal distribution, lateral spread, microsatellites, mixedwood, niche, organic soil, SSR, stratification

3.5 Introduction

Mixedwood forests of white spruce (Sw; *Picea glauca* (Moench) Voss) and trembling aspen (Pt; *Populus tremuloides* Michx.) may possess ecological advantages over monospecific Sw stands in the utilization of belowground resources. Mixedwood forests are common throughout the Boreal Forest Region of Ontario (Rowe & Halliday 1972). Traditional silvicultural practices have attempted to create monocultures of historically more desirable conifer species throughout this forest region. However, mixedwood forests may be more productive overall, in part, due to advantageous belowground dynamics (Kelty *et al.* 1992; Man & Lieffers 1999; Kelty 2006).

Belowground interactions are important to understanding mixedwood forest dynamics, but information on this topic is limited (Jose *et al.* 2006) . Mixedwood Sw and Pt forests may exhibit a higher degree of soil resource exploitation compared to pure Sw forests. Competitive reduction may occur in mixtures of Sw and Pt through ―avoidance” strategies (Novoplansky 2009), leading to vertical stratification of roots, with Sw assumed to be more shallowly rooted. Aspen may facilitate resource capture for Sw roots in mixedwood forests. Litter from hardwood trees, such as Pt, is more readily decomposable (Gordon 1983) and less acidic than Sw litter; this may improve the growing environment for Sw, particularly in upper soil layers.

Elucidating a tree's ―zone of influence” (*i.e.*, the area under its influence) is important to understanding competitive interactions (Casper *et al.* 2003). In mixedwood forests, the mechanisms of competitive reduction and facilitation may lead to a wider distribution of Sw roots in shallow soils, creating a larger shallow soil ―zone of influence” per spruce tree. If vertical stratification does indeed occur, spruce roots growing in the upper soil layer in the vicinity of a Pt neighbour may experience decreased competition and thus grow further laterally. Also, if soil enrichment does occur in mixedwood forests, particularly in upper soil layers, this may impart an incentive for spruce to preferentially exploit more ―profitable” upper soil layers (Hodge 2009). Larger ―zones of influence” per spruce tree may confer additional advantages to Sw such as improved resistance to windthrow (Stokes *et al.* 1996) and increased capacity to intercept precipitation.

Previous research upon the lateral distribution of Sw roots has mainly been descriptive or anecdotal. Excavations of individual Sw root systems by Bannan (1940) noted the maximum extent of roots. Strong and La Roi (1983) observed maximum root extents and also noted that fine roots were —concentrated in a band outside the tree crown”. These studies involved full or partial excavations of a limited number of individual root systems. The restricted sample size in these studies limits the inferences that may be drawn about typical rooting behaviours. Uncertainty remains regarding Sw fine root lateral distribution that is *generally* present within a wider population.

It was hypothesized that white spruce fine roots in mixedwood stands will extend further than those in pure Sw stands. The objectives of this research were to determine i) the maximum extent of Sw lateral roots in mixedwood and pure Sw stands, ii) how white spruce root prevalence in upper soil layers varies with distance from tree stems, and iii) the influence of stand type upon this distribution *i.e.*, pure Sw or mixedwood. These goals were aided by simple sequence repeat (SSR) DNA profiling technology, enabling intraspecific differentiation of roots and leaves.

3.6 Materials and Methods

3.6.1 Study Location

Research was conducted at the Fallingsnow Ecosystem Project (FEP) site in northwestern Ontario (48°10'N, 89°49'W), 60 km southwest of Thunder Bay, Ontario (Lautenschlager *et al.* 1997). The site location is depicted in Figure 3-1. This research site consists of four blocks ranging from 28 to 52 ha, established in 1993 to study ecological effects of conifer release alternatives. The site is located in the transition zone between the Boreal and Great lakes-St. Lawrence forest zones (Rowe & Halliday 1972), at an elevation of approximately 400 m (Blocks 3 and 4) and 500 m (Block 2). Mean annual precipitation is 845 mm; mean annual temperature is 2.1 °C. Slope exposure is SE in Blocks 3 and 4, and NE in Block 2. The blocks were harvested in 1986-1989 and planted with white spruce (Sw); trembling aspen (Pt) regenerated naturally. Suppression of Pt occurred with varying degrees of success. Currently the site contains even aged monospecific stands of Sw and Pt, as well as mixedwood stands of these species in various proportions. Amongst plots used in this study, density ranges from 1840 to 2901 stems ha^{-1} for Sw and 0 to 4049 stems ha^{-1} for Pt; basal area ranges from 14 to 23 m^2 ha^{-1} for Sw and 0 to 9.2 m^2 ha^{-1} for Pt. The presence of these even aged stands of varying species proportion makes this site ideal for the research presented in this paper. Blocks 2, 3 and 4 were used in this study.

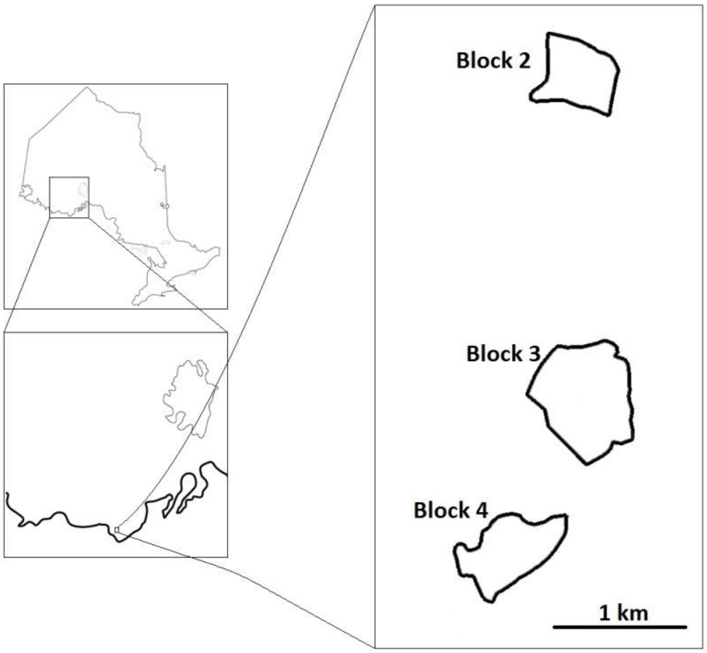

Figure 3-1. Fallingsnow Ecosystem Project site[2].

It is worth emphasizing that these stands are not of natural origin, and accordingly the dynamics between these two species will differ from natural mixedwood stands. In particular, forest succession did not occur in a normal manner with Sw coming up beneath a relatively established Pt canopy. Rather, Sw was often given a ―head start” through the use of Pt suppression techniques, generally leading to a much smaller size difference between the two species than might otherwise be observed in nature.

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[2] *Modified from:* Map of Ontario. St. Catharines, Ontario: Brock University Map Library. Available: Brock University Map Library Controlled Access http://www.brocku.ca/maplibrary/maps/outline/Ontario/ontario2.pdf (Accessed February 21, 2011).

3.6.2 Plot Selection

This study is integrated within a larger research project currently in progress. Within this larger project, 45 seven metre radius plots representing a spectrum of stand types ranging from pure Sw to pure Pt stands were randomly established in 2008. During the summer of 2009, species, diameter at breast height (dbh) and location within the plot were recorded for all trees having a dbh ≥ 6 cm; the same data were collected for smaller trees (2 cm ≤ dbh < 6 cm) within a radius of 3.5 m from plot centre. Tree heights and crown dimensions were measured for several representative trees per plot. Heights for remaining trees were calculated using a height-diameter equation (Sharma & Parton 2007). Crown dimensions for remaining trees were calculated through regression, taking into account dbh, density and species mixture composition (unpublished data). Plots were assigned names based on an alphanumeric grid system.

For this study, a subsample of 6 plots was selected in each block, three representing pure Sw stands and three representing mixedwood stands[3]. Plot categorization was based on the relative importance value (RIV; Curtis & McIntosh 1951) of conifer and hardwood trees having a dbh ≥ 2 cm. Relative importance value was calculated as the sum of density and basal area per hectare (BAH) of the subject tree type, each expressed as a percentage of the total. The maximum RIV is 200. Pure Sw plots were defined as having a RIV of

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[3] Plots representing pure Pt stands were also selected for future work.

> 170 for conifers. Mixedwood plots were defined as having a RIV between 30 and 170 for conifers.

All pure Sw plots identified were selected (3 per block). Several mixedwood plots were available per block. Mixedwood plots were selected based on criteria designed to minimize differences between plots in terms of total basal area and density of all trees. Large differences in site occupation were undesirable since this could potentially confound observation of stand composition effects. Mixedwood plots were selected that had a density and BAH in between the averages observed for the pure Sw and pure Pt plots, to the greatest extent possible. Although no pure Pt plots were used in the current study, it was important to ensure similarity of the mixedwood plots to both types of monospecific plots for appropriate comparisons in other root dynamics research that will be reported at a later date. Plot attributes are summarized in Table 3-1. Layout of a typical plot is depicted in Figure 3-2.

Table 3-1. Selected mean plot attributes. Standard deviations are presented in parentheses.

Plot Attributes:	Block	Pure white spruce plots		Mixedwood plots	
		White spruce	Trembling aspen	White spruce	Trembling aspen
Density (stems ha^{-1})	2	2901 (357)	-	2533 (1012)	1472 (487)
	3	2251 (369)	194 (194)	1992 (1243)	4049 (1476)
	4	1840 (228)	194 (234)	2641 (521)	2793 (2793)
Basal Area (m^2 ha^{-1})	2	20 (5)	-	17 (4)	3.6 (2.8)
	3	23 (1)	0.9 (0.9)	14 (6)	9.2 (5.1)
	4	15 (8)	0.7 (0.7)	14 (1)	7.9 (3.6)
Relative Importance Value (RIV)	2	184 (13) *	15 (13) *	133 (34) *	66 (34) *
	3	188 (10) *	11 (10) *	99 (34) *	100 (34) *
	4	189 (11) *	10 (11) *	127 (35) *	72 (35) *
Average Tree Height (m)	2	6 (0.5)	-	6.3 (0.3)	5.9 (1.3)
	3	7.7 (0.4)	7.7 (3.9) **	7.2 (0.9)	6.4 (1.3)
	4	6.2 (1.2)	5.5 (0.3) **	6.9 (0.1)	8.8 (1.3)
Mean crown radius (m)	2	1.21 (0.02)	-	1.15 (0.02)	
	3	1.4 (0.1)	-	1.28 (0.06)	
	4	1.22 (0.16)	-	1.19 (0.03)	

* RIV values are for Conifers and Hardwoods, which includes species with a minimal presence such as balsam fir and white birch.

** Average heights for plots where species exist.

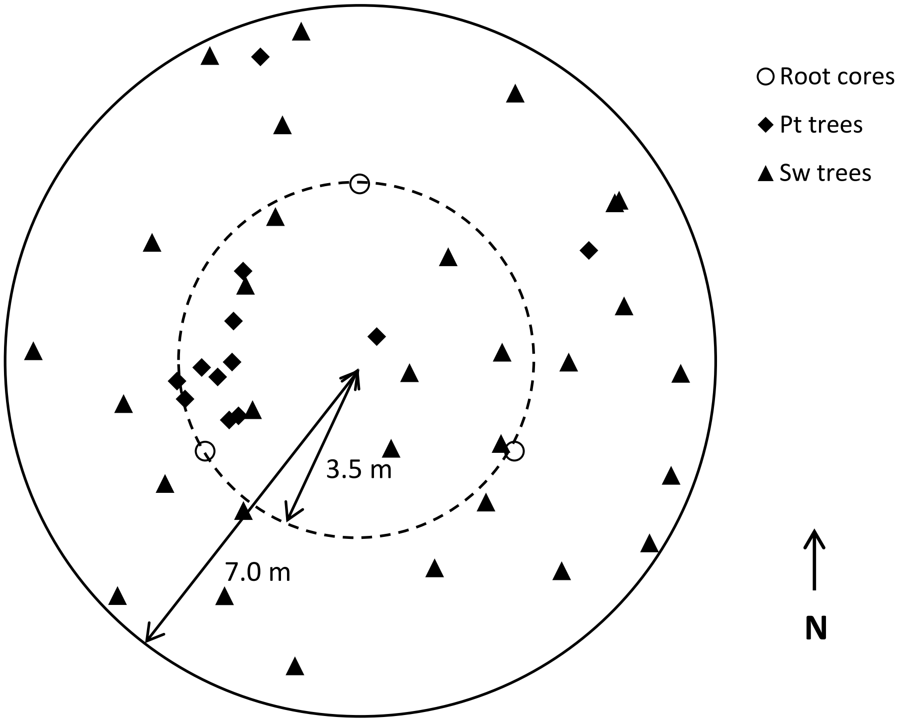

Figure 3-2. Typical plot layout, Plot 2D5 (mixedwood plot type).

3.6.3 Soil Characteristics

Soil samples for physical and chemical analyses were collected from the organic layer (F/H; Soil Classification Working Group 1998) and from the upper 40 cm of mineral soil (mainly Bm; Soil Classification Working Group 1998) from all 45 plots in Blocks 2, 3 and 4 during the summer of 2009. Soil types were assigned according to the northwestern Ontario forest ecosystem classification system (NWO-FEC) (Sims *et al.* 1997). Soil sample collection occurred only to a depth of approximately 40 cm; therefore NWO-FEC soil types are approximate. All soils were assumed to be deep (> 100 cm, based on past exploratory soil pit excavations, Meyer 2011 personal communication) for purposes of keying by the NWO-FEC. Soil types were mainly S3 (16 plots), with one plot being S4 and another S6. Moisture regime ranged from dry to fresh. In the organic layer of Block 3, pH was significantly lower ($p = 0.013$) in pure Sw plots (mean 4.9, range 4.7-5.1) compared to mixedwood plots (mean 5.8, range 5.4 to 6.2). Mineral soil pH levels were comparable between plot types. Within each block, textural class was similar between plot types. Sand content ranged from 29 to 62%; silt content ranged from 30 to 51%. Block 4 had significantly higher levels of clay ($p = 0.046$, mean = 16.4%) compared to Block 2 (7.1%); clay content in Block 3 (11.8%) was not significantly different from either block. Available nutrient levels (N, P, K) were similar between stand types, in both the organic layer and in the B layer.

3.6.4 Foliage and root sample collection

Foliage samples (~2 g) were collected of either buds or juvenile leaves for all Sw trees having a dbh ≥ 6.0 cm during the spring of 2010. Young tissue was collected to ensure the best possible quality of DNA extractions. Foliage was dried immediately using silica gel desiccant (28-200 mesh, 1:10 tissue: silica) at room temperature(Chase & Hills 1991).

Root samples were collected during June 2010. In each plot, three soil cores were collected at a distance of 3.5 m and azimuths of 0°, 120° and 240° from plot centre. To ensure accurate delineation between organic and mineral layers, rectangular sections (~7.5 cm x 15 cm) of organic layers were extracted by hand using a knife. Mineral soil root samples were collected using a modified ice auger having a steel coring tube of inner diameter 67 mm. Root samples were divided by soil depth: organic, 0-5 cm, 5-15 cm and then 15-40 cm. Coring continued until encumbered by rocks. Root samples were stored at -18°C. To aid root identification, at each sample point, a brief survey of the plant community was conducted noting relative abundance of each species within ~3 m.

3.6.5 Sample processing

Roots were separated from soil via the floatation method using a 1 mm sieve (Böem 1979). Roots were sorted using a stereomicroscope into three categories: Sw roots, Pt roots and —other” roots. Classification was based upon colour, morphology and the aboveground species survey. Roots were then spread out and suspended in water in a shallow transparent tray and scanned to obtain estimates of root length using WinRHIZO software (Regent Instruments Inc., Quebec City, Quebec). Roots were then dried overnight at room temperature in small paper envelopes and were further dried for ~ 1 week in plastic re-sealable bags with silica gel. Fine roots (d ≤ 2 mm) were separated from larger roots and then fine roots of Sw from the organic layer were selected for DNA analysis. For each sample point, Sw root fragments from the organic layer were spread out evenly on letter size paper (8.5 x 11 inches) and then 15 fragments (length ≥ ~2-3 cm) were randomly sampled, for a total of 45 Sw root fragment samples per plot.

3.6.6 Simple Sequence Repeat DNA analysis

DNA extraction and simple sequence repeat (SSR) amplification were performed at the University of Guelph (Newmaster Cryptic Diversity Lab) after some initial training and selection of markers at the Lakehead University Paleo-

DNA laboratory. Foliage and root DNA were extracted using plant DNeasy® 96 kits (QIAGEN group, Mississauga, Ontario). Simple sequence repeat markers UAPgCA91 developed by Hodgetts *et al.* (2001), and PGL14 developed by Rajora *et al.* (2001) were selected for analysis since they were highly informative in previous studies by these authors. Another SSR marker was initially selected (PGL13, Rajora *et al.* 2001) but was later rejected due to a low success rate in DNA amplification. Polymerase chain reaction (PCR) DNA amplification was performed separately for each SSR marker, based upon methods modified from Rajora *et al* (2001). Amplification took place in a total volume of 10 µl containing ~20 ng DNA, 0.2 mM dNTPs, 1.5 mM $MgCl_2$, 5 pmol of both forward and reverse primers, 2 µg of BSA, 1 x reaction buffer and 0.2 U of Platinum® *Taq* DNA Polymerase (Invitrogen Inc, Carlsbad, California). Forward primers were fluorescently labelled with dyes 6-FAM (UAPgCA91) and VIC (PGL14). Temperature cycling consisted of an initial denaturing stage at 95°C for 2 min; followed by 43 cycles of 95°C for 30 sec, an annealing stage at 50°C for PGL14 or 62°C for UAPgCA91 for 1 min, extension at 72°C for 2 min; followed by a final extension phase at 72°C for 5 min. Pooled reactions from each primer set were run on a 3730 DNA analyzer (Applied Biosystems, Foster city, California).

Analysis of SSR data was performed using Peak Scanner® software (Applied Biosystems). Allele sizes were assigned for each marker for both foliage and root samples. Root fragments were matched to originating trees by comparison of allele sizes for the two SSR markers. Occasionally (30 times) matches were made with only one SSR marker due to a DNA amplification failure for root samples, but only when such matches were unequivocal. Reference to the original electropherograms was made in cases of ambiguous results. An example of matching tree and root fragment electropherograms is presented in Figure 3-3.

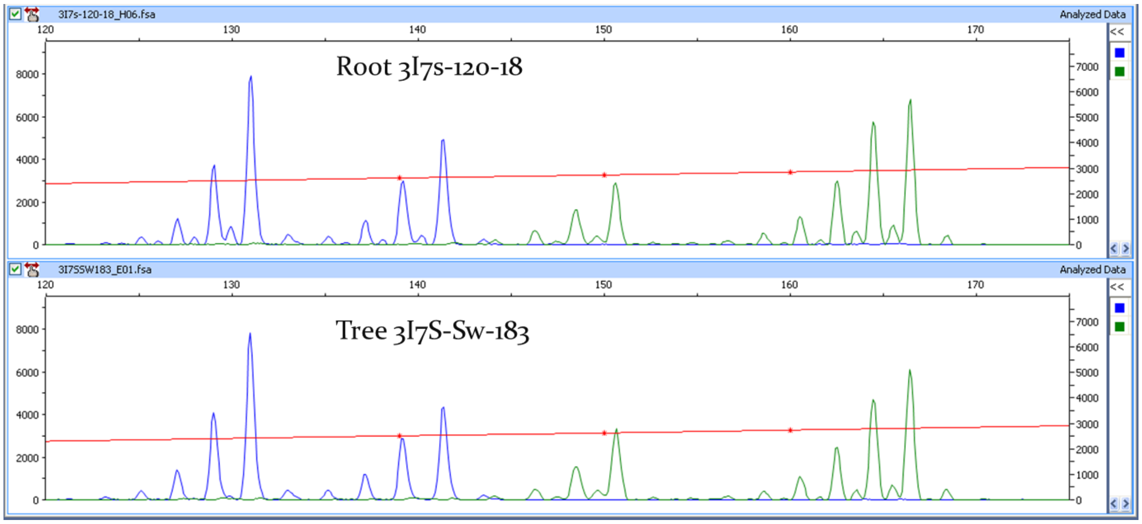

Figure 3-3. Matching electropherograms of a Sw root fragment and a Sw tree.

3.6.7 Data Analysis

Prior to statistical modelling, the data were categorized by distance class and adjusted to reduce noise. Tree-root matches were considered separately for each plot. Distances associated with each tree-root match were calculated and each match was assigned a distance class category: 0.5 - ≤ 2.0 m, 2.0 - ≤ 3.5 m *etc.*, resulting in a root match count per distance class. Root counts per distance class were adjusted by dividing by the sum of Sw basal area present at that distance class from sampling cores (Equation 3-1). The purpose of this adjustment was to partially account for random variation in stem distribution between plots, thereby reducing noise in the statistical model. Basal area has also been used by other authors to adjust fine root attributes (Schmid & Kazda 2002; Bolte & Villanueva 2006). This procedure limited the noise introduced by extremes in root counts arising from chance agglomerations of trees in particular distance classes. Total sapwood area might provide a better correlation since it transports the resource acquired by the fine roots (Shinozaki *et al.* 1964), however, such an analysis was beyond the scope of this study. Across all plots, average Sw fine root length was correlated with plot Sw basal area ($R^2 = 0.63$, $p < 0.001$) (Figure 3-4); this observation formed the rationale for using basal area to adjust root counts. Finally, proportional adjusted root counts per distance class were calculated (Equation 3-2). Proportions were used rather than absolute counts to eliminate the confounding effects of 1) differences in the number of root DNA analysis failures between plots, 2) differences in the total number of fragments analyzed. (For several plots, a larger number of root fragments were sampled). From this point onwards, ―roots” will refer to proportional adjusted root count.

$$\text{Adjusted Root Count}(\mathit{distance\ class}) = \frac{\text{Root Count}(\mathit{distance\ class})}{\text{Sw basal area}(\mathit{distance\ class})}$$

Equation 3-1

$$\text{Proportional Adjusted Root Count}(\mathit{distance\ class}) = \frac{\text{Adjusted Root Count}(\mathit{distance\ class})}{\sum \text{Adjusted Root Count}}$$

Equation 3-2

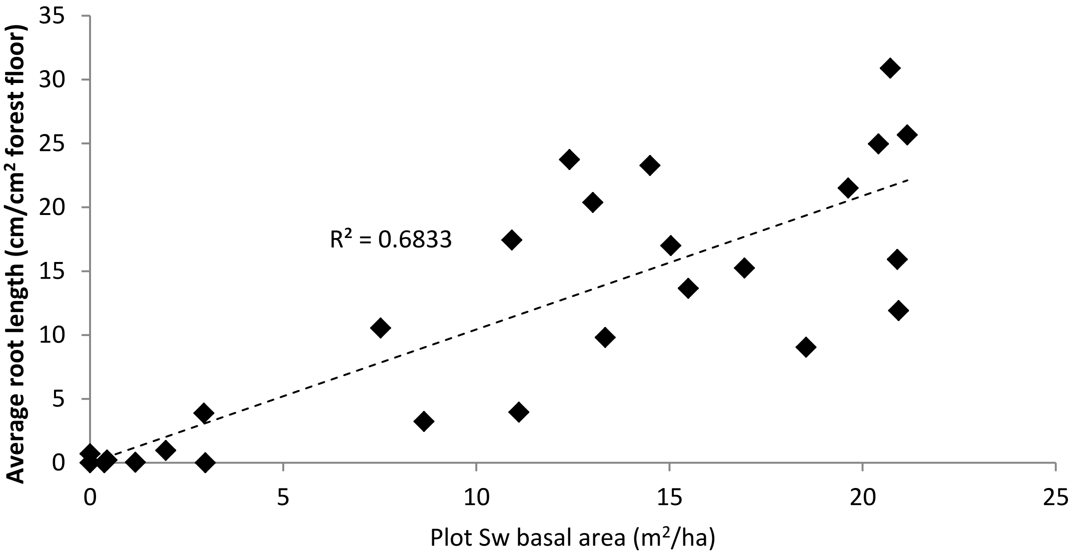

Figure 3-4. Average Sw fine root length vs. basal area per hectare for 26 plots (n = 26, pure Sw, pure Pt and mixedwood plots).

Soil type may affect lateral root distribution. As summarized by Sutton (1969), root distribution of spruces may be impacted by the soil moisture regime, with drier soils resulting in deeper roots. Soil texture may also impact root distribution. Finer textured soils may impede the growth of roots. Coarse textured soils are associated with decreased moisture availability (Sims *et al.* 1997), and a deeper rooting tendency (Jackson *et al.* 2000). Soil types according to the NWO-FEC system were not regarded as a suitable way of comparing site soil quality since most plots were similar, with all plots but two having soil types S1-S3. Additionally, these rudimentary soil type classifications may not be the best predictors of differential rooting habits since, as described by Carmean (1996), they are poorly related to site quality.

To address potential variability introduced into this experiment from differing soil qualities, clay content was examined since this soil characteristic varied significantly amongst the plots. Plots were placed into two equal sized soil texture categories on basis of clay content in the B mineral layer: low clay content (3.5-10%; 4 mixedwood, 5 pure Sw) and high clay content (11-41%; 5 mixedwood, 4 pure Sw). These categories were used to investigate effects that clay may have upon lateral distribution of Sw roots in this experiment. To search for such effects, a simple model was used having the factors distance class (five levels) and soil texture class (low clay, high clay). In this model, the interaction of distance class with clay content class was not significant ($p = 0.969$), therefore clay content of plots was not considered in further statistical analyses. (By design, all main effect factors except distance class have no significance in this experimental design ($p = 1.00$), since the predicted variable of proportional adjusted root count represents a proportion summing to 1 across levels of distance class. For factors other than distance class, only interaction effects with distance may have significance).

Proportional adjusted root count data were analyzed in an ANOVA statistical model having three factors: Block ($i = 2,3,4$), plot type (j = mixedwood, pure Sw) and distance class ($k = 1,2,3,4,5$), all fixed effect factors in a fully factorial design. An experimental unit was defined as a distance class of a plot. Normality and homogeneity of variance were assessed numerically and visually. Normality tests failed ($p < 0.001$). Visual inspection revealed that the problem lies with a high level of kurtosis (kurtosis = 2.096, Figure 3-5). This problem is being driven by observations from distal distance classes, where residuals are predictably quite small since the observed values are low or zero. Additionally, problems may exist due to a rather small sample size (n = 9). For similar reasons, variances were not homogeneously distributed (Levene's test, $p < 0.001$). Variances were greater at proximal distance classes where measured values are much larger, an expected issue with this type of study (see Figure 3-6). Square root transformations were attempted without success. However, F tests in ANOVA are robust to heterogeneity of variance; this homogeneity problem is not likely to strongly affect results (Glass *et al.* 1972).

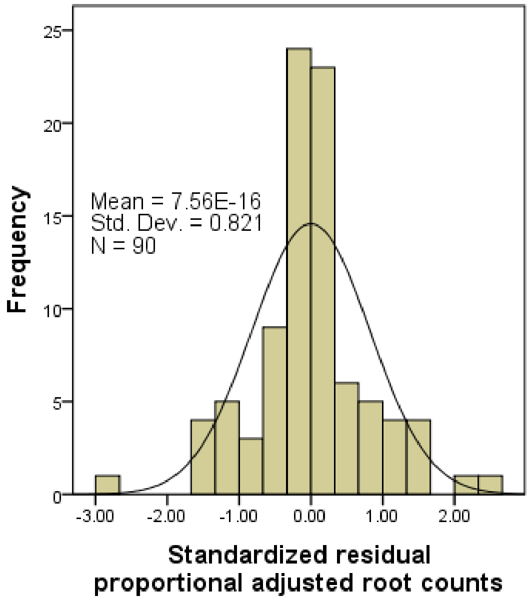

Figure 3-5. Histogram of standardized residual for proportional adjusted root counts.

3.7 Results

3.7.1 SSR analysis

Simple sequence repeat DNA profiles were determined for all Sw trees having a dbh ≥ 6.0 cm in the eighteen plots (530 trees). Within each plot, trees possessed unique genotypes for one or both SSR markers. Occasionally, trees had matching SSR DNA profiles but upon reference to stem map information, these were determined to be forked stem individuals. In several cases, one SSR marker could not be determined; in these instances, differentiation between individuals was still possible using the other SSR marker. Allele sizes ranged from 130-178 base pairs (bp) for PGL14, and 106-236 bp for UAPgCA91. Allelic frequency data are presented in Table 3-2. For UAPgCA91, allele size 142 had the highest frequency (0.104); for PGL14, allele size 152 had the highest frequency (0.110).

A total of 870 root fragments were analyzed, resulting in one or two locus genotypes for 825 root fragments. Occasionally only one SSR marker yielded results. Of these genotyped root fragments, matches to trees were found for 615 fragments.

Table 3-2. Simple sequence repeat locus, allele size and observed frequency in Sw trees.

Locus	Allele size	Frequency	Locus	Allele size	Frequency
UAPgCA91	106	0.002		184	0.007
	110	0.008		186	0.002
	114	0.011		188	0.003
	116	0.022		190	0.001
	118	0.054		192	0.002
	120	0.003		194	0.008
	124	0.001		196	0.001
	126	0.031		198	0.002
	128	0.053		200	0.002
	130	0.068		204	0.005
	132	0.062		212	0.002
	134	0.053		236	0.002
	136	0.038	PGL14	130	0.002
	138	0.017		132	0.003
	140	0.033		134	0.004
	142	0.104		136	0.031
	144	0.056		138	0.072
	146	0.041		140	0.103
	148	0.035		142	0.041
	150	0.034		144	0.040
	152	0.015		146	0.027
	154	0.031		148	0.040
	156	0.026		150	0.082
	158	0.013		152	0.110
	160	0.021		154	0.066
	162	0.014		156	0.076
	164	0.011		158	0.046
	166	0.012		160	0.059
	168	0.012		162	0.042
	170	0.009		164	0.034
	172	0.016		166	0.043
	174	0.020		168	0.013
	176	0.011		170	0.026
	178	0.008		172	0.017
	180	0.006		174	0.012
	182	0.010		176	0.003
...	…	…		178	0.009

3.7.2 Root vertical distribution

Across all plots, mean Sw fine root length (*i.e.*, root length of all Sw trees as measured through image analysis with WinRHIZO software) was found to be highest in the organic layer and decreased with depth. Root length was calculated in terms of cm of root length per cm^2 forest floor. Mean fine root length by layer was found to be 0.43 cm cm^{-2} in the organic layer and then 0.35, 0.28 and 0.11 cm cm^{-2} at depths of 0-5cm, 5-15cm and 15-40 cm, respectively.

3.7.3 Root lateral distribution

The mean tree to soil core distance was 5.3 m for mixed plots and 5.4 m for pure Sw plots, an insignificant difference ($p = 0.34$). The mean tree-root match distance was 2.3 m for mixed plots and 2.2 for pure Sw plots, an insignificant difference ($p = 0.58$). Across all plots, 80% of tree-root matches were within < 3.2 m of tree stems; 95% were within < 4.4 m. The average of the maximum extent of roots was 4.3 m for mixedwood plots and 5.0 m for pure Sw plots, an insignificant difference ($p = 0.31$), with an overall average of 4.7 m. The furthest distance recorded across all plots was 7.2 m. It is important to note that tree-root matches for distances in excess of 3.5 m are underrepresented since the minimum soil core-plot edge distance was 3.5 m.

Main effects of mixture type and block were not significant ($p > 0.05$). Interaction effect of block and mixture type also was not significant. This was expected by virtue of the model design; results were tabulated on a proportion basis across levels of distance class. By definition, average proportional root count across all levels of factors not involving distance class will be equal to 1 divided by 5, or 0.2, since there are 5 levels for distance class. Distance class, however, was significant ($p < 0.001$). White spruce root prevalence decreased with increasing distance from stems, following an inverse relationship, as presented in Figure 3-6.

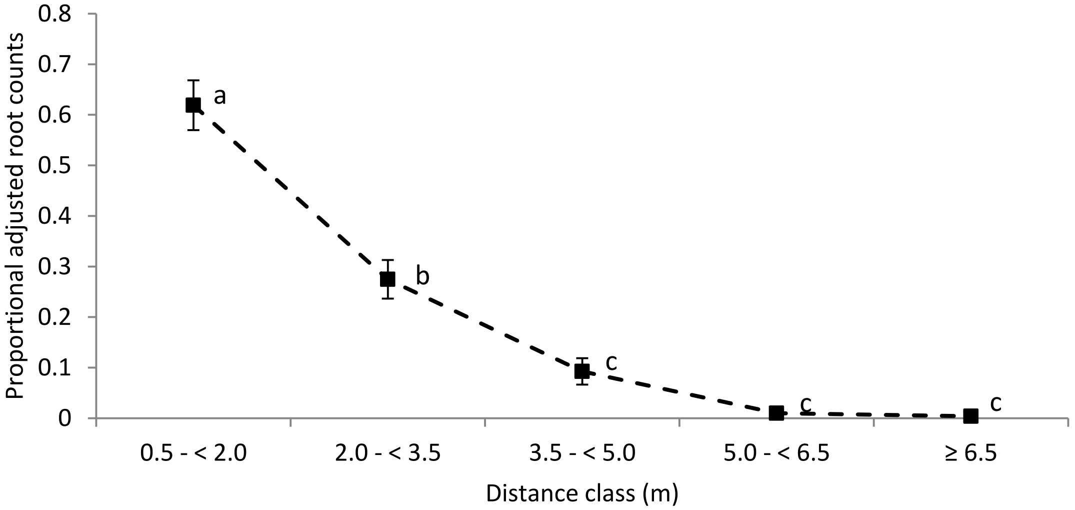

Figure 3-6. White spruce proportional adjusted root count decreases with distance from tree stem. Error bars represent 1 S.E.; letters indicate significant differences (Tukey's HSD test).

There was a significant ($p = 0.034$) interaction with block and distance class. Generally, Blocks 3 and 4 were more similar to each other than to Block 2. Between distance classes 1 and 2, root prevalence decreased significantly in Block 2 and 4 but not in Block 3. Between distance class 2 and 3, root prevalence decreased significantly in Block 3 but not in Blocks 2 and 4. Figure 3-7 illustrates this relationship.

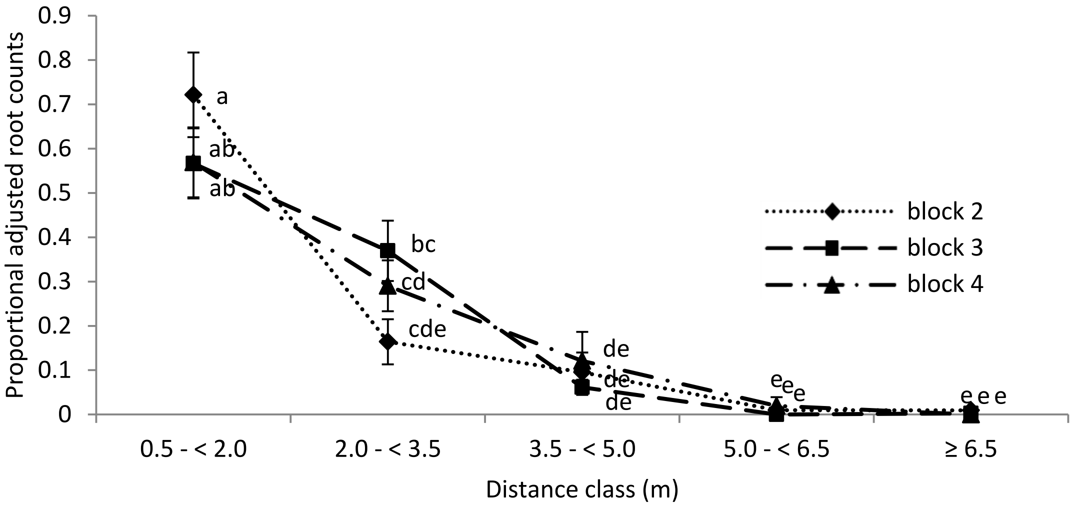

Figure 3-7. Lateral distribution of Sw fine roots in the three blocks. Error bars represent 1 S.E.; letters indicate significant differences (Tukey's HSD test).

The interaction of factors distance class and plot type was significant (p = 0.004). The interaction effect is evident in the first two distance classes. Between distance classes 1 and 2, root prevalence decreased significantly in both plot types but decreased to a greater degree in pure Sw plots. In pure Sw plots, root prevalence at distance class 2 did not differ significantly from root prevalence at the next furthest distance class; however, in mixedwood plots root prevalence was significantly greater in distance class 2 compared with 3. This result is presented in Figure 3-8.

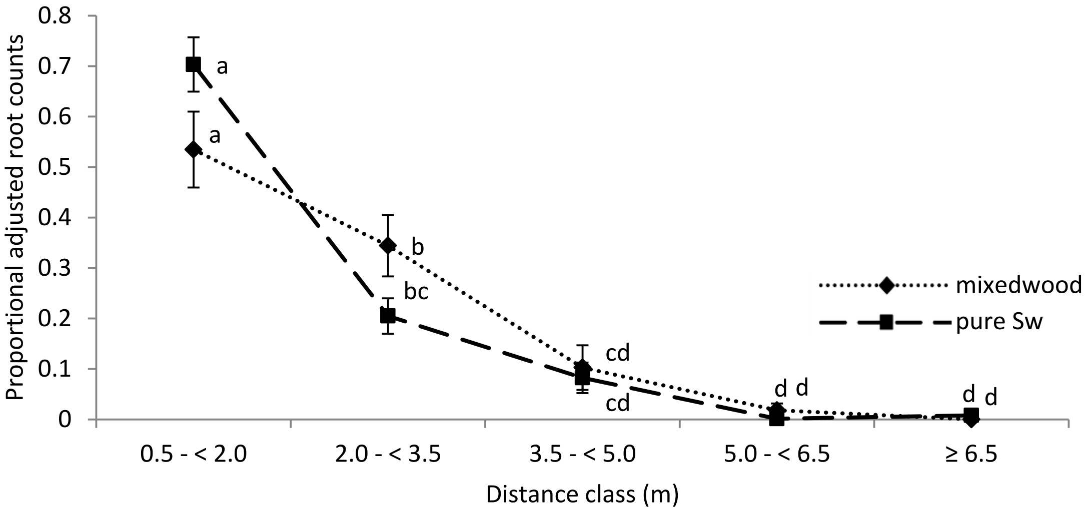

Figure 3-8. Lateral distribution of Sw fine roots in mixedwood and pure Sw plot types. Error bars represent 1 S.E.; letters indicate significant differences (Tukey's HSD test).

Although the three way interaction of factors block, plot type and distance class was not significant (p = 0.099), examination of this relationship reveals that the interaction of plot type and distance class appears to be more pronounced in Blocks 3 and 4, whereas it seems to be much weaker or non-existent in Block 2. This non-significant trend is described by Figure 3-9.

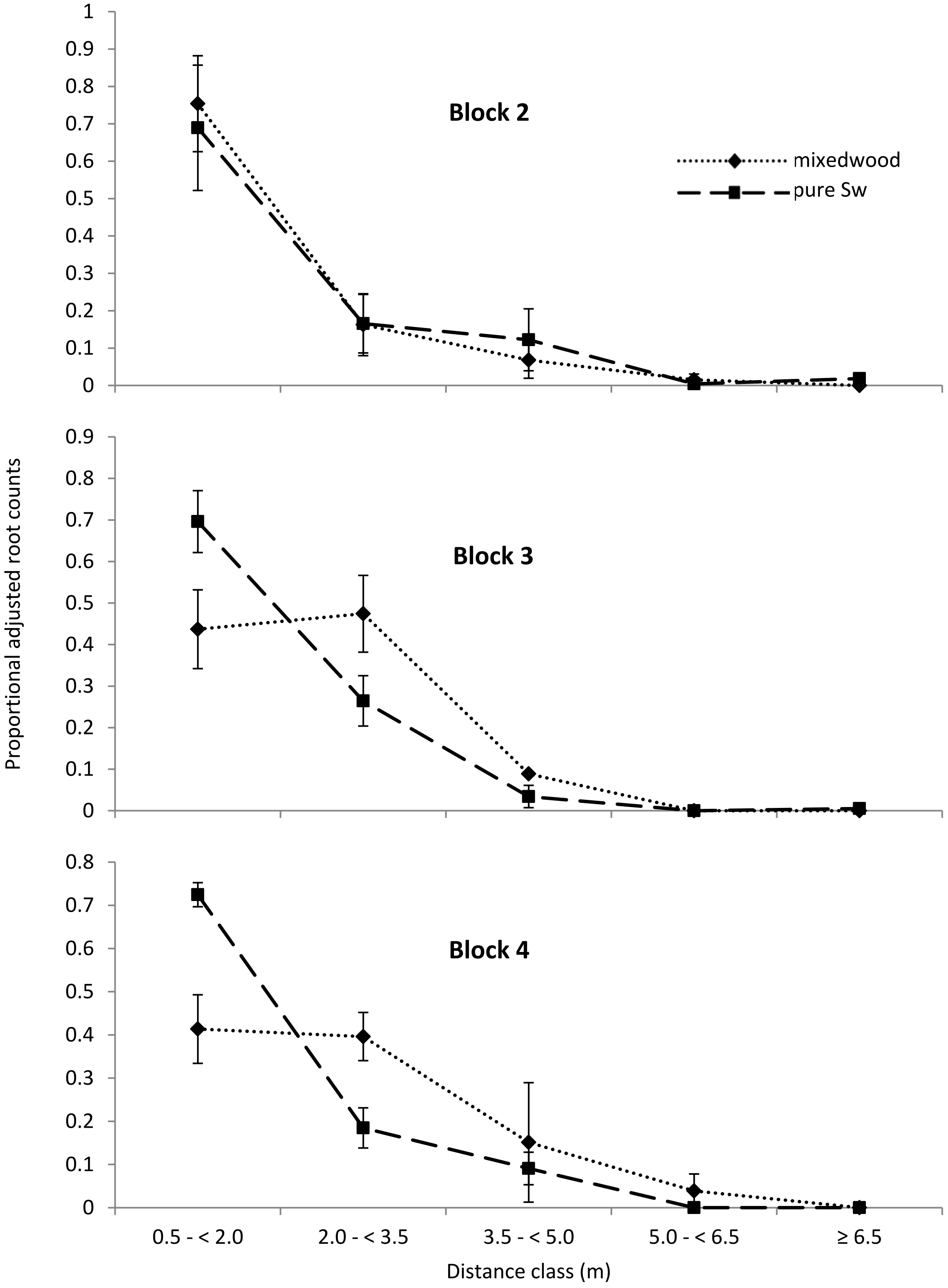

Figure 3-9. Lateral distribution of Sw fine roots by block and mixture type. This non-significant three way interaction suggests that factors mixture and distance class might only interact in Blocks 3 and 4. Error bars represent 1 S.E.

3.8 Discussion

3.8.1 SSR markers as a root mapping tool

The SSR marker UAPgCA91 proved to be very useful for intraspecific identification, having 48 separate alleles across a wide range of allele sizes from 106 to 236 bp. Hodgetts *et al.* (2001), the developers of this marker, noted only 8 alleles across a range of 118-158 bp. This is not surprising since this study determined alleles in a much larger population, 530 Sw individuals vs. 10 studied by Hodgetts *et al.* (2001). The usefulness of this marker was further enhanced by a relatively uniform distribution of allele sizes. No one allele was dominant in the results, with allele size 142 bp having the greatest frequency at 0.104. This marker did, however, show greater susceptibility to —stutter” effects during PCR DNA amplification than marker PGL14.

The SSR marker PGL14 was also useful for intraspecific identification, although it was not as informative as UAPgCA91. Allele sizes ranged from 130-178; 25 allele sizes existed in total. As with UAPgCA91, a greater number of alleles across a wider range were noted for PGL14 than has been reported in the literature. Rajora *et al.* (2001), the developers of this marker, reported 18 allele sizes over a range of 136-180 bp in a random sampling of 32 Sw individuals. As with the former marker, this marker demonstrated a relatively uniform distribution of alleles. No one allele was dominant in the results, with allele size 152 bp having the greatest frequency at 0.110.

3.8.2 Root vertical distribution

Although the focus of this study was upon lateral distribution, some vertical distribution data was analyzed to support the sampling protocol. For root lateral distribution results, only roots from the organic surface layer were considered to reduce the scale of the experiment. It was assumed that a large portion of Sw fine roots would be present in the organic surface layer and that roots in this layer would provide a reasonable representation of the general lateral distribution. This assumption is supported by observations by Strong & La Roi (1983) who found that Sw concentrates roots in the organic surface layer. The results from this experiment agree with this assumption. It was observed that Sw fine root length per unit of forest floor in both mixedwood and pure Sw plots was greatest in the organic surface layer, and decreased with depth.

3.8.3 Lateral distribution – Distance relationship

Root prevalence was noted to decrease with distance, following an inverse relationship. This observation lends support to forest stand competition models which assume the influence of neighbouring trees is inversely related to their distance, *e.g.* Hegyi's index (Hegyi 1974) for modelling competition in jack pine stands. This observation is important because it extends to belowground systems the concept of competition being inversely related to distance between competitors.

3.8.4 Lateral distribution – affected by plot type

The significant interaction with distance class and plot type suggests a subtle trend towards a wider lateral reach of Sw roots in mixedwood plots. This supports the main hypothesis of this paper. However, support for the hypothesis would be stronger if this interaction was more obvious, *i.e.*, if, within a specific distal distance class, Sw root prevalence was significantly greater in mixedwood compared to pure Sw plots.

There are a number of possible explanations for why Sw trees in mixedwood plots have greater lateral reach. Differing preferred niches may contribute to greater lateral reach in mixedwood plots. White spruce may be a superior competitor to Pt in the upper soil layers, displacing Pt to deeper layers; conversely, Pt may be a superior competitor in deeper soils displacing Sw roots to the upper soil layers.

This trend may simply reflect differences in aboveground crown dimensions. Strong & La Roi (1983) noted an increase in root concentration in a region just beyond the extent of the crown; if crowns are wider in mixedwood plots, this may cause wider root lateral distributions as roots reach out to the edges of wider crowns. However, the concept of wider crowns resulting in wider lateral reach was not supported by the evidence. The opposite was observed, with pure Sw plots having wider Sw crowns, although this result was not significant ($p = 0.09$).

Root self/non-self discrimination may affect lateral reach. Self/non-self discrimination is the ability of some species' roots to discern and respond to the identity of neighbouring roots. It has been observed experimentally that certain species will tend to abort growth in the direction of a same-species neighbour and may accelerate growth towards neighbours of a different species (Falik *et al.* 2003; de Kroon 2007; Semchenko *et al.* 2007). Self/non-self discrimination behaviour could explain wider Sw lateral reach in mixedwood plots, in such plots neighbours are more likely to be of a different species. It is unknown if this behaviour exists in Sw; this question warrants further study.

Facilitation of Sw resource acquisition by Pt litter may be occurring in mixedwood plots, particularly in organic soil layers (*i.e.*, F and/or Ah), leading to preferential exploitation of organic layers and wider lateral reach. This concept presents the most convincing explanation for wider Sw lateral reach since it is supported by observations. It was noted that organic layer pH was significantly less acidic in mixedwood plots compared to pure spruce plots (Block 3 only). It may be that Sw trees in mixedwood plots more intensively forage the organic layer for resources since this layer is more hospitable than in pure Sw plots.

Additionally, there may be a sub effect of microsite variability within the forest floor. It is supposed that higher quality Pt aspen litter is responsible for favourable pH conditions (and a dominance of Ah surface layers) in the mixedwood plots and that acidic spruce litter is responsible for acidifying the soil. However, Sw and Pt litter deposition may follow different patterns. Spruce needles have comparatively lower surface area and size, making them less susceptible to being spread by the wind. Consequently, the area directly beneath the crown of Sw trees may experience greater deposition of Sw needles (and more dominance of an F surface layer). This may create patterns of high acidity directly beneath Sw crowns, and lower acidity in areas outside of

Sw crowns, that may be more greatly impacted by Pt litter. Wider Sw lateral reach in mixedwood plots could simply be a result of Sw roots exploiting higher quality soils just outside the area influenced by the Sw tree.

The root distributions described by this mapping method represented generalized distributions that may be expected from an average representative tree on a given plot, with root presence at a given distance averaged around the entirety of the tree. With this in mind, it is important to remember that lateral roots of a single individual are likely to be distributed in a highly irregular manner with roots from that tree being present at one coring location while perhaps none might be found in an adjacent excavation. Occasionally, cores placed near a particular tree resulted in no root fragment matches to that tree. It should not be assumed that roots from a given individual were distributed evenly within a given distance class.

3.8.5 Lateral distribution – block effect re-examined

Block did not significantly affect mixture – distance interactions in this experiment. However, similarities were noted between Blocks 3 and 4, where mixture-distance interaction was more pronounced, compared to Block 2 where mixture-distance interactions seemed to be weaker or non-existent. Differences between blocks were examined to explore possible explanations for this discrepancy. Slope exposure may contribute to differing rooting behaviours between the blocks. Blocks 3 and 4 share a common SE slope exposure; slope exposure in Block 2 is NE. Soils in Blocks 3 and 4 may experience greater solar heating than in Block 2. Soil temperature has a large impact on rooting behaviours of Sw and Pt (Landhausser *et al.* 2001; McMichael & Burke 2002), and could potentially be responsible for differences observed between blocks.

Examining Sw tree height may shed light on differences between Blocks 3 and 4 compared to Block 2, since lateral distribution may be related to tree height. In a study by Strong & La Roi (1983), maximal lateral root spread of Sw roots increased with age and height amongst a series of four trees. There was considerable variation in average Sw tree height per plot (range: 5.1-8.0 m), but no significant variation between blocks. However, when plots are sorted into two equal sized height classes containing short trees (average Sw height 5.1-6.5 m) and tall trees (average Sw height 6.8-8.0 m), Block 2 contains *only* —short” tree plots whereas Blocks 3 and 4 contain combinations of “short” tree and —tall” tree plots. (As a side note, these height classes were not related to plot type, with relatively even distributions of plot types in —short” tree plots (4 mixedwood, 5 pure Sw) and ”tall” tree plots (5 mixedwood, 4 pure Sw).)

Relative height of Sw trees was not originally considered as a factor in this experiment. As a theoretical exercise, a model was considered having the original factors distance class and plot type, introducing a third factor of Sw height class (H) having two levels (—short” and —tall”). This model discards the factor Block, assuming that the effect of block is mostly to do with tree heights. The resulting model is an unbalanced design and contains a large spatial bias, *i.e.*, most —short” tree plots are agglomerated in Block 2. Therefore, the results from this exercise are speculative and must be evaluated with caution. The three way interaction of factors height class, distance class and plot type was found to be significant (p = 0.003). Specifically, the effect of distance class depended upon plot type, but only for the —tall‖ height class. In —tall‖ tree plots, root prevalence in pure Sw plots decreased significantly between distance class 0.5 - < 2.0 m and 2.0 - < 3.5 m; in mixedwood plots root prevalence did not significantly differ between these distance classes. There was no interaction of distance class and plot type amongst plots in the “short” category. These relationships are illustrated in Figure 3-10.

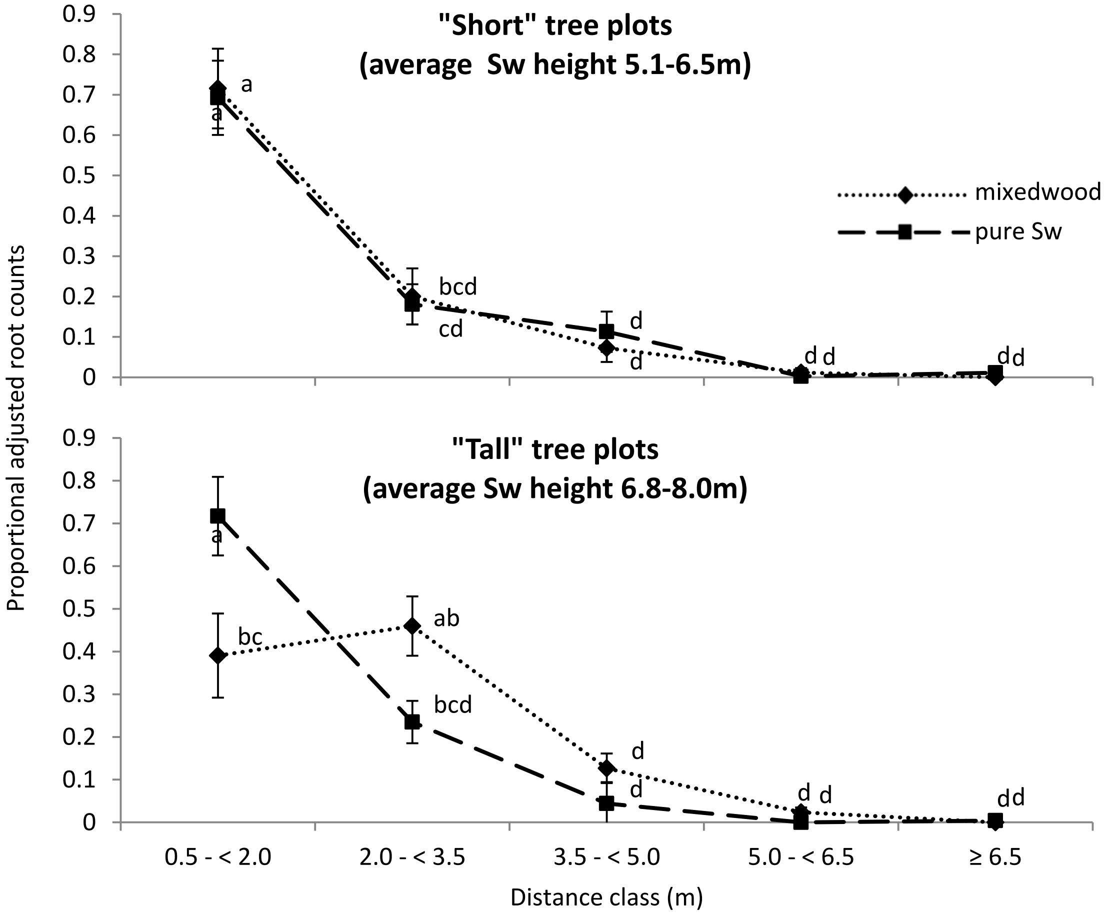

Figure 3-10. Lateral distribution of Sw fine roots in “short” and “talL” tree plots, separated by plot type. Significant interactions exist between distance class and plot type, but only in “tall” tree plots. Error bars represent 1 S.E.; letters indicate significant differences (Tukey’s HSD test).

The pattern displayed in Figure 3-10 is remarkably similar to the pattern observed for the three way interaction of block, distance class and plot type (Figure 3-9). In particular, the three way interaction of block, distance class and plot type for Block 2 appears to be similar to the –short” tree plot in Figure 3-10; Blocks 3 and 4 appear to be similar to the —tall" tree plot. This suggests that differences between Block 2 and the other blocks with regards to distance class – plot type interactions may be related to Sw height.

It is of course possible that some intrinsic difference between the blocks is responsible for Block 2 having both shorter trees *and* an apparent lack of distance class – plot type interaction. In this case, tree height might have no effect upon distance class – plot type interactions. A thorough investigation of the effect of tree height upon lateral distribution is beyond the scope of this study. Experimental design in similar future investigations should therefore pay close attention to relative tree heights.

3.9 Conclusions

Fine roots of white spruce trees at the FEP site were primarily found near tree stems, with 80% of fine roots being within 3.2 m of the originating stem. Maximum extent of white spruce roots was on average 4.2 m, and was not affected by plot type. Lateral distribution of Sw fine roots follows an inverse curve pattern, dropping off quickly with distance. Plot type affected the lateral distribution of Sw roots, with trees in mixedwood plots demonstrating a subtle trend towards a wider reaching lateral root distribution. Root prevalence in pure

Sw plots dropped off more quickly with distance from tree stems. Stem density of Sw at the FEP site was within a fairly narrow range. Future research may address the effect of stem density upon lateral distribution of Sw fine roots.

Wider distribution of Sw roots in mixedwood plots may be a result of facilitative benefits provided by the presence of Pt trees. Organic layer pH was less acidic in mixedwood plots in one block, presumably due to the presence of Pt litter. The spatial variation of organic soil layer pH *within* mixedwood plots is unknown; speculatively, pH increases due to Pt litter might be more pronounced in areas not directly beneath Sw crowns. More work is needed to explicitly determine facilitative effects of Pt litter and its potential role in creating wider Sw lateral reach.

Speculative analysis of tree height data suggest that tree height may affect Sw root lateral distribution. Specifically, wider distributions of Sw roots might only occur amongst the taller trees in Blocks 3 and 4. Tree height should be considered as a factor in the planning and execution of future investigations of Sw lateral reach.

Root mapping via SSR technology proved to be an effective tool for mapping Sw fine root lateral distribution. It allows for plot-level characterization of fine root lateral distribution, while being minimally destructive. Despite controlling for heterogeneous tree distributions on plots, significant variability in results limited the potential resolution of lateral distributions. Resolution of lateral distributions might be improved through more intensive sampling per unit area of forest.

3.10 Acknowledgements

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4 Thesis conclusions

This study revealed only limited evidence of reduced belowground competition in mixedwood forests of Sw and Pt, in the form of altered Sw horizontal root distribution. Some suggestion was also found to support the concept of facilitative production. Similar future investigations may be improved through suggestions contained in this section.

Vertical distributions of Sw and Pt fine roots were unchanged between monospecific and mixedwood plots. Vertical stratification of fine roots was not observed. Stratification, if present, would have provided strong evidence for spatial separation of belowground niches, and thus reduction of competition.

Tantalizing suggestions of behaviour changes were noted, however, in the case of Pt root attributes, that might be related to a process of stratification. Trembling aspen roots were thinner in mixedwood plots, *i.e.*, they had higher SRL, which may suggest the adoption of a more exploratory foraging strategy. This shift would be expected if stratification did indeed occur with Pt shifting away from organic soils to less nutrient rich mineral soils. It is unknown, however, if such reasoning is factually supported, since stratification was not observed. Also, sampling intensity was insufficient to determine SRL on a per-depth basis. This information would confirm the assumption of SRL being associated with exploration of less nutrient rich mineral soil.

Horizontal distribution of Sw roots was influenced by plot types, subtly trending towards a wider distribution in organic soils of mixedwood plots. This supports the concept of spatial niche separation between Sw and Pt in mixedwood plots, with Sw expanding its exploitation of shallow organic soils in the mixedwood condition. This concept would enjoy greater support, however, if this effect was paired with a reduction of Pt roots in those same organic layers, which was not (significantly) observed.

There is some evidence to suggest that in pure Sw plots, a portion of the realized niche of Sw in organic layers comes at the expense of other understory species otherwise present in mixedwood and pure Pt stands. Significant decreases in —other” species root presence were noted in pure Sw organic layers. The exact mechanism driving this reduction in other species was not determined by this study. Two possible explanations of this effect could lie in a greater competitiveness of Sw roots or changes to the organic layer brought about by Sw litter, in the form of acidification, potentially excluding acid intolerant plants. The latter explanation seems more likely due to the observed acidification. Future work may provide better and more complete explanations.

Resource acquisition was probably facilitated by Pt litter in organic layers of mixedwood and pure Pt plots of Block 3. This facilitation, in the form of less acidic pH leading to improved growing conditions, is assumed to be the result of Pt litter, although this theory was not tested directly. Future work would do well to elucidate the precise impact of Pt litter upon soil conditions, and the related implications for the understory plant community.

Conclusions reached in this study are constrained by a number of factors. Fine roots, *i.e.*, those responsible for absorption of water and nutrients, were arbitrarily assumed to be all roots lesser than 2 mm in diameter. A more refined definition of absorbing roots based upon actual physiological functions would be preferred. Comparisons were made at one specific point of time in the spring, and at a specific age of approximately 20 years. Rooting patterns may vary over a whole growing season; studying such patterns may reveal the presence of a more temporally nuanced reduction of competition. Measurements taken of these same forests when they are older, when competition for soil resources becomes more intense, may also present differing findings.

Measurements in this study were characterized by large relative standard errors. This may have constrained our ability to detect any patterns in the data, if they exist. As might be expected, relative standard errors increased with depth, since the prevalence of roots decreased with depth, and their distribution became more erratic. Improvements may be made to the sampling regime in this type of experiment by collecting more samples, particularly at deeper mineral layers, and by collecting smaller samples of the organic layer. Roots and soil from mineral layers could be pooled together. This improvement does not need to add much burden to the processing of root samples. From our experience, the organic layer was by far the most difficult layer to separate roots from soil, requiring many hours of labour, whereas mineral soil layers were processed with relative ease. Root prevalence in organic layers was usually intense; smaller samples could likely be collected without having much impact on the accuracy of each sampling point. By collecting more frequent, but smaller, samples of the organic layer, root and soil sorting efforts for this difficult layer could be focussed on reducing noise due to spatial variability of roots.

This altered field sample collection regime would also likely improve the efficiency of the horizontal distribution experiment. White spruce root fragments were subsampled from the organic samples, up to a maximum of 15 fragments. Often there were considerably more fragments available than were sampled, so collecting smaller samples from the field per sampling point is unlikely to affect the results in this experiment if it were repeated with the same system of three sampling points per plot.

However, if the horizontal distribution experiment was repeated with subsampling of Sw root fragments occurring from this new enlarged set of sampling points, more accurate horizontal distributions might be described, since the experiment would capture more of the spatial variability present on the plots. The total number of subsampled Sw root fragments could be maintained by reducing the subsample quantity per sample point. In this manner, less effort would be expended confirming multiple matches to individual trees that happen to be close to a sample point, and more effort would be spent assessing the nature of a *typical* horizontal distribution for that area of forest. This would improve the generalizability of the findings to a plot level. For example, instead of discovering that in a particular plot, 15 matches were found in the 0.5-1.5 m distance category, based on matches to one tree within one hole, we might discover 15 matches in the 0.5-1.5 m category from 5 different holes, with each hole revealing 3 matches to a tree 0.5-1.5 m away. In each case, we would uncover 15 matches in the 0.5-1.5 m distance category, but in the first case the finding is based on one tree only but in the second case, our observation is based on roots from five different trees and forms a better case for claiming that the observed distribution is typical of the plot.

It is important to restate that future work should be cognizant of nearby influences upon plots. As observed in the horizontal distribution study, roots can sometimes reach out quite far; the furthest distance recorded for Sw fine roots was 7.2 m, with maximum reach per plot being on average 4.7 m. When it is considered that sampling holes were only 3.5 m away from the plot edge, it becomes obvious that what surrounded these plots mattered, since many trees outside the plot may reach sampling points. Future work may avoid this confounding factor by both accounting for the forest mixture type beyond the plot, and by creating larger plots to minimize the possibility of sampling roots belonging to trees not under consideration in the plot. Additionally, from anecdotal observation in the field it was clear that Pt litter may spread a great distance; although not noticed in this study, it is conceivable that Pt litter may have a measurable impact upon the soils in a plot considered to be pure Sw if there are Pt trees in the vicinity.

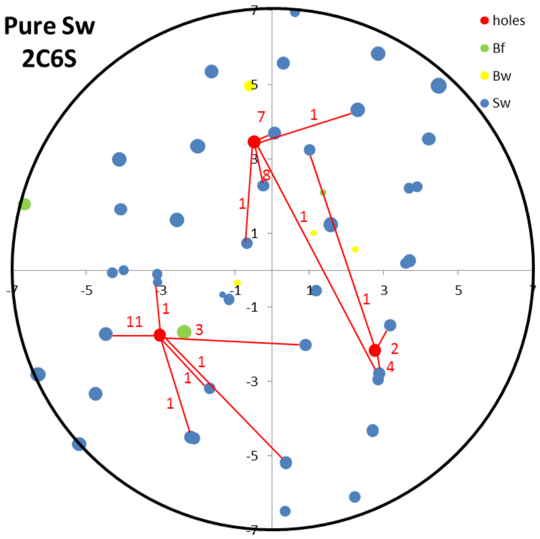
The ability to characterize the prevalence of roots at a particular distance from tree stems is of great significance. This information is more informative than simply knowing the maximum extent of roots, since it allows us to know how far away, and with what intensity, a given tree’s belowground influence may extend. Such knowledge may inform our assumptions regarding belowground competition in stand growth projection models, complementing what is known regarding aboveground competition for light, enabling more accurate predictions of future forest growth. This work is merely a starting point, far more information would be required to tailor such predictions to the myriad possible combinations of factors affecting belowground systems.

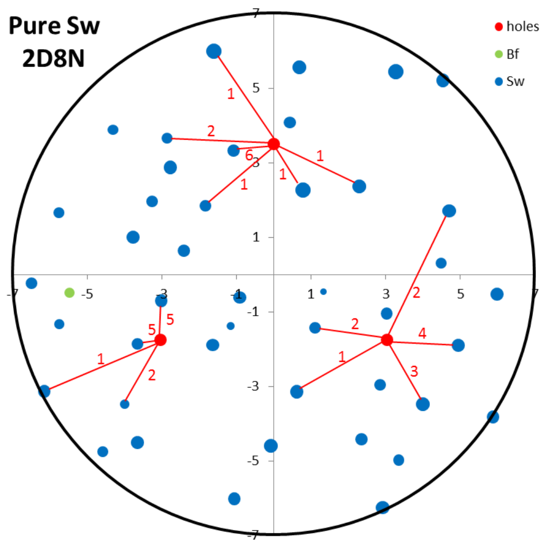
APPENDICES

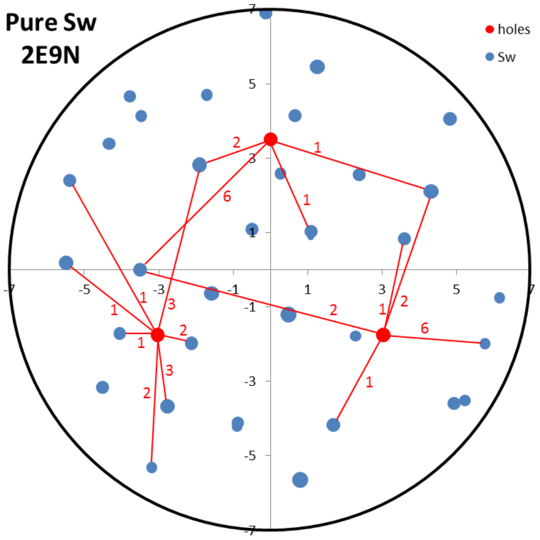
APPENDIX I

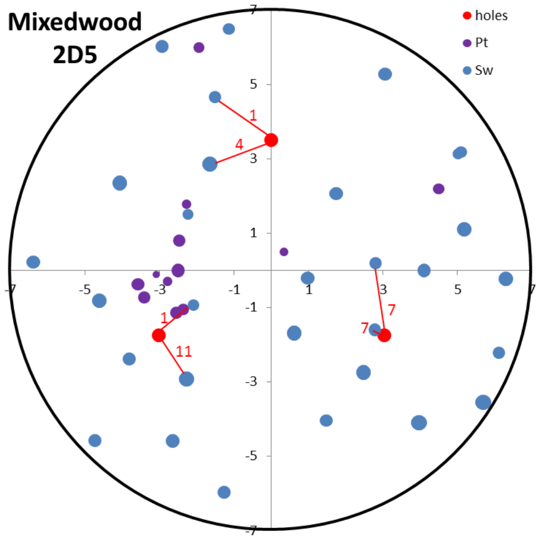
ROOT FRAGMENT – TREE STEM MAPS

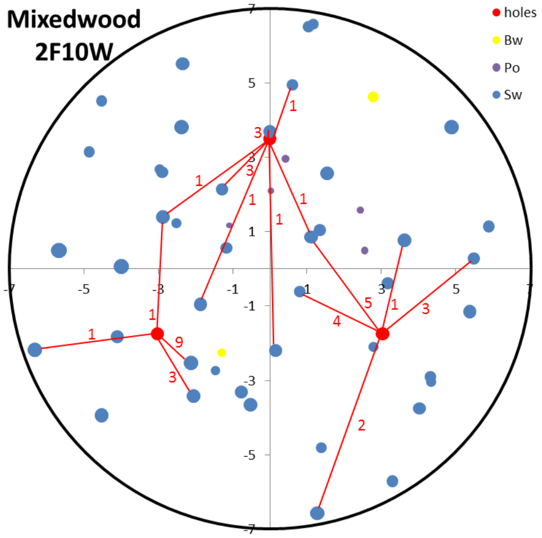
Plots were radius 7m. Plot names start with the block number followed by a grid reference identifier. Diameters of tree stems are not to scale, but relative sizes are correct. Roots were excavated from three sample points per plot (red circles). Red lines signify a match between the SSR profile of a root fragment(s) and a Sw tree. Numbers beside red lines signify the quantity of root fragments having that match.







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Bw
Po
Sw
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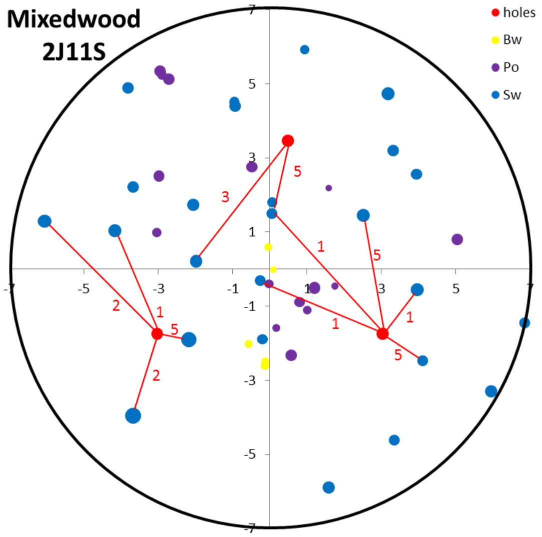
-1
-3
-5
-7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Po
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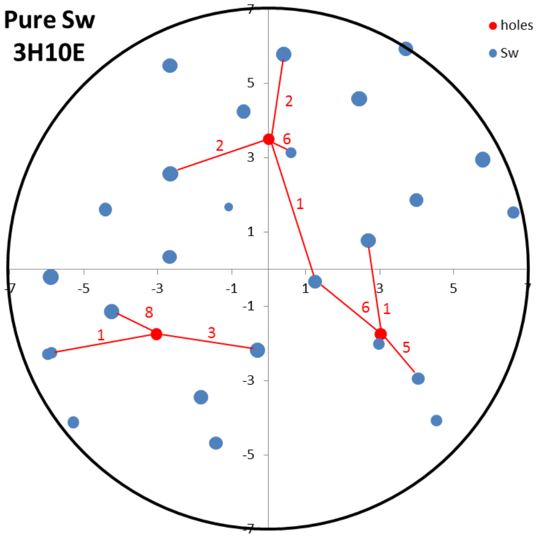
-7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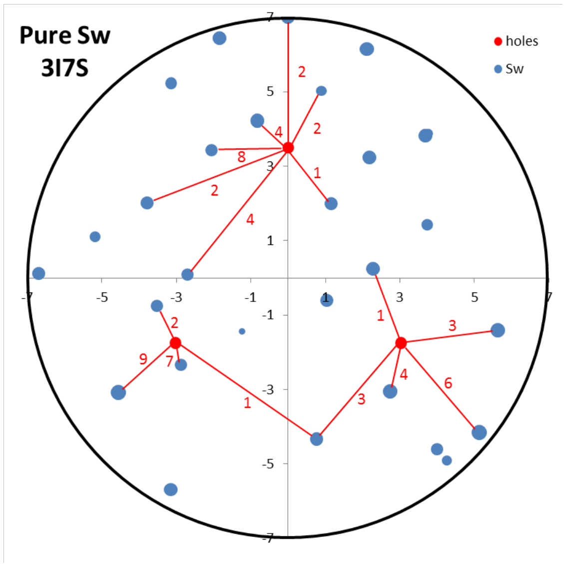
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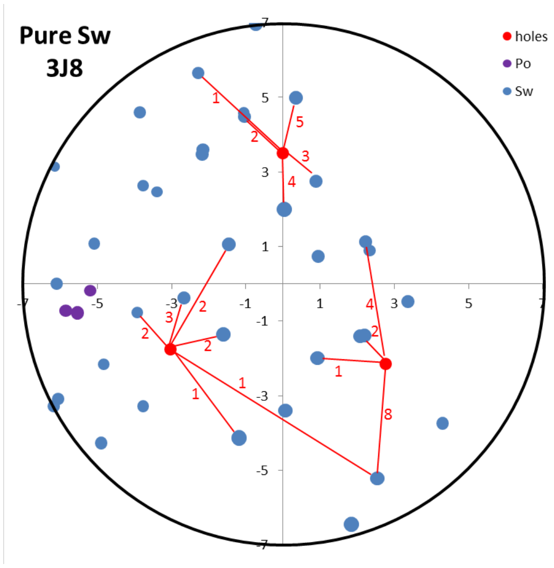
-7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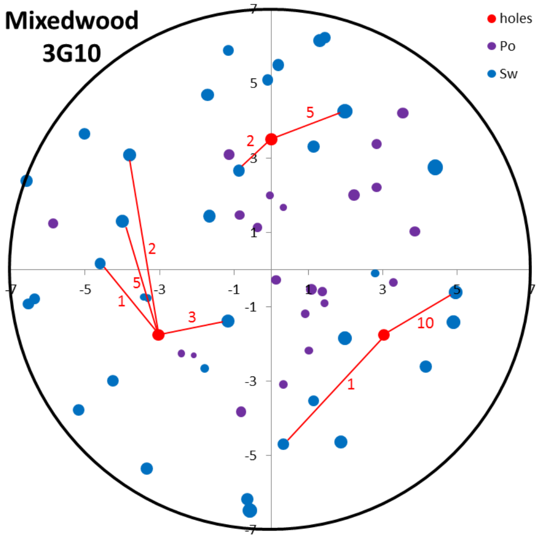
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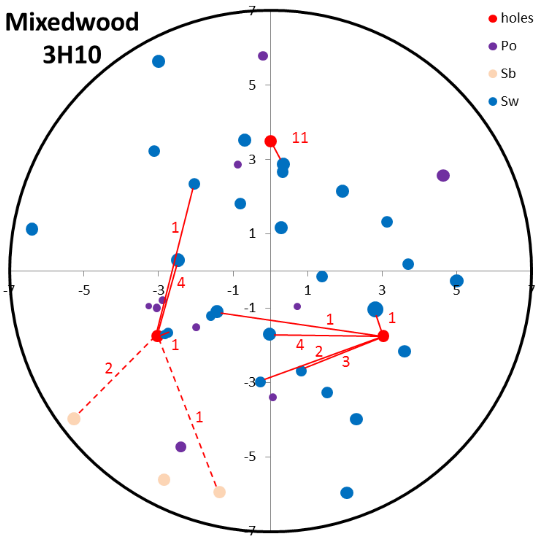
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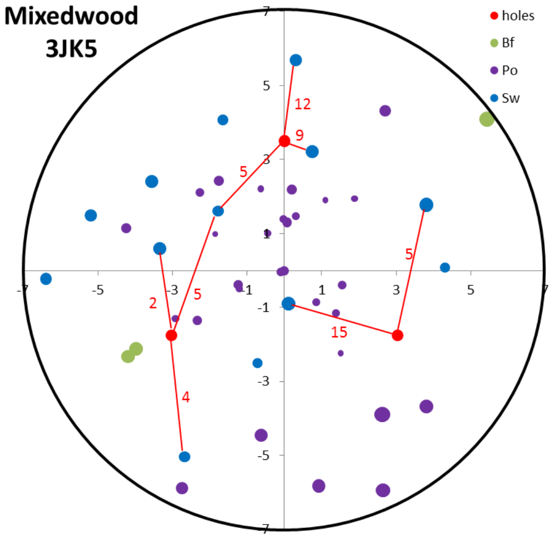
1
4
2
3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Bf
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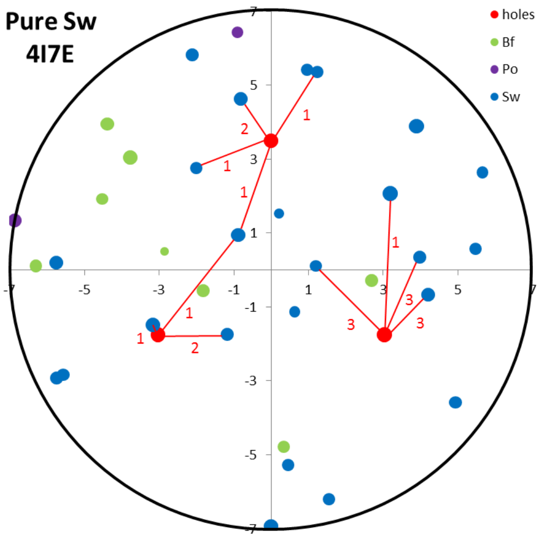
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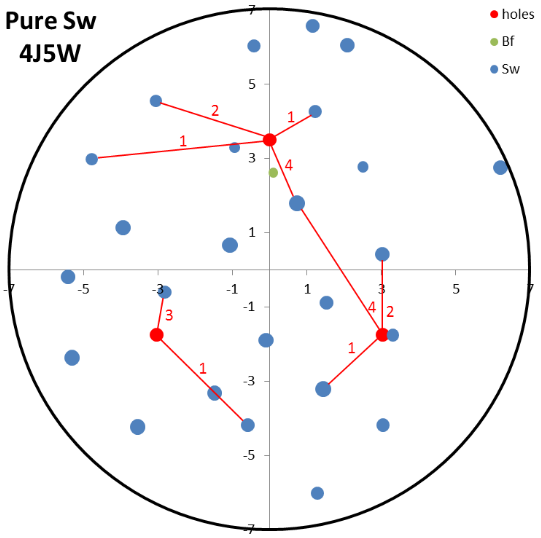
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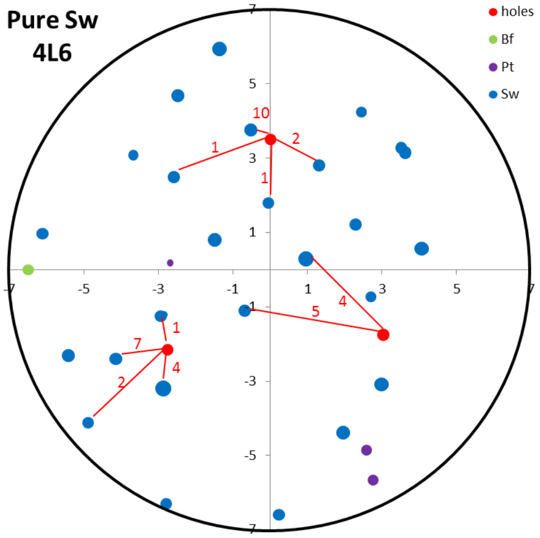
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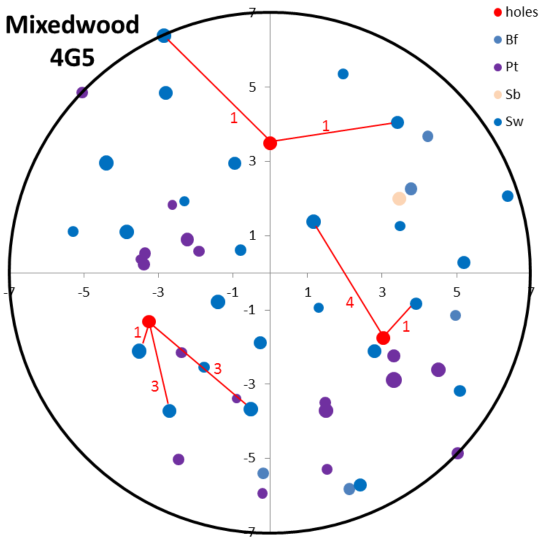
1
7
4
2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3
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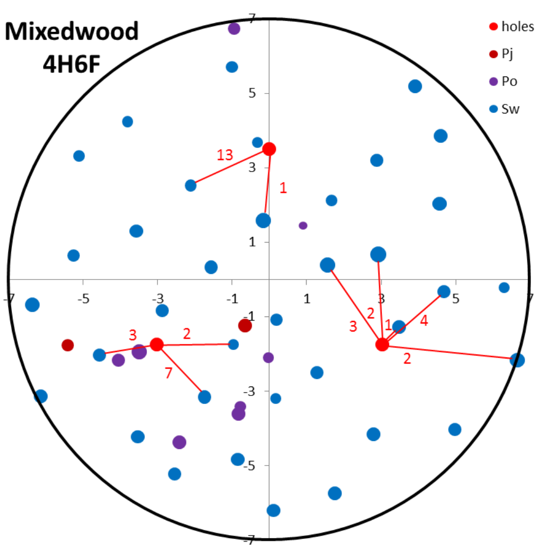
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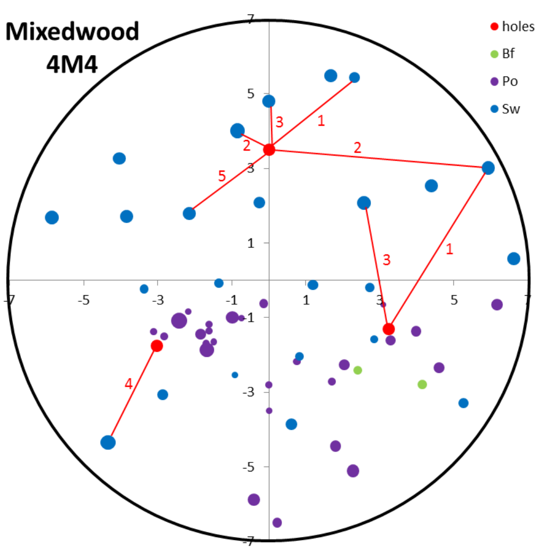
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Bf
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-1
1
3
5
7
3
1
2
2
5
3
1
4

APPENDIX II

STEM MAP DATA: MIXEDWOOD AND PURE SW PLOTS

Spp is species, Azi and Dist are azimuth and distance from plot centre, DBH is diameter at breast height at the end of the 2009 growing season. Species codes: Bf, balsam fir; Bw, white birch; Pj, jack pine; Pt, trembling aspen; Sw, white spruce.

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
Mixedwood Plots				
Plot 2D5				
205	Pt	268	3.1	2.6
239	Pt	342	6.3	6.6
318	Pt	270	2.5	9.6
321	Pt	246	2.8	7.7
322	Pt	246	2.6	7.2
323	Pt	258	3.5	8
325	Pt	264	3.6	9.1
326	Pt	264	2.8	4.5
327	Pt	288	2.6	8.5
476	Pt	308	2.9	4.5
545	Pt	64	5	7
571	Pt	34	0.6	3.6
89	Sw	30	6.1	9.6
154	Sw	136	5.7	13
218	Sw	92	6.3	12
232	Sw	40	2.7	9.8
240	Sw	226	6.6	9.1
242	Sw	122	6.7	14
245	Sw	334	6.7	8.7
319	Sw	246	2.3	7.5
320	Sw	218	3.7	12
328	Sw	304	2.7	6.5
329	Sw	330	3.3	12
330	Sw	342	4.9	8.6
331	Sw	350	6.6	7.6
332	Sw	300	4.7	12
333	Sw	272	6.4	9.7
334	Sw	260	4.7	12
335	Sw	238	4.5	9.5
336	Sw	210	5.3	11
337	Sw	192	6.1	8.9
384	Sw	78	5.3	12
461	Sw	110	6.5	8.5
464	Sw	120	3.2	8.6
471	Sw	86	2.8	8.5
472	Sw	138	3.7	12
513	Sw	58	5.9	6.5
533	Sw	58	6	7.6
534	Sw	160	4.3	8.6
695	Sw	102	1	9.7
873	Sw	90	4.1	10
883	Sw	160	1.8	12
Plot 2F10W				
258	Bw	210	2.6	4.2
792	Bw	31	5.4	7.1
722	Pt	79	2.6	3.2
723	Pt	57	2.9	3.1
766	Pt	317	1.6	2.2
767	Pt	1	2.1	2.5
768	Pt	8	3	3.5
219	Sw	9	6.6	8
220	Sw	79	6	8.4
260	Sw	10	6.7	6.8
261	Sw	337	6	11
262	Sw	133	5.5	9
263	Sw	127	3.5	6
264	Sw	208	3.1	5.1
265	Sw	150	6.6	8.5
266	Sw	169	6.7	11
589	Sw	211	4	11
771	Sw	243	2.1	10
772	Sw	296	1.3	8.2
773	Sw	296	2.8	5.8
774	Sw	296	3.2	11

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
777	Sw	52	1.7	8.9
778	Sw	31	3	5.2
779	Sw	31	3	11
780	Sw	97	3.2	8.6
781	Sw	127	1	7.7
782	Sw	127	1	7.4
783	Sw	176	2.2	9.5
784	Sw	188	3.7	11
785	Sw	193	3.4	10
786	Sw	164	5	7.1
787	Sw	102	5.5	11
788	Sw	124	5.2	7.8
789	Sw	87	5.5	8.9
790	Sw	78	3.7	10
791	Sw	52	6.2	13
793	Sw	7	5	7.8
794	Sw	360	3.7	9.7
795	Sw	328	4.5	12
796	Sw	312	3.9	7.8
797	Sw	271	4	13
798	Sw	275	5.7	14
799	Sw	303	5.8	7.5
800	Sw	246	4.5	10
801	Sw	229	6	12
802	Sw	220	3.3	12
804	Sw	251	6.7	12
998	Sw	125	5.3	6.2
999	Sw	312	4	6.1
Plot 2J11S				
540	Bw	196	2.1	4
558	Bw	100	0.1	3.1
664	Bw	356	0.6	4.6
674	Bw	183	2.6	4.9
675	Bw	183	2.5	4.4
383	Pt	331	6.1	9.5
384	Pt	331	6	6.8
386	Pt	332	5.8	8.9
582	Pt	184	0.4	5.7
665	Pt	113	1.3	10
666	Pt	36	2.7	2.8
667	Pt	105	1.8	3.6
668	Pt	138	1.2	7.8
669	Pt	138	1.5	5.2
670	Pt	166	2.4	9.3
671	Pt	174	1.6	4.2
682	Pt	81	5.1	8.7
684	Pt	350	2.8	8.6
690	Pt	310	3.9	9
695	Pt	288	3.2	6.8
385	Sw	322	6.2	9.6
520	Sw	310	2.7	10
596	Sw	276	2	11
624	Sw	220	0.4	8.5
662	Sw	2	1.5	8.9
663	Sw	2	1.8	7.4
672	Sw	186	1.9	7.6
676	Sw	165	6.1	11
677	Sw	144	5.7	7.8
678	Sw	121	4.8	8.6
679	Sw	119	6.8	10
680	Sw	102	7	8.2
681	Sw	98	4	11
683	Sw	57	4.7	8.8
685	Sw	34	5.7	12
686	Sw	46	4.6	9.1
687	Sw	348	4.5	9.8
689	Sw	9	6	6.6
691	Sw	301	4.3	8.9
692	Sw	348	4.6	8
693	Sw	282	6.2	12
696	Sw	229	2.9	16
697	Sw	223	5.4	17
866	Sw	60	2.9	12
1000	Sw	186	1.9	5.3
Plot 3G10				
30	Pt	116	1.2	7.5
330	Pt	113	1.5	5.9
484	Pt	96	3.3	5.5
601	Pt	155	2.4	4.6
601	Pt	156	2.6	4.5
666	Pt	122	1.7	4.4
668	Pt	142	1.5	5.1
801	Pt	227	3.3	3.9

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
802	Po	222	3.1	2.2
806	Po	155	0.3	6.6
928	Po	342	1.2	5.5
933	Po	330	1.7	6.2
936	Po	11	1.7	3.6
937	Po	359	2	4.2
944	Po	340	3.3	7.8
950	Po	48	3	9.1
951	Po	48	3.3	7.1
954	Po	40	4.4	7
955	Po	40	5.5	8.6
965	Po	282	6	6.7
975	Po	192	3.9	7.5
983	Po	75	4	7.1
984	Po	52	3.6	6.6
35	Sw	220	1.8	11
478	Sw	92	2.8	4.8
669	Sw	258	3.5	3.8
672	Sw	214	3.2	5.8
805	Sw	257	3.4	3.9
935	Sw	342	2.8	9.9
945	Sw	311	2.2	11
952	Sw	19	3.5	11
953	Sw	25	4.7	15
956	Sw	13	6.4	8.5
957	Sw	12	6.3	12
958	Sw	2	5.5	9.9
959	Sw	359	5.1	8.3
960	Sw	340	5	11
961	Sw	349	6	7.9
962	Sw	306	6.2	9
963	Sw	309	4.9	11
964	Sw	290	7	10
966	Sw	288	4.2	12
967	Sw	272	4.6	8.8
968	Sw	263	6.4	7.9
969	Sw	262	6.6	9
970	Sw	235	5.2	8.6
971	Sw	212	6.3	11
972	Sw	234	6.4	9.5
974	Sw	185	6.5	14
976	Sw	176	4.7	9.9
977	Sw	162	3.7	7.5
978	Sw	158	5	12
979	Sw	122	4.9	11
980	Sw	106	5.1	13
981	Sw	97	5	13
982	Sw	58	5.2	17
Plot 3H10				
871	Po	254	3.4	3
914	Po	233	2.5	4.3
915	Po	252	3.2	4.6
916	Po	255	3	4.1
921	Po	179	3.4	4.1
939	Po	207	5.3	7.7
946	Po	143	1.2	3.5
949	Po	61	5.3	11
938	Sb	233	6.6	11
940	Sb	207	6.3	10
941	Sb	193	6.1	10
901	Sw	14	1.2	11
902	Sw	42	2.9	11
904	Sw	7	2.9	11
905	Sw	336	2	9
907	Sw	349	3.6	12
911	Sw	277	2.5	13
912	Sw	233	1.8	12
913	Sw	233	2	6.6
918	Sw	239	3.2	7
919	Sw	239	3.3	6.2
920	Sw	181	1.7	11
922	Sw	185	3	8
923	Sw	163	2.8	7.9
925	Sw	96	1.4	8.9
926	Sw	67	3.4	9.7
927	Sw	110	3	17
930	Sw	93	5	12
932	Sw	316	4.5	9
934	Sw	280	6.5	11
942	Sw	161	6.3	10
943	Sw	150	4.6	11
947	Sw	121	4.2	11
948	Sw	87	3.7	9.6

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
Plot 3JK5				
164	Bf	242	4.5	14
165	Bf	241	4.8	13
700	Bf	53	6.8	18
166	Po	324	3	7.3
168	Po	285	4.4	7.4
169	Po	205	6.5	11
173	Po	298	2.1	2.2
174	Po	240	2.7	6.5
360	Po	336	1.1	3.7
370	Po	248	0.1	4.9
484	Po	344	2.3	3.3
497	Po	188	4.5	12
694	Po	32	5.1	10
698	Po	171	5.9	13
699	Po	156	6.5	14
850	Po	253	1.3	6.7
851	Po	134	5.3	14
852	Po	135	1.2	4.7
853	Po	30	2.2	2.9
856	Po	248	1.3	3.7
857	Po	104	1.6	5.5
859	Po	146	4.7	18
861	Po	130	1.8	4.5
863	Po	3	1.3	7.1
866	Po	359	1.4	4.7
867	Po	44	2.7	3.7
869	Po	146	2.7	2.8
871	Po	12	1.5	4.5
875	Po	0	0	6.4
877	Po	5	2.2	7.1
972	Po	246	3.2	4
167	Sw	286	5.4	11
170	Sw	268	6.4	10
175	Sw	3	5.7	11
684	Sw	338	4.4	8.5
685	Sw	280	3.4	12
687	Sw	304	4.3	12
691	Sw	13	3.3	13
693	Sw	208	5.7	9.1
696	Sw	312	2.4	9.4
858	Sw	89	4.3	7.7
862	Sw	65	4.2	15
870	Sw	173	0.9	14
876	Sw	196	2.6	7.4
Plot 4G5				
185	Bf	103	5.1	6.7
186	Bf	160	6.2	8.1
187	Bf	49	5.6	7.3
821	Bf	59	4.4	8.5
173	Pj	118	3.1	15
175	Po	195	3.5	5
176	Po	279	3.4	8.3
177	Po	274	3.4	8.1
178	Po	276	3.5	5.1
181	Po	131	4.4	14
183	Po	157	3.8	7.5
184	Po	158	4	12
184	Po	120	5.2	12
193	Po	124	4	8.9
199	Po	134	7	8.2
202	Po	164	5.5	6.5
205	Po	182	5.9	6.5
301	Po	228	3.2	6.9
375	Po	292	2.4	10
814	Po	314	7	7.4
815	Po	206	5.6	7.4
850	Po	305	3.2	5.1
910	Sb	60	4	11
172	Sw	342	3.1	9.3
174	Sw	188	1.9	9.4
182	Sw	72	6.7	7.1
189	Sw	87	5.2	9.5
191	Sw	40	5.3	9.4
194	Sw	102	4	8.2
200	Sw	188	3.7	12
204	Sw	239	4.1	12
207	Sw	70	3.7	6.3
291	Sw	241	1.6	12
299	Sw	20	5.7	6.6
306	Sw	286	4	12
398	Sw	304	5.3	12
496	Sw	282	5.4	6.8

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
498	Sw	216	4.6	11
817	Sw	157	6.2	9.1
818	Sw	126	1.6	5.6
822	Sw	308	1	7.5
836	Sw	310	3	5.9
842	Sw	215	3.1	7.1
847	Sw	330	5.6	10
865	Sw	40	1.8	11
914	Sw	122	6	7.7
918	Sw	127	3.5	10
999	Sw	336	7	12
Plot 4H6F				
731	Pj	252	5.7	8.6
807	Pj	208	1.4	10
282	Po	352	6.8	8
323	Po	209	5	9.8
356	Po	241	4	13
357	Po	242	4.6	9
362	Po	193	3.7	10
369	Po	218	7.3	15
736	Po	193	3.5	6.7
789	Po	32	1.7	3.5
810	Po	181	2.1	6.2
283	Sw	92	6.3	6.2
312	Sw	277	5.3	8.5
322	Sw	282	1.6	9.2
325	Sw	77	3	13
328	Sw	163	6	11
342	Sw	110	3.7	9.8
352	Sw	50	6	11
354	Sw	320	3.3	7.5
361	Sw	66	5	11
380	Sw	177	3.2	5.8
397	Sw	209	3.6	9.4
625	Sw	350	5.8	7.4
720	Sw	355	3.7	6.3
721	Sw	264	6.4	11
725	Sw	243	6.9	9.7
727	Sw	76	1.6	12
729	Sw	318	5.7	6.8
730	Sw	246	5	9
733	Sw	254	3	9.1
735	Sw	354	1.6	13
738	Sw	206	5.8	8.9
741	Sw	220	5.5	9.3
744	Sw	38	2.7	7.5
747	Sw	129	6.4	9.2
748	Sw	94	4.7	9.1
749	Sw	190	4.9	9.2
750	Sw	153	2.8	8.4
752	Sw	108	7	12
769	Sw	209	2	6.4
772	Sw	146	5	10
776	Sw	290	3.8	9.7
782	Sw	179	6.2	9
790	Sw	42	4.3	9
815	Sw	170	1.1	7.8
Plot 4M4				
87	Bf	135	3.4	5.1
57	Bw	124	5	6.5
28	Po	180	3.5	3
51	Po	184	5.9	10
55	Po	158	4.8	8.8
56	Po	156	5.6	11
67	Po	178	6.5	6.5
69	Po	117	5.2	8
72	Po	161	2.3	4.1
74	Po	180	2.8	3.5
78	Po	148	3.2	4.4
80	Po	138	3.1	7.4
82	Po	102	3.2	2.2
85	Po	216	1.3	3
89	Po	194	0.6	3.2
91	Po	225	1.4	11
92	Po	193	0.6	5.2
94	Po	242	3.2	4.7
95	Po	246	2.7	17
96	Po	246	3.4	3.6
313	Po	225	2.4	4
338	Po	230	2.1	3.6
363	Po	249	2.3	2.6
375	Po	232	2.4	8
398	Po	248	2.6	5.8

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
722	Po	234	2	3.2
724	Po	96	6.2	8.5
755	Po	116	3.7	7.2
759	Po	222	2.5	13
49	Sw	286	6.1	14
50	Sw	223	4.2	8
63	Sw	122	6.2	6.9
66	Sw	171	3.9	9.2
70	Sw	225	6.2	15
88	Sw	200	2.7	2.8
90	Sw	158	2.2	4.5
318	Sw	294	4.2	11
341	Sw	85	6.6	11
350	Sw	360	4.8	12
371	Sw	60	5.1	12
372	Sw	63	6.7	12
723	Sw	267	1.4	6.2
739	Sw	266	3.4	5.6
743	Sw	17	5.7	11
756	Sw	23	5.9	8.1
757	Sw	96	1.2	7.5
758	Sw	348	4.1	14
760	Sw	353	2.1	9
761	Sw	310	2.8	12
762	Sw	51	3.3	13
763	Sw	94	2.7	5.8
764	Sw	119	3.3	4.2
765	Sw	352	2.1	2.2
Pure Sw plots				
2C6S				
244	Bf	285	6.9	9.8
303	Bf	33	2.5	2.8
474	Bf	235	2.9	13
302	Bw	48	1.5	2.5
304	Bw	76	2.3	2.6
315	Bw	353	5	7.5
589	Bw	250	1	3.1
88	Sw	236	1.4	7.4
158	Sw	176	5.2	10
200	Sw	264	3.1	5.9
201	Sw	156	2.2	9.2
202	Sw	177	6.5	7.5
204	Sw	249	4.8	12
219	Sw	205	5	9.3
298	Sw	354	2.3	8.6
299	Sw	329	3.9	13
300	Sw	1	3.7	10
301	Sw	52	2	13
305	Sw	87	3.6	8.1
306	Sw	86	3.7	9.7
307	Sw	59	4.3	7.7
308	Sw	60	4.5	7.6
309	Sw	50	5.5	11
311	Sw	26	6.5	14
312	Sw	42	6.7	15
313	Sw	3	5.6	11
314	Sw	5	7	6.7
316	Sw	343	5.6	12
317	Sw	306	5.1	13
439	Sw	208	3.6	8.6
440	Sw	206	5	10
451	Sw	134	4	9.8
454	Sw	136	4.1	7.6
475	Sw	270	4	6.6
483	Sw	235	5.8	12
508	Sw	292	4.4	9.6
516	Sw	160	6.5	8.6
518	Sw	115	1.3	8.2
520	Sw	115	3.5	9.4
536	Sw	244	1.5	2.6
552	Sw	317	1	8.6
558	Sw	268	3.1	7
566	Sw	148	5.1	10
578	Sw	17	3.4	8.1
598	Sw	298	2.9	13
891	Sw	246	6.9	14
899	Sw	228	7	13
Plot 2D8N				
506	Bf	265	5.5	6.7
198	Bw	220	1.8	3.7
569	Bw	109	1.4	2.6
93	Sw	111	5.3	11
96	Sw	285	3.9	11

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
195	Sw	236	1.1	10
196	Sw	221	2.5	10
197	Sw	257	3.1	11
199	Sw	285	2.5	9.5
200	Sw	142	1.8	8.8
241	Sw	243	6.9	10
243	Sw	224	6.6	8.1
254	Sw	268	6.5	9
255	Sw	155	6.9	12
282	Sw	19	2.4	16
283	Sw	315	2.6	8.8
284	Sw	44	3.3	12
285	Sw	109	3.2	9.3
286	Sw	70	5	11
287	Sw	86	4.5	7.8
288	Sw	41	6.9	12
290	Sw	95	6	11
291	Sw	31	6.4	14
292	Sw	6	4.1	9.2
293	Sw	316	4	12
294	Sw	342	3.5	9.5
295	Sw	322	4.7	7.6
296	Sw	345	6.2	14
297	Sw	7	5.6	12
434	Sw	219	5.8	12
443	Sw	123	7	11
445	Sw	301	3.8	8.8
447	Sw	152	5	10
449	Sw	181	4.6	12
459	Sw	190	6.1	11
479	Sw	169	3.2	11
486	Sw	257	5.9	7.2
522	Sw	136	4.1	9.1
525	Sw	229	5.3	5.9
540	Sw	243	4.1	9.5
596	Sw	146	6	7.8
856	Sw	312	5.8	6.9
880	Sw	131	5.3	12
895	Sw	286	6	7.7
Plot 2E9N				
391	Sw	109	6.1	6.4
392	Sw	211	6.2	6.2
394	Sw	50	6.3	9.1
396	Sw	192	4.3	6.1
504	Sw	248	1.7	12
506	Sw	9	4.2	8.6
516	Sw	158	1.3	13
524	Sw	227	2.9	9.1
525	Sw	294	5.9	8
527	Sw	270	3.5	9.8
529	Sw	359	6.9	9.2
552	Sw	321	6	7.5
556	Sw	172	5.7	13
562	Sw	64	4.8	11
568	Sw	13	5.6	11
583	Sw	126	6.1	8.7
586	Sw	336	1.2	8.7
587	Sw	308	5.5	8.5
600	Sw	158	4.5	9.9
604	Sw	320	5.4	7.7
605	Sw	192	4.2	7.6
608	Sw	247	4.4	8.5
611	Sw	272	5.5	11
615	Sw	6	2.6	7.1
628	Sw	77	3.7	8.6
638	Sw	217	4.6	11
639	Sw	47	1.5	8.8
643	Sw	326	3.4	11
645	Sw	43	3.5	8.8
770	Sw	51	1.4	2.3
Plot 3H10E				
124	Po	129	1.7	2.6
138	Po	174	4.6	13
118	Sw	277	2.7	14
119	Sw	188	2.2	16
120	Sw	105	1.3	13
121	Sw	74	2.8	15
122	Sw	327	2	5.5
123	Sw	208	3.9	14
125	Sw	314	3.7	17
126	Sw	11	3.2	8
127	Sw	351	4.3	14

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
128	Sw	28	5.2	17
129	Sw	32	7	14
130	Sw	4	5.8	17
131	Sw	334	6.1	16
132	Sw	65	4.4	13
133	Sw	63	6.5	17
134	Sw	77	6.8	11
135	Sw	124	3.6	9
136	Sw	126	5	11
137	Sw	132	6.1	9.3
139	Sw	197	4.9	13
140	Sw	232	6.7	9.7
141	Sw	255	4.4	16
142	Sw	249	6.3	9.4
143	Sw	249	6.4	9.3
144	Sw	268	5.9	17
145	Sw	290	4.7	12
Plot 3I7S				
179	Sw	30	2.3	12
180	Sw	298	4.3	12
181	Sw	34	3.9	13
183	Sw	138	4.1	15
184	Sw	139	6.1	11
185	Sw	104	5.8	15
186	Sw	282	5.3	7.9
187	Sw	258	3.6	11
188	Sw	271	6.7	12
189	Sw	236	5.5	16
190	Sw	129	6.6	18
192	Sw	209	6.5	13
193	Sw	170	4.4	13
194	Sw	139	6.5	7.1
865	Sw	329	6.1	10
866	Sw	344	6.7	13
868	Sw	360	7	14
869	Sw	19	6.5	15
870	Sw	10	5.1	8
871	Sw	44	5.4	6.8
872	Sw	44	5.3	13
873	Sw	69	4	10
874	Sw	231	3.7	11
875	Sw	272	2.7	10
876	Sw	329	4	11
877	Sw	44	5.3	13
877	Sw	349	4.3	14
878	Sw	84	2.3	14
879	Sw	120	1.2	12
Plot 3J8				
356	Po	268	5.2	9.5
359	Po	263	5.9	10
362	Po	262	5.6	12
358	Sw	246	5.3	8.6
361	Sw	52	1.2	12
363	Sw	259	4	8.5
364	Sw	229	6.5	11
365	Sw	179	3.4	13
366	Sw	306	4.2	7.9
367	Sw	306	1.8	13
368	Sw	98	3.4	10
371	Sw	230	2.1	13
372	Sw	229	5	9.5
373	Sw	196	4.3	16
374	Sw	354	7	13
375	Sw	282	5.2	9.4
377	Sw	338	6.1	11
378	Sw	305	4.6	8.5
381	Sw	320	6	9.5
382	Sw	154	5.8	13
383	Sw	69	2.5	8.9
385	Sw	329	4.2	11
386	Sw	124	2.5	12
387	Sw	155	2.2	13
389	Sw	63	2.5	12
390	Sw	270	6.1	11
391	Sw	328	4.1	11
392	Sw	347	4.7	9.8
393	Sw	297	6.9	6.8
394	Sw	164	6.7	15
395	Sw	4	5	13
397	Sw	242	7	9.5
399	Sw	243	6.8	9.5
400	Sw	347	4.6	11
689	Sw	131	5.7	11

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
864	Sw	1	2	14
865	Sw	18	2.9	11
Plot 4I7E				
40	Bf	280	2.9	4
41	Bf	253	1.9	8.1
44	Bf	96	2.7	7.8
211	Bf	293	4.9	6.5
215	Bf	271	6.3	7.4
272	Bf	176	4.8	6.6
306	Bf	309	4.9	9.8
646	Bf	312	5.9	8.3
793	Po	281	7	8.9
36	Sw	84	5.5	7.2
38	Sw	126	6.1	7.3
39	Sw	175	5.3	7.1
42	Sw	214	2.1	8.5
45	Sw	151	1.3	6.1
46	Sw	85	1.2	6.3
216	Sw	243	6.5	8
217	Sw	180	6.9	9.5
218	Sw	243	6.3	7.5
271	Sw	166	6.4	7.1
391	Sw	324	3.4	7.1
393	Sw	45	5.5	11
620	Sw	8	1.5	5
622	Sw	85	4	8.2
623	Sw	13	5.5	6.8
629	Sw	350	4.7	8.2
636	Sw	57	3.8	12
637	Sw	10	5.5	7.1
642	Sw	340	6.2	7.6
647	Sw	65	6.3	6.3
792	Sw	245	3.5	9.8
794	Sw	272	5.8	8.9
795	Sw	99	4.3	8.5
Plot 4J5W				
387	Bf	2	2.6	4.9
309	Sw	82	3.1	11
319	Sw	156	3.5	13
336	Sw	16	4.4	8.7
339	Sw	168	6.1	9
389	Sw	118	3.8	8.5
392	Sw	22	1.9	13
615	Sw	302	1.3	13
617	Sw	326	5.5	8.1
618	Sw	183	1.9	12
619	Sw	258	2.9	9.6
631	Sw	268	5.4	12
632	Sw	188	4.2	11
633	Sw	302	5.6	8
634	Sw	246	5.8	13
635	Sw	144	5.2	9.3
645	Sw	220	5.5	13
649	Sw	204	3.6	12
768	Sw	344	3.4	6.3
773	Sw	356	6.1	9.1
777	Sw	120	1.8	10
796	Sw	42	3.7	6.9
797	Sw	66	6.8	11
798	Sw	19	6.4	11
799	Sw	10	6.7	9.7
Plot 4L6				
745	Bf	270	6.5	11
53	Po	154	6.3	9.7
54	Po	152	5.5	9.5
307	Po	274	2.7	4.1
47	Sw	156	4.8	15
48	Sw	240	4.8	14
59	Sw	222	4.3	21
62	Sw	247	5.9	13
64	Sw	212	1.3	12
315	Sw	25	3.1	12
317	Sw	298	1.7	16
347	Sw	178	6.6	12
351	Sw	347	6.1	16
355	Sw	204	6.9	11
358	Sw	310	4.8	8.3
376	Sw	49	4.8	13
383	Sw	279	6.2	12
385	Sw	332	5.3	13
386	Sw	136	4.3	16
394	Sw	82	4.1	16
395	Sw	247	3.1	3.9

Tree #	Spp.	Azi. (°)	Dist. (m)	DBH (cm)
396	Sw	352	3.8	15
719	Sw	230	6.4	10
728	Sw	73	1	18
732	Sw	47	4.8	12
740	Sw	358	1.8	11
742	Sw	314	3.6	13
753	Sw	30	4.9	9.9
754	Sw	358	1.8	6.3
775	Sw	105	2.8	9.5
778	Sw	247	3.2	11
785	Sw	62	2.6	11

APPENDIX III

SSR ALLELE SIZES FOR SW TREES (FOLIAGE)

Stars denote a locus profile occurring more than once within a plot. All trees white spruce unless otherwise noted.

	allele sizes (base pairs)				
tree #	PGL14 green		UAPgCA91 blue		notes
Plot 4L6					
315	132*	140*	132	154	
383	132*	140*	134	154	
355	136	146	146	150	
753	136	152	142	190	
47	136	162	132*	132*	
386	138	140	136	176	
785	138	152	146*	146*	
775	138	156	134	134	
728	138	158	146	176	
358	140	150	132*	132*	
385	140	152	116	116	
376	140*	156*	130*	130*	forked stem
732	140*	156*	130*	130*	forked stem
394	142	158	130*	130*	
740	142*	172*	140*	156*	forked stem
754	142*	172*	140*	156*	forked stem
742	148	176	126	138	
719	150	164	126	126	
48	150*	172*	146*	146*	forked stem
62	150*	172*	146*	146*	forked stem
396	152	172	160*	160*	
351	154	154	160*	160*	
59	154	172	142*	142*	
347	156	164	176	176	
64	158	170	142	196	
317	160	166	136	146	
778	168	172	142*	142*	
Plot 4H6F					
815	136	136	178	178	
772	138	148	142*	142*	
721	138	170	136	148	
729	140	142	152	152	
741	140	154	140	140	
727	140	156	118	172	
735	140	164	142	148	
397	142*	150*	130*	130*	
354	142*	150*	150	150	
782	142	154	132	158	
342	142	160	130*	130*	
283	144	148	130	184	
750	144	150	154*	154*	
744	144	152	142*	142*	
322	144	154	126	144	
769	144	170	142	194	
790	146	160	126*	142*	
361	148	156	130*	130*	
752	148*	160*	126*	142*	
625	148*	160*	140	158	
367	148	162	130	148	
730	150	154	118	176	
776	150	156	114	142	
325	150	164	144	144	
364	152	152	116	116	
749	152*	152*	132	160	
312	152*	152*	148	148	
352	152	156	146	154	
720	152	160	154*	154*	
733	154	172	136	144	
748	160	160	142	170	
747	162*	162*	126	134	
328	162*	162*	142	146	
725	164	168	146	146	
738	164	174	130*	130*	
Plot 4I7E					
642	138	158	132	132	
636	140	150	116	116	
629	140	152	174	174	
393	140*	164*	144	144	
42	140*	164*	170	170	
647	144	154	134*	160*	
46	146	164	142	142	
36	148	154	158	158	
622	150	158	130*	130*	
271	150	172	126	126	
795	152	152	106	106	unusual blue peak, very strong
391	152	156	144	172	
792	152	158	136	160	
216	152*	166*	118*	132*	forked stem
218	152*	166*	118*	132*	forked stem

allele sizes (base pairs)

tree	PGL14		UAPgCA91		
#	green		blue		notes
217	152	170	142	172	
794	152	172	130	198	
624	152	174	130*	130*	
623	154*	178*	134*	160*	forked stem
637	154*	178*	134*	160*	forked stem
38	158	158	154	166	
45	160	168	116	118	
39	166	166	154	154	
Plot 4J5W					
649	136	156	148	148	
796	138	138	132*	132*	
632	138	144	126	134	
309	138	150	134	174	
645	138*	152*	128	148	
799	138*	152*	130	198	
339	138*	158*	128*	128*	
768	138*	158*	164	164	
392	140	144	130	136	
336	140	150	118	118	
619	140	152	120	172	
630	140	162	132*	132*	
617	142	142	236	236	
631	146	150	150	150	
635	146*	158*	118	130	
798	146*	158*	142	172	
633	146	170	136	136	
618	148	154	130	156	
773	150	150	126	176	
777	150	162	138	192	
319	150	166	140	156	
389	152	166	128*	128*	
797	154*	154*	114	114	
634	154*	154*	126	150	
615	160	164	140	150	
Plot 4G5					
498	136	136	146	150	
172	136	156	130	162	
191	138	140	170	170	
496	138	150	150	150	
174	138	158	140	148	
842	138	164	132*	132*	
914	138	172	142	160	
194	140	152	130	152	
847	140*	156*	138	158	
817	140*	156*	174	174	
200	140	160	130	144	
291	140	166	118	162	green 140 very large
918	146*	156*	116	142	
865	146*	156*	132*	132*	
306	146	160	132	142	
910	148	160	110	110	unusual blue peak
182	150	150	128	170	
398	150	158	118	170	blue 118 very large and strong
189	150	162	130	150	
299	152	158	152	156	
822	152	160	142	166	
204	156	156	136	168	
999	158	162	134	164	
207	164	170	118	118	
Plot 4M4					
371	140	160	148*	148*	
762	140	168	148*	148*	
66	140	170	148	200	
757	142	152	142*	142*	
723	142*	156*	144	144	
49	142*	156*	154	154	
372	142*	156*	158	186	
63	148	156	118	132	
758	150	154	148	174	
760	150*	156*	132	132	
350	150*	156*	158	158	
70	150	160	128	132	
756	150	164	130	148	
743	150	164	148*	148*	
310	150	174	136	136	
318	152	152	fail	fail	
50	152	160	142	148	
761	154	160	114	144	
341	156	156	142*	142*	
Plot 3J8					
397	136	136	118*	118*	
399	136*	138*	118*	118*	
376	138*	138*	130	142	
864	138	150	142	166	
368	138	156	130	134	
381	138	160	164	164	
392	138*	170*	140*	140*	
400	138*	170*	140	158	
865	138	172	128	152	
373	140	140	168	168	
367	140	152	118*	118*	
689	140	154	fail	fail	
380	140*	156*	142*	142*	forked stem
386	140*	156*	142*	142*	forked stem

allele sizes (base pairs)

tree #	PGL14 green		UAPgCA91 blue		notes
366	140*	166*	152*	152*	probably forked stem
378	140*	166*	fail	fail	probably forked stem
383	142*	152*	136	172	
389	142*	152*	136	174	
358	142	156	152	168	
365	144	166	174	174	
385	146*	160*	142*	142*	forked stem
391	146*	160*	142*	142*	forked stem
375	146	164	152*	152*	
363	148	152	134	134	
390	150	150	128	128	
372	150*	158*	118	132	
394	150*	158*	156	156	
395	150	172	154	154	
371	152*	152*	118	142	
361	152*	152*	134	144	
377	152	158	134	154	
382	152	170	fail	fail	
364	152	174	118	144	
393	154	154	140*	140*	
374	156	156	162	162	
387	162	162	130	200	
Plot 3H10					
901	132	140	132	176	
932	136	160	132	136	
922	138	142	142	142	
938	140	146	110*	110*	black spruce
930	140	152	132	166	
907	140*	154*	130*	174*	
908	140*	154*	130*	174*	
948	140*	156*	174	174	
947	140*	156*	fail	fail	
911	140	166	fail	fail	
934	142	170	136*	136*	
912	144*	156*	194*	194*	forked stem
913	144*	156*	194*	194*	forked stem
931	144	160	148*	148*	
941	148	148	110*	110*	black spruce
940	148	170	110*	110*	black spruce
918	150*	160*	126*	126*	forked stem
919	150*	160*	126*	126*	forked stem
926	150	174	184	184	
902	152	152	148	182	
905	152	156	148*	148*	
909	152	160	154	154	
920	156	164	142	164	
942	156	178	126	150	
903	158*	166*	134*	134*	forked stem
904	158*	166*	134*	134*	forked stem
927	158*	166*	136*	136*	
943	162	162	144	144	
925	164	164	140	156	
923	166	166	114	128	
924	fail	fail	140	140	four green alleles: 136, 150, 158, 170
Plot 3I7S					
870	134	162	114	144	
875	138	138	144	150	
181	138	150	118	134	
866	138	156	164	164	
879	140	148	118	130	
180	142	152	182	182	
185	142	166	160	160	
184	144*	150*	172*	172*	forked stem
194	144*	150*	172*	172*	forked stem
188	146	154	130	172	
349	146	176	142	150	
186	148	152	130	142	
187	148	164	fail	fail	
873	150	156	142*	142*	
874	150	160	132	132	
868	150*	162*	144	144	
869	150*	162*	152	152	
183	150	166	132	142	
878	150	168	142*	142*	
872	152*	152*	162	162	probably forked stem
871	152*	152*	fail	fail	probably forked stem
876	152	164	128	148	
192	152	166	118	118	
189	154	160	130	130	
179	154*	162*	128	128	
190	154*	162*	138	138	
193	154	170	136	136	
865	164	168	142*	142*	
Plot 3JK5			*	*	
691	136	154	130	130	
870	138	138	116	162	
167	140	148	118	142	
696	140	156	118	150	
687	140	164	118	126	
175	142	154	134	158	
862	148	148	154	154	
685	150	156	156	164	

	allele sizes (base pairs)				
tree	PGL14		UAPgCA91		
#	green		blue		notes
858	150	166	132	132	
876	152*	152*	118	120	
170	152*	152*	136	144	
684	152	164	176	176	
693	162	162	138	144	
Plot 3G10					
967	130	130	140	168	
980	136*	150*	142*	142*	forked stem
981	136*	150*	142*	142*	forked stem
971	138	150	162	204	
982	138	156	134*	134*	
957	140	146	142*	156*	
979	140	150	142	164	
953	140*	154*	132	132	
978	140*	154*	150	150	
935	140	156	146	146	
958	140*	166*	142*	142*	forked stem
959	140*	166*	142*	142*	forked stem
960	142	142	134*	134*	
964	142*	158*	138*	138*	
956	142*	158*	142*	156*	
968	144*	148*	118*	136*	forked stem
969	144*	148*	118*	136*	forked stem
966	144	162	132	186	
952	150	158	118	146	
973	150*	164*	116*	146*	forked stem
974	150*	164*	116*	146*	forked stem
976	152	152	154	180	
945	152	178	fail	fail	
977	154	166	142*	142*	
972	156	166	132	146	
963	158	158	140	150	
35	158	174	138	150	
667	160	166	116	116	
970	160	174	128	128	
961	164	164	138*	138*	
962	166	178	118	150	
Plot 3H10E					
119	136	150	152	152	
130	136	174	118*	118*	
144	138	138	146	146	
139	138	144	118*	118*	
126	138	156	130	130	
142	138*	158*	118*	132*	forked stem
143	138*	158*	118*	132*	forked stem
135	138*	170*	182*	182*	forked stem
136	138*	170*	182*	182*	forked stem
121	140	152	126	126	
133	140	154	128	128	
132	140*	158*	138	148	
127	140*	158*	184	184	
125	142	148	142*	142*	
140	142	158	132	146	
118	144	148	130	136	
123	144	156	126	142	
129	148	152	142	172	
134	148	154	fail	fail	
141	148	166	142*	142*	
137	152	152	144*	144*	
120	152	158	130	184	
145	152	160	144*	144*	
128	154	154	212	212	
131	156	156	134	134	
Plot 2D5					
332	134	162	118	172	
464	138	140	144	144	
333	138	154	136	144	
232	138	162	fail	fail	
320	140	140	fail	fail	
242	140	160	128	142	
331	142	142	fail	fail	
89	142	154	128	136	
218	142*	160*	128*	128*	
328	142*	160*	fail	fail	
471	144*	154*	128*	128*	
873	144*	154*	132	150	
154	146	162	144	168	
472	148	148	124	134	
337	148	178	142*	142*	
534	150	150	126	126	
883	152*	152*	116	116	
240	152*	152*	136	136	
245	152	162	fail	fail	
695	154*	154*	118	128	
336	154*	154*	142	168	
319	154	162	fail	fail	
513	154	174	146*	146*	
329	156	156	fail	fail	
335	156	162	142*	142*	
334	156	172	156	156	
330	156	174	134	134	
461	166	166	144	156	
384	170	170	fail	fail	
533	174	174	146*	146*	

	allele sizes (base pairs)				
tree #	PGL14 green		UAPgCA91 blue		notes
Plot 2E9N					
600	136	160	148	204	
645	138	138	118	118	
568	138	142	116	148	
394	138	146	156*	156*	
556	138	148	130	134	
529	138	150	128	132	
538	138	158	fail	fail	
504	138	178	128	138	
400	140	140	128*	148*	
638	140	156	142*	142*	
615	140	158	138	138	
527	140*	160*	142*	142*	
525	140*	160*	144*	144*	
392	140	162	118	132	
552	140*	168*	134*	144*	forked stem
604	140*	168*	134*	144*	forked stem
608	140	170	130	154	
551	142	142	156*	156*	
530	144	170	142*	142*	
495	146*	160*	130	130	
583	146*	160*	130	204	
396	150*	150*	142*	150*	forked stem
605	150*	150*	142*	150*	forked stem
628	150	156	162	162	
391	152	152	128	170	
639	152*	158*	128*	148*	forked stem
770	152*	158*	128*	148*	forked stem
611	152	160	166	166	
524	154	160	144*	144*	
562	154	164	144*	144*	
516	154	166	120	136	
586	156	156	132	132	
506	156	172	194	194	
587	160	160	128*	128*	
643	166	166	128*	128*	
Plot 2D8N					
243	136	136	126*	136*	
525	136	138	126*	136*	
282	136	144	166	182	
96	136	154	150	178	
196	138*	138*	188	188	
199	138*	138*	fail	fail	
254	138	140	114	114	
286	138	144	fail	fail	
434	138	150	128	142	
292	140	144	116	144	
293	140	144	fail	fail	
294	140*	152*	128	156	
295	140*	152*	160	160	
895	140*	152*	fail	fail	
449	140	170	116	194	
596	140	172	138	192	
479	142	146	172	172	
296	144	170	144	144	
255	146*	162*	178	178	
284	146*	162*	130	178	
297	148	148	168	178	
486	148	156	126	154	
93	148	162	116	204	
540	150	154	142	174	
200	150	160	fail	fail	
283	152	156	134*	142*	
880	152	164	132	142	
197	152	168	154	168	
522	154	160	130	176	
285	154	172	fail	fail	
291	156	156	134	134	
290	156	160	148	148	
241	156	168	136	146	
856	156	170	134*	142*	
447	160*	160*	118	118	
445	160*	160*	134	152	
443	160	174	144	162	
459	166*	166*	128	134	
287	166*	166*	156	156	
288	170	170	140	180	
195	178	178	160	160	
Plot 2C6S					
598	134	152	fail	fail	
311	136*	140*	134*	134*	
314	136*	140*	134*	134*	
891	138	146	116	146	
516	138	150	174	174	
317	138	162	128	166	
309	140	140	130*	130*	
307	140*	148*	126	170	
310	140*	148*	142	158	
899	140	160	128	142	
439	140	162	144	144	
451	142*	166*	132*	132*	forked stem
454	142*	166*	132*	132*	forked stem
219	144*	144*	140*	160*	forked stem
440	144*	144*	140*	160*	forked stem
508	144	152	118	140	
298	144	154	126	146	

552	144	156	130	142	

	allele sizes (base pairs)				
tree #	PGL14 green		UAPgCA91 blue		notes
316	144	166	134	164	
312	146	160	128	128	
518	148	158	136	162	
483	150	150	128	140	
313	150	156	128	180	
520	150	158	130	136	
201	150	160	146	146	
299	150	170	150	204	
305	152*	154*	150*	150*	forked stem
306	152*	154*	150*	150*	forked stem
301	152	156	fail	fail	
88	152	162	144	156	
558	152	166	fail	fail	
308	152*	168*	118	136	
566	152*	168*	130	146	
578	154	154	138	154	
300	154	158	148	148	
475	154*	164*	162	166	forked stem
523	154*	164*	fail	fail	forked stem
204	156	162	156	156	
158	158	170	180	180	
202	160	160	130*	130*	
2J11S					
689	134	152	132*	132*	
596	136	136	132	154	
692	136*	150*	114*	144*	
687	136*	150*	114*	144*	
866	138	140	162	182	
696	138	142	142	180	
683	140	140	174	174	
520	140	158	132*	132*	
662	140*	162*	118*	126*	forked stem
663	140*	162*	118*	126*	forked stem
672	140*	162*	154*	154*	
676	142	156	140	166	
693	144*	144*	134	134	
385	144*	144*	144	156	
677	146	156	130	134	
691	148	152	132*	132*	
697	148	178	146	160	
681	150	158	136	174	
694	150	170	132	142	
678	152	152	150	178	
680	152	162	154*	154*	
686	152*	166*	128	146	
685	152*	166*	140	140	
679	156	156	126	132	
624	160	170	144	188	
2F10W					
793	136*	138*	118	142	
775	136*	138*	144*	144*	
794	136	156	130	142	
265	138	140	136	144	
783	138	142	118	132	
785	138	154	142	146	
261	138	162	144*	144*	
266	140	144	140	142	
788	140*	150*	116*	142*	
998	140*	150*	116*	142*	
790	140	152	140*	140*	
220	140	152	160	160	
219	140	156	134*	150*	
260	140	156	fail	fail	
771	140*	160*	128	156	
777	140*	160*	130	140	
263	140	162	130	146	
787	140*	164*	130	130	
262	140*	164*	140*	140*	
789	142	152	134*	150*	
784	144	152	fail	fail	Four blue alleles 120, 134, 150, 166
797	146	158	140	176	
259	146	160	158	172	
779	148	168	130*	144*	
798	150	160	118	184	
589	150	162	114	134	
786	150	168	132	132	
776	152*	152*	146*	146*	
774	152*	152*	158	168	
800	152	152	174	182	
780	152	154	146*	146*	
804	152	160	134	142	
772	154	154	128*	128*	
801	154	162	130*	144*	
781	154*	166*	128*	128*	
782	154*	166*	128*	128*	
796	156*	164*	134*	154*	
999	156*	164*	134*	154*	
799	156	176	128	136	
802	158	158	166	166	
795	158	164	168	168	
791	158	172	150	150	

APPENDIX IV

SSR ALLELE SIZES FOR SW ROOT FRAGMENTS

Root fragment numbers are coded as plot—hole azimiuth—fragment number. —Failmeans that no signal was detected.

root fragment #	allele sizes (base pairs) PGL14 green		UAPgCA91 blue		notes
2C6S-0-1	154	154	148	148	
2C6S-0-2	fail	fail	fail	fail	
2C6S-0-3	154	158	148	148	
2C6S-0-4	144	154	126	146	
2C6S-0-5	154	158	148	148	
2C6S-0-6	144	154	126	146	
2C6S-0-7	140	148	142	160	
2C6S-0-8	144	154	126	146	
2C6S-0-9	154	154	148	148	
2C6S-0-10	154	158	148	148	
2C6S-0-11	144	154	126	146	
2C6S-0-12	144	156	130	142	
2C6S-0-13	fail	fail	fail	fail	
2C6S-0-14	154	158	148	148	
2C6S-0-15	144	154	126	146	
2C6S-0-16	154	154	148	148	
2C6S-0-17	150	170	126	150	
2C6S-0-18	144	154	126	146	
2C6S-0-19	fail	fail	fail	fail	
2C6S-0-20	144	154	126	146	
2C6S-0-21	fail	fail	132	132	
2C6S-0-22	144	154	126	146	
2C6S-120-1	154	154	fail	fail	
2C6S-120-2	fail	fail	fail	fail	
2C6S-120-3	166	166	fail	fail	
2C6S-120-4	fail	fail	fail	fail	
2C6S-120-5	fail	fail	fail	fail	
2C6S-120-6	fail	fail	fail	fail	
2C6S-120-7	150	158	130	136	
2C6S-120-8	142	166	132	132	
2C6S-120-9	142	166	132	132	
2C6S-120-10	152	152	fail	fail	
2C6S-120-11	150	150	132	132	
2C6S-120-12	142	166	132	132	
2C6S-120-13	150	158	130	136	
2C6S-120-14	142	166	132	132	
2C6S-240-1	156	162	156	156	
2C6S-240-2	156	162	156	156	
2C6S-240-3	156	162	156	156	
2C6S-240-4	152	166	156	162	
2C6S-240-5	150	166	fail	fail	
2C6S-240-6	150	160	146	146	
2C6S-240-7	156	162	156	156	
2C6S-240-8	150	150	156	156	
2C6S-240-9	150	160	148	148	
2C6S-240-10	156	162	156	156	
2C6S-240-11	156	162	156	156	
2C6S-240-12	140	162	144	144	
2C6S-240-13	156	162	156	156	
2C6S-240-14	150	160	146	146	
2C6S-240-15	156	162	156	156	
2C6S-240-16	156	162	156	156	
2C6S-240-17	144	144	140	160	
2C6S-240-18	158	170	180	180	
2C6S-240-19	156	162	156	156	
2C6S-240-20	156	162	156	156	
2D5-0-1	156	174	134	134	
2D5-0-2	138	156	fail	fail	Green also 166
2D5-0-3	156	156	132	192	
2D5-0-4	156	156	132	192	
2D5-0-5	156	156	132	192	
2D5-0-6	fail	fail	fail	fail	
2D5-0-7	150	156	132	192	
2D5-120-1	144	154	128	128	
2D5-120-2	138	140	144	144	
2D5-120-3	144	154	128	128	

	allele sizes (base pairs)				
root fragment #	PGL14 green		UAPgCA91 blue		notes
2D5-120-4	144	154	128	128	
2D5-120-5	138	140	114	144	
2D5-120-6	138	140	144	144	
2D5-120-7	144	154	128	128	
2D5-120-8	144	154	128	128	
2D5-120-9	144	154	128	128	
2D5-120-10	138	140	144	144	
2D5-120-11	138	140	144	144	
2D5-120-12	144	154	128	128	
2D5-120-13	138	140	144	144	
2D5-120-14	fail	fail	fail	fail	
2D5-120-15	138	140	144	144	
2D5-240-1	140	140	204	204	
2D5-240-2	140	140	204	204	
2D5-240-3	154	162	128	144	
2D5-240-4	140	140	116	204	
2D5-240-5	140	140	116	204	
2D5-240-6	fail	fail	fail	fail	
2D5-240-7	140	140	204	204	
2D5-240-8	140	140	204	204	
2D5-240-9	140	140	116	204	
2D5-240-10	140	140	206	206	
2D5-240-11	fail	fail	fail	fail	
2D5-240-12	140	140	138	204	
2D5-240-13	140	140	134	206	
2D5-240-14	fail	fail	fail	fail	
2D5-240-15	140	140	204	204	
2D8N-0-1	fail	fail	fail	fail	
2D8N-0-2	140	152	128	156	
2D8N-0-3	144	170	144	144	
2D8N-0-4	136	144	166	182	
2D8N-0-5	152	156	134	142	
2D8N-0-6	140	152	160	160	
2D8N-0-7	140	152	128	156	
2D8N-0-8	140	152	128	156	
2D8N-0-9	140	152	128	156	
2D8N-0-10	146	162	130	178	
2D8N-0-11	fail	fail	126	154	
2D8N-0-12	fail	fail	128	128	
2D8N-0-13	140	152	160	160	
2D8N-0-14	140	152	128	156	
2D8N-0-15	140	152	128	156	
2D8N-120-1	148	162	116	204	
2D8N-120-2	fail	fail	fail	fail	
2D8N-120-3	148	162	116	204	
2D8N-120-4	152	164	132	142	
2D8N-120-5	142	146	172	172	
2D8N-120-6	152	164	132	132	
2D8N-120-7	fail	fail	fail	fail	
2D8N-120-8	150	160	128	128	
2D8N-120-9	138	144	fail	fail	
2D8N-120-10	148	162	116	204	
2D8N-120-11	138	144	fail	fail	
2D8N-120-12	fail	fail	fail	fail	
2D8N-120-13	150	160	128	128	
2D8N-120-14	148	162	116	206	
2D8N-120-15	152	162	132	132	
2D8N-240-1	150	154	142	174	
2D8N-240-2	156	166	136	146	
2D8N-240-3	152	168	154	168	
2D8N-240-4	fail	fail	fail	fail	
2D8N-240-5	150	154	142	174	
2D8N-240-6	152	168	154	168	
2D8N-240-7	136	138	126	136	
2D8N-240-8	152	166	154	168	
2D8N-240-9	150	154	142	174	
2D8N-240-10	136	138	126	136	
2D8N-240-11	150	154	142	174	
2D8N-240-12	fail	fail	fail	fail	
2D8N-240-13	152	168	154	168	
2D8N-240-14	152	168	154	168	
2D8N-240-15	150	154	142	174	
2E9N-0-1	152	166	128	128	
2E9N-0-2	140	160	142	142	
2E9N-0-3	fail	fail	fail	fail	
2E9N-0-4	152	166	128	128	
2E9N-0-5	152	166	128	164	
2E9N-0-6	154	164	144	144	
2E9N-0-7	154	164	128	144	
2E9N-0-8	152	158	128	148	
2E9N-0-9	fail	fail	fail	fail	

	allele sizes (base pairs)				
root fragment #	PGL14 green		UAPgCA91 blue		notes
2E9N-0-10	140	160	142	142	
2E9N-0-11	140	160	142	142	
2E9N-0-12	140	160	142	142	
2E9N-0-13	140	160	142	142	
2E9N-0-14	166	166	142	142	
2E9N-0-15	140	160	142	142	
2E9N-120-1	152	154	128	170	
2E9N-120-2	156	168	136	148	
2E9N-120-3	152	154	128	170	
2E9N-120-4	136	160	148	206	
2E9N-120-5	152	154	128	170	
2E9N-120-6	156	168	136	148	
2E9N-120-7	140	156	128	134	
2E9N-120-8	152	154	128	170	
2E9N-120-9	140	160	142	142	
2E9N-120-10	154	164	144	144	
2E9N-120-11	154	164	144	144	
2E9N-120-12	140	160	142	142	
2E9N-120-13	152	154	128	170	
2E9N-120-14	150	156	162	162	
2E9N-120-15	152	154	128	170	
2E9N-240-1	140	160	144	144	
2E9N-240-2	140	156	142	142	
2E9N-240-3	140	156	142	142	
2E9N-240-4	152	166	128	128	
2E9N-240-5	140	162	118	132	
2E9N-240-6	160	160	144	144	
2E9N-240-7	140	170	130	154	
2E9N-240-8	160	160	fail	fail	
2E9N-240-9	fail	fail	fail	fail	
2E9N-240-10	140	156	142	142	
2E9N-240-11	152	160	166	166	
2E9N-240-12	152	166	128	128	
2E9N-240-13	140	162	118	132	
2E9N-240-14	152	166	128	128	
2E9N-240-15	160	160	144	144	
2F10W-0-1	140	160	128	156	
2F10W-0-2	136	156	130	142	
2F10W-0-3	fail	fail	fail	fail	
2F10W-0-4	136	156	130	142	
2F10W-0-5	fail	fail	138	138	
2F10W-0-6	140	160	130	140	
2F10W-0-7	136	156	130	142	
2F10W-0-8	138	142	118	132	
2F10W-0-9	136	136	118	142	
2F10W-0-10	138	138	144	144	
2F10W-0-11	138	138	144	144	
2F10W-0-12	fail	fail	fail	fail	
2F10W-0-13	152	152	158	168	
2F10W-0-14	fail	fail	fail	fail	
2F10W-0-15	138	138	144	144	
2F10W-120-1	140	144	140	140	
2F10W-120-2	142	152	134	150	
2F10W-120-3	140	144	140	140	
2F10W-120-4	140	160	130	140	
2F10W-120-5	140	160	130	140	
2F10W-120-6	142	152	134	150	
2F10W-120-7	140	152	138	138	
2F10W-120-8	140	160	130	140	
2F10W-120-9	154	166	fail	fail	
2F10W-120-10	142	152	134	150	
2F10W-120-11	154	166	128	128	
2F10W-120-12	130	130	140	140	
2F10W-120-13	140	160	130	140	
2F10W-120-14	154	166	128	128	
2F10W-120-15	154	166	128	128	
2F10W-240-1	150	158	166	166	
2F10W-240-2	150	158	166	166	
2F10W-240-3	150	158	166	166	
2F10W-240-4	150	162	114	134	
2F10W-240-5	150	162	114	134	
2F10W-240-6	152	164	158	168	
2F10W-240-7	158	158	166	166	
2F10W-240-8	fail	fail	fail	fail	
2F10W-240-9	158	158	166	166	
2F10W-240-10	150	158	166	166	
2F10W-240-11	150	158	166	166	
2F10W-240-12	150	162	114	134	
2F10W-240-13	150	158	166	166	
2F10W-240-14	152	160	134	142	
2F10W-240-15	150	158	166	166	

	allele sizes (base pairs)				
root fragment #	PGL14 green		UAPgCA91 blue		notes
2J11S-0-1	140	162	118	126	
2J11S-0-2	140	162	118	126	
2J11S-0-3	152	152	fail	fail	
2J11S-0-4	140	162	118	126	
2J11S-0-5	136	138	132	154	
2J11S-0-6	140	170	142	166	
2J11S-0-7	140	162	118	126	
2J11S-0-8	140	140	142	166	
2J11S-0-9	152	152	128	128	
2J11S-0-10	140	162	118	126	
2J11S-0-11	136	138	132	154	
2J11S-0-12	136	138	132	154	
2J11S-0-13	152	152	128	128	
2J11S-0-14	fail	fail	fail	fail	
2J11S-0-15	140	170	142	166	
2J11S-120-1	150	158	134	174	
2J11S-120-2	138	140	162	182	
2J11S-120-3	152	152	150	178	
2J11S-120-4	138	140	164	182	
2J11S-120-5	138	154	136	136	
2J11S-120-6	138	140	164	182	
2J11S-120-7	152	152	150	178	
2J11S-120-8	170	170	144	188	
2J11S-120-9	fail	fail	fail	fail	
2J11S-120-10	140	162	118	126	
2J11S-120-11	138	140	164	182	
2J11S-120-12	152	152	150	178	
2J11S-120-13	152	152	150	178	
2J11S-120-14	152	152	150	176	
2J11S-120-15	138	140	164	182	
2J11S-240-1	138	142	142	180	
2J11S-240-2	148	178	146	160	
2J11S-240-3	138	142	142	180	
2J11S-240-4	138	142	142	180	
2J11S-240-5	150	170	132	142	
2J11S-240-6	148	178	146	160	
2J11S-240-7	fail	fail	fail	fail	
2J11S-240-8	fail	fail	fail	fail	
2J11S-240-9	fail	fail	fail	fail	
2J11S-240-10	fail	fail	fail	fail	
2J11S-240-11	138	138	fail	fail	
2J11S-240-12	138	142	142	180	
2J11S-240-13	144	144	134	144	
2J11S-240-14	144	144	134	144	
2J11S-240-15	138	142	142	180	
3G10-0-1	fail	fail	fail	fail	
3G10-0-2	140	154	132	132	
3G10-0-3	178	178	fail	fail	
3G10-0-4	fail	fail	fail	fail	
3G10-0-5	140	156	146	146	
3G10-0-6	fail	fail	fail	fail	
3G10-0-7	fail	fail	fail	fail	
3G10-0-8	fail	fail	142	142	
3G10-0-9	140	154	132	132	
3G10-0-10	140	156	146	146	
3G10-0-11	fail	fail	fail	fail	
3G10-0-12	140	154	132	132	
3G10-0-13	140	154	132	132	
3G10-0-14	140	154	132	132	
3G10-0-15	140	140	fail	fail	
3G10-120-1	136	150	142	142	
3G10-120-2	fail	fail	fail	fail	
3G10-120-3	136	150	142	142	
3G10-120-4	136	136	142	142	
3G10-120-5	136	136	fail	fail	
3G10-120-6	136	150	140	140	
3G10-120-7	fail	fail	fail	fail	
3G10-120-8	136	136	fail	fail	
3G10-120-9	152	152	fail	fail	
3G10-120-10	136	136	fail	fail	
3G10-120-11	136	136	142	142	
3G10-120-12	136	150	142	142	
3G10-120-13	136	150	142	142	
3G10-120-14	fail	fail	fail	fail	
3G10-120-15	fail	fail	fail	fail	
3G10-240-1	156	178	144	164	
3G10-240-2	158	174	138	152	
3G10-240-3	158	158	140	150	
3G10-240-4	144	162	132	188	
3G10-240-5	156	156	136	136	
3G10-240-6	144	162	132	188	
3G10-240-7	144	162	132	188	

	allele sizes (base pairs)				
root fragment #	PGL14 green		UAPgCA91 blue		notes
3G10-240-8	158	174	138	152	
3G10-240-9	158	158	fail	fail	
3G10-240-10	158	158	140	150	
3G10-240-11	144	162	132	188	
3G10-240-12	158	174	138	152	
3G10-240-13	130	130	fail	fail	
3G10-240-14	156	178	144	164	
3G10-240-15	144	162	132	188	
3H10-0-1	158	166	134	134	
3H10-0-2	158	166	134	134	
3H10-0-3	158	166	134	134	
3H10-0-4	158	166	134	134	
3H10-0-5	158	166	134	134	
3H10-0-6	158	166	134	134	
3H10-0-7	158	166	134	134	
3H10-0-8	158	166	134	134	
3H10-0-9	158	166	134	134	
3H10-0-10	158	166	134	134	
3H10-0-11	158	166	134	134	
3H10-0-12	158	166	134	134	
3H10-0-13	158	166	134	134	
3H10-0-14	158	166	134	134	
3H10-0-15	136	140	fail	fail	
3H10-120-1	158	166	fail	fail	
3H10-120-2	138	142	142	142	
3H10-120-3	166	166	114	128	
3H10-120-4	156	164	142	164	
3H10-120-5	166	166	114	128	
3H10-120-6	166	166	114	128	
3H10-120-7	156	156	fail	fail	
3H10-120-8	156	164	142	164	
3H10-120-9	fail	fail	fail	fail	
3H10-120-10	fail	fail	fail	fail	
3H10-120-11	138	142	142	142	
3H10-120-12	158	166	136	136	
3H10-120-13	156	164	142	164	
3H10-120-14	156	164	142	164	
3H10-120-15	144	156	194	194	
3H10-240-1	140	166	142	142	
3H10-240-2	fail	fail	fail	fail	
3H10-240-3	152	160	156	156	
3H10-240-4	fail	fail	fail	fail	
3H10-240-5	fail	fail	fail	fail	
3H10-240-6	140	166	142	142	
3H10-240-7	fail	fail	fail	fail	
3H10-240-8	140	146	110	110	
3H10-240-9	140	140	fail	fail	
3H10-240-10	140	146	110	110	
3H10-240-11	150	160	126	126	
3H10-240-12	144	156	110	194	
3H10-240-13	148	148	fail	fail	
3H10-240-14	140	166	142	142	
3H10-240-15	140	166	140	140	
3H10E-0-1	138	156	130	130	
3H10E-0-2	138	156	130	130	
3H10E-0-3	138	156	130	130	
3H10E-0-4	142	148	142	142	
3H10E-0-5	142	148	fail	fail	
3H10E-0-6	138	156	130	130	
3H10E-0-7	136	172	118	118	
3H10E-0-8	fail	fail	fail	fail	
3H10E-0-9	fail	fail	fail	fail	
3H10E-0-10	142	148	142	144	
3H10E-0-11	152	158	130	184	
3H10E-0-12	136	136	fail	fail	
3H10E-0-13	138	156	130	130	
3H10E-0-14	fail	fail	fail	fail	
3H10E-0-15	138	156	130	130	
3H10E-120-1	152	158	130	184	
3H10E-120-2	138	170	184	184	
3H10E-120-3	152	158	130	184	
3H10E-120-4	152	158	130	184	
3H10E-120-5	fail	fail	fail	fail	
3H10E-120-6	fail	fail	fail	fail	
3H10E-120-7	138	170	136	184	
3H10E-120-8	138	170	184	184	
3H10E-120-9	fail	fail	fail	fail	
3H10E-120-10	152	158	fail	fail	
3H10E-120-11	138	170	184	fail	
3H10E-120-12	152	158	130	184	
3H10E-120-13	138	170	136	184	

	allele sizes (base pairs)				
root fragment #	PGL14 green		UAPgCA91 blue		notes
3H10E-120-14	140	152	126	126	
3H10E-120-15	152	158	128	184	
3H10E-240-1	fail	fail	fail	fail	
3H10E-240-2	138	158	118	132	
3H10E-240-3	136	136	fail	fail	
3H10E-240-4	148	166	142	142	
3H10E-240-5	148	166	fail	fail	
3H10E-240-6	148	166	142	142	
3H10E-240-7	fail	fail	fail	fail	
3H10E-240-8	fail	fail	fail	fail	
3H10E-240-9	148	166	142	142	
3H10E-240-10	148	166	142	142	
3H10E-240-11	148	166	142	142	
3H10E-240-12	136	136	152	152	
3H10E-240-13	136	136	152	152	
3H10E-240-14	148	166	142	142	
3H10E-240-15	148	166	142	142	
3I7S-0-1	150	162	144	144	
3I7S-0-2	146	176	142	150	
3I7S-0-3	134	162	114	144	
3I7S-0-4	134	162	114	144	
3I7S-0-5	138	138	114	144	
3I7S-0-6	152	152	128	148	
3I7S-0-7	152	164	128	148	
3I7S-0-8	150	162	144	144	
3I7S-0-9	fail	fail	fail	fail	
3I7S-0-10	152	152	128	148	
3I7S-0-11	140	140	144	144	
3I7S-0-12	152	164	128	148	
3I7S-0-13	fail	fail	142	142	
3I7S-0-14	146	176	142	150	
3I7S-0-15	148	148	fail	fail	
3I7S-0-16	138	138	144	150	
3I7S-0-17	146	178	142	150	
3I7S-0-18	152	164	128	148	
3I7S-0-19	138	138	144	150	
3I7S-0-20	146	178	150	150	
3I7S-0-21	152	164	128	148	
3I7S-0-22	154	162	128	140	
3I7S-0-23	152	164	128	148	
3I7S-0-24	142	152	182	182	
3I7S-0-25	146	178	142	150	
3I7S-0-26	152	164	128	148	
3I7S-0-27	134	134	144	144	
3I7S-0-28	150	150	fail	fail	
3I7S-0-29	138	138	148	150	
3I7S-0-30	142	142	182	182	
3I7S-120-1	fail	fail	132	142	
3I7S-120-2	fail	fail	fail	fail	
3I7S-120-3	154	162	138	138	
3I7S-120-4	154	162	138	138	
3I7S-120-5	fail	fail	fail	fail	
3I7S-120-6	142	142	fail	fail	
3I7S-120-7	fail	fail	fail	fail	
3I7S-120-8	fail	fail	fail	fail	
3I7S-120-9	150	168	142	142	
3I7S-120-10	154	162	138	138	
3I7S-120-11	fail	fail	fail	fail	
3I7S-120-12	fail	fail	fail	fail	
3I7S-120-13	154	162	138	142	
3I7S-120-14	154	162	138	138	
3I7S-120-15	150	166	132	142	
3I7S-120-16	154	170	136	136	
3I7S-120-17	154	170	136	136	
3I7S-120-18	150	166	132	142	
3I7S-120-19	142	166	162	162	
3I7S-120-20	fail	fail	fail	fail	
3I7S-120-21	150	164	132	142	
3I7S-120-22	142	166	160	160	
3I7S-120-23	fail	fail	136	136	
3I7S-120-24	154	154	fail	fail	
3I7S-120-25	154	160	138	138	
3I7S-120-26	154	154	136	136	
3I7S-120-27	142	166	162	162	
3I7S-120-28	154	162	138	138	
3I7S-120-29	162	162	138	138	
3I7S-120-30	fail	fail	fail	fail	
3I7S-240-1	148	164	fail	fail	
3I7S-240-2	150	160	132	132	
3I7S-240-3	150	160	132	132	
3I7S-240-4	154	160	130	130	
3I7S-240-5	150	160	132	132	

root fragment #	allele sizes (base pairs)				
	PGL14 green		UAPgCA91 blue		notes
3I7S-240-6	154	168	136	136	
3I7S-240-7	150	156	118	128	
3I7S-240-8	154	154	130	130	
3I7S-240-9	148	164	fail	fail	
3I7S-240-10	150	160	132	132	
3I7S-240-11	154	160	130	130	
3I7S-240-12	fail	fail	fail	fail	
3I7S-240-13	150	160	132	132	
3I7S-240-14	150	160	132	132	
3I7S-240-15	154	160	130	162	
3I7S-240-16	154	170	130	130	
3I7S-240-17	154	158	130	130	
3I7S-240-18	148	148	fail	fail	
3I7S-240-19	154	160	fail	fail	
3I7S-240-20	154	160	130	130	
3I7S-240-21	154	160	130	130	
3I7S-240-22	154	160	130	130	
3I7S-240-23	158	158	fail	fail	
3I7S-240-24	fail	fail	fail	fail	
3I7S-240-25	154	160	130	130	
3I7S-240-26	154	154	130	130	
3I7S-240-27	fail	fail	fail	fail	
3I7S-240-28	154	154	130	162	
3I7S-240-29	154	160	130	130	
3I7S-240-30	150	160	132	132	
3J8-0-1	138	172	128	128	
3J8-0-2	150	172	154	154	
3J8-0-3	138	170	140	158	
3J8-0-4	150	172	156	156	
3J8-0-5	138	170	140	156	
3J8-0-6	138	150	142	166	
3J8-0-7	150	172	156	156	
3J8-0-8	138	172	128	152	
3J8-0-9	138	150	142	166	
3J8-0-10	138	150	142	166	
3J8-0-11	150	172	156	156	
3J8-0-12	150	172	154	154	
3J8-0-13	152	158	134	154	
3J8-0-14	138	150	142	166	
3J8-0-15	138	172	128	152	
3J8-120-1	152	170	146	146	
3J8-120-2	142	152	136	172	
3J8-120-3	142	152	136	172	
3J8-120-4	140	156	142	142	
3J8-120-5	152	170	fail	fail	
3J8-120-6	140	156	142	142	
3J8-120-7	152	170	fail	fail	
3J8-120-8	152	170	fail	fail	
3J8-120-9	152	170	fail	fail	
3J8-120-10	152	170	114	148	
3J8-120-11	162	162	130	200	
3J8-120-12	142	152	136	172	
3J8-120-13	152	170	148	148	
3J8-120-14	142	152	136	172	
3J8-120-15	152	170	148	148	
3J8-240-1	138	140	130	142	
3J8-240-2	152	170	118	142	
3J8-240-3	138	140	130	142	
3J8-240-4	140	152	118	118	
3J8-240-5	140	148	134	134	
3J8-240-6	fail	fail	fail	fail	
3J8-240-7	152	152	118	142	
3J8-240-8	fail	fail	fail	fail	
3J8-240-9	140	140	168	206	
3J8-240-10	140	152	118	118	
3J8-240-11	fail	fail	fail	fail	
3J8-240-12	fail	fail	fail	fail	
3J8-240-13	138	140	130	142	
3J8-240-14	152	152	118	142	
3J8-240-15	148	152	134	134	
3JK5-0-1	136	154	130	130	
3JK5-0-2	142	154	134	160	
3JK5-0-3	142	154	134	160	
3JK5-0-4	fail	fail	fail	fail	
3JK5-0-5	136	154	130	130	
3JK5-0-6	142	154	134	160	
3JK5-0-7	136	154	130	130	
3JK5-0-8	142	154	134	160	
3JK5-0-9	142	154	134	160	
3JK5-0-10	136	154	130	130	
3JK5-0-11	140	156	118	152	

	allele sizes (base pairs)				
root fragment #	PGL14 green		UAPgCA91 blue		notes
3JK5-0-12	142	154	134	160	
3JK5-0-13	fail	fail	fail	fail	
3JK5-0-14	140	156	118	152	
3JK5-0-15	fail	fail	fail	fail	
3JK5-0-16	142	154	134	158	
3JK5-0-17	136	154	130	130	
3JK5-0-18	140	156	118	152	
3JK5-0-19	142	154	134	160	
3JK5-0-20	142	154	134	158	
3JK5-0-21	142	154	134	158	
3JK5-0-22	136	154	130	130	
3JK5-0-23	140	156	118	152	
3JK5-0-24	142	154	134	160	
3JK5-0-25	136	154	130	130	
3JK5-0-26	142	154	134	160	
3JK5-0-27	136	154	130	130	
3JK5-0-28	fail	fail	fail	fail	
3JK5-0-29	140	156	118	152	
3JK5-0-30	136	154	130	130	
3JK5-120-1	fail	fail	fail	fail	
3JK5-120-2	148	148	154	154	
3JK5-120-3	138	140	162	162	
3JK5-120-4	fail	fail	fail	fail	
3JK5-120-5	148	148	154	154	
3JK5-120-6	138	140	162	162	
3JK5-120-7	138	140	162	162	
3JK5-120-8	fail	fail	fail	fail	
3JK5-120-9	148	148	154	154	
3JK5-120-10	fail	fail	fail	fail	
3JK5-120-11	138	140	162	162	
3JK5-120-12	138	140	162	162	
3JK5-120-13	138	140	162	162	
3JK5-120-14	138	140	162	162	
3JK5-120-15	fail	fail	fail	fail	
3JK5-120-16	fail	fail	fail	fail	
3JK5-120-17	138	140	162	162	
3JK5-120-18	138	140	162	162	
3JK5-120-19	fail	fail	fail	fail	
3JK5-120-20	148	148	154	154	
3JK5-120-21	fail	fail	fail	fail	
3JK5-120-22	138	140	162	162	
3JK5-120-23	138	140	162	162	
3JK5-120-24	138	140	162	162	
3JK5-120-25	fail	fail	fail	fail	
3JK5-120-26	fail	fail	fail	fail	
3JK5-120-27	138	140	162	162	
3JK5-120-28	138	140	162	162	
3JK5-120-29	138	140	162	162	
3JK5-120-30	148	148	154	154	
3JK5-240-1	fail	fail	fail	fail	
3JK5-240-2	fail	fail	fail	fail	
3JK5-240-3	fail	fail	fail	fail	
3JK5-240-4	140	156	118	152	
3JK5-240-5	140	156	118	152	
3JK5-240-6	140	156	118	152	
3JK5-240-7	fail	fail	fail	fail	
3JK5-240-8	fail	fail	fail	fail	
3JK5-240-9	fail	fail	fail	fail	
3JK5-240-10	140	156	118	152	
3JK5-240-11	fail	fail	fail	fail	
3JK5-240-12	fail	fail	fail	fail	
3JK5-240-13	fail	fail	fail	fail	
3JK5-240-14	fail	fail	fail	fail	
3JK5-240-15	162	162	138	144	
3JK5-240-16	156	156	156	164	
3JK5-240-17	fail	fail	fail	fail	
3JK5-240-18	162	162	138	144	
3JK5-240-19	140	156	118	152	
3JK5-240-20	162	162	138	144	
3JK5-240-21	fail	fail	fail	fail	
3JK5-240-22	140	162	126	126	
3JK5-240-23	fail	fail	fail	fail	
3JK5-240-24	fail	fail	fail	fail	
3JK5-240-25	140	162	126	148	
3JK5-240-26	fail	fail	fail	fail	
3JK5-240-27	fail	fail	fail	fail	
3JK5-240-28	162	162	138	144	
3JK5-240-29	150	156	156	164	
3JK5-240-30	fail	fail	fail	fail	
4G5-0-1	fail	fail	fail	fail	
4G5-0-2	fail	fail	fail	fail	
4G5-0-3	158	158	134	164	

	allele sizes (base pairs)				
root fragment #	PGL14 green		UAPgCA91 blue		notes
4G5-0-4	fail	fail	fail	fail	
4G5-0-5	140	140	fail	fail	
4G5-0-6	154	170	130	142	
4G5-0-7	138	140	154	170	
4G5-0-8	140	152	118	162	
4G5-0-9	fail	fail	fail	fail	
4G5-0-10	fail	fail	fail	fail	
4G5-0-11	fail	fail	fail	fail	
4G5-0-12	fail	fail	fail	fail	
4G5-0-13	156	170	130	142	
4G5-0-14	fail	fail	fail	fail	
4G5-0-15	152	170	118	162	
4G5-120-1	146	156	132	132	
4G5-120-2	160	160	134	148	
4G5-120-3	162	162	134	148	
4G5-120-4	fail	fail	fail	fail	
4G5-120-5	162	162	134	148	
4G5-120-6	fail	fail	fail	fail	
4G5-120-7	fail	fail	fail	fail	
4G5-120-8	fail	fail	fail	fail	
4G5-120-9	146	146	132	132	
4G5-120-10	146	156	132	132	
4G5-120-11	162	162	134	148	
4G5-120-12	140	152	130	152	
4G5-120-13	162	162	134	148	
4G5-120-14	fail	fail	fail	fail	
4G5-120-15	146	156	132	132	
4G5-240-1	156	156	136	168	
4G5-240-2	140	160	130	144	
4G5-240-3	140	160	130	144	
4G5-240-4	140	160	130	144	
4G5-240-5	136	138	146	150	
4G5-240-6	fail	fail	fail	fail	
4G5-240-7	136	160	126	148	
4G5-240-8	136	138	146	150	
4G5-240-9	fail	fail	fail	fail	
4G5-240-10	136	138	146	150	
4G5-240-11	fail	fail	fail	fail	
4G5-240-12	fail	fail	fail	fail	
4G5-240-13	fail	fail	fail	fail	
4G5-240-14	fail	fail	fail	fail	
4G5-240-15	fail	fail	fail	fail	
4H6F-0-1	142	150	150	150	
4H6F-0-2	142	150	150	150	
4H6F-0-3	142	150	150	150	
4H6F-0-4	142	150	150	150	
4H6F-0-5	142	150	150	150	
4H6F-0-6	140	164	142	148	
4H6F-0-7	142	150	fail	fail	
4H6F-0-8	142	150	150	150	
4H6F-0-9	fail	fail	fail	fail	
4H6F-0-10	142	150	150	150	
4H6F-0-11	142	150	fail	fail	
4H6F-0-12	142	150	150	150	
4H6F-0-13	142	150	150	150	
4H6F-0-14	142	150	fail	fail	
4H6F-0-15	142	150	150	150	
4H6F-120-1	150	164	144	144	
4H6F-120-2	148	160	126	142	
4H6F-120-3	160	162	142	170	
4H6F-120-4	160	162	142	170	
4H6F-120-5	142	160	130	130	
4H6F-120-6	140	156	118	172	
4H6F-120-7	fail	fail	fail	fail	
4H6F-120-8	156	156	118	170	
4H6F-120-9	fail	fail	fail	fail	
4H6F-120-10	160	162	142	170	
4H6F-120-11	140	156	118	172	
4H6F-120-12	fail	fail	fail	fail	
4H6F-120-13	148	160	126	142	
4H6F-120-14	150	164	144	144	
4H6F-120-15	160	162	142	170	
4H6F-240-1	150	154	118	176	
4H6F-240-2	142	150	130	130	
4H6F-240-3	150	154	118	176	
4H6F-240-4	142	150	130	130	
4H6F-240-5	150	154	118	176	
4H6F-240-6	142	142	130	130	
4H6F-240-7	142	142	130	130	
4H6F-240-8	142	142	fail	fail	
4H6F-240-9	142	142	130	130	
4H6F-240-10	142	150	130	130	

root fragment #	allele sizes (base pairs)				notes
	PGL14 green		UAPgCA91 blue		
4H6F-240-11	142	150	130	130	
4H6F-240-12	142	142	fail	fail	
4H6F-240-13	fail	fail	fail	fail	
4H6F-240-14	144	168	fail	fail	
4H6F-240-15	144	170	142	196	
4I7E-0-1	140	154	142	142	
4I7E-0-2	140	154	142	142	
4I7E-0-3	154	178	134	160	
4I7E-0-4	140	154	fail	fail	
4I7E-0-5	152	174	130	130	
4I7E-0-6	140	152	174	174	
4I7E-0-7	140	152	174	174	
4I7E-0-8	140	154	142	142	
4I7E-0-9	152	156	144	170	
4I7E-0-10	fail	fail	fail	fail	
4I7E-0-11	fail	fail	fail	fail	
4I7E-0-12	fail	fail	fail	fail	
4I7E-0-13	fail	fail	fail	fail	
4I7E-0-14	fail	fail	fail	fail	
4I7E-0-15	fail	fail	fail	fail	
4I7E-120-1	146	164	142	142	
4I7E-120-2	fail	fail	fail	fail	
4I7E-120-3	150	158	130	130	
4I7E-120-4	150	158	130	130	
4I7E-120-5	fail	fail	fail	fail	
4I7E-120-6	140	150	116	116	
4I7E-120-7	fail	fail	fail	fail	
4I7E-120-8	152	152	fail	fail	
4I7E-120-9	150	158	130	130	
4I7E-120-10	152	152	fail	fail	
4I7E-120-11	146	164	142	142	
4I7E-120-12	146	164	142	142	
4I7E-120-13	152	152	fail	fail	
4I7E-120-14	fail	fail	fail	fail	
4I7E-120-15	fail	fail	fail	fail	
4I7E-240-1	fail	fail	fail	fail	
4I7E-240-2	140	164	170	170	
4I7E-240-3	152	172	128	128	
4I7E-240-4	fail	fail	fail	fail	
4I7E-240-5	fail	fail	fail	fail	
4I7E-240-6	140	164	168	168	
4I7E-240-7	fail	fail	fail	fail	
4I7E-240-8	fail	fail	fail	fail	
4I7E-240-9	152	158	160	160	
4I7E-240-10	fail	fail	fail	fail	
4I7E-240-11	fail	fail	fail	fail	
4I7E-240-12	fail	fail	fail	fail	
4I7E-240-13	fail	fail	fail	fail	
4I7E-240-14	fail	fail	fail	fail	
4I7E-240-15	fail	fail	fail	fail	
4J5W-0-1	140	144	130	136	
4J5W-0-2	136	166	126	176	
4J5W-0-3	fail	fail	fail	fail	
4J5W-0-4	136	166	126	174	
4J5W-0-5	fail	fail	136	136	
4J5W-0-6	140	144	130	136	
4J5W-0-7	140	144	130	136	
4J5W-0-8	154	164	132	132	
4J5W-0-9	140	144	130	136	
4J5W-0-10	fail	fail	fail	fail	
4J5W-0-11	140	150	118	118	
4J5W-0-12	136	166	126	174	
4J5W-0-13	142	142	236	236	
4J5W-0-14	142	142	236	236	
4J5W-0-15	136	164	fail	fail	
4J5W-120-1	138	140	138	192	
4J5W-120-2	138	140	138	192	
4J5W-120-3	138	140	138	192	
4J5W-120-4	150	164	140	156	
4J5W-120-5	140	144	130	136	
4J5W-120-6	138	150	134	174	
4J5W-120-7	140	144	130	136	
4J5W-120-8	fail	fail	fail	fail	
4J5W-120-9	140	144	130	136	
4J5W-120-10	138	140	138	192	
4J5W-120-11	138	140	138	192	
4J5W-120-12	fail	fail	fail	fail	
4J5W-120-13	140	144	130	136	
4J5W-120-14	138	150	134	174	
4J5W-120-15	fail	fail	fail	fail	
4J5W-240-1	fail	fail	fail	fail	

	allele sizes (base pairs)				
root fragment #	PGL14 green		UAPgCA91 blue		notes
4J5W-240-2	fail	fail	fail	fail	
4J5W-240-3	fail	fail	fail	fail	
4J5W-240-4	fail	fail	fail	fail	
4J5W-240-5	fail	fail	fail	fail	
4J5W-240-6	140	152	120	170	
4J5W-240-7	fail	fail	fail	fail	
4J5W-240-8	fail	fail	fail	fail	
4J5W-240-9	140	152	120	172	
4J5W-240-10	fail	fail	fail	fail	
4J5W-240-11	166	166	fail	fail	
4J5W-240-12	138	144	126	134	
4J5W-240-13	148	150	148	148	
4J5W-240-14	140	152	120	170	
4J5W-240-15	fail	fail	fail	fail	
4L6-2-0-1	132	140	132	154	
4L6-2-0-2	152	172	160	160	
4L6-2-0-3	148	176	126	138	
4L6-2-0-4	152	172	160	160	
4L6-2-0-5	152	172	160	160	
4L6-2-0-6	152	172	160	160	
4L6-2-0-7	152	172	160	160	
4L6-2-0-8	fail	fail	160	160	
4L6-2-0-9	152	172	160	160	
4L6-2-0-10	142	172	140	156	
4L6-2-0-11	132	140	132	156	
4L6-2-0-12	152	172	160	160	
4L6-2-0-13	152	172	160	160	
4L6-2-0-14	152	172	160	160	
4L6-2-0-15	152	172	160	160	
4L6-2-120-1	158	172	142	198	
4L6-2-120-2	138	158	146	176	
4L6-2-120-3	138	158	146	176	
4L6-2-120-4	158	172	142	198	
4L6-2-120-5	158	158	146	176	
4L6-2-120-6	fail	fail	fail	fail	
4L6-2-120-7	fail	fail	fail	fail	
4L6-2-120-8	138	158	146	176	
4L6-2-120-9	138	158	146	176	
4L6-2-120-10	158	172	138	144	
4L6-2-120-11	138	158	fail	fail	
4L6-2-120-12	138	138	fail	fail	
4L6-2-120-13	138	158	146	176	
4L6-2-120-14	fail	fail	fail	fail	
4L6-2-120-15	158	172	142	198	
4L6-2-240-1	150	172	146	146	
4L6-2-240-2	150	164	126	126	
4L6-2-240-3	150	172	146	146	
4L6-2-240-4	154	172	142	142	
4L6-2-240-5	154	172	142	142	
4L6-2-240-6	154	172	142	142	
4L6-2-240-7	154	172	142	142	
4L6-2-240-8	150	172	146	146	
4L6-2-240-9	150	172	146	146	
4L6-2-240-10	150	172	146	146	
4L6-2-240-11	172	172	146	146	
4L6-2-240-12	fail	fail	fail	fail	
4L6-2-240-13	172	172	146	146	
4L6-2-240-14	172	172	142	142	
4L6-2-240-15	150	164	126	126	
4M4-0-1	142	156	158	184	
4M4-0-2	154	160	114	144	
4M4-0-3	154	160	114	144	
4M4-0-4	154	160	114	144	
4M4-0-5	150	156	160	160	
4M4-0-6	154	160	114	144	
4M4-0-7	150	164	130	148	
4M4-0-8	154	160	114	144	
4M4-0-9	150	156	116	160	
4M4-0-10	150	154	148	174	
4M4-0-11	150	154	148	174	
4M4-0-12	150	156	160	160	
4M4-0-13	142	142	156	184	
4M4-0-14	fail	fail	fail	fail	
4M4-0-15	fail	fail	fail	fail	
4M4-120-1	fail	fail	fail	fail	
4M4-120-2	146	158	142	142	
4M4-120-3	fail	fail	fail	fail	
4M4-120-4	fail	fail	fail	fail	
4M4-120-5	146	158	142	142	
4M4-120-6	138	168	fail	fail	
4M4-120-7	142	156	156	184	

root fragment #	allele sizes (base pairs) PGL14 green		UAPgCA91 blue		notes
4M4-120-8	138	168	148	148	
4M4-120-9	152	152	142	142	
4M4-120-10	146	158	142	142	
4M4-120-11	152	152	142	144	
4M4-120-12	146	158	fail	fail	
4M4-120-13	138	168	148	148	
4M4-120-14	152	160	136	136	Green also 166
4M4-120-15	fail	fail	fail	fail	
4M4-240-1	150	160	128	132	
4M4-240-2	152	160	136	172	
4M4-240-3	148	162	142	168	
4M4-240-4	fail	fail	fail	fail	
4M4-240-5	152	152	fail	fail	
4M4-240-6	152	160	136	170	
4M4-240-7	152	160	136	172	
4M4-240-8	150	160	128	132	
4M4-240-9	fail	fail	fail	fail	
4M4-240-10	150	160	128	132	
4M4-240-11	160	160	132	132	
4M4-240-12	152	160	136	170	
4M4-240-13	148	162	142	168	
4M4-240-14	148	162	142	166	
4M4-240-15	152	160	136	172	
2C6S-0-1	154	154	148	148	

APPENDIX V

ROOT LENGTH DATA

White spruce root length

Depth	**Adjusted root length m m^{-2} (m^2 ha^{-1})$^{-1}$**
mixedwood plots	
plot 2D5	
organic	12.96
0-5 cm	36.92
5-15 cm	50.23
15-40 cm	38.67
plot 2F10W	
organic	20.88
0-5 cm	23.67
5-15 cm	5.54
15-40 cm	1.55
plot 2J11S	
organic	34.61
0-5 cm	21.29
5-15 cm	52.85
15-40 cm	missing
plot 3G10	
organic	39.04
0-5 cm	17.88
5-15 cm	28.71
15-40 cm	12.96
plot 3H10	
organic	43.24
0-5 cm	22.10
5-15 cm	18.84
15-40 cm	3.96
plot 3JK5	
organic	67.02
0-5 cm	41.91
5-15 cm	42.45
15-40 cm	4.31
plot 4G5	
organic	46.75
0-5 cm	60.41
5-15 cm	46.46
15-40 cm	5.95
plot 4H6F	
organic	94.93
0-5 cm	31.14
5-15 cm	21.87
15-40 cm	12.57
plot 4M4	
organic	11.40
0-5 cm	19.64
5-15 cm	7.26
15-40 cm	6.49
pure Sw plots	
plot 2C6S	
organic	31.84
0-5 cm	37.84
5-15 cm	21.64
15-40 cm	18.23
plot 2D8N	
organic	67.44
0-5 cm	34.84
5-15 cm	45.77
15-40 cm	24.42
plot 2E9N	
organic	62.24
0-5 cm	93.95
5-15 cm	32.70
15-40 cm	3.41
plot 3H10E	
organic	37.68
0-5 cm	25.23
5-15 cm	11.82
15-40 cm	4.28
plot 3I7S	
organic	62.74
0-5 cm	38.30
5-15 cm	17.15
15-40 cm	4.14
plot 3J8	
organic	37.44
0-5 cm	19.45
5-15 cm	missing
15-40 cm	missing
plot 4I7E	
organic	15.00
0-5 cm	7.90
5-15 cm	13.45
15-40 cm	8.21
plot 4J5W	
organic	41.29
0-5 cm	62.30
5-15 cm	33.30
15-40 cm	19.68
plot 4L6	
organic	61.98
0-5 cm	28.14
5-15 cm	21.87
15-40 cm	9.33

Trembling aspen root length

Depth	Adjusted root length m m^{-2} (m^2 ha^{-1})$^{-1}$
mixedwood plots	
plot 2D5	
organic	9.15
0-5 cm	8.57
5-15 cm	0.00
15-40 cm	0.00
plot 2F10W	
organic	0.00
0-5 cm	18.67
5-15 cm	0.00
15-40 cm	0.00
plot 3G10	
organic	12.62
0-5 cm	1.55
5-15 cm	0.00
15-40 cm	0.00
plot 4G5	
organic	17.01
0-5 cm	17.81
5-15 cm	5.83
15-40 cm	1.54
plot 3H10	
organic	26.55
0-5 cm	0.00
5-15 cm	0.00
15-40 cm	0.00
plot 4H6F	
organic	15.41
0-5 cm	0.00
5-15 cm	4.37
15-40 cm	0.00
plot 2J11S	
organic	26.15
0-5 cm	5.41
5-15 cm	39.63
15-40 cm	missing
plot 3JK5	
organic	8.48
0-5 cm	0.00
5-15 cm	0.00
15-40 cm	0.00
plot 4M4	
organic	11.86
0-5 cm	21.97
5-15 cm	3.45
15-40 cm	0.00
pure Pt plots	
plot 2E4NW	
organic	55.52
0-5 cm	5.34
5-15 cm	2.75
15-40 cm	0.00
plot 3E5E	
organic	3.86
0-5 cm	missing
5-15 cm	missing
15-40 cm	missing
plot 4E8	
organic	28.60
0-5 cm	8.88
5-15 cm	7.98
15-40 cm	6.84
plot 2I9S	
organic	108.60
0-5 cm	27.19
5-15 cm	21.47
15-40 cm	9.49
plot 3J13W	
organic	18.24
0-5 cm	23.32
5-15 cm	2.87
15-40 cm	missing
plot 2K7SW	
organic	7.34
0-5 cm	0.00
5-15 cm	0.00
15-40 cm	0.00
plot 4M3W	
organic	3.66
0-5 cm	7.90
5-15 cm	missing
15-40 cm	missing
plot 4N4	
organic	10.62
0-5 cm	3.81
5-15 cm	2.75
15-40 cm	3.58

“Other” root length

Depth	Root length (m m^{-2})
mixedwood plots	
plot 2D5	
organic	3.35
0-5 cm	9.33
5-15 cm	7.43
15-40 cm	7.61
plot 2F10W	
organic	1.51
0-5 cm	2.1
5-15 cm	1.55
15-40 cm	1.77
plot 3G10	
organic	8.34
0-5 cm	5.36
5-15 cm	6.87
15-40 cm	3.65
plot 4G5	
organic	3.77
0-5 cm	9.15
5-15 cm	9.22
15-40 cm	2.4
plot 3H10	
organic	4.6
0-5 cm	2.05
5-15 cm	1.78
15-40 cm	0.33
plot 4H6F	
organic	4.16
0-5 cm	8.05
5-15 cm	4.76
15-40 cm	2.29
plot 2J11S	
organic	5.33
0-5 cm	2.2
5-15 cm	6.31
15-40 cm	missing
plot 3JK5	
organic	13.04
0-5 cm	7.43
5-15 cm	8.42
15-40 cm	3.32
plot 4M4	
organic	2.91
0-5 cm	4.2
5-15 cm	0.58
15-40 cm	2.4
pure Pt plots	
plot 2E4NW	
organic	10.32
0-5 cm	1.54
5-15 cm	2.81
15-40 cm	1.09
plot 3E5E	
organic	35.15
0-5 cm	missing
5-15 cm	missing
15-40 cm	missing
plot 4E8	
organic	1.81
0-5 cm	1.92
5-15 cm	4.06
15-40 cm	1.71
plot 2I9S	
organic	30.98
0-5 cm	9.48
5-15 cm	6.95
15-40 cm	2.66
plot 3J13W	
organic	8.23
0-5 cm	3.95
5-15 cm	0.09
15-40 cm	missing
plot 2K7SW	
organic	18.45
0-5 cm	17.51
5-15 cm	12.09
15-40 cm	3.46
plot 4M3W	
organic	9.5
0-5 cm	3.07
5-15 cm	missing
15-40 cm	missing
plot 4N4	
organic	4.25
0-5 cm	7.1
5-15 cm	5.23
15-40 cm	1.89
pure Sw plots	
plot 2C6S	
organic	4.15
0-5 cm	1.87
5-15 cm	1.15
15-40 cm	0.3
plot 2D8N	
organic	3.85
0-5 cm	2.02
5-15 cm	8.29
15-40 cm	8.05
plot 2E9N	
organic	4.1
0-5 cm	12.6
5-15 cm	4.05
15-40 cm	0.61
plot 3H10E	
organic	1.73
0-5 cm	0.22
5-15 cm	0.57
15-40 cm	0
plot 4I7E	
organic	4.38
0-5 cm	6.56
5-15 cm	6.64
15-40 cm	2.24
plot 3I7S	
organic	6.65
0-5 cm	5.54
5-15 cm	0.81
15-40 cm	0.14
plot 4J5W	
organic	1.9
0-5 cm	7.92
5-15 cm	3.47
15-40 cm	0.55
plot 3J8	
organic	4.26
0-5 cm	4.06
5-15 cm	missing
15-40 cm	missing
plot 4L6	
organic	3.31
0-5 cm	0.66
5-15 cm	0.86
15-40 cm	1.08

APPENDIX VI

ROOT MASS DATA

White spruce root mass

Depth	Adjusted root mass g m^{-2} $(m^2\ ha^{-1})^{-1}$
mixedwood plots	
plot 2D5	
organic	1.37
0-5 cm	3.32
5-15 cm	3.96
15-40 cm	3.09
plot 2F10W	
organic	2.74
0-5 cm	2.58
5-15 cm	0.61
15-40 cm	0.17
plot 3G10	
organic	6.95
0-5 cm	2.44
5-15 cm	2.67
15-40 cm	0.75
plot 4G5	
organic	5.57
0-5 cm	9.52
5-15 cm	4.46
15-40 cm	0.48
plot 3H10	
organic	1.69
0-5 cm	3.07
5-15 cm	4.29
15-40 cm	0.65
plot 4H6F	
organic	11.66
0-5 cm	3.19
5-15 cm	2.48
15-40 cm	1.76
plot 2J11S	
organic	5.76
0-5 cm	3.39
5-15 cm	5.10
15-40 cm	missing
plot 3JK5	
organic	10.53
0-5 cm	4.08
5-15 cm	8.12
15-40 cm	0.34
plot 4M4	
organic	1.44
0-5 cm	3.18
5-15 cm	0.46
15-40 cm	0.61
pure Sw plots	
plot 2C6S	
organic	2.55
0-5 cm	3.61
5-15 cm	1.69
15-40 cm	2.88
plot 2D8N	
organic	8.20
0-5 cm	3.96
5-15 cm	6.74
15-40 cm	2.82
plot 2E9N	
organic	7.94
0-5 cm	8.19
5-15 cm	4.04
15-40 cm	0.19
plot 3H10E	
organic	4.17
0-5 cm	3.67
5-15 cm	1.34
15-40 cm	0.52
plot 4I7E	
organic	2.67
0-5 cm	1.33
5-15 cm	1.62
15-40 cm	2.82
plot 3I7S	
organic	5.58
0-5 cm	3.08
5-15 cm	2.27
15-40 cm	0.66
plot 4J5W	
organic	4.48
0-5 cm	6.85
5-15 cm	6.19
15-40 cm	3.65
plot 3J8	
organic	5.09
0-5 cm	2.21
5-15 cm	missing
15-40 cm	missing
plot 4L6	
organic	6.44
0-5 cm	3.91
5-15 cm	2.01
15-40 cm	0.67

Trembling aspen root mass

Depth	Adjusted root mass $g\ m^{-2}\ (m^2\ ha^{-1})^{-1}$
mixedwood plots	
plot 2D5	
organic	0.23
0-5 cm	0.37
5-15 cm	0.00
15-40 cm	0.00
plot 2F10W	
organic	0.00
0-5 cm	0.51
5-15 cm	0.00
15-40 cm	0.00
plot 3G10	
organic	0.44
0-5 cm	0.04
5-15 cm	0.00
15-40 cm	0.00
plot 4G5	
organic	0.84
0-5 cm	1.31
5-15 cm	2.36
15-40 cm	0.31
plot 3H10	
organic	1.00
0-5 cm	0.00
5-15 cm	0.00
15-40 cm	0.00
plot 4H6F	
organic	0.77
0-5 cm	0.00
5-15 cm	0.21
15-40 cm	0.00
plot 2J11S	
organic	1.20
0-5 cm	0.23
5-15 cm	1.77
15-40 cm	missing
plot 3JK5	
organic	0.57
0-5 cm	0.00
5-15 cm	0.00
15-40 cm	0.00
plot 4M4	
organic	1.66
0-5 cm	2.27
5-15 cm	0.33
15-40 cm	0.00
pure Pt plots	
plot 2E4NW	
organic	4.71
0-5 cm	0.51
5-15 cm	0.54
15-40 cm	0.00
plot 3E5E	
organic	0.57
0-5 cm	missing
5-15 cm	missing
15-40 cm	missing
plot 4E8	
organic	1.68
0-5 cm	0.47
5-15 cm	0.59
15-40 cm	0.34
plot 2I9S	
organic	5.39
0-5 cm	3.02
5-15 cm	2.33
15-40 cm	0.52
plot 3J13W	
organic	0.88
0-5 cm	1.39
5-15 cm	1.05
15-40 cm	missing
plot 2K7SW	
organic	1.02
0-5 cm	0.00
5-15 cm	0.00
15-40 cm	0.00
plot 4M3W	
organic	0.59
0-5 cm	1.28
5-15 cm	missing
15-40 cm	missing
plot 4N4	
organic	0.49
0-5 cm	0.25
5-15 cm	0.10
15-40 cm	0.14

“Other” root mass

Depth	Root mass (g m^{-2})
mixedwood plots	
plot 2D5	
organic	16.7
0-5 cm	69.1
5-15 cm	56.2
15-40 cm	90.5
plot 2F10W	
organic	13.7
0-5 cm	21.2
5-15 cm	14.7
15-40 cm	19.0
plot 3G10	
organic	65.5
0-5 cm	49.0
5-15 cm	39.5
15-40 cm	13.6
plot 4G5	
organic	17.8
0-5 cm	42.8
5-15 cm	51.2
15-40 cm	12.9
plot 3H10	
organic	43.6
0-5 cm	16.4
5-15 cm	27.6
15-40 cm	5.5
plot 4H6F	
organic	28.6
0-5 cm	49.2
5-15 cm	21.5
15-40 cm	17.0
plot 2J11S	
organic	60.6
0-5 cm	20.6
5-15 cm	80.8
15-40 cm	missing
plot 3JK5	
organic	90.0
0-5 cm	37.7
5-15 cm	51.6
15-40 cm	41.4
plot 4M4	
organic	17.4
0-5 cm	40.2
5-15 cm	11.9
15-40 cm	36.3
pure Pt plots	
plot 2E4NW	
organic	82.6
0-5 cm	9.3
5-15 cm	19.5
15-40 cm	8.3
plot 3E5E	
organic	136.8
0-5 cm	missing
5-15 cm	missing
15-40 cm	missing
plot 4E8	
organic	7.5
0-5 cm	13.9
5-15 cm	32.7
15-40 cm	6.6
plot 2I9S	
organic	140.2
0-5 cm	44.0
5-15 cm	39.0
15-40 cm	8.8
plot 3J13W	
organic	80.3
0-5 cm	29.3
5-15 cm	4.5
15-40 cm	missing
plot 2K7SW	
organic	122.9
0-5 cm	135.4
5-15 cm	81.1
15-40 cm	49.9
plot 4M3W	
organic	86.6
0-5 cm	49.5
5-15 cm	missing
15-40 cm	missing
plot 4N4	
organic	30.4
0-5 cm	74.1
5-15 cm	105.5
15-40 cm	13.9
pure Sw plots	
plot 2C6S	
organic	64.7
0-5 cm	28.8
5-15 cm	7.8
15-40 cm	6.0
plot 2D8N	
organic	21.4
0-5 cm	17.2
5-15 cm	18.6
15-40 cm	26.7
plot 2E9N	
organic	51.5
0-5 cm	57.8
5-15 cm	12.9
15-40 cm	3.8
plot 3H10E	
organic	18.8
0-5 cm	1.1
5-15 cm	7.7
15-40 cm	0.0
plot 4I7E	
organic	20.8
0-5 cm	36.1
5-15 cm	26.5
15-40 cm	14.2
plot 3I7S	
organic	36.6
0-5 cm	21.1
5-15 cm	3.4
15-40 cm	0.3
plot 4J5W	
organic	8.1
0-5 cm	67.5
5-15 cm	16.6
15-40 cm	2.0
plot 3J8	
organic	22.7
0-5 cm	14.2
5-15 cm	missing
15-40 cm	missing
plot 4L6	
organic	44.7
0-5 cm	15.5
5-15 cm	18.2
15-40 cm	19.7