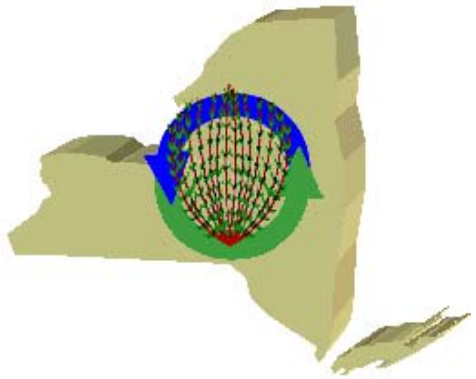

Short-Rotation Woody Crops Program

at

State University of New York

College of Environmental Science & Forestry

Biomass Power for Rural Development Technical Report:

EFFECT OF SLOW-RELEASE NITROGEN FERTILIZATION ON ABOVEGROUND BIOMASS PRODUCTION OF FIVE *SALIX* CLONES AND ONE *POPULUS* CLONE IN A SHORT-ROTATION INTENSIVE CULTURE (SRIC) BIOENERGY PLANTATION

Interim Program Report

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Submitted to:

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NOTICE

This report was originally submitted by Benjamin D. Ballard as a thesis in partial fulfillment of the requirements for the Master of Science Degree at the State University of New York College of Environmental Science and Forestry.

ABSTRACT

Short-rotation woody crop plantations of fast-growing trees, such as willow and poplar, can be grown as alternative sources of clean, renewable energy. These intensive culture systems have high nutrient demands. Application of N at three rates, (100, 200, and 300 kg N/ha) as slow-release urea and a control were used to evaluate the impact of fertilization on second-year yields of five willow clones and one poplar clone in three plantations across New York State. Regression equations were developed to estimate standing biomass. Willow clone SV1 and poplar clone NM6 benefited from fertilization, reaching yields as high as 20.3 and 21.6 o.d. Mg/ha by the second year of the rotation, respectively. The responses of the other four willow clones were confounded greatly by weeds and unmeasured site factors, though there was some benefit from fertilization. Tree biomass response to fertilization differed by site and was a function of survival, weeds, and the interactions with site and microsite variations. Fertilizing at rates above 100 kg N/ha for a three-year rotation are recommended only when additional site data indicate a need.

INTRODUCTION

The use of wood for energy production has received more attention in recent decades as alternative sources of clean, renewable energy are being explored. The desire to increase the use of renewable fuels, international pressure to reduce carbon dioxide emissions, and increasing public concern for the environment are making dedicated short-rotation bioenergy plantations of willow and poplar, also known as short rotation woody crops (SRWC), viable sources of energy (Ballard et al., 1998). SRWCs could also become an alternative crop for farmers, contributing to economic revitalization in rural communities.

The continued burning of fossil fuels, such as coal, has sparked concerns over acidic deposition and global warming. Compared with burning coal, SO_x and NO_x emissions, both precursors to acidic deposition, are reduced when coal is co-fired with wood. The tremendous growth potential of willow bioenergy plantations and the rapid sequestering of CO_2 from the atmosphere help offset CO_2 inputs to the atmosphere.

The first experiments to determine the biomass yield potential of willows using short-rotation-intensive-culture (SRIC) techniques were established in 1987 at the SUNY College of Environmental Science and Forestry's (ESF) Genetics Field Station at Tully, New York. (White et al., 1988). Favorable initial results led to additional experiments at the Genetics Field Station and on other sites across New York State, Pennsylvania, Vermont, and Wisconsin (Ballard et al., 1998).

The information gained from the initial studies at SUNY-ESF, coupled with research efforts at the University of Toronto and information from Europe on *Salix* culture, has resulted in development of a willow bioenergy production system that is being piloted at a commercial scale across New York (Ballard et al., 1998).

The Willow Bioenergy System

Commercial willow bioenergy plantations are planted in a “double-row system” based on a Swedish design. This system has all of the components of a silvicultural system, including establishment/regeneration, tending, and harvesting, and also incorporates many of the methods used in agricultural systems. Site preparation utilizes conventional agricultural practices, including plowing and discing. Part of the tending phase includes roto-tilling and the use of herbicides to control weeds. Cuttings (25 cm-long sticks) are planted at a density of approximately 15,000 stools per hectare (60 x 70 x 150-cm spacing). Cuttings sprout soon after planting and are coppiced (cut back) in the first winter. The following spring, stools re-sprout, producing multiple stems (3 to 15+ stems per stool). Trees are generally harvested on a 3- to 4-year rotation. After harvest, the stools re-sprout, as they did after the initial coppice. Further details of the production system can be found in Kopp et al. (1997).

The system is continually improving, and additional cultural treatments still need to be assessed. Substantial research has already been conducted in the area of *Salix* culture in Europe and the United States. Tree spacing or density, rotation length, irrigation, fertilization, genetic improvement, pest management, deployment patterns, and site preparation continue to be areas of research and development.

This research focused on fertilization and measurement of short-rotation willow and poplar bioenergy crops. Chapter 2 addresses the measurement aspect, specifically, non-destructive methods of estimating standing woody biomass. Chapter 3 examines the use of slow-release nitrogen (urea) as a potential method of fertilization. The non-destructive biomass estimation work detailed in Chapter 2 allowed for monitoring of the crop throughout the rotation to evaluate response to fertilization (Chapter 3).

The practice of nitrogen (N) fertilization is widespread in agriculture and forestry, and in many instances, it will be beneficial, or necessary, to fertilize SRWCs with nitrogen. As commercialization of willow bioenergy crops moves forward, there is an operational need to inform farmers about fertilization requirements of the crop. There are many potential sources of nutrients for fertilization of bioenergy crops. SUNY-ESF recently established studies to explore various fertilization methods and rates to obtain preliminary recommendations about nitrogen fertilization (e.g., slow-release urea) for farmers interested in growing the crop. A related study was established to compare and evaluate slow-release urea, composted poultry manure, and limed biosolids as potential sources of nitrogen fertilizer (Adegbidi, 1999).

Objectives

There were two main objectives for this research: (1) to develop non-destructive biomass estimation procedures for assessing pre-harvest responses to fertilization and (2) to determine the effects of slow-release

nitrogen fertilization on SRWC yields based on second-year data to aid in the refinement of general and/or clone-specific fertilization recommendations. Meeting the first objective was necessary to complete the second.

ASSESSMENT OF TREE RESPONSE TO FERTILIZATION.

Introduction

SRWC systems are continually evolving, and many cultural treatments are being improved through research and commercialization projects. One obstacle to the development of the system as a viable commercial crop is the high cost of production. Improving yields is a common objective of research. High yields lead to greater uptake and removal of nutrients, which in turn require fertilization to maintain those yields. Fertilization is an important part of the total cost of production, as high as 20 to 30% (Johansson and Rosenqvist, 1995; Kelkjoer, 1995; Strauss, 1995). Nearly all anthropogenic NH_4-fertilizer is derived from atmospheric nitrogen through the Haber-Bosch process ($N_2 + 3H_2 \rightarrow 2NH_3 + H^+ \rightarrow NH_4^+$), an exceptionally energy intensive process requiring electricity and often involving the burning of fossil fuels. If SRWCs are to be grown as an alternative fuel to decrease dependency on fossil fuels, alternative sources of fertilization (e.g., organic amendments), or reduction of the reliance on commercial inorganic fertilizers is necessary. One approach to reducing fertilization costs while maintaining relatively high yields is to determine the minimum amount of fertilization required to maintain desired yields.

Choosing a fertilization rate that will maintain high levels of yield requires adequate nutrients available for plant growth. As the concentration of plant available nutrients in the soil increases, plant growth increases to an asymptote. Further additions to the soil system result in excessive nutrient concentration which may become toxic and reduce growth. The concentration at which plant growth levels off is defined as the "sufficiency range" and represents the concentration of nutrient at which another factor, nutrient or otherwise (e.g., moisture, sunlight, etc.), limits plant growth. This phenomenon is described by Liebig's law of the minimum (1843) and the concept of the limiting factor, which states "plant production can be no greater than that level allowed by the growth factor present in the lowest amount relative to the optimum amount for that factor" (as referenced in Brady and Weil, 1996). Until the limiting factor is increased, the growth of the plant is hindered. This theoretical "sufficiency range" is illustrated in Figure 1.1 (adapted from Brady and Weil, 1996).

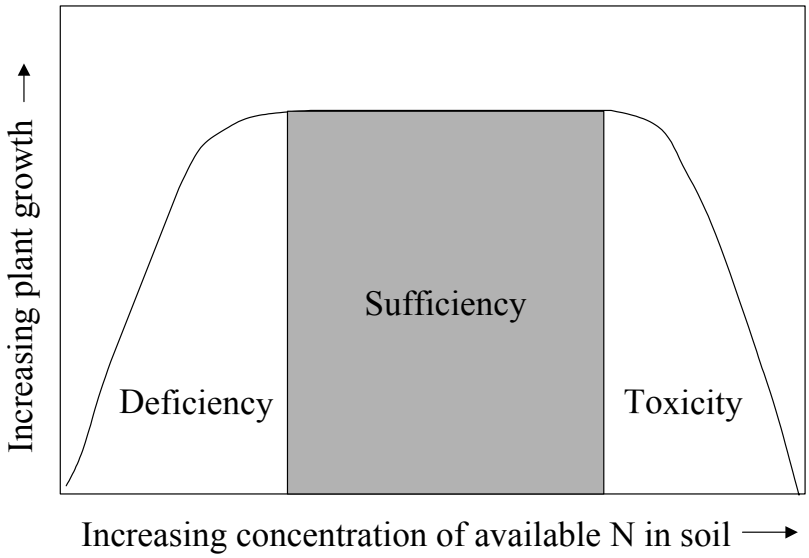

Figure 1.1. Theoretical plant growth response to changing concentration of available nitrogen. Adapted from Brady and Weil, 1996.

Stated another way, as the N fertilization rate increases, and the concentration of available N increases, aboveground biomass should increase to a point beyond which additional N fertilization will not increase biomass. This response could be characterized by the exponential saturation function: biomass = $I + A(1 - e^{vTRT})$ (described in methods section below).

The objectives of the fertilization trials were to determine the effects of slow-release nitrogen fertilization on SRWC yields based on second-year data to aid in the refinement of general and/or clone-specific fertilization recommendations. The following hypotheses were tested:

1. Fertilization does not increase aboveground tree biomass compared to unfertilized trees.

a) A single application of slow-release nitrogen (urea) fertilizer at four successively increasing rates should result in an aboveground growth response that is asymptotic for individual clones if the "sufficiency range" was reached.

b) Alternatively, if the sufficiency range was not reached (i.e., the four fertilization rates were still within the "deficiency range" of the plants), the response would be linear.

Differences among clones are expected and are not considered as a hypothesis. Factors such as site, soil characteristics (within and between sites), and competition from non-target vegetation (e.g., weed or herbaceous vegetation) would be potential sources of variability in biomass response that would be characterized or assessed in evaluating the hypotheses.

Materials and Methods

Study Sites

The study was conducted at three sites across New York State. The sites were located at King Ferry (KF), Somerset (S), and Tully (T), New York (Figure 1.2).

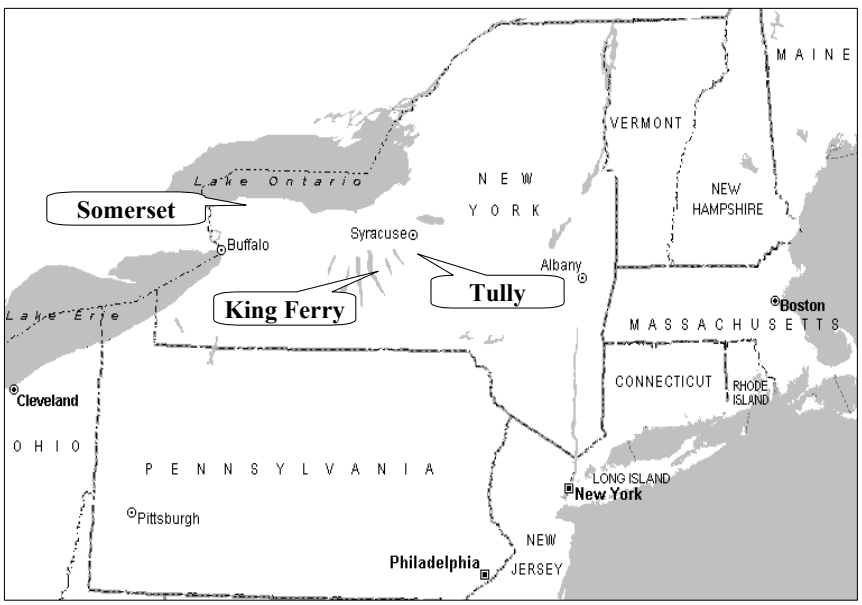

Figure 1.2. Location of the fertilization trial plantings in New York State: King Ferry, Somerset, and Tully. Base map from Microsoft© Automap Streets Plus.

King Ferry

The study site was an agricultural field located on the east shore of Cayuga Lake near the Milliken Power Station on property owned by New York State Electric and Gas (NYSEG) Power Company. The site is between the villages of King Ferry and Lansing, NY, in Tompkins County. Until site preparation began in the fall of 1994, the site had not been in agricultural production for several years. In spring 1995, a clone-site trial was established at this location, and the fertilization treatments for experimental plots were established in spring 1996 (Figure 1.3).

The soils at this site are Glossoboric Hapludalfs of the Lansing and Conesus series. Formed in glacial till, the series consist of very deep, well drained to moderately well drained gravelly silt loams with 3 to 8 percent slopes (Neeley, 1965; USDA-NRCS, 1998). The range of baseline soil characteristics is reported in Table 1.1.

Table 1.1. Range of soil characteristics found at the three study sites.

SITE	Texture	pH	OM (g/kg)	CEC $cmol_c$ /kg
King Ferry	clay/clay loam	5.2 - 6.8	38 - 50	10 – 18.1
Somerset	clay	5.4 - 6.8	34 - 42	9.5 -15.1
Tully†	loam/clay loam	5.1 - 5.5	50 - 67	15.2 - 20.1

SITE	N (g/kg)	P (mg/kg)	K (mg/kg)	Ca (mg/kg)	Mg (mg/kg)
King Ferry	1.3 – 1.9	17.8 - 31.7	65 - 339	1135 - 3165	141 – 393
Somerset	1.1 – 1.4	21.7 - 48.5	65 – 133	958 – 1962	134 – 114
Tully†	1.7 – 2.3	4.7 - 16.0	51 - 153	679 - 1469	38 – 114

† Note: with the exception of Tully, data represent baseline conditions; Tully data were collected mid-treatment during the second year of the rotation.
Soil was analyzed following the methods of Bickelhaupt and White (1982).
Complete data are in Appendix 7 and

Appendix 8.

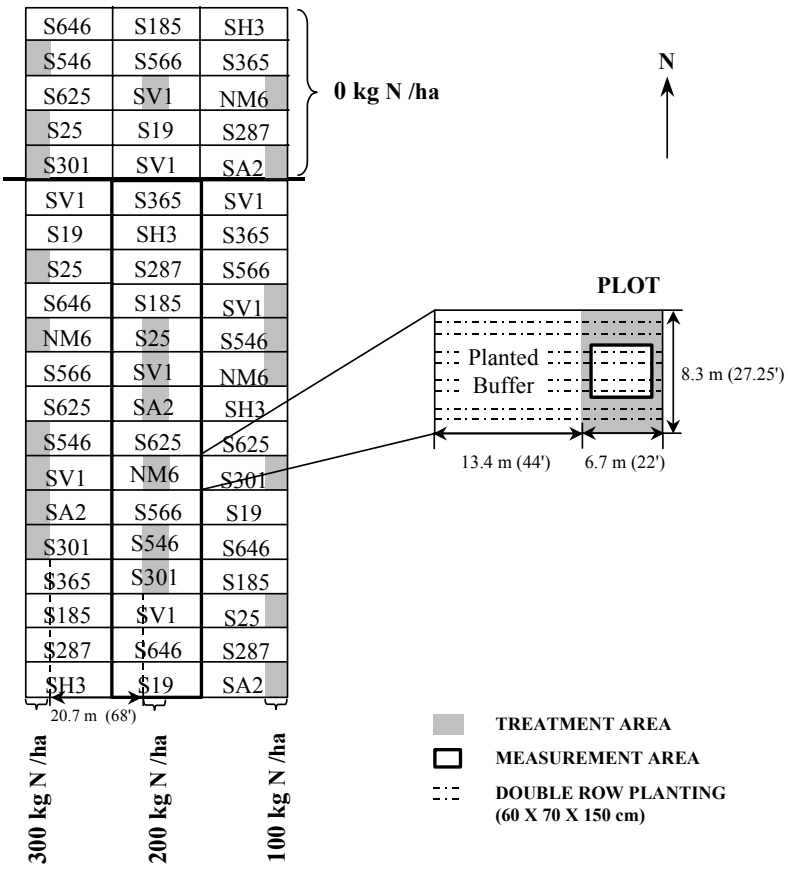

Figure 1.3. Plot and treatment layout at Milliken Power Station, King Ferry, NY.

Somerset

The study site was an agricultural field on the southern shore of Lake Ontario in western New York State near the Kintigh Power Station, which is operated by NYSEG Power Company. Prior to site preparation, the site was under agriculture production. Site preparation on the area was completed in autumn 1994. In spring 1995, a clone-site trial was established at this location; the fertilization treatments for experimental plots were established in spring 1996 (Figure 1.4). Two control plots were established at this location because an on-site evaluation revealed important differences across the site for the original control. In particular, the drainage in the original control was much poorer compared to the rest of the site.

The soils at this site are a Glossaquic Hapludalf of the Collamer series and a Mollic Endoaqualf of the Madalin series. The Collamer series consists of very deep, moderately well drained (MWD) soils formed in silty glacio-lacustrine sediments. Slopes are nearly level (0 to 5 percent) on these lake plains. The Madalin series consists of very deep, poorly drained (PD) soils with slopes ranging between 0 and 3 percent (Higgins et al., 1972; USDA-NRCS, 1998). The range of baseline soil characteristics is reported in Table 1.1.

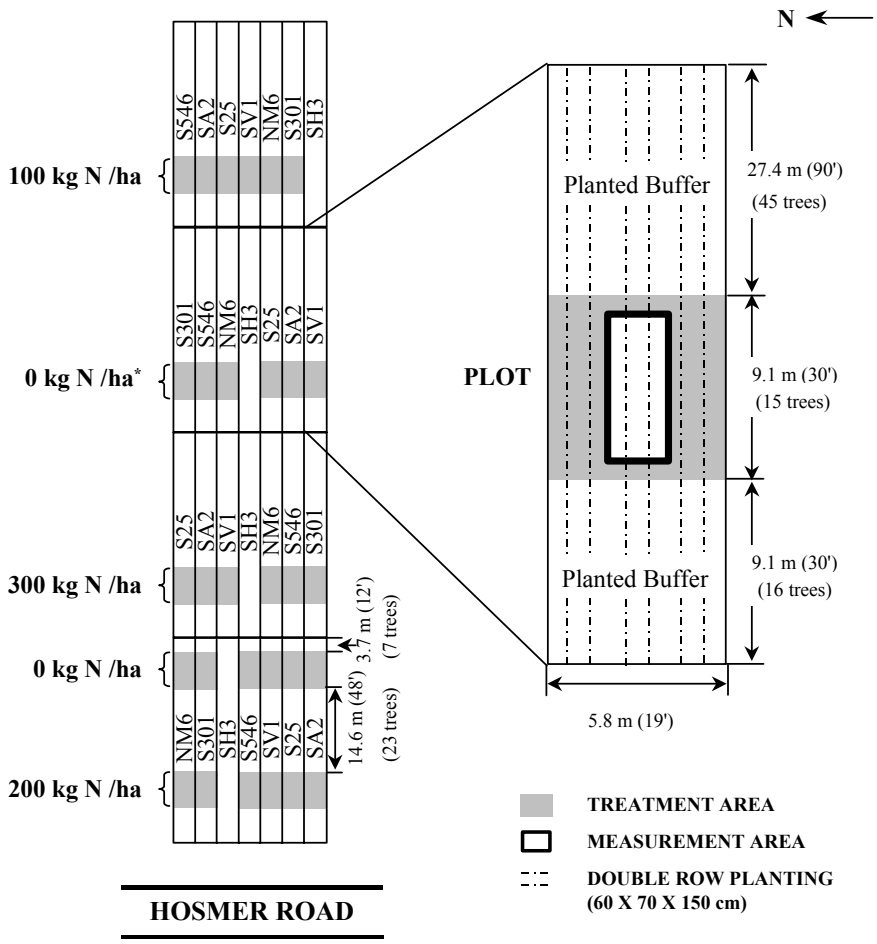

Figure 1.4. Plot and treatment layout at Kintigh Power Station, Somerset, NY. Note: The treatment labeled "0 kg N/ha*" indicates the original control that was excluded due to microsite differences in drainage patterns.

Tully

The study was superimposed on part of a bioenergy demonstration planting at SUNY-ESF's Genetic Field Station. The experimental area was an agricultural farm until the 1920's when it became a state tree nursery run by the New York State Department of Environmental Conservation (NYS DEC). In the 1950's the land was transferred to SUNY-ESF and has since been used for genetic field experiments. Until the summer of 1994 when site preparation for the demonstration planting began, the site was largely occupied by a Norway maple plantation

interspersed with areas of non-woody vegetation. The demonstration planting was established in 1995, and the fertilization treatments for experimental plots were established in spring 1996 (Figure 1.5).

The soil at this site is a Glossoboric Hapludalf of the Palmyra series. The Palmyra series consists of deep, well drained to somewhat excessively drained soils formed in glacial outwash. They are nearly level soils formed in loamy material overlying calcareous, stratified gravel and sand (Hutton and Rice, 1977; USDA-NRCS, 1998). The range of second-year soil characteristics is reported in Table 1.1.

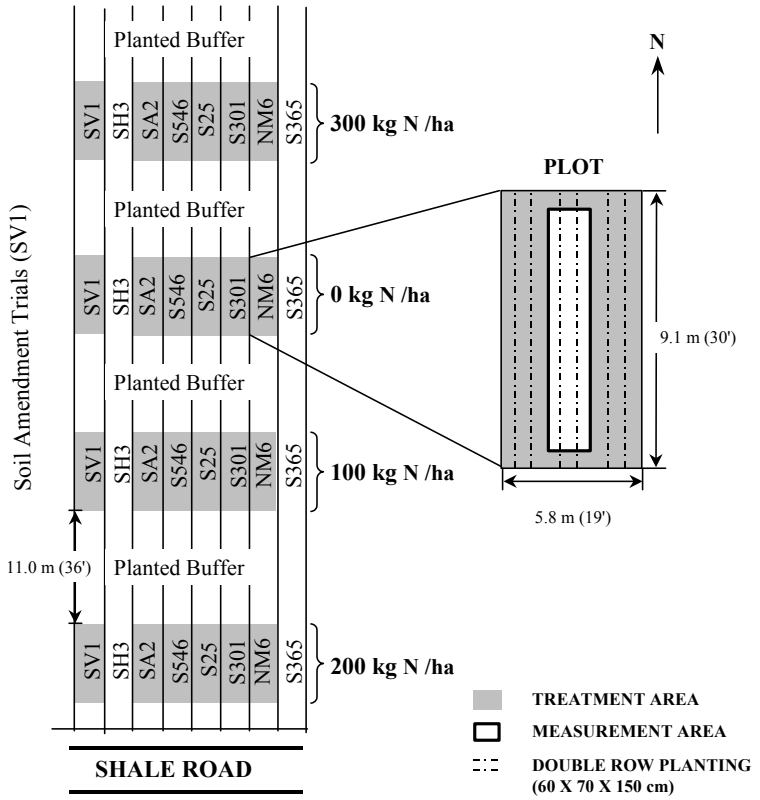

Figure 1.5. Plot and treatment layout at Tully Genetic Field Station, Tully, NY.

Plant Material

Five clones of willow and one clone of hybrid poplar were used in this study (Table 1.2). Unrooted cuttings were obtained from cutting orchards at the SUNY-ESF Genetic Field Station in Tully, NY.

Table 1.2. Parentage and origin of willow and poplar clones used in this study.

CLONE	PARENTAGE	ORIGIN
NM6	*Populus nigra* x *P. maximowiczii*.	Ontario Ministry of Natural Resources.
S25	*S. eriocephala* 16 x *S. eriocephala* 276.	University of Toronto
S301	*S. exigua* 62 x *S. eriocephala* 276.	University of Toronto.
S546	*S. eriocephala* 16 x *S. eriocephala* 24.	University of Toronto.
SA2	*S. alba* var. *sanquinea*.	Novi Sad, Yugoslavia.
SV1	*Salix dasyclados*.	Brantford, Ontario, Canada

Experimental Layout

For each of the six clones in the fertilization trial, the experimental design was quantitative treatments of fertilizer in a completely randomized design with three replicates (sites). Fertilization treatments of slow-release N fertilizer (sulfur-coated urea; i.e., Osmocote, 38 g N/kg) were superimposed on the existing plantings at the rates of 0, 100, 200, 300 kg N/ha. Fertilization treatments were replicated (sites = replicate), but due to constraints of the existing studies treatments were not replicated on each site (i.e., there were four fertilization treatments and three replicates for each clone for a total of twelve plots per clone and a grand total of 72 plots (Figure 1.3, 3.4, and 3.5)).

Plot sizes were constrained by existing treatments (clone-site trials) to 52.8 square meters at the Tully and Somerset sites and 55.6 square meters at the King Ferry site. To maintain appropriate buffers a minimum of 20 meters between treatment plots was used.

In addition, second-year data for clone SV1 were used from a concurrent fertilization amendment trial at SUNY-ESF's Genetic Field Station (Adegbidi, 1999). The experimental design was quantitative treatments of fertilizer in a randomized complete block design. Fertilization treatments, the same as those used in the current study, were applied in three blocks at the same time as those in the current study providing twelve additional plots of clone SV1 at Tully.

Plantation Establishment

Prior to planting in spring 1995, each site was sprayed with Roundup^{TM} (glyphosate), plowed, disced, and capped with herbicide [Goal, oxyfluorfen, at 2.24 kg active ingredient per hectare at Tully and King Ferry in fall 1994 and Simazine, 2-Chloro-4,6-Bis (Ethyl Amino)-S-Triazine, at 0.74 and 0.37 kg active ingredient per ha in fall 1994 and spring 1995, respectively, at Somerset]. Site preparation at Tully also included first bulldozing Norway maple stumps as well as raking after plowing and discing.

The sites were all planted in spring 1995 and grew for one growing season. The trees were then coppiced between December 1995, and January 1996. Treatments of a single application of the four fertilization rates (0, 100, 200, 300 kg N/ha) were applied early in the growing season in 1996 on one-year old root systems. Fertilizer was hand broadcast. Landscape edging was installed soon after application to minimize surface movement of fertilizer in areas that were prone to erosion.

Measurements

Diameter Measurements for Estimation of Stem Biomass

Biomass was estimated for the second year of the rotation (in 1997) using a non-destructive estimation technique (clone-specific logarithmic regression equations). Unless otherwise noted, all reported tree biomass estimates are for the second year of the rotation. Field diameter measurements were collected for use in the prediction equations; stem diameter was measured at 30 cm from the base of the stool (Figure 1.6). Stem biomass was estimated for every stem in the measurement plot using clone-specific logarithmic regression equations (without a bias correction) and summed for total plot biomass. Total plot biomass was expressed as biomass yield (o.d. Mg/ha at a given point in time) using the measurement plot area and appropriate unit conversions. Additionally, survival adjusted (**SADJ**) biomass yields were calculated by dividing total plot biomass by the number of live stools in the measurement plot. This average biomass per stool was converted to a per hectare basis using the theoretical growing space per stool (0.682 square meters).

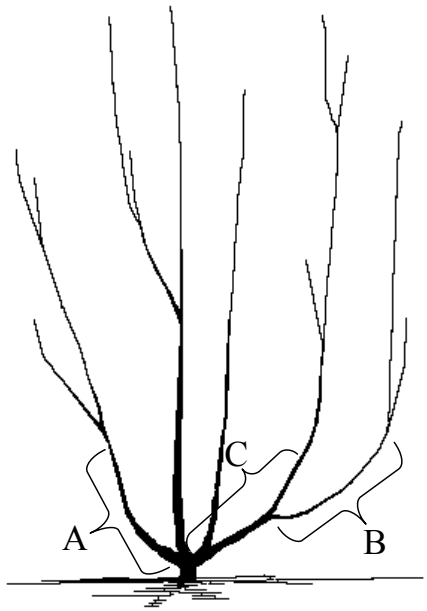

Figure 1.6. Measurement of stem diameter was made at 30 cm (brackets) from the base of the stool following the curvature of the stem (A). Secondary branches forking below 30 cm were measured from the base of the fork (B), while the main stem of a fork was measured from the base of the stool (C).

Assessment of Weed Competition

Weed biomass was measured as an indicator of weed competition annually during the growing season. A systematic random sample of three weed plots with dimensions 30 x 75cm (first-year, 1996) and 30 x 30cm (second-year, 1997) was collected from the base of trees within the fertilization measurement plots. Weed plots were centered at the base of a tree with one edge of the plot bordering the tree. Weeds were cut at ground level, placed in a paper bag, and oven dried at 65°C. Oven-dry samples were removed from the bags and weighed. Oven-dry biomass was converted to a per hectare basis for analysis using the weed plot areas above (Appendix 5).

The purpose of weed competition assessment was to explain variability in tree biomass yield response to fertilization. Note: weeds were cut at Somerset (7/18/96) to reduce competition after weed samples were collected that year.

Survival Assessment

Tree survival was assessed in measurement plots prior to fertilization. Thereafter, annual survival measurements were taken concurrently with stem measurements for biomass estimation. Additionally, frost heave was assessed in spring 1996, to identify plots that were heavily affected (Appendix 5). In some instances, dead cuttings were also replanted by field crews during the 1995 growing season. When survival was assessed that winter, identifiable replants were recorded (Appendix 5).

Assessment of Soil Moisture

Three randomly located soil moisture measurements were taken per plot in the top 6 cm of soil with a Theta Probe during the first growing season of the rotation (Appendix 7). Moisture readings (volts) were converted to m^3/m^3 using the generalized equation in the Theta Probe manual (Delta-T Devices, Ltd., 1996). More intensive soil moisture measurements were planned (e.g., at greater depths and varying moisture conditions), but due to faulty equipment, that was not possible.

Foliar Nutrient Sampling

Foliage was sampled in late August within the treatment plots in 1996 using a procedure equivalent to the foliar sampling Standard Operating Procedure (ESF Willow Bioenergy Program, 1998, Appendix 9). In 1997, foliar sampling was conducted in conjunction with foliar biomass sampling (see the following section for the

procedure). Foliar nutrient concentration was determined following the laboratory procedures outlined below and was used as an indicator of uptake and nutrient status of the plant.

Estimation of Foliar Biomass and Corresponding Woody Biomass

Foliar biomass was sampled concurrently with foliar nutrient sampling between the last week of August and first week of September 1997. A simple random sample of three border stools (all stems on each stool) was selected from non-measurement stools within the treatment area of each plot. All foliage was removed from each sample stool and bagged. Samples were weighed and then placed in the oven at 65°C on the day of collection, or placed in a freezer until they could be transported and placed in the oven. Oven-dry weight was recorded and was used for estimating foliar biomass (Appendix 6). Note that for the S546 control plot at King Ferry, only two dry weights were obtained. Dry weights were also used to calculate nitrogen content of the foliage (Appendix 6). Woody biomass of the three foliar sampled stools was also estimated using biomass equations and stem diameter measurements, according to the procedures outlined above (Appendix 6).

Soil Sampling

Pre-treatment soil samples were collected at King Ferry and Somerset (Tully data were unavailable) in summer 1995 using an AMS 10-cm diameter soil auger at a depth of 0-15 cm. Additional soil samples were collected from treatment plots of SV1 and NM6 the second year of the rotation (summer 1997), in conjunction with another study. Soil was analyzed using the laboratory procedures outlined below. Laboratory data are reported in Appendix 7 and

Appendix 8.

Laboratory

All laboratory analyses were conducted by the soil fertility laboratory at SUNY-ESF in Syracuse, NY, under the direction of Donald Bickelhaupt.

Plant Tissue Analysis

Plant tissues (foliar samples) were oven-dried at 65^0C to constant weight and ground in a Wiley mill to pass through a 2-mm screen. Each ground sample was stored in a glass bottle and redried before analyses. The macro-Kjeldahl method was used to determine the total N concentration in 0.5-gram foliar subsamples. The dry ash procedure was used for destruction of organic matter and determination of ash percent. The ash was dissolved in 6 N HCl and the solution diluted to a final volume of 100 ml. Concentration of K, Ca and Mg were determined by atomic absorption using a Perkin-Elmer 3030B spectrophotometer. Concentration of P was determined by the ammonium molybdate vanadate method using a Milton Roy Company Spectronic 1201 (Bickelhaupt and White, 1982).

Soil Analysis

Soil samples were air-dried, passed through a 2-mm sieve and thoroughly mixed. Subsamples of 20 grams were taken for cation extraction using 1N ammonium acetate at pH 7.0. Potassium, Ca and Mg concentrations in the solution were determined using a Perkin-Elmer 3030B atomic absorption spectrophotometer. Two-gram subsamples were used for determination of P by the Truog method utilizing the Milton Roy Company Spectronic 1201. The macro-Kjeldahl method was used to determine the total N concentration in 10-g soil subsamples. Soil pH was determined in 2:1 soil:water suspension with an Orion Research Digital Ionalyzer Model 601A using 20-g subsamples of soil in 40 ml H_20. Organic matter was determined by loss on ignition with approximately 35-g subsamples of oven dried soil at 105^0C. Using a 10-g subsample, soil CEC was determined by the ammonium saturation method using 1N ammonium acetate at pH 7.0. All results were reported on an oven dried (105^oC) basis (Bickelhaupt and White, 1982).

Statistical Procedures

Since it was expected that clonal response would be different, rigorous comparison of responses among clones was not the focus of the experiment. Several methods were used to determine the response to fertilization for the six clones in the study. Initial assessment involved comparing fertilized versus non-fertilized treatment for each clone to evaluate the general benefit to tree growth from fertilization. To evaluate specific responses, response curves for individual clones at each site were fit. Since generalized fertilization recommendations were the ultimate objective of the study, two methods of generalization were considered: 1) pooling the three sites together for each clone and 2) pooling all six clones together for each site. When sites were pooled together, site was isolated in the error term sum of squares using PROC GLM in SAS (SAS Institute, 1997). Since clone x site x trt interactions were potentially important, caution was used in interpreting "generalized" results (i.e., essentially main effects). Due to the limitations of the experimental design, interactions could not be tested statistically. Instead, data for each clone by site were examined for potential trends, using caution due to the lack of replication on sites. Unless otherwise noted, statistically significant results were reported using a Type I error rate of $\alpha = 0.05$.

Assessment of an asymptotic biomass response to fertilization (using SADJ yields)

The theoretical model of biomass response to fertilization, as described by an exponential saturation function, was fitted using the Quasi-Newton and Simplex non-linear estimation methods (StatSoft, 1997). The initial starting values were set to various values and the tolerance criterion for convergence was 10^{-5} units of absolute magnitude of each parameter. All estimation results for this non-linear model were checked by plotting the estimated functions together with the raw data. The exponential saturation function considered was biomass = $I + A\,(1 - e^{v * TRT})$ (modified from Spain, 1982; Figure 1.7 provides example curves), where biomass is SADJ oven-dry biomass yield (Mg /ha), I is the intercept (biomass yield without fertilization), A is the additional biomass resulting from fertilization to reach the asymptote ($I + A$ = asymptote), e is Euler's number (2.71828…),

v is the rate of ascent (how quickly the asymptote is reached), and *TRT* is the fertilization rate (kg N/ha). This function was selected because each fitted coefficient was biologically meaningful. Site-specific response curves for each clone were fit in an attempt to assess site and clonal differences for biomass yield response to fertilization. The three sites were then pooled by clone to fit a generalized response curve using the same non-linear model, and finally, the model was fit for all clones pooled by site.

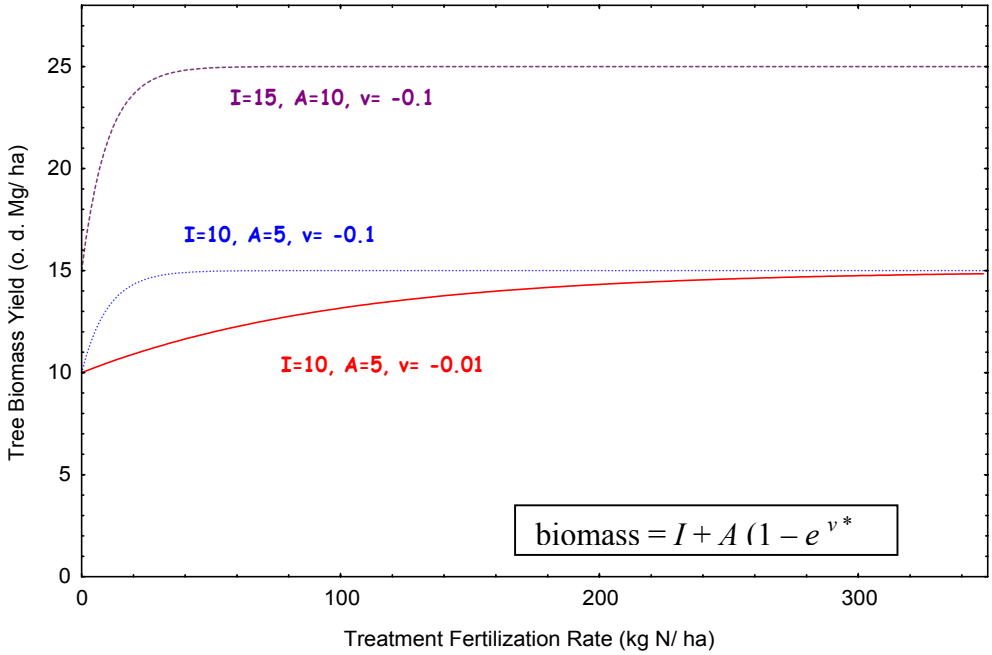

Figure 1.7. Various curves of the non-linear exponential saturation function.

Assessment of cubic, quadratic, and linear responses to fertilization (using SADJ yields)

A least-squares regression approach using polynomials was used to characterize the response to fertilization (SADJ biomass yields). The four equally spaced quantitative rates of fertilizer allowed for a maximum of a third-order polynomial (cubic) to be fit. The cubic (turning), quadratic (curvature) and linear (increasing or decreasing trend) components of the response were evaluated. The multiple regression using the polynomial models was conducted using PROC REG in SAS (SAS Institute, 1997). To avoid collinearity among predictor variables (i.e., among TRT, TRT^2 and TRT^3), the distance from the mean fertilization rate (150 kg N/ha) was used as the primary predictor variable (Neter et al., 1996). For the clones that had only a significant linear trend, the regression was run again using TRT as the predictor variable, as opposed to the distance from the mean fertilization rate, to establish the coefficient for the intercept of the regression.

Clones that did not have a significant cubic, quadratic or linear regression trend by site (likely due to the small sample size) were pooled and then analyzed together by site. Differences in site were evaluated to explain response, or lack thereof, by attempting to fit a cubic, quadratic, and linear regression for the pooled clones.

Results and Discussion

Biomass Response to Fertilization

There was considerable variation in tree biomass response to fertilization as illustrated in Figure 1.8. Variation was observed from site to site, as well as within sites (i.e., microsite variation; demonstrated below in the multi-clone analysis by site). The impacts of weeds and survival were important. Of particular importance was the effect that survival had on biomass yields. A strong correlation between survival and plot yields was evident for every clone (see Table 1.4). The proportion of trees surviving was a function of site preparation, herbicide damage, and weed competition. Due to the strong influence that survival had on tree biomass yields (o.d. Mg /ha), survival adjusted yields (SADJ) were considered when assessing response to fertilization (see Measurements section above). These confounding factors, survival, weeds, site and microsite variation, are discussed below.

Survival, a Confounding Factor

It is necessary to discuss survival before analyzing the response to fertilization due to its potential impact on yield estimates. Tree survival was highly correlated with tree biomass for every clone except S546. Tree survival was also highly correlated with weed biomass for several clones (Table 1.3). Significant correlation for survival and unadjusted biomass yield are reported in Table 1.4. The positive correlation between survival and tree biomass is illustrated in Figure 1.8. When tree survival was high, tree biomass was also high. Adjustment of biomass yields for survival had the most impact on the site with the poorest survival (i.e., King Ferry), as illustrated in Figure 1.9 and Figure 1.10.

Table 1.3. Pearson correlations (R) for second-year weed biomass and first-year survival.

CLONE	R	p-value	n
NM6	-0.44	0.14	12
S25	-0.91	0.0001*	12
S301	-0.71	0.01*	12
S546	-0.63	0.03*	12
SA2	-0.86	0.0003*	12
SV1	-0.84	0.001*	24

*Significant correlations are indicated.

Table 1.4. Pearson correlations (R) for second year unadjusted tree biomass yield and second-year survival.

CLONE	R	p-value	n
NM6	0.77	0.003*	12
S25	0.59	0.04*	12
S301	0.72	0.008*	12
S546	0.47	0.12	12
SA2	0.68	0.01*	12
SV1	0.66	0.0004*	24

*Significant correlations are indicated.

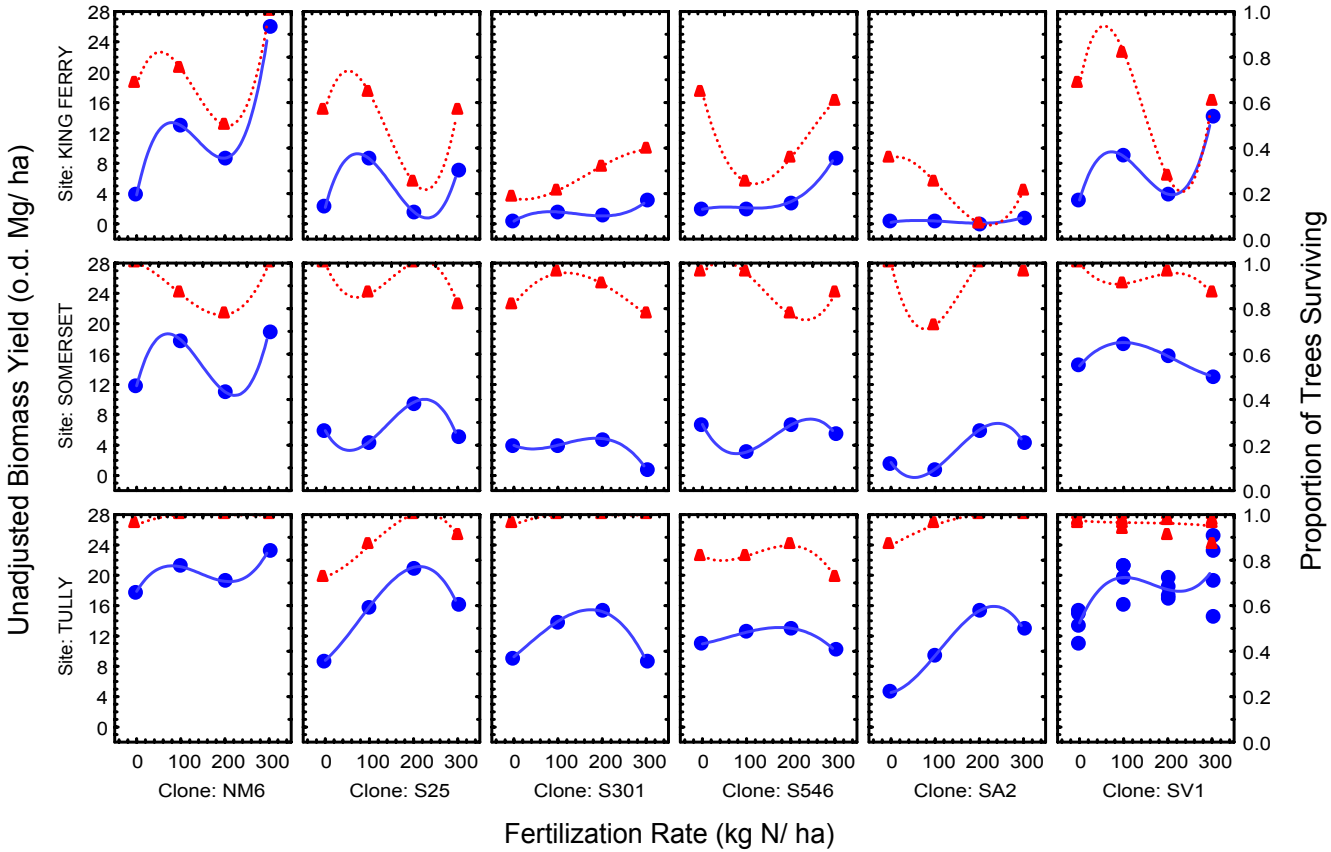

Figure 1.8. Unadjusted biomass yield (—•—) and corresponding survival at the end of the second year of the rotation (- -▲- -). Points were connected with smoothed lines to help illustrate the relationship between biomass yield and survival.

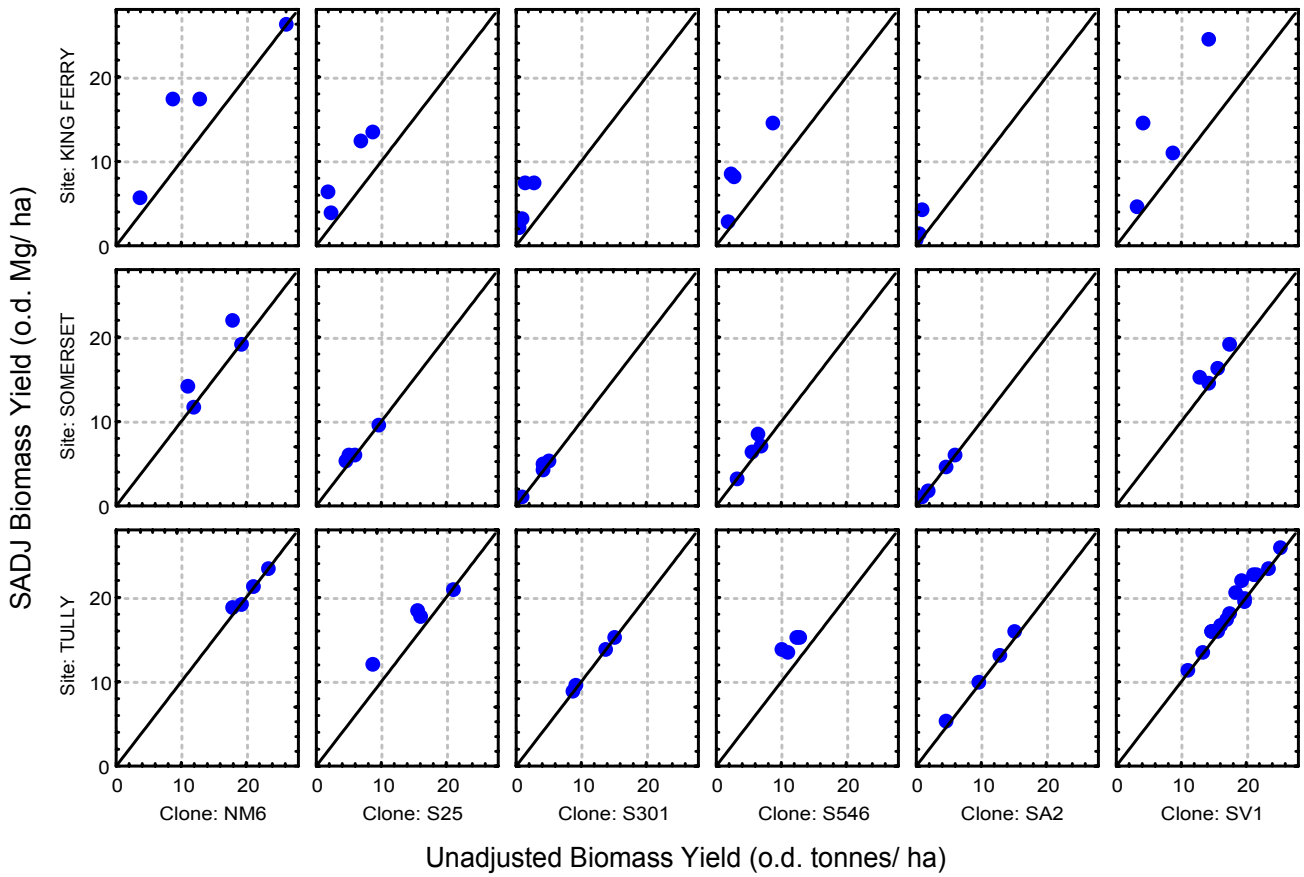

Figure 1.9. SADJ biomass yields versus unadjusted biomass yields. A 1:1 line was used to illustrate the change in biomass yield estimates by adjusting for survival.

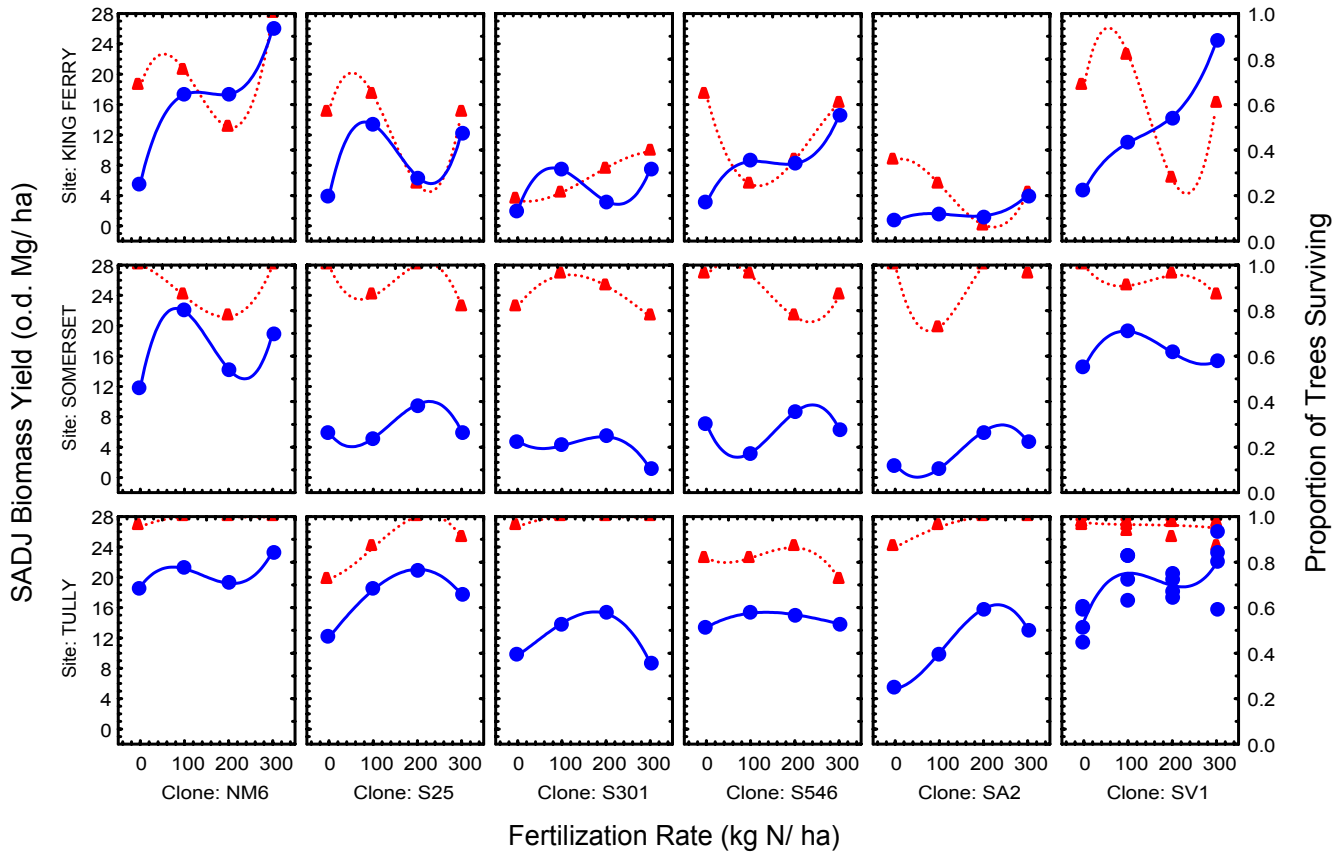

Figure 1.10. SADJ biomass yield (—●—) and corresponding survival at the end of the second year of the rotation (- -▲- -). Points were connected with smoothed lines to help illustrate the relationship between SADJ biomass yield and survival.

Weed Competition, a Confounding Factor

Weed biomass was used as an indicator of weed competition. Weed biomass is plotted with the corresponding tree biomass in Figure 1.11 and illustrates the variability of weed biomass. Weed biomass was highly correlated with tree survival (Table 1.3) and tree biomass yield (Table 1.5 and Table 1.6). At King Ferry, poor site preparation and poor tree survival exacerbated the weed problem and was clearly a confounding factor at this site. Weeds at Somerset were not as severe as at King Ferry, though they were a source of competition. The Somerset site was mowed annually to help reduce weed competition, which proved quite effective. The Tully site had excellent site preparation, and weeds were negligible throughout the planting.

Table 1.5. Pearson correlations (R) for second-year unadjusted tree biomass yield and first-year weed biomass.

CLONE	R	p-value	N
NM6	-0.30	0.35	12
S25	-0.57	0.05*	12
S301	-0.63	0.03*	12
S546	-0.74	0.006*	12
SA2	-0.47	0.12	12
SV1	-0.41	0.05*	24

*Significant correlations are indicated.

Table 1.6. Pearson correlations (R) for second year unadjusted tree biomass yield and second-year weed biomass.

CLONE	R	p-value	n
NM6	-0.64	0.02*	12
S25	-0.58	0.05*	12
S301	-0.47	0.12	12
S546	-0.92	0.0001*	12
SA2	-0.51	0.09	12
SV1	-0.58	0.003*	24

*Significant correlations are indicated.

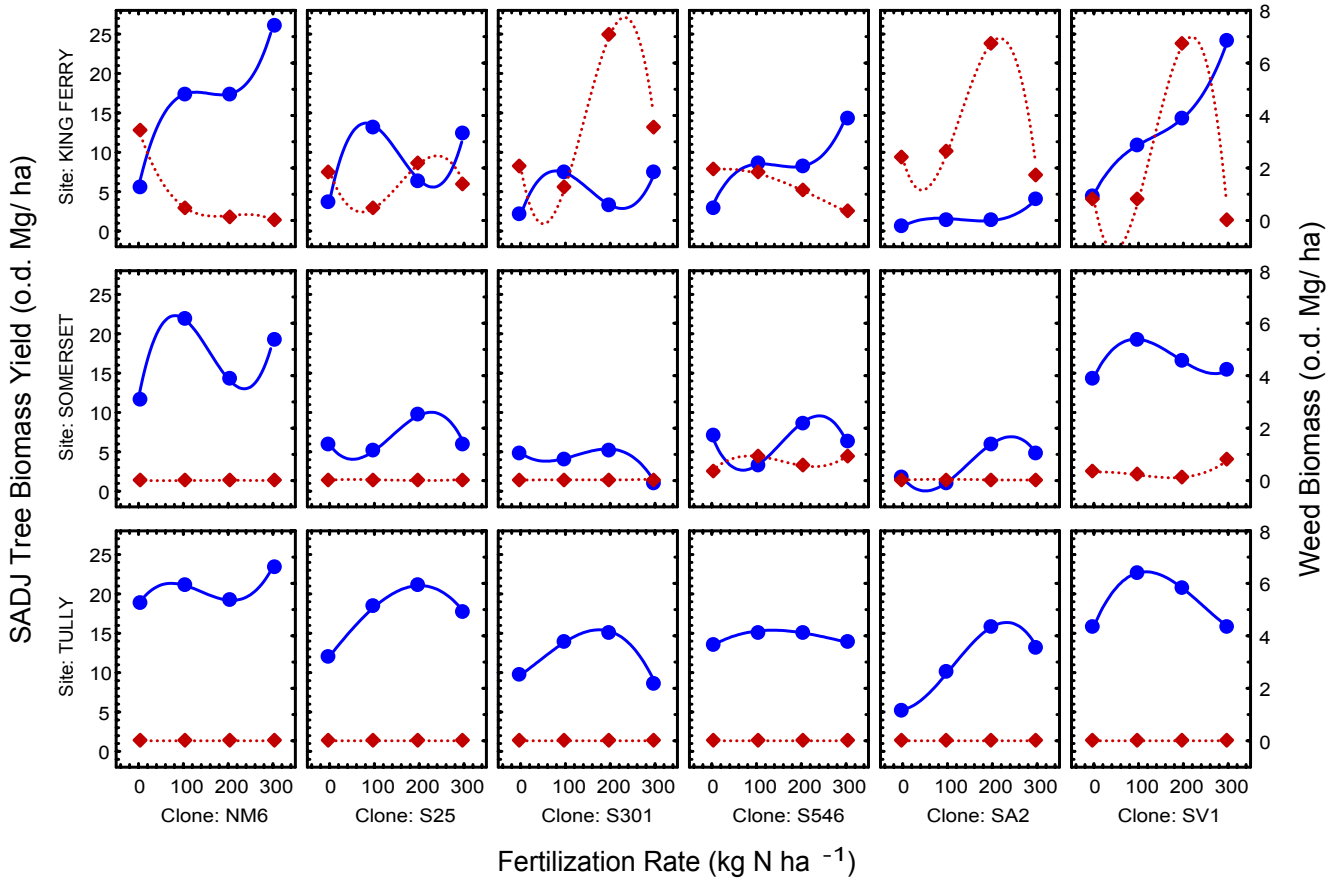

Figure 1.11. SADJ tree biomass yield (—•—) and corresponding annual dry weed biomass yield (second-year - - ♦ - -). Points were connected with smoothed lines to help illustrate the relationship between biomass yield and weed biomass yield.

The unexpected response to fertilization by some clones/treatments was due in part to weed competition, coupled with other site factors. Figure 1.11 illustrates that as weed biomass increased, tree biomass decreases, and vice versa. Tree response to fertilization was altered by these factors. The effectiveness of fertilization was reduced due to weed competition and should be considered when making fertilization recommendations. Fertilization at high rates, especially on sites that have poor weed control is not recommended. Additionally, sites with poor survival, which are often encroached upon by weeds, should not be fertilized at high rates.

Tree Biomass Response

Fertilized plots had higher biomass yields than non-fertilized treatments for four of the six clones in the study. The effect of fertilization was significant for clones NM6, SA2, and SV1 (i.e., non-fertilized versus fertilized treatments differed; data from three sites pooled;

Table 1.7). The effect of fertilization was marginally significant (p-value = 0.06) for clone S25, but not for S301 and S546.

In addition to this general evaluation of the response to fertilization, the exponential saturation curve was used to evaluate the hypothesis that a single application of slow-release nitrogen (urea) fertilizer at increasing fertilization rates would result in an aboveground growth response that is asymptotic for individual clones if the "sufficiency range" was reached. Alternatively, if the sufficiency range was not reached (i.e., the four fertilization rates were still within the "deficiency range" of the plants), the response would be linear. Least-squares regression was used to evaluate the linear, cubic, and quadratic trends.

Table 1.7. ANOVA for clonal biomass response to fertilization (three sites pooled).

ANOVA

----------NM6----------

Source	df	Sum of Squares	Mean Square	F value	p-value
Model	5	235.67	47.13	3.01	0.11
TRT	3	194.20	64.74	4.13	0.07*
Non-fert. vs. fert.	1	141.21	141.21	9.01	0.02**
SITE	2	41.44	20.72	1.32	0.33
Error	6	94.02	15.67		
Total	11	329.69		n= 12	

----------S25----------

Source	df	Sum of Squares	Mean Square	F value	p-value
Model	5	304.16	60.83	5.84	0.03*
TRT	3	55.90	18.63	1.79	0.25
Non-fert. vs. fert.	1	55.70	55.70	5.35	0.06*
SITE	2	248.27	124.13	11.93	0.01**
Error	6	62.45	10.41		
Total	11	366.62		n= 12	

----------S301----------

Source	df	Sum of Squares	Mean Square	F value	p-value
Model	5	170.59	34.12	4.6	0.05**
TRT	3	20.58	6.86	0.92	0.48
Non-fert. vs. fert.	1	8.02	8.02	1.08	0.34
SITE	2	150.01	75.01	10.11	0.01**
Error	6	44.51	7.42		
Total	11	215.10		n= 12	

Table 1.7 (cont'd)

----------S546----------

Source	df	Sum of Squares	Mean Square	F value	p-value
Model	5	164.90	32.98	3.37	0.09*
TRT	3	25.77	8.59	0.88	0.50
Non-fert. vs. fert.	1	15.25	15.25	1.56	0.26
SITE	2	139.13	69.56	7.11	0.03**
Error	6	58.70	9.78		
Total	11	223.60		n= 12	

----------SA2----------

Source	df	Sum of Squares	Mean Square	F value	p-value
Model	5	250.09	50.02	10.36	0.01**
TRT	3	55.97	18.66	3.86	0.07*
Non-fert. vs. fert.	1	34.20	34.20	7.08	0.04**
SITE	2	194.12	97.06	20.1	0.002**
Error	6	28.97	4.83		
Total	11	279.06		n= 12	

----------SV1----------

Source	df	Sum of Squares	Mean Square	F value	p-value
Model	5	328.84	65.77	5.34	0.004**
TRT	3	232.58	77.53	6.29	0.004**
Non-fert. vs. fert.	1	195.23	195.23	15.85	0.001**
SITE	2	96.27	48.13	3.91	0.04**
Error	18	221.77	12.32		
Total	23	550.61		n= 24	

*, ** Statistically significant p-values are highlighted, $\alpha = 0.10$ and 0.05, respectively.

Exponential Saturation

The non-linear exponential saturation model for individual clones on each site was subject to a great deal of variability. Several clones fit the model reasonably well on some sites; however, others did not (Table 1.8). The actual responses of many of the clones on each of the three sites did not fit the theoretical response to fertilization. Either the responses were not asymptotic, or there were too few data points for a single clone on a specific site. The fit of the exponential saturation function should be interpreted with caution; three coefficients were estimated using only four data points when considering an individual clone on a single site, with the exception of clone SV1.

In several instances, fitting the exponential saturation curve for a specific clone on a specific site required the removal of "unusual" observations. Unusual observations were only removed if the model could not be fit with the point left in and there was a legitimate reason for removing the point (e.g., severe weed competition, poor survival, etc.). The validity of this procedure may be questioned since only *three* data points were used to fit the non-linear model (Table 1.8; "unusual" observations removed to allow the model to be fit are noted). For two clones, SA2 at King Ferry and SV1 at Somerset, the exponential saturation function was fit with and without a treatment removed to illustrate the "improved" fit. What this indicated was that for those clones that required removal of "unusual" points the response could not be characterized by the non-linear exponential saturation model. Conceptually, model coefficients are biologically meaningful and could be used to compare clones, sites, and interaction with adequate replication on sites.

The nature of this study requires generalization—across sites by clone, or across clones by site. Therefore, the curves fit for individual clones across the three sites and for individual sites across clones were considered (data were pooled, yielding more points and a more realistic fit). [Note: Heilman and Xie (1993) did not find a significant interaction for clones x fertilization response for the poplar in their study, though it is likely that interaction will be important in many cases. Pooling clone data could be problematic.] The results from these procedures are presented in Table 1.9. The unusual observations that were removed when fitting a function for site-specific, clone-specific data were not removed when the data were pooled across sites by clone or across clones by site. The only exception was the 300 kg N ha^{1} treatment for clone S301 at Somerset, which had severe weed and survival problems.

Table 1.8. Coefficients and model fits by clone and site for the non-linear exponential saturation model† using SADJ yields. The number of observations for each fit was four (n = 4), unless otherwise noted.

CLONE	SITE‡	Coefficients *I*	*A*	*v*	R^2	n	NOTES
NM6	KF	6.28	27.71	-0.004	0.91	4	
NM6	S	11.83	6.19	-0.319	0.56	4	
NM6	T	18.78	46.91	0.000	0.54	4	
S25	KF	3.81	6.93	-0.335	0.57	4	
S25	S	5.63	1.93	-0.008	0.15	4	
S25	T	12.06	7.20	-0.024	0.86	4	
S301	KF	2.01	4.04	-0.352	0.51	4	
S301	S	4.54	20.98	0.000	0.18	3	300 kg N/ha trt. removed (weeds & poor survival)
S301	T	9.70	6.10	-0.012	1.00	3	300 kg N/ha trt. removed
S546	KF	3.33	71.19	-0.001	0.88	4	
S546	S	5.81	25.68	0.000	0.04	4	
S546	T	13.40	1.35	-0.328	0.55	4	
SA2	KF	0.49	25.89	-0.0005	0.99	3	200 kg N/ha trt. removed (survival poor)
SA2	KF	0.36	434.9	-0.00002	0.76	4	200 kg N/ha trt. not removed
SA2	S	1.29	23.83	-0.001	0.58	4	
SA2	T	5.13	9.92	-0.009	0.87	4	
SV1	KF	4.11	176.28	-0.0004	0.96	4	
SV1	S	14.44	3.44	-0.309	0.67	3	300 kg N/ha trt. removed
SV1	S	14.44	2.58	-0.278	0.37	4	300 kg N/ha trt. not removed
SV1	T	15.88	5.78	-0.326	0.91	3	300 kg N/ha trt. removed
SV1	T	14.31	25.69	-0.001	0.64	12	(data from Adegbidi, 1999)
SV1	T	14.18	6.25	-0.266	0.49	16	(including Adegbidi's data)

† Exponential saturation function: Biomass = $I + A\,(1 - e^{v * TRT})$ (modified from Spain, 1982), where biomass is SADJ oven-dry biomass yield (Mg /ha), *I* is the intercept (biomass yield without fertilization), *A* is the additional biomass resulting from fertilization to reach the asymptote (*I* + *A* = asymptote), *e* is Euler's number (2.71828…), *v* is the rate of ascent (how quickly the asymptote is reached).

‡ Sites: King Ferry (KF), Somerset (S), and Tully (T)

The exponential saturation function fits by clone (pooling data from all three sites) were generally poorer (i.e., lower R^2; Table 1.9), with the exception of clone NM6 and SV1, than the fits for individual sites. The general trends of the fit by clone (three sites pooled) were consistent with the results for individual clones at each site, however. NM6 and SV1 could be characterized by an exponential saturation function with reasonable confidence. A linear fit was considered as a plausible alternative in the next section (0).

Table 1.9. Coefficients and fits by clone and site for the non-linear exponential saturation model†.

CLONE	SITE‡	*Coefficients* *I*	*A*	*v*	R^2	n
NM6	All	12.33	9.23	-0.010	0.43	16
S25	All	7.26	4.98	-0.241	0.15	16
S301§	All	5.52	2.68	-0.301	0.09	15
S546	All	7.74	14.62	-0.001	0.11	16
SA2	All	2.36	7.27	-0.005	0.18	16
SV1	All	12.74	7.56	-0.012	0.37	28
All	KF	3.87	26.96	-0.002	0.29	24
All	S	7.62	3.11	-0.007	0.31	23
All	T	12.89	5.26	-0.029	0.24	36

† Exponential saturation function: Biomass = $I + A\,(1 - e^{v * TRT})$ (modified from Spain, 1982), where biomass is SADJ oven-dry biomass yield (Mg /ha), *I* is the intercept (biomass yield without fertilization), *A* is the additional biomass resulting from fertilization to reach the asymptote ($I + A$ = asymptote), *e* is Euler's number (2.71828…), *v* is the rate of ascent (how quickly the asymptote is reached).

‡ Sites: King Ferry (KF), Somerset (S), and Tully (T)

§ S301, 300 kg N/ha treatment at Somerset was removed due to severe weed competition and poor survival.

Least-squares Regression: Cubic, Quadratic, and Linear Trend Evaluation

The second approach used to describe the responses to fertilization was a regression approach. Four fertilization treatments would permit up to a cubic polynomial to be fit to describe the response. Least-squares regression was used to describe the cubic, quadratic, and linear trends, and the results of the regression analyses are presented below. Trends for each clone on each site were considered first, then for each clone across three sites, and finally, groups of clones across sites were considered. Cubic and quadratic trends were not evaluated for individual clones at each site due to the limited amount of data (i.e., four data points).

Regression results for significant linear trends by clone at each site are reported in Table 1.10. There was a strong linear trend for clones NM6, S546, and SV1 at King Ferry and a weaker, significant trend for SV1 at Tully.

The linear trends for clones (data for the three sites pooled) are presented in

Table 1.7 and Figure 1.12. SV1 was the only clones that exhibited a significant linear trend when data for sites were combined and the error for sites was accounted for. NM6 and SA2 exhibited a marginally significant linear trend (p-values = 0.07). The variability of this pooled data was high, as explained by site and microsite differences, weed competition, and survival (partially corrected by SADJ yields).

Table 1.10. Least-squares regression results for linear trends† in clonal biomass response to fertilization by clone and site.

CLONE	SITE‡	Linear Trend (p-value)	Intercept (std. error)	Slope Coeff. (std. error)	R^2	n
NM6	KF	0.056*	7.4 (2.8)	0.061 (0.015)	0.89	4
NM6	S	0.60	--	--	--	4
NM6	T	0.26	--	--	--	4
S25	KF	0.47	-	-		4
S25	S	0.68	-	-		4
S25	T	0.33	-	-		4
S301	T	0.93	-	-		4
S301	S	0.32	-	-		4
S301	KF	0.43	-	-		4
S546	KF	0.06*	3.4 (1.7)	0.034 (0.009)	0.82	4
S546	S	0.80	-	-		4
S546	T	0.82	-	-		4
SA2	KF	0.13	-	-		4
SA2	S	0.24	-	-		4
SA2	T	0.16	-	-		4
SV1	KF	0.02*	4.2 (1.65)	0.063 (0.009)	0.96	4
SV1	S	0.99	--	--	--	4
SV1	T	0.01*	15.7 (1.3)	0.021 (0.007)	0.38	16

† Simple linear regression model: $Y_i = \beta_0 + \beta_1 > (X_i) + \varepsilon_i$, where Y_i is the value of the response variable (biomass yield) in the *i*th trial; β_0 and β_1 are parameters (intercept and slope, respectively); X_i is the value of the predictor variable (fertilization rate) in the *i*th trial; and ε_I is a random error term, $\varepsilon_i \sim N(0,\sigma^2)$.

‡ Sites: King Ferry (KF), Somerset (S), and Tully (T)

* Significant linear trends for clones NM6 and SV1; there were no significant linear trends for the other four clones; S546 at King Ferry was marginally significant.

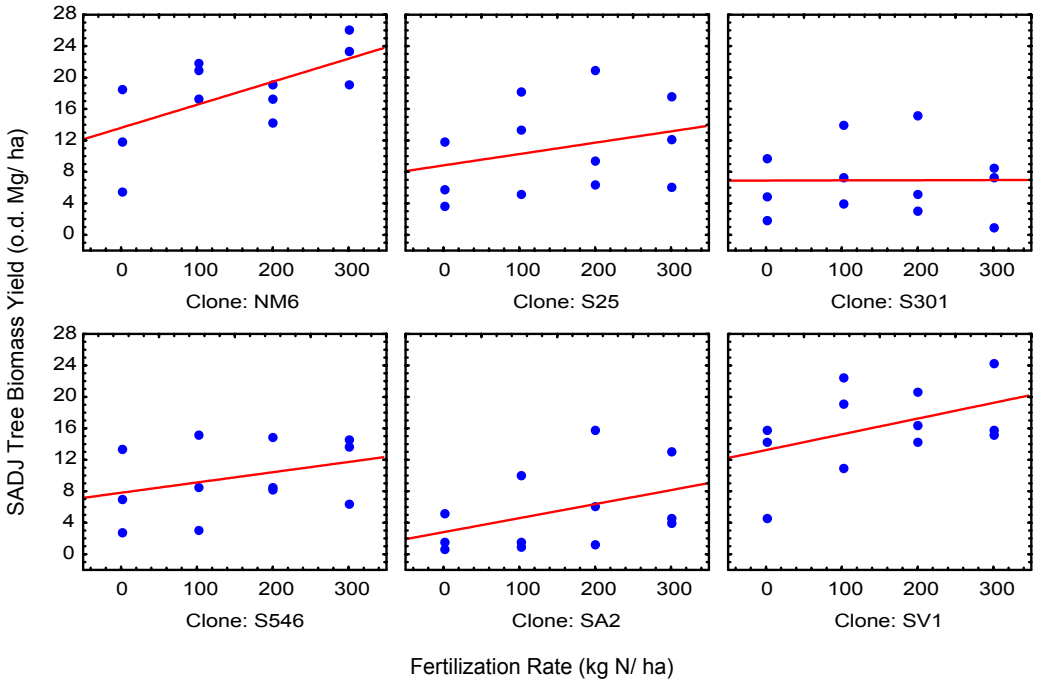

Figure 1.12. Linear trends for pooled site data by clone. The linear trend for SV1 was significant (p-value = 0.004) and marginally significant for NM6 and SA2 (p-values = 0.07).

Foliar Nutrient Concentration

Foliar nutrients were monitored and considered in the analysis of tree biomass response to fertilization. Foliar nitrogen concentration should represent nutrients available to the plant (uptake). Foliar nitrogen concentration is a function of available nitrogen in the soil and the factors influencing uptake. If trees took up and used fertilizer but sufficiency was *not* reached, foliar nitrogen should have increased as woody biomass and fertilization rate increased (a positive slope, or the front part of the curve in Figure 1.13). However, if trees took up and used fertilizer and sufficiency *was* reached, foliar nitrogen should have increased as woody biomass leveled off and fertilization rate increased (zero slope, or the plateau in Figure 1.13).

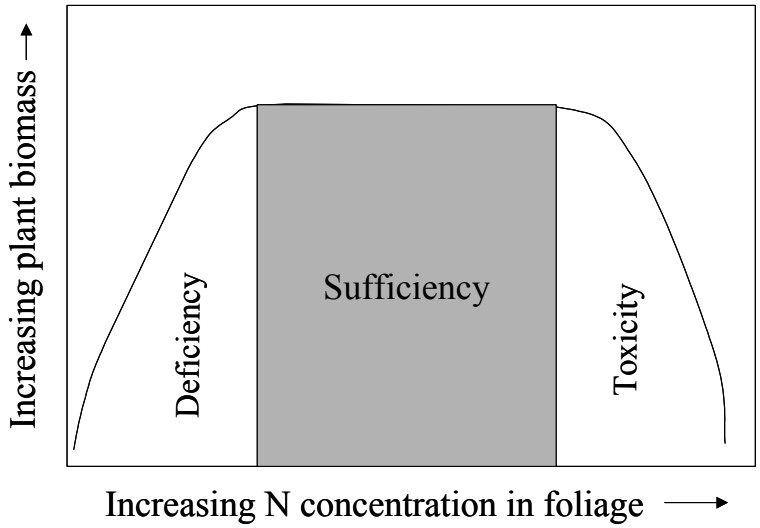

Figure 1.13. Theoretical relationship between plant growth and the concentration of nitrogen in foliage. Adapted from Brady and Weil (1996).

Foliar nitrogen concentration was significantly correlated with tree biomass for every clone the year of fertilization. With the exception of clone SV1, tree biomass was significantly correlated the second year of the rotation as well (Table 1.11). Note: caution is required when considering the first-year foliar nitrogen concentrations from Tully. Fertilization treatments for eighteen samples from Tully were mislabeled during processing in the lab; treatments for those samples were identified by using discriminant/classification analysis.

Table 1.11. Pearson correlations (R) for first- and second-year unadjusted tree biomass yield with foliar nitrogen concentrations from the corresponding year (data from three sites pooled).

CLONE	First-year		Second-year		n
	R	p-value	R	p-value	
NM6	0.68†(3)	0.02*	0.76	0.004*	12
S25	0.76	0.004*	0.90	0.0001*	12
S301	0.77†(4)	0.003*	0.71	0.01*	12
S546	0.65†(4)	0.02*	0.79	0.002*	12
SA2	0.88†(3)	0.0001*	0.59	0.04*	12
SV1	0.70†(4)	0.0001*	0.15	0.5	24

† Fertilization treatments for eighteen samples from Tully were mislabeled in the lab; treatments for these samples were identified by using discriminant/classification analysis. Numbers in parentheses indicate the number of samples that were relabeled using this approach.
* Significant p-values are indicated.

There was a strong correlation between foliar nitrogen concentrations at the end of the first growing season following fertilization and the fertilization rates applied. This suggested that NM6, S25, S546, and SV1 trees took up fertilizer (i.e., as the treatment rates increased, the concentration of nitrogen in foliage also increased; Table 1.12). There was not a significant correlation between foliar nitrogen concentration and fertilization rate for the other three clones S301 and SA2, suggesting that the trees did not take up fertilizer in proportion to the rates applied. These trees likely took up some fertilizer. When considering the exploratory nature of the correlation analysis, an R = 0.46 (p-value = 0.13) for clone SA2 indicated a marginally significant trend. Differences among sites may have confounded these results. Unfortunately, due to the small sample size for individual sites and the issue of mislabeled samples (at Tully) a more detailed interpretation was not possible.

Table 1.12. Pearson correlations (R) for fertilization treatment and first-year foliar nitrogen concentrations† by clone (data from three sites pooled).

CLONE	SITE	R	p-value	n
NM6†(3)	ALL	0.54	0.07*	12
S25	ALL	0.54	0.07*	12
S301†(4)	ALL	0.29	0.36	12
S546†(4)	ALL	0.69	0.01*	12
SA2†(3)	ALL	0.46	0.13	12
SV1†(4)	ALL	0.69	0.0001**	24

† Fertilization treatments for eighteen samples from Tully were mislabeled in the lab; treatments for these samples were identified by using discriminant/classification analysis. Numbers in parentheses indicate the number of samples that were relabeled using this approach.
*, ** Significant p-values are highlighted, $\alpha = 0.10$ and 0.05, respectively.

Results for Willow Clone SV1

Using R-squared as the criterion, the linear regression described the fertilization response of willow clone SV1 as well as the exponential saturation function did (Table 1.13). Cubic and quadratic trends were evaluated, but were not significant for clone SV1 at individual sites or combined (Table 1.14). The fit of the exponential saturation function indicated a plateau for pooled data (i.e., all sites combined; Figure 1.14). The linear trend resulting from the regression analysis for pooled data indicated a significant positive trend (i.e., as fertilization rate increased, biomass increased, Figure 1.15). The examination of responses by site was considered more closely to explain the high variably in response to fertilization.

Table 1.13. Linear regression and exponential saturation fits for clone SV1.

		Exponential Saturation† Coefficients			Fit	Significant Linear Fits‡	
CLONE	SITE§	I	A	v	R^2	R^2	n
SV1	ALL	12.7	7.6	-0.01	0.37	0.46¶	24
SV1	KF	4.1	176.3	-0.001	0.96	0.96	4
SV1	S	14.4	2.6	-0.27	0.37	--	4
SV1	T	14.2	6.3	-0.27	0.49	0.38	16

† Exponential saturation function: Biomass = $I + A\,(1 - e^{v * TRT})$ (modified from Spain, 1982), where biomass is SADJ oven-dry biomass yield (Mg /ha), *I* is the intercept (biomass yield without fertilization), *A* is the additional biomass resulting from fertilization to reach the asymptote ($I + A$ = asymptote), *e* is Euler's number (2.71828…), *v* is the rate of ascent (how quickly the asymptote is reached).

‡ Simple linear regression model: $Y_i = \beta_0 + \beta_1 > (X_i) + \varepsilon_i$, where Y_i is the value of the response variable (SADJ biomass yield) in the *i*th trial; β_0 and β_1 are parameters (intercept and slope, respectively); X_i is the value of the predictor variable (fertilization rate) in the *i*th trial; and ε_i is a random error term, $\varepsilon_i \sim N(0,\sigma^2)$.

§ Sites: King Ferry (KF), Somerset (S), and Tully (T).

¶ Site was included in the regression models as a predictor variable when data from all sites were combined.

Table 1.14. Summary of p-values for the least-squares polynomial regression used to evaluate linear, quadratic and cubic trends for clone SV1.

SITE†	Model‡	Models Highest-order Predictor	p-value	n
ALL§	Cubic	TRT^3	0.08	24
	Quadratic	TRT^2	0.38	24
	Linear	TRT	0.001*	24
KF	Cubic	TRT^3	--	4
	Quadratic	TRT^2	0.54	4
	Linear	TRT	0.019*	4
S	Cubic	TRT^3	--	4
	Quadratic	TRT^2	0.83	4
	Linear	TRT	0.99	4
T	Cubic	TRT^3	0.08	16
	Quadratic	TRT^2	0.31	16
	Linear	TRT	0.010*	16

† Sites: King Ferry (KF), Somerset (S), and Tully (T).

‡ Polynomial regression models: $Y_i = \beta_0 + \beta_1>(X_i) + \beta_2>(X^2_i) + \beta_3>(X^3_i) + \varepsilon_i$, where Y_i is the value of the response variable (biomass yield) in the *i*th trial; β_0, β_1, β_2, and β_3 are parameters (intercept, linear (slope), quadratic (curvature), and cubic (turning), respectively); X_i is the value of the predictor variable (TRT = fertilization rate – 150 kg N/ha) in the *i*th trial; and ε_I is a random error term, $\varepsilon_i \sim N(0,\sigma^2)$. As the model is reduced, the predictor variable and corresponding parameter are removed (e.g., when the cubic is reduced to a quadratic, $\beta_3>(X^3_i)$ is removed from the model).

§ Site was included in the regression models as a predictor variable when data from all sites were combined.

* Significant p-values are highlighted.

Note: a cubic model could not be evaluated for KF and S due to the small sample size.

Though the hypothesized response was an exponential saturation curve, site differences were confounding factors (i.e., the trends of fertilization response by SV1 differed by site). There was a significant positive linear trend for SV1 at King Ferry and Tully (p-value = 0.01 and 0.02, respectively; Table 1.10); there was not a significant linear trend at Somerset (likely due to microsite variation (e.g., drainage differences)).

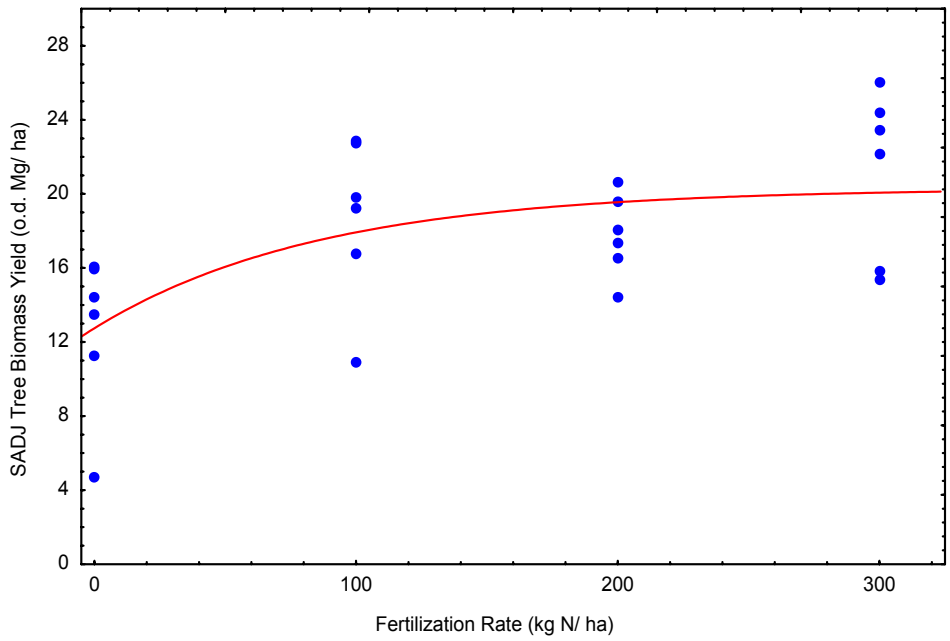

Figure 1.14. Non-linear fit of the exponential saturation model using pooled data across three sites for clone SV1 (R^2 = 0.37, n = 24).

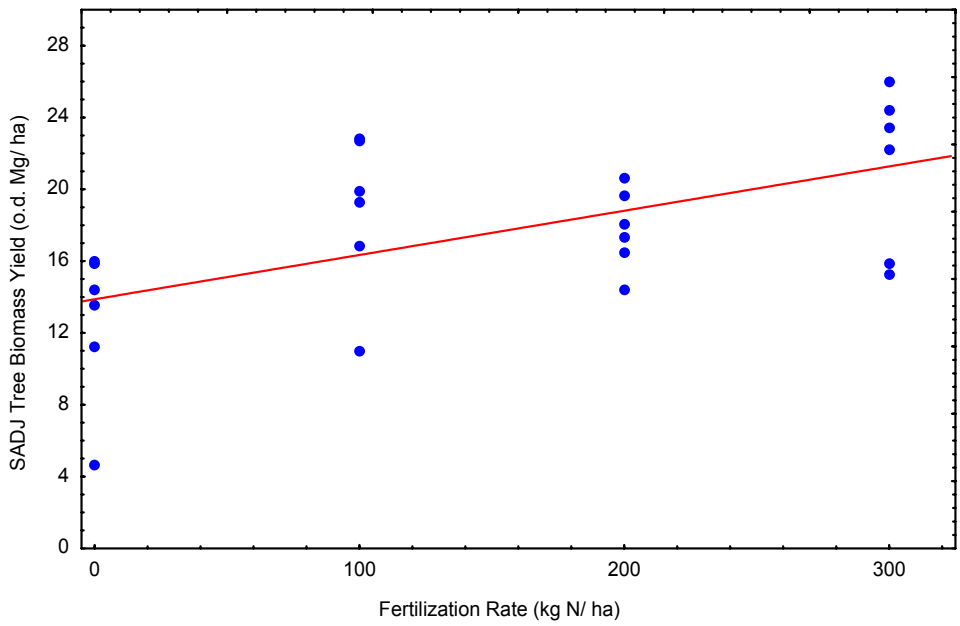

Figure 1.15. Linear fit using pooled data across three sites for clone SV1 (R^2 = 0.33, n = 24, p-value = 0.003).

The small sample sizes at individual sites did not allow for statistical testing of site differences. Caution was used in interpreting results for an individual clone at a particular site. High R-squared values for linear regressions, or fit of the exponential saturation function should only be used to indicate potential trends. Fortunately, for clone SV1 at Tully, twelve additional plots (three blocks for each treatment) were available for the analysis (Adegbidi, 1999).

The exponential saturation fit for SV1 at Tully was good (i.e., 49% of the variation in tree biomass yield was explained with the exponential saturation function) and suggested that growth reached a plateau. The number

of observations at Tully allowed for more confident statements to be made. However, the resulting fit was not useful in characterizing the response between 0 and 100 kg N/ha, due to the large interval between treatments or data points, as illustrated in Figure 1.16. For example, the resulting curve in this case jumped up to the plateau immediately (just above a fertilization rate of zero) because there are no data points for fertilization rates between 0 and 100 kg N/ha. A more realistic response would be a more gradual curve, as indicated in Figure 1.16. Fertilizing at 100 kg N/ha would be adequate for clone SV1 given the site conditions at Tully (i.e., additional nitrogen fertilization would not have increased yields without addition of some other limiting factor).

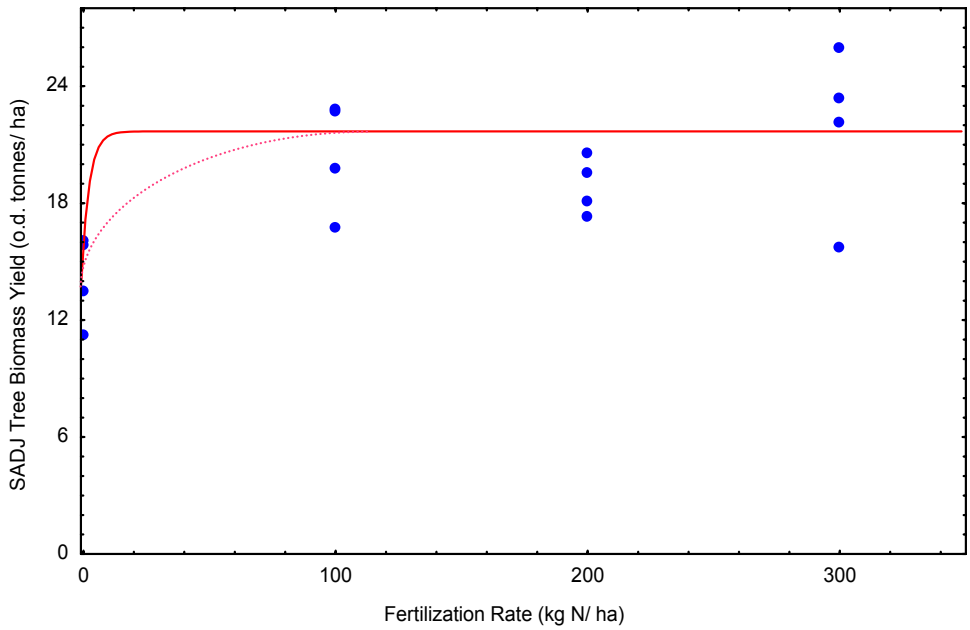

Figure 1.16. Non-linear fit of the exponential saturation model for willow clone SV1 at Tully ($R^2 = 0.49$, n = 16). Note: The dashed line represents a hypothetical response/fit.

From the plots in Figure 1.17 it is fairly clear, even with only four data points, that there were confounding factors (e.g., weeds, microsite differences in drainage) at Somerset that masked any positive response to fertilization. That would have explained the non-significant linear trend and the poor fit for the exponential saturation function. Even with high weed competition at King Ferry, there was clearly a positive response to fertilization, and the response did not level off. Though the exponential saturation function had a high R^2 value, the response was linear; the coefficients for the exponential saturation fit a nearly straight line (Table 1.13 and Figure 1.17).

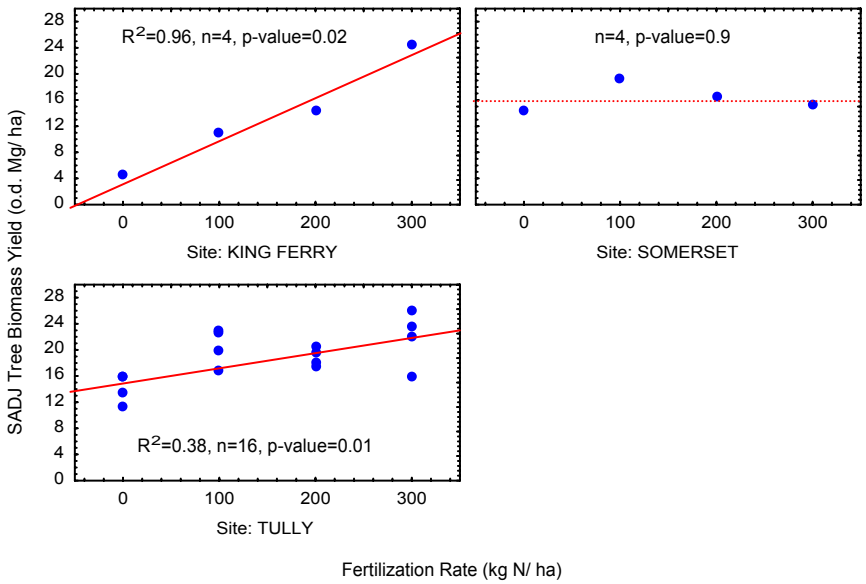

Figure 1.17. Linear trends for willow clone SV1 by site.

The evidence presented thus far for clone SV1 suggests that original null hypothesis that fertilization does not increase aboveground tree biomass compared to unfertilized trees is false (at least at some sites). At King Ferry, tree biomass continued to increase as fertilization rate increased, which was best described by a linear function, indicating the plants were still within the "deficiency range" for nitrogen. At Tully, the response could be best described with an exponential saturation (asymptotic) model, suggesting that "sufficiency range" was reached. Somerset poses a different problem, since neither of the hypothesized response curves was observed. The non-significant linear trend at Somerset would indicate that the response was not different from zero; therefore, the trees were within the "sufficiency range" because other (confounding) factors were limiting growth.

Results for Poplar Clone NM6

There was a significant linear trend for poplar clone NM6 pooled across three sites (R^2 = 0.38,

Table 1.15 and

Table 1.6). NM6 had a marginally significant positive linear trend at King Ferry (p-value = 0.056), but not at the other two sites (

Table 1.15 and Figure 1.18). Cubic and quadratic trends were evaluated, but were not significant for clone NM6 at individual sites (

Table 1.15). The cubic trend across the three sites (data pooled) was marginally significant (p-value = 0.08) when site was included in the model. The cubic trends could not be evaluated at individual sites due the small sample size. A cubic trend would suggest that factors other than fertilization were influencing growth. Differences among sites were not unexpected, though detailed examination of those potential differences was limited for NM6 due to the small sample sizes. The focus should be on pooled data across sites, recognizing that site differences must be accounted for.

Table 1.15. Summary of p-values for the least-squares polynomial regression used to evaluate linear, quadratic and cubic trends for clone NM6.

SITE†	Model‡	Models Highest-order Predictor	p-value	n
ALL§	Cubic	TRT^3	0.08	12
	Quadratic	TRT^2	0.70	12
	Linear	TRT	0.03*	12
KF	Cubic	TRT^3	--	4
	Quadratic	TRT^2	0.80	4
	Linear	TRT	0.056*	4
S	Cubic	TRT^3	--	4
	Quadratic	TRT^2	0.76	4
	Linear	TRT	0.60	4
T	Cubic	TRT^3	--	4
	Quadratic	TRT^2	0.76	4
	Linear	TRT	0.26	4

† Sites: King Ferry (KF), Somerset (S), and Tully (T).

‡ Polynomial regression models: $Y_i = \beta_0 + \beta_1>(X_i) + \beta_2>(X^2_i) + \beta_3>(X^3_i) + \varepsilon_i$, where Y_i is the value of the response variable (biomass yield) in the *i*th trial; β_0, β_1, β_2, and β_3 are parameters (intercept, linear (slope), quadratic (curvature), and cubic (turning), respectively); X_i is the value of the predictor variable (TRT = fertilization rate – 150 kg N/ha) in the *i*th trial; and ε_I is a random error term, $\varepsilon_i \sim N(0,\sigma^2)$. As the model is reduced, the predictor variable and corresponding parameter are removed (e.g., when the cubic is reduced to a quadratic, $\beta_3>(X^3_i)$ is removed from the model).

§ Site was included in the regression models as a predictor variable when data from all sites were combined.

* Significant p-values are highlighted.

Note: a cubic model could not be evaluated for KF and S due to the small sample size.

The significant linear trend for NM6 pooled across three sites was likely influenced by the stronger linear trend at King Ferry. The strong linear trend and the "good" fit with the exponential saturation function (essentially a straight line) at King Ferry both indicated an increase in tree growth with fertilization rate. The variance explained by the exponential saturation function for data pooled across site was slightly higher, though comparable, to that of the linear regression (R^2 = 0.43 versus 0.38;

Table 1.6). It was hypothesized that tree growth would level off as fertilization rate increased (i.e., reached saturation). The slightly better fit with the exponential saturation function was not inconsistent with this hypothesis (Figure 1.19), though the response at King Ferry would suggest that tree growth did not level of at that site.

Table 1.16. Linear regression and exponential saturation fits for clone NM6.

CLONE	SITE§	Exponential Saturation† Coefficients I	A	v	Fit R^2	Significant Linear Fit‡ R^2	n
NM6	ALL	12.33	9.23	-0.010	0.43	0.38¶	12
NM6	KF	6.28	27.71	-0.004	0.91	0.89	4
NM6	S	11.83	6.19	-0.319	0.56	--	4
NM6	T	18.78	46.91	0.000	0.54	--	4

† Exponential saturation function: Biomass = $I + A\,(1 - e^{v * TRT})$ (modified from Spain, 1982), where biomass is SADJ oven-dry biomass yield (Mg /ha), I is the intercept (biomass yield without fertilization), A is the additional biomass resulting from fertilization to reach the asymptote ($I + A$ = asymptote), e is Euler's number (2.71828…), v is the rate of ascent (how quickly the asymptote is reached).

‡ Simple linear regression model: $Y_i = \beta_0 + \beta_1 > (X_i) + \varepsilon_i$, where Y_i is the value of the response variable (SADJ biomass yield) in the ith trial; β_0 and β_1 are parameters (intercept and slope, respectively); X_i is the value of the predictor variable (fertilization rate) in the ith trial; and ε_i is a random error term, $\varepsilon_i \sim N(0,\sigma^2)$.

§ Sites: King Ferry (KF), Somerset (S), and Tully (T).

¶ Site was included in the regression models as a predictor variable when data from all sites were combined.

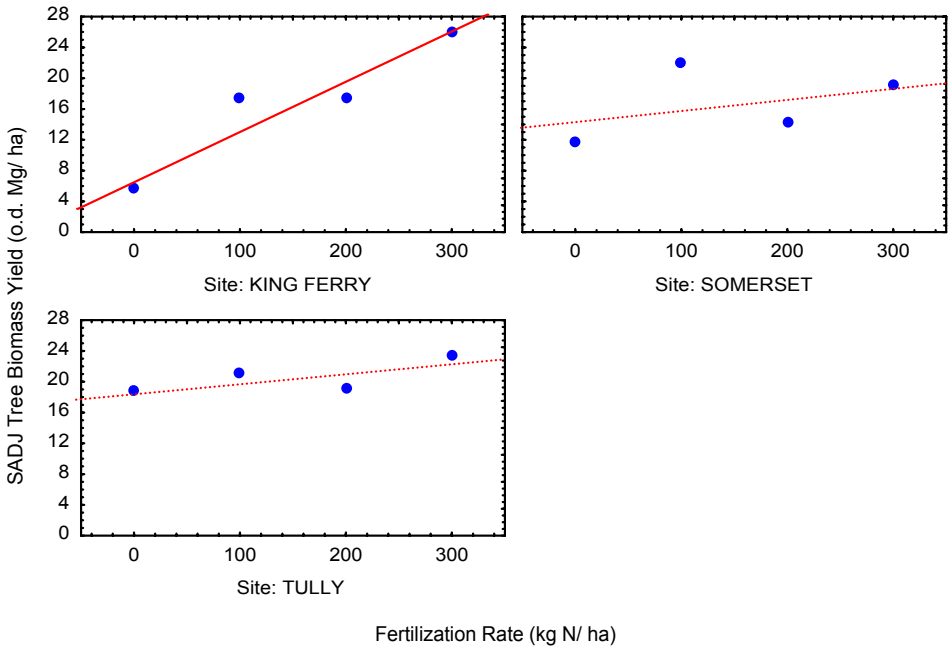

Figure 1.18. Linear trends for NM6 by site. The linear trend was only marginally significant at the King Ferry site (p-value = 0.06).

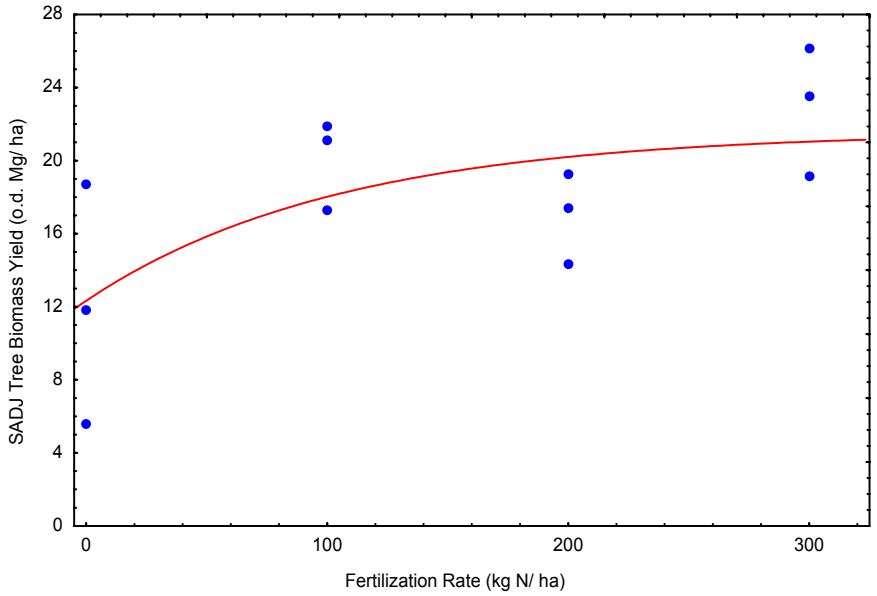

Figure 1.19. Non-linear fit of the exponential saturation model using pooled data across three sites for clone NM6 ($R^2 = 0.43$, n = 16).

Results for Willow Clones S25, S301, S546, and SA2

When considered individually, these four willow clones did not exhibit significant linear trends by site (Table 1.10 and

Table 1.167). Note: the results reported in

Table 1.167 and

Table 1.18 were obtained using “TRT – 150 kg N/ha” as the source variable to avoid collinearity among predictor variables (see Methods 0).

Fertilization response was likely influenced by site differences, so it seems reasonable to evaluate the three sites for the clones that responded similarly to fertilization in an attempt to characterize those differences. There was a positive response to fertilization for clone SA2 when site was accounted for. With the exception of the linear trend for clone SA2, neither the cubic, quadratic, nor linear trend was significant for these clones individually when data were pooled from the three sites (

Table 1.167).

When the four clones S25, S301, S546, and SA2 were combined across sites (all clones and all sites pooled, accounting for site in the model) the linear trend was significant, but the cubic and quadratic trends were not (

Table 1.18). This suggested that there was a benefit to fertilization. When the group of four clones was considered at individual sites (clones pooled by site) the cubic trend was significant at King Ferry and Somerset, and the quadratic trend was significant at Tully (

Table 1.18).

Table 1.167. Summary of p-values for least-squares polynomial regressions† for cubic, quadratic and linear trends for the group of four willow clones S25, S301, S546, and SA2 by site.

CLONE	SITE§	Cubic	Quadratic	Linear
		p-value of highest-order predictor‡		
S25	ALL	0.74	0.35	0.26
S301	ALL	0.85	0.24	0.98
S546	ALL	0.93	0.97	0.22
SA2	ALL	0.46	0.52	0.03*

† Polynomial regression models: $Y_i = \beta_0 + \beta_1>(X_i) + \beta_2>(X^2_i) + \beta_3>(X^3_i) + \varepsilon_i$, where Y_i is the value of the response variable (biomass yield) in the *i*th trial; β_0, β_1, β_2, and β_3 are parameters (intercept, linear (slope), quadratic (curvature), and cubic (turning), respectively); X_i is the value of the predictor variable (TRT = fertilization rate – 150 kg N/ha) in the *i*th trial; and ε_I is a random error term, $\varepsilon_i \sim N(0,\sigma^2)$. As the model is reduced, the predictor variable and corresponding parameter are removed (e.g., when the cubic is reduced to a quadratic, $\beta_3>(X^3_i)$ is removed from the model).
‡ Reported p-values are for the highest order predictor in the regression (e.g., TRT^3 for the cubic regression).
§ Site was included in the regression models as a predictor variable when data from all sites were combined.
* Significant p-values are highlighted.

Table 1.18. Summary of p-values for least-squares polynomial regressions† for cubic, quadratic and linear trends for willow clones S25, S301, S546, and SA2.

CLONE	SITE‡	Cubic	Quadratic	Linear
		p-value of highest-order predictor§		
ALL FOUR	ALL¶	0.99	0.18	0.04*
ALL FOUR	KF	0.08	0.90	0.052*
ALL FOUR	S	0.025*	0.59	0.59
ALL FOUR	T	0.61	0.036*	0.17

† Polynomial regression models: $Y_i = \beta_0 + \beta_1>(X_i) + \beta_2>(X^2_i) + \beta_3>(X^3_i) + \varepsilon_i$, where Y_i is the value of the response variable (biomass yield) in the *i*th trial; β_0, β_1, β_2, and β_3 are parameters (intercept, linear (slope), quadratic (curvature), and cubic (turning), respectively); X_i is the value of the predictor variable (TRT = fertilization rate – 150 kg N/ha) in the *i*th trial; and ε_I is a random error term, $\varepsilon_i \sim N(0,\sigma^2)$. As the model is reduced, the predictor variable and corresponding parameter are removed (e.g., when the cubic is reduced to a quadratic, $\beta_3>(X^3_i)$ is removed from the model).
‡ Sites: King Ferry (KF), Somerset (S), and Tully (T).
§ Reported p-values are for the highest order predictor in the regression (e.g., TRT^3 for the cubic regression).
¶ Site was included in the regression models as a predictor variable when data from all sites were combined.
* Significant p-values are highlighted.

For King Ferry, a significant linear trend was indicated for the four willow clones combined (p-value=0.052). The cubic trend at King Ferry was also marginally significant (p-value = 0.08). Somerset had a significant cubic trend (p-value = 0.025), and Tully had a significant quadratic trend (p-value = 0.04). This suggests that there were important differences among sites for these clones.

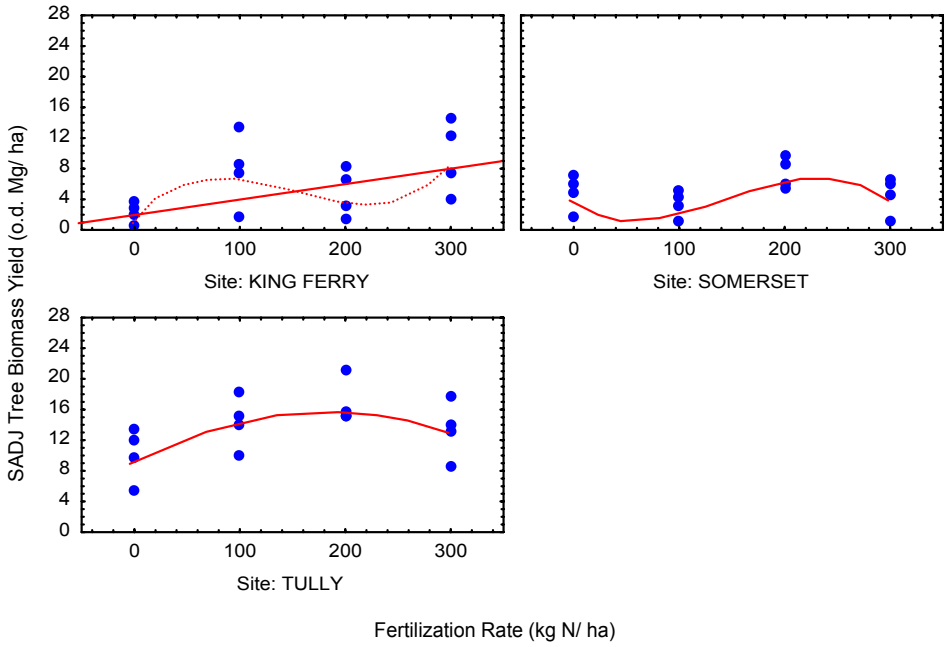

Figure 1.20. Curvilinear trend for clones S25, S301, S546, and SA2 by site.

The curvilinear trends for these four willow clones by site have important implications. There were clearly confounding factors at each site, as discussed previously (i.e., survival, weeds, and microsite variation). An important confounding factor at Somerset was microsite variation. There was a decrease in growth at the 100 kg N/ha fertilization rate at Somerset (Figure 1.0). This area was spatially the furthest away from the other three treatment strips, and there was a poorly drained area between them. Additionally, weeds were an issue at this site; specifically, weed biomass response to fertilization at the 300 kg N/ha fertilization rate (Figure 1.1).

At King Ferry, there was a considerable amount of variation in tree biomass yields and there was a decrease in biomass yield for the 200 kg N/ha treatment strip (Figure 1.0; marginally significant cubic trend, p-value = 0.08). Weeds were a serious concern at King Ferry, and the pattern indicated higher weed competition at the 200 kg N/ha treatment strip (Figure 1.192). The decrease for the 300 kg N/ha treatment level for Tully (Figure 1.0) was also likely due to microsite variation. There is little reason to suspect that the decrease at 300 kg N/ha was due to N toxicity; it is likely, however, that available soil moisture or nutrients may have been less in the area where the 300 kg N/ha treatment was applied.

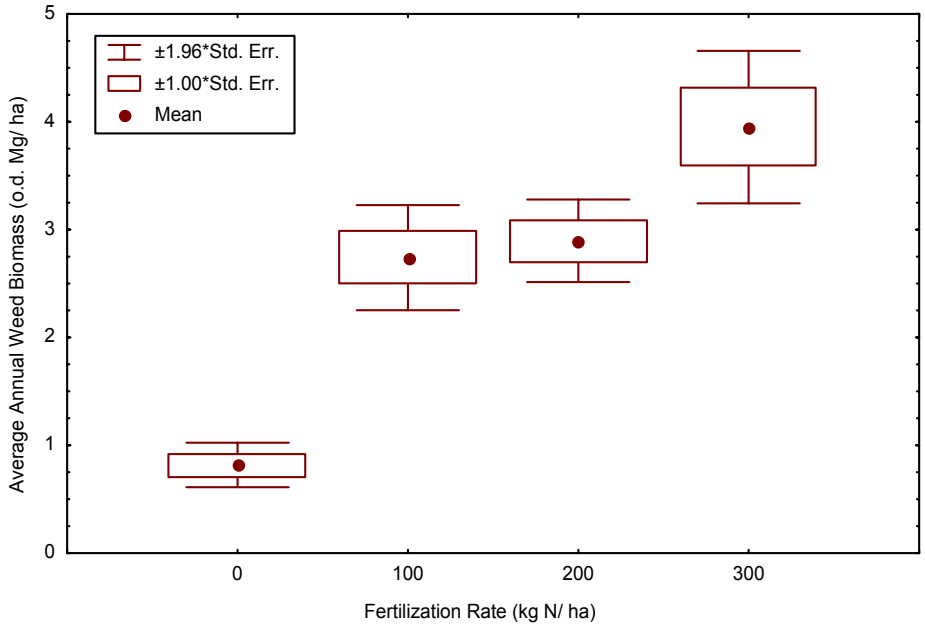

Figure 1.21. First-year average annual weed biomass for the six clones by treatment at Somerset, NY.

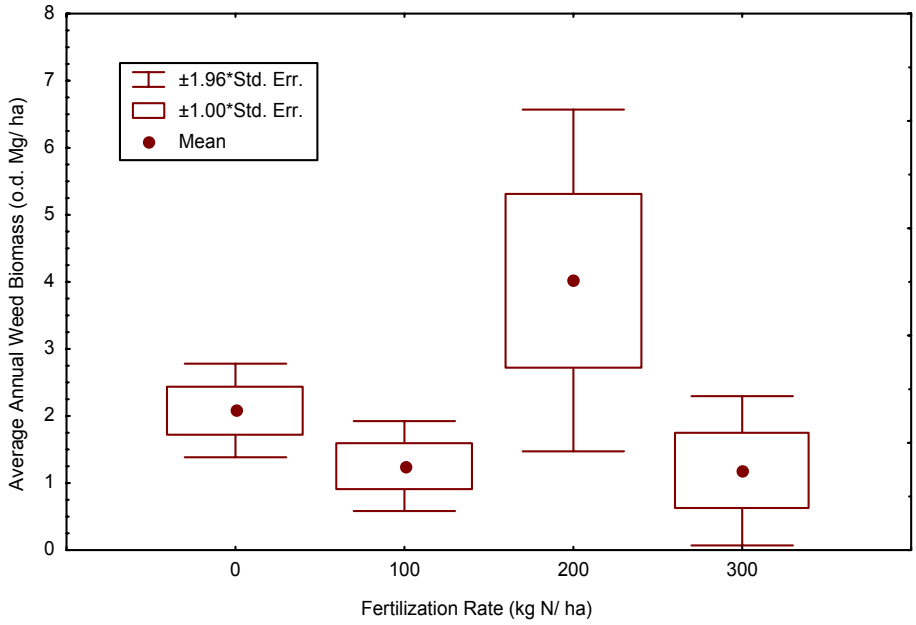

Figure 1.192. Second-year average annual weed biomass for the six clones by treatment at King Ferry, NY.

Given the impact that confounding factors had on tree biomass response to fertilization, there was little evidence to refute the original hypothesis that fertilization does not increase aboveground tree biomass compared to unfertilized trees for these four clones. There was some evidence to suggest that fertilization did benefit tree growth; there was a positive linear trend when all four clones were combined across the three sites, and clone SA2 exhibited a significant linear trend when site were combined. However, the evidence for clones S25, S301, S546, and was weak since the responses for individual clones were neither asymptotic, to indicate that sufficiency was reached, nor were they linear, which would have indicated that the plants had not yet reached sufficiency for nitrogen. When the four clones were combined, King Ferry had a significant linear trend, but the cubic trend was

also deemed important. At King Ferry and Somerset weed competition undoubtedly hampered the uptake of fertilizer by the trees, affected survival, and variably reduced tree growth through competition for other nutrients, water, and sunlight.

Conclusions

Biomass Response to Fertilization

Fertilized plots had higher biomass yields than non-fertilized treatments for four of the six clones in the study NM6, S25, SA2, and SV1. There was evidence to refute the hypothesis that fertilization does not increase aboveground tree biomass compared to unfertilized trees. The evidence presented for clone SV1 refuted this hypothesis; however, responses differed by site. At King Ferry, tree biomass continued to increase as fertilization rate increased, which was described best by a linear curve, indicating the plants were still within the "deficiency range" for nitrogen. At Tully, the response could be best described with an exponential saturation (asymptotic) model, suggesting that "sufficiency range" was reached; i.e., something else was limiting growth. Somerset presented a different problem, since neither of the hypothesized response curves was observed. The non-significant linear trend at Somerset indicated that tree response to fertilization was not different than zero; therefore, the trees were within the "sufficiency range" because other (confounding) factors were limiting growth.

It was hypothesized that that tree growth would level off as fertilization rate increased (i.e., reached saturation), the slightly better fit with the exponential saturation function that was observed for poplar clone NM6 (sites pooled) was consistent with that hypothesis. Site differences could not be adequately characterized for NM6 due to limitations of the data. There was a significant linear trend for all three sites combined and at King Ferry. Trees of NM6 appeared to benefit from fertilization at King Ferry and had not yet reached sufficiency; though, no doubt, other factors were impacting growth. Results for NM6 at Somerset and Tully indicated that there was little response in growth to fertilization. So with respect to the hypothesis, trees of clone NM6 at Somerset and Tully were within the sufficiency range (i.e., something else was limiting growth).

Willow clone SA2 demonstrated a significant linear trend when sites were pooled and site differences were accounted for, adding evidence to refute the hypothesis that fertilization does not increase aboveground tree biomass compared to unfertilized trees. Given the impact that confounding factors had on tree biomass response to fertilization for clones S25, S301, and S546, there was insufficient evidence to support or refute the hypothesis. The responses of these three willow clones to fertilization were neither asymptotic, to indicate that sufficiency was reached, nor were they linear, which would have indicated that the plants had not yet reached sufficiency for nitrogen. At King Ferry and Somerset weed competition undoubtedly hampered the uptake of fertilizer by the trees, affected survival, and variably reduced tree growth through competition for other nutrients, water, and sunlight. At Tully, an unmeasured factor was influencing tree biomass yields.

It was clear that tree biomass response to fertilization was a function of survival, weed competition, site and microsite variation, and their interactions. This study failed to isolate each of these components, due in part to limitations in the experimental design.

Recommended fertilization schemes based on these results would include extensive site preparation to eliminate, or at least substantially reduce, weed competition. Unless weeds are controlled, fertilizer, energy, and money will be wasted. Fertilization rates for conditions similar to those presented here above 100 kg N/ha for the three years of the rotation following planting are not recommended; responses either leveled off, or were limited by other factors. Additional consideration to determining a biologically and economically optimal fertilization scheme should be given in the near future (e.g., an extension of this work and of Adegbidi (1999)). Maintaining adequate annual growth rates in SRWC plantations throughout the entire rotation will likely require multiple applications of inorganic amendments, in contrast to organic fertilizers. Adegbidi (1999) suggested that a single application of organic amendment would be adequate for one rotation. The fertilization rates applied once at the beginning of the rotation in this study are within the range of *annual* fertilization rates. Many of the recommended rates (literature review) suggest fertilization annually at 10 – 200 kg N/ha.

Future work should focus on interactions among clone, survival, weed competition, site and microsite variation, by increasing the number of replications used within and across sites for various clones. Future fertilization trials should narrow the increments of the fertilization rates (e.g., use 50 kg N/ha increments rather than 100), and fertilization treatments should be applied randomly to plots rather than in strips. Utilization of the

exponential saturation curve with a well-designed experiment (e.g., replicated trials on each of several sites) will prove very useful, since each coefficient is biologically meaningful. Additionally, a monitoring tool, such as foliar nutrient concentrations, for diagnosing plant nutritional needs should be improved. A tool of this type will be useful in tailoring fertilization schemes for individual sites.

CONCLUSIONS

The current studies demonstrated a tool for estimating standing biomass at various stages in the life of a SRWC plantation and the application of that tool to evaluate the effects of fertilization of SRWCs with slow-release nitrogen. The use of regression equations was an attractive alternative to destructively sampling experimental plots or waiting until the plantation was harvested at the end of the rotation. Using regression estimators allowed for monitoring of the crop throughout the rotation to evaluate response to fertilization.

After evaluating various regression estimators for the prediction of biomass for one poplar and five willow bioenergy crops, the logarithmic regression estimator was selected as one of the best, using typical regression evaluation criteria. The logarithmic estimator, based on stem diameter, explained a high degree of variability in stem dry weight (i.e., high R^2 values, with low error). Predictions for the logarithmic regression had relatively low error; MSEP and PEP for logarithmic regressions was among the lowest of the models evaluated in the model development and selection.

Stool-based regression estimators were as good as stem-based regression estimators. Regression equations based solely on diameter could adequately estimate tree biomass. Generalizing by clone (all clones combined) worked well for several clones. Yet, clone-specific models were far better than the generalized equations for NM6 and SV1. Clone-specific equations should be used whenever possible; though, generalized equations may yield reasonable approximations. Telenius and Verwijst (1995) reported that for regression equations that were generalized for clone or site, estimates often deviated by less than 10% from the stand-specific equations. Performance of both the logarithmic and non-linear regressions was reasonable. Error variance increased as diameter increased when using the non-linear regression model, suggesting that a weighting procedure should be considered in the future. Additionally, future work should include more intensive sampling of stems of various ages to develop age-specific estimators and quantify the loss of accuracy by using age-generalized estimators in these plantations.

Using the regression equations to monitor the effects of fertilization for SRWCs demonstrated that the relatively simple concepts of Liebig (1843; e.g., law of the minimum) could help explain response to fertilization with slow-release nitrogen. Growth of the trees was not necessarily limited by nitrogen. The “expected” positive growth response or exponential saturation response was not observed for all clones or sites. The limiting factors were manifested at different sites at different treatment levels due to site differences.

Fertilization increased aboveground tree biomass of clone SV1, although responses differed by site. At King Ferry, tree biomass continued to increase as fertilization rate increased, indicating that the plants were still within the “deficiency range” for nitrogen. At Tully, the response was asymptotic, implying that something else was limiting growth. Somerset presented a different problem, since neither of the hypothesized response curves was observed. There was no growth response to fertilization by SV1 at Somerset because other confounding factors were limiting growth.

Tree growth essentially leveled off as fertilization rate increased for poplar clone NM6 (sites pooled), though this generalized response was partially due to the grouping of sites. A very strong positive linear growth response was observed at King Ferry, indicating that trees benefited from fertilization and had not yet reached sufficiency. There was little response in growth of NM6 trees to fertilization at Somerset and Tully, illustrating that other possible factors were limiting growth.

Confounding factors greatly impacted tree growth for clones S25, S301, S546, and SA2, minimizing the benefits of fertilization. At King Ferry and Somerset, weed competition undoubtedly hampered the uptake of fertilizer by the trees, affected survival, and variably reduced tree growth through competition for other nutrients, water, and sunlight. At Tully, an unmeasured factor was influencing tree biomass yields.

It was clear that tree biomass response to fertilization was a function of survival, weed competition, site and microsite variation, and their interactions. This study failed to isolate each of these components, due in part to limitations in the experimental design. Hence, future work should focus on interactions of clones, survival, weed competition, and site and microsite variation, by increasing the number of replications used within and across sites for various clones.

Recommended fertilization schemes based on these results would include extensive site preparation to eliminate, or at least substantially reduce, weed competition. Resources will be wasted unless weeds are controlled. Fertilization rates above 100 kg N/ha, for conditions similar to those presented here, for the three years

of the rotation following planting, are not recommended; responses either leveled off, or were limited by other factors. Additional consideration to determining a biologically and economically optimal fertilization scheme should be given in the near future [e.g., an extension of this work and of Adegbidi (1999)].

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APPENDICES

Appendix 1. Basic statistics of stem diameter (mm), measured at 30 cm from the base of the stool, for the complete, model-selection, and validation data sets.

CLONE/Data Set	Variable	n	Stem Diameter (mm) Mean	Minimum	Maximum	Std. Error
GENERAL (All)	Diameter	516	10.35	2.91	43.41	0.24
GENERAL (Model-selection)	Diameter	248	10.14	2.93	36.59	0.34
GENERAL (Validation)	Diameter	268	10.53	2.91	43.41	0.35
NM6 (All)	Diameter	57	13.60	3.81	43.41	1.16
NM6 (Model-selection)	Diameter	24	14.49	3.81	36.59	1.69
NM6 (Validation)	Diameter	33	12.95	3.93	43.41	1.58
S25 (All)	Diameter	73	11.72	3.05	25.12	0.57
S25 (Model-selection)	Diameter	34	11.59	4.85	24.61	0.77
S25 (Validation)	Diameter	39	11.83	3.05	25.12	0.83
S301 (All)	Diameter	60	10.68	3.02	23.30	0.69
S301 (Model-selection)	Diameter	27	10.35	3.02	22.67	1.10
S301 (Validation)	Diameter	33	10.94	3.17	23.30	0.90
S546 (All)	Diameter	101	9.44	2.93	19.99	0.45
S546 (Model-selection)	Diameter	50	9.16	2.93	19.89	0.66
S546 (Validation)	Diameter	51	9.71	2.95	19.99	0.62
SA2 (All)	Diameter	94	8.23	2.91	18.88	0.34
SA2 (Model-selection)	Diameter	45	8.32	4.12	17.81	0.45
SA2 (Validation)	Diameter	49	8.15	2.91	18.88	0.51
SV1 (All)	Diameter	131	10.23	2.97	27.14	0.47
SV1 (Model-selection)	Diameter	68	9.72	2.97	25.99	0.60
SV1 (Validation)	Diameter	63	10.77	3.13	27.14	0.73
WILLOW (All)	Diameter	459	9.94	2.91	27.14	0.23
WILLOW (Model-selection)	Diameter	224	9.68	2.93	25.99	0.31
WILLOW (Validation)	Diameter	235	10.19	2.91	27.14	0.33

Appendix 2. Basic statistics of oven dry weight (g, 65°C) for the complete, model-selection, and validation data sets.

CLONE/Data Set	Variable	n	Dry Weight (g) Mean	Minimum	Maximum	Std. Error
GENERAL (All)	Dry Weight	516	71.00	1.18	1572.7	5.86
GENERAL (Model-selection)	Dry Weight	248	65.70	1.45	1084.8	7.28
GENERAL (Validation)	Dry Weight	268	75.90	1.18	1572.7	9.05
NM6 (All)	Dry Weight	57	152.76	2.42	1572.7	38.92
NM6 (Model-selection)	Dry Weight	24	157.82	2.42	1084.8	51.06
NM6 (Validation)	Dry Weight	33	149.07	3.04	1572.7	56.70
S25 (All)	Dry Weight	73	74.18	1.29	412	9.69
S25 (Model-selection)	Dry Weight	34	68.85	3.65	412	14.32
S25 (Validation)	Dry Weight	39	78.82	1.29	340.72	13.29
S301 (All)	Dry Weight	60	68.07	1.45	316.04	10.48
S301 (Model-selection)	Dry Weight	27	69.39	1.45	316.04	16.10
S301 (Validation)	Dry Weight	33	66.99	1.71	310.01	13.99
S546 (All)	Dry Weight	101	49.10	1.35	246.24	5.76
S546 (Model-selection)	Dry Weight	50	46.19	1.54	246.24	8.32
S546 (Validation)	Dry Weight	51	51.95	1.35	202.29	8.04
SA2 (All)	Dry Weight	94	29.37	1.18	213.91	3.75
SA2 (Model-selection)	Dry Weight	45	27.87	3.6	153.77	4.52
SA2 (Validation)	Dry Weight	49	30.75	1.18	213.91	5.92
SV1 (All)	Dry Weight	131	81.76	2.49	665.4	11.69
SV1 (Model-selection)	Dry Weight	68	69.55	2.49	564.13	13.99
SV1 (Validation)	Dry Weight	63	94.95	2.58	665.4	19.04
WILLOW (All)	Dry Weight	459	60.85	1.18	665.4	4.28
WILLOW (Model-selection)	Dry Weight	224	55.83	1.45	564.13	5.62
WILLOW (Validation)	Dry Weight	235	65.63	1.18	665.4	6.41

Appendix 3. Raw data for biomass equation development: diameter (mm) measured at 30 cm from the base of the stool, oven dry weight (g, 65°C), and average height of the stool (cm).

SPLIT‡	CLONE	SITE†	AGE (yr)	STOOL SIZE§	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
selection	SV1	KF	1	S	2	2.97	2.49	75
selection	SV1	T	1	L	16	3.56	3.36	290
selection	SV1	T	1	L	10	3.85	3.23	290
selection	SV1	S	1	S	1	3.91	3.09	125
selection	SV1	KF	1	S	5	4.03	4.45	75
selection	SV1	KF	1	M	7	4.04	3.33	150
selection	SV1	S	1	M	1	4.22	3.83	185
selection	SV1	T	1	S	3	4.67	5.48	160
selection	SV1	S	1	L	1	4.71	3.93	155
selection	SV1	KF	1	M	11	5.54	8.45	150
selection	SV1	S	1	L	8	5.58	8.87	155
selection	SV1	T	1	S	1	5.83	11.04	160
selection	SV1	S	1	L	7	5.83	6	155
selection	SV1	T	1	L	8	5.87	10.89	290
selection	SV1	T	1	M	6	5.91	11.26	185
selection	SV1	S	1	L	16	6.09	9.28	155
selection	SV1	S	1	M	5	6.17	11.06	185
selection	SV1	T	1	M	13	6.27	15.69	185
selection	SV1	T	1	M	3	6.44	18.46	185
selection	SV1	T	1	L	2	6.51	12.31	290
selection	SV1	KF	1	L	4	6.81	12.25	165
selection	SV1	T	1	M	14	7.02	15.97	185
selection	SV1	KF	1	L	14	7.09	20.27	165
selection	SV1	T	1	M	5	7.16	18.18	185
selection	SV1	KF	1	L	9	7.27	18.45	165
selection	SV1	KF	1	L	6	7.33	19.38	165
selection	SV1	T	1	M	1	7.43	17.94	185
selection	SV1	KF	1	M	2	7.53	23.71	150
selection	SV1	KF	1	M	10	8.04	23.8	150
selection	SV1	KF	1	M	3	8.15	25.59	150
selection	SV1	KF	1	M	9	8.33	26.92	150
selection	SV1	KF	1	L	19	8.43	24.99	165
selection	SV1	T	1	M	15	8.44	38.28	185
selection	SV1	T	1	M	2	8.8	34.65	185
selection	SV1	KF	1	M	6	8.85	27.09	150
selection	SV1	S	1	M	2	9.06	35.9	185
selection	SV1	KF	1	L	2	9.06	33.14	165
selection	SV1	S	1	L	3	9.32	35.19	155
selection	SV1	S	1	L	13	9.46	33.17	155
selection	SV1	KF	1	M	1	9.7	42.78	150
selection	SV1	T	1	M	12	9.85	44.49	185
selection	SV1	KF	1	L	3	10.04	38.26	165

Appendix 3 (cont.)

SPLIT[‡]	CLONE	SITE[†]	AGE (yr)	STOOL SIZE[§]	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
selection	SV1	T	1	L	5	10.06	42.72	290
selection	SV1	S	1	L	10	10.12	35.67	155
selection	SV1	KF	1	M	8	10.16	46.92	150
selection	SV1	T	1	L	9	10.62	50.88	290
selection	SV1	KF	1	L	22	10.66	49.13	165
selection	SV1	KF	1	L	23	10.78	49.65	165
selection	SV1	S	1	M	3	10.95	43.47	185
selection	SV1	T	1	M	7	10.97	63.65	185
selection	SV1	KF	1	L	16	11.28	56.03	165
selection	SV1	T	2	L	7	11.47	59.15	
selection	SV1	T	1	S	2	11.48	67.64	160
selection	SV1	T	1	L	6	11.77	65.32	290
selection	SV1	T	1	M	8	11.98	61.83	185
selection	SV1	KF	1	L	20	12.64	72.07	165
selection	SV1	T	2	L	2	12.84	69.2	
selection	SV1	T	2	M	6	13.08	79.06	
selection	SV1	T	1	L	4	13.5	95.52	290
selection	SV1	T	1	L	7	15.53	161.12	290
selection	SV1	T	2	S	2	15.76	143.78	
selection	SV1	T	2	M	4	19.16	297.11	
selection	SV1	T	2	L	5	19.4	261.66	
selection	SV1	T	2	L	9	19.66	302.99	
selection	SV1	S	2	M	4	21.4	306.1	
selection	SV1	T	2	L	12	22.2	564.13	
selection	SV1	T	2	L	1	22.66	393.7	
selection	SV1	T	2	M	2	25.99	523.86	
validation	SV1	KF	1	S	4	3.13	2.58	75
validation	SV1	KF	1	S	3	3.81	3.86	75
validation	SV1	S	1	L	15	3.86	2.8	155
validation	SV1	KF	1	L	5	3.91	4.22	165
validation	SV1	T	1	M	11	4.61	5.11	185
validation	SV1	KF	1	S	6	4.64	6.15	75
validation	SV1	T	1	L	11	5	4.58	290
validation	SV1	KF	1	S	1	5.4	8.93	75
validation	SV1	S	1	S	2	5.84	5.89	125
validation	SV1	S	1	M	4	5.98	8.93	185
validation	SV1	T	1	S	5	6	11.7	160
validation	SV1	S	1	L	9	6.05	11.57	155
validation	SV1	S	1	S	4	6.1	9.76	125
validation	SV1	S	1	L	14	6.37	9.39	155
validation	SV1	S	1	S	3	6.53	12.5	125
validation	SV1	T	1	M	10	6.58	16.01	185
validation	SV1	T	1	S	4	6.62	16.11	160
validation	SV1	S	1	L	11	6.63	12.14	155

Appendix 3 (cont.)

SPLIT[‡]	CLONE	SITE[†]	AGE (yr)	STOOL SIZE[§]	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
validation	SV1	S	1	L	5	6.66	11.71	155
validation	SV1	S	1	S	5	6.82	13.82	125
validation	SV1	KF	1	M	12	7.26	21.17	150
validation	SV1	KF	1	L	17	7.8	26.25	165
validation	SV1	KF	1	L	12	8.12	22.62	165
validation	SV1	S	1	L	12	8.21	17.88	155
validation	SV1	KF	1	M	5	8.51	32.82	150
validation	SV1	KF	1	L	21	8.68	26.31	165
validation	SV1	T	1	L	1	8.69	28.99	290
validation	SV1	S	1	M	7	8.78	29	185
validation	SV1	KF	1	L	24	8.98	31.61	165
validation	SV1	KF	1	L	18	9.07	29.32	165
validation	SV1	KF	1	L	15	9.19	38.02	165
validation	SV1	S	1	L	4	9.44	28.78	155
validation	SV1	KF	1	L	10	9.51	29.82	165
validation	SV1	KF	1	L	1	9.52	38.43	165
validation	SV1	S	1	M	6	9.68	30.25	185
validation	SV1	S	1	L	2	10.28	36.86	155
validation	SV1	T	2	L	13	10.32	50.46	
validation	SV1	S	1	L	6	10.37	40.54	155
validation	SV1	KF	1	L	13	10.46	47.9	165
validation	SV1	KF	1	L	8	10.51	46.8	165
validation	SV1	KF	1	L	11	10.54	47.13	165
validation	SV1	S	2	M	1	10.71	62.9	
validation	SV1	T	1	L	12	11.33	56.04	290
validation	SV1	KF	1	L	7	11.41	53.12	165
validation	SV1	T	1	M	4	11.64	67.85	185
validation	SV1	T	1	L	13	11.96	59.27	290
validation	SV1	T	1	M	9	13.11	91.2	185
validation	SV1	T	1	L	3	13.49	91.51	290
validation	SV1	T	2	S	3	13.57	107.84	
validation	SV1	T	1	L	14	14.43	122.76	290
validation	SV1	T	2	M	5	15.08	81.58	
validation	SV1	T	1	L	15	15.27	130.57	290
validation	SV1	T	2	L	8	16.12	201.34	
validation	SV1	S	2	M	2	17.28	242.2	
validation	SV1	T	2	L	10	17.3	188.81	
validation	SV1	T	2	L	6	17.33	253.9	
validation	SV1	S	2	M	3	17.49	248.2	
validation	SV1	T	2	M	3	22.31	366.39	
validation	SV1	T	2	L	4	22.88	406.92	
validation	SV1	T	2	M	1	23.55	456.4	
validation	SV1	T	2	S	1	24.89	579.6	
validation	SV1	T	2	L	3	26.01	665.4	

Appendix 3 (cont.)

SPLIT[‡]	CLONE	SITE[†]	AGE (yr)	STOOL SIZE[§]	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
validation	SV1	T	2	S	4	27.14	569.02	
selection	S25	S	1	L	2	4.85	3.65	145
selection	S25	T	1	L	15	4.88	5.14	220
selection	S25	T	1	L	19	5.72	8.76	220
selection	S25	T	1	L	3	6.02	10.78	220
selection	S25	S	1	M	4	6.21	7.03	95
selection	S25	S	1	S	1	6.71	9.97	95
selection	S25	S	1	S	2	6.73	9.32	95
selection	S25	T	1	L	16	9.4	31.27	220
selection	S25	S	1	L	3	9.49	21.21	145
selection	S25	S	1	L	8	9.87	26.41	145
selection	S25	S	1	L	6	9.94	28.64	145
selection	S25	T	1	L	2	10.12	40.88	220
selection	S25	T	1	L	7	10.52	37.33	220
selection	S25	S	1	L	1	10.78	31.51	145
selection	S25	T	1	L	4	10.89	48.88	220
selection	S25	T	1	M	8	11.03	40.41	225
selection	S25	T	1	M	9	11.23	47.19	225
selection	S25	T	1	L	13	11.38	51.95	220
selection	S25	T	1	S	1	11.43	50.11	190
selection	S25	T	1	L	18	11.64	51.8	220
selection	S25	T	1	M	5	11.89	58.25	225
selection	S25	T	1	M	1	12	58.3	225
selection	S25	T	1	L	8	12.01	64.2	220
selection	S25	T	1	M	3	12.32	59.05	225
selection	S25	T	2	S	6	12.41	72.3	
selection	S25	T	2	L	16	12.68	69.03	
selection	S25	T	1	L	9	13.05	73.29	220
selection	S25	T	1	L	10	13.59	86.67	220
selection	S25	T	1	L	12	15.15	99.75	220
selection	S25	T	2	L	9	17.04	101.75	
selection	S25	T	2	L	4	17.49	117.59	
selection	S25	T	2	L	2	20.5	239.26	
selection	S25	T	2	L	1	20.52	267.08	
selection	S25	T	2	M	1	24.61	412	
validation	S25	S	1	M	6	3.05	1.29	95
validation	S25	T	1	S	2	4.85	5.53	190
validation	S25	S	1	S	3	5.05	3.21	95
validation	S25	S	1	M	5	5.15	5.13	95
validation	S25	T	1	L	17	5.26	7.19	220
validation	S25	S	1	M	3	5.47	5.01	95
validation	S25	T	1	M	2	6.19	10.1	225
validation	S25	S	1	L	4	7.2	16.02	145
validation	S25	T	1	M	7	7.54	13.96	225

Appendix 3 (cont.)

SPLIT[‡]	CLONE	SITE[†]	AGE (yr)	STOOL SIZE[§]	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
validation	S25	S	1	M	2	7.94	14.85	95
validation	S25	S	1	M	1	8.11	17.88	95
validation	S25	T	1	M	10	8.28	22.5	225
validation	S25	T	1	S	3	9.85	36.98	190
validation	S25	T	1	S	4	10.47	42.55	190
validation	S25	S	1	L	5	10.52	32.19	145
validation	S25	S	1	L	7	10.54	32.82	145
validation	S25	T	1	S	5	10.92	45.62	190
validation	S25	T	1	L	14	10.93	45.45	220
validation	S25	T	1	L	21	10.98	49.8	220
validation	S25	T	1	L	6	11.07	52.2	220
validation	S25	T	1	L	1	11.68	59.04	220
validation	S25	T	1	L	5	11.82	60.07	220
validation	S25	S	2	M	4	12.06	64.4	
validation	S25	T	1	M	6	12.15	54.12	225
validation	S25	T	1	M	4	12.23	76.23	225
validation	S25	T	1	L	20	12.6	70.73	220
validation	S25	T	1	L	11	13.82	92.13	220
validation	S25	S	2	M	2	14.15	100.69	
validation	S25	S	2	M	3	14.19	87.2	
validation	S25	T	2	L	11	14.31	79.89	
validation	S25	S	2	M	1	16.14	153.9	
validation	S25	T	2	L	13	16.49	96.07	
validation	S25	T	2	S	2	17.14	174.16	
validation	S25	T	2	S	4	17.7	187.76	
validation	S25	T	2	L	6	18.04	197.27	
validation	S25	T	2	S	1	18.27	199.43	
validation	S25	T	2	L	15	19.93	231.08	
validation	S25	T	2	L	8	24.01	288.99	
validation	S25	T	2	M	3	25.12	340.72	
selection	S546	S	1	L	12	2.93	1.79	120
selection	S546	S	1	L	3	3.09	1.54	120
selection	S546	T	1	M	14	3.47	1.88	175
selection	S546	S	1	M	7	3.55	2.69	140
selection	S546	S	1	L	24	3.98	3.73	120
selection	S546	S	1	L	23	4.02	3.22	120
selection	S546	T	1	L	7	4.35	4.2	220
selection	S546	S	1	L	6	4.4	3.5	120
selection	S546	T	1	M	11	4.72	3.84	175
selection	S546	T	1	L	11	4.78	4.4	220
selection	S546	T	1	L	23	5.01	5.39	220
selection	S546	S	1	L	2	5.05	6.1	120
selection	S546	T	1	L	22	5.15	4.81	220
selection	S546	T	1	M	12	5.34	6.17	175

Appendix 3 (cont.)

SPLIT[‡]	CLONE	SITE[†]	AGE (yr)	STOOL SIZE[§]	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
selection	S546	S	1	L	8	5.8	9.08	120
selection	S546	T	1	M	3	6.28	10.95	175
selection	S546	T	1	M	2	6.38	10.64	175
selection	S546	S	1	L	9	6.7	14	120
selection	S546	S	1	L	1	6.89	12.41	120
selection	S546	S	1	L	20	6.92	15.72	120
selection	S546	S	1	L	14	7.02	12.59	120
selection	S546	S	1	L	7	7.36	15.31	120
selection	S546	S	1	M	8	7.45	18.14	140
selection	S546	T	1	S	7	7.53	15.99	130
selection	S546	S	1	L	22	7.55	20.3	120
selection	S546	T	1	M	4	7.55	16.86	175
selection	S546	S	1	M	3	7.63	21.03	140
selection	S546	T	2	L	11	8.24	17.26	
selection	S546	T	1	M	5	8.58	29.12	175
selection	S546	S	1	L	18	8.63	32.11	120
selection	S546	T	1	L	17	9.08	29.84	220
selection	S546	T	1	M	1	10.41	44.81	175
selection	S546	T	1	S	5	10.54	47.75	130
selection	S546	T	1	M	8	11.26	47.46	175
selection	S546	T	1	L	2	11.46	51.18	220
selection	S546	S	2	M	1	11.96	65.4	
selection	S546	T	1	L	19	12.29	53.95	220
selection	S546	T	1	L	16	12.66	74.73	220
selection	S546	T	2	M	6	13.4	82.43	
selection	S546	T	2	M	3	13.8	69.33	
selection	S546	T	1	L	10	14.02	82.8	220
selection	S546	T	2	M	1	14.17	81.02	
selection	S546	T	1	L	6	15	111.47	220
selection	S546	T	2	L	5	15.34	97.75	
selection	S546	T	1	L	18	15.63	123.15	220
selection	S546	T	1	L	13	15.73	127.39	220
selection	S546	T	2	L	10	16.59	104.91	
selection	S546	S	2	M	2	18.85	224.5	
selection	S546	T	2	M	5	19.71	218.45	
selection	S546	T	2	M	2	19.89	246.24	
validation	S546	S	1	M	5	2.95	1.35	140
validation	S546	S	1	L	11	3.49	2.93	120
validation	S546	S	1	M	4	3.56	2.63	140
validation	S546	T	1	L	24	4.05	3.68	220
validation	S546	S	1	M	6	4.38	4.97	140
validation	S546	S	1	L	15	4.48	5.19	120
validation	S546	T	1	M	13	4.61	3.73	175
validation	S546	T	1	M	7	5.01	6.49	175

Appendix 3 (cont.)

SPLIT‡	CLONE	SITE†	AGE (yr)	STOOL SIZE§	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
validation	S546	T	1	S	2	5.34	6.41	130
validation	S546	S	1	L	5	5.47	8.02	120
validation	S546	T	1	L	21	5.63	5.86	220
validation	S546	S	1	M	9	5.68	9.03	140
validation	S546	S	1	L	16	6.08	6.75	120
validation	S546	S	1	L	19	6.71	12.96	120
validation	S546	S	1	L	10	6.98	14.55	120
validation	S546	S	1	L	21	6.99	15.26	120
validation	S546	S	1	L	17	7.08	13.71	120
validation	S546	T	1	L	12	7.45	14.59	220
validation	S546	T	1	S	3	7.58	16.38	130
validation	S546	S	1	L	4	7.7	17.59	120
validation	S546	S	1	L	25	7.81	17.69	120
validation	S546	T	1	S	6	7.83	18.24	130
validation	S546	T	1	L	9	8.11	18.98	220
validation	S546	S	1	M	1	8.16	19.58	140
validation	S546	T	1	S	1	8.18	23.12	130
validation	S546	S	1	L	13	8.22	22.45	120
validation	S546	T	1	M	6	8.99	33.4	175
validation	S546	S	1	M	2	9.02	31.83	140
validation	S546	T	1	M	10	9.17	35.72	175
validation	S546	T	2	S	2	9.44	33.52	
validation	S546	T	2	L	4	9.9	35.03	
validation	S546	T	1	S	4	10.22	38.98	130
validation	S546	T	1	L	14	10.31	38.68	220
validation	S546	T	1	L	4	11.45	60.46	220
validation	S546	T	1	L	5	12.17	63.98	220
validation	S546	T	1	L	8	12.79	77.82	220
validation	S546	T	1	L	20	12.94	77.84	220
validation	S546	T	2	L	3	12.98	62.91	
validation	S546	T	1	M	9	13.01	79.55	175
validation	S546	T	1	L	15	13.05	66.45	220
validation	S546	S	2	M	4	13.61	88.8	
validation	S546	T	1	L	3	13.88	98.96	220
validation	S546	T	1	L	1	15.13	106.56	220
validation	S546	T	2	L	2	15.84	141.13	
validation	S546	T	2	L	7	15.99	141.28	
validation	S546	T	2	S	1	16.03	123.52	
validation	S546	T	2	L	1	16.47	167.63	
validation	S546	S	2	M	3	17.27	171	
validation	S546	T	2	L	8	17.69	186.85	
validation	S546	T	2	L	6	18.57	193.05	
validation	S546	T	2	L	9	19.99	202.29	
selection	S301	S	1	S	2	3.02	1.45	60

Appendix 3 (cont.)

SPLIT‡	CLONE	SITE†	AGE (yr)	STOOL SIZE§	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
selection	S301	S	1	S	1	3.21	2.17	60
selection	S301	T	1	S	5	3.25	2.19	140
selection	S301	T	1	M	5	3.81	3.1	220
selection	S301	S	1	M	2	4.1	4.3	70
selection	S301	T	1	S	4	4.87	7.74	140
selection	S301	T	1	L	4	4.88	6.53	180
selection	S301	S	1	L	4	5.39	8.31	105
selection	S301	T	1	S	2	5.76	10.74	140
selection	S301	T	1	L	7	8.38	24.1	180
selection	S301	T	1	S	3	8.49	21.67	140
selection	S301	T	2	S	4	9	24.86	
selection	S301	T	2	L	12	9.05	26.94	
selection	S301	T	2	M	7	9.56	25.5	
selection	S301	T	2	M	8	10.47	29.74	
selection	S301	T	1	M	4	11.05	44.96	220
selection	S301	T	1	S	1	11.15	53.87	140
selection	S301	T	1	M	2	11.31	74.78	220
selection	S301	T	2	S	2	12.57	91.32	
selection	S301	T	2	S	1	13.11	98.1	
selection	S301	T	2	S	3	13.53	83.86	
selection	S301	T	2	L	2	15.97	137.53	
selection	S301	T	2	L	3	17.23	149.33	
selection	S301	T	2	L	7	18.52	202.71	
selection	S301	T	2	M	2	19.56	187.83	
selection	S301	T	2	L	10	19.58	233.93	
selection	S301	T	2	M	1	22.67	316.04	
validation	S301	S	1	M	1	3.17	1.71	70
validation	S301	S	1	S	3	3.63	4.04	60
validation	S301	T	1	L	10	3.9	3.51	180
validation	S301	S	1	M	4	4	2.92	70
validation	S301	S	1	M	3	4.36	4.32	70
validation	S301	T	1	M	6	4.51	4.31	220
validation	S301	S	1	L	1	5.38	7.38	105
validation	S301	S	1	L	2	6.48	12.12	105
validation	S301	S	1	L	3	6.73	10.92	105
validation	S301	T	2	S	5	8.02	20.56	
validation	S301	T	1	L	3	8.62	27.03	180
validation	S301	T	1	L	5	9.26	26.91	180
validation	S301	T	2	L	5	9.96	27.2	
validation	S301	T	1	L	9	10.63	46.31	180
validation	S301	T	2	L	11	10.63	32.03	
validation	S301	T	1	L	6	10.69	44.81	180
validation	S301	T	1	L	2	11.04	45.36	180
validation	S301	T	1	L	8	11.1	54.83	180

Appendix 3 (cont.)

SPLIT‡	CLONE	SITE†	AGE (yr)	STOOL SIZE§	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
validation	S301	T	2	L	14	11.17	48.28	
validation	S301	T	2	L	15	11.23	50.28	
validation	S301	T	1	L	1	12.53	68.1	180
validation	S301	T	2	L	13	12.76	56	
validation	S301	T	1	M	3	12.81	50.93	220
validation	S301	T	2	M	5	13.84	73.2	
validation	S301	T	1	M	1	13.87	83.65	220
validation	S301	S	2	M	1	14.54	112.5	
validation	S301	T	2	L	6	14.64	90.53	
validation	S301	T	2	M	4	15.27	90.25	
validation	S301	S	2	M	2	15.45	122	
validation	S301	S	2	M	3	15.46	109	
validation	S301	T	2	L	1	20.61	284.28	
validation	S301	T	2	L	4	21.49	285.26	
validation	S301	T	2	M	3	23.3	310.01	
selection	SA2	T	1	S	7	4.12	3.76	115
selection	SA2	S	1	L	9	4.48	4.48	125
selection	SA2	S	1	S	1	4.92	3.6	65
selection	SA2	T	1	M	14	5.05	5.36	130
selection	SA2	T	1	M	5	5.25	7.41	130
selection	SA2	T	1	L	15	5.29	5.97	175
selection	SA2	T	1	S	4	5.33	7.28	115
selection	SA2	T	1	M	12	5.7	7.33	130
selection	SA2	T	1	M	11	5.8	7.89	130
selection	SA2	T	1	S	5	5.85	8.83	115
selection	SA2	T	1	M	9	5.95	10.06	130
selection	SA2	T	2	L	8	6.33	8.51	
selection	SA2	T	1	L	16	6.48	11.01	175
selection	SA2	S	1	L	7	6.59	8.7	125
selection	SA2	T	1	L	8	6.61	14.76	175
selection	SA2	T	1	M	7	6.64	13.44	130
selection	SA2	S	1	M	4	6.73	9.58	110
selection	SA2	T	1	M	10	6.76	9.91	130
selection	SA2	T	1	M	8	6.9	14.53	130
selection	SA2	S	1	L	3	7.16	13.65	125
selection	SA2	S	1	L	4	7.52	14.45	125
selection	SA2	T	1	L	11	7.53	18.14	175
selection	SA2	T	1	L	10	7.83	15.82	175
selection	SA2	T	1	S	1	7.87	21.71	115
selection	SA2	T	1	L	19	7.9	18.19	175
selection	SA2	T	1	M	1	8.14	21.27	130
selection	SA2	T	1	M	3	8.25	21.38	130
selection	SA2	T	1	L	3	8.27	22.68	175
selection	SA2	T	1	L	17	8.4	23.32	175

Appendix 3 (cont.)

SPLIT‡	CLONE	SITE†	AGE (yr)	STOOL SIZE§	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
selection	SA2	T	2	L	13	8.57	24.99	
selection	SA2	T	1	L	14	8.61	22.3	175
selection	SA2	T	1	L	13	8.67	26.64	175
selection	SA2	T	2	M	2	9.03	21.14	
selection	SA2	T	2	L	15	9.98	25.7	
selection	SA2	S	2	M	5	9.99	30.7	
selection	SA2	T	1	L	1	10.08	38.69	175
selection	SA2	T	2	S	1	11.48	45.97	
selection	SA2	T	2	L	5	11.81	62.39	
selection	SA2	T	1	L	18	12.11	59.5	175
selection	SA2	S	2	M	1	12.33	54.5	
selection	SA2	T	2	L	6	12.47	70.34	
selection	SA2	T	1	L	7	12.57	73.38	175
selection	SA2	T	2	M	3	14.32	90.55	
selection	SA2	T	2	L	2	14.99	100.35	
selection	SA2	T	2	M	1	17.81	153.77	
validation	SA2	S	1	M	8	2.91	1.18	110
validation	SA2	S	1	S	3	3.69	1.59	65
validation	SA2	S	1	S	4	3.78	1.86	65
validation	SA2	S	1	M	5	3.81	3.09	110
validation	SA2	T	1	S	9	3.93	2.92	115
validation	SA2	T	1	M	2	4.41	4.35	130
validation	SA2	T	1	S	8	4.64	4.15	115
validation	SA2	T	1	L	6	4.73	4.89	175
validation	SA2	S	1	M	2	4.82	4.07	110
validation	SA2	T	1	S	6	4.85	4.95	115
validation	SA2	T	1	M	13	5.05	4.99	130
validation	SA2	S	1	L	1	5.21	4.34	125
validation	SA2	T	1	L	4	5.61	6.93	175
validation	SA2	S	1	M	1	5.72	6.22	110
validation	SA2	T	1	S	3	5.74	8.6	115
validation	SA2	T	2	L	11	6.06	9.85	
validation	SA2	S	1	M	6	6.09	7.53	110
validation	SA2	S	1	L	6	6.44	11.53	125
validation	SA2	T	1	L	2	6.67	13.29	175
validation	SA2	T	2	L	4	6.67	12	
validation	SA2	T	1	S	2	6.7	13.34	115
validation	SA2	T	1	L	9	7.06	13.91	175
validation	SA2	T	1	M	6	7.22	15.33	130
validation	SA2	T	2	M	6	7.52	13.28	
validation	SA2	T	2	M	5	7.57	12.12	
validation	SA2	S	1	L	2	7.76	14.51	125
validation	SA2	S	1	M	3	7.77	14.92	110
validation	SA2	T	2	L	9	7.77	14.71	

Appendix 3 (cont.)

SPLIT[‡]	CLONE	SITE[†]	AGE (yr)	STOOL SIZE[§]	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
validation	SA2	S	1	L	8	8	16.04	125
validation	SA2	T	1	M	4	8.23	21.46	130
validation	SA2	T	2	M	4	8.46	17.33	
validation	SA2	S	1	M	7	8.47	19.75	110
validation	SA2	S	1	L	5	8.52	26.52	125
validation	SA2	T	1	L	20	8.65	20.79	175
validation	SA2	T	1	L	12	9.34	33.19	175
validation	SA2	T	1	L	5	10.02	35.8	175
validation	SA2	T	2	L	16	10.14	33.64	
validation	SA2	T	2	L	14	10.15	39.17	
validation	SA2	S	2	M	3	10.37	39.6	
validation	SA2	T	2	S	2	11.09	34.99	
validation	SA2	T	2	L	10	11.53	57.94	
validation	SA2	T	2	L	3	12.1	63.57	
validation	SA2	T	2	M	7	12.98	78	
validation	SA2	S	2	M	2	13.61	82.1	
validation	SA2	T	2	L	12	13.77	95.79	
validation	SA2	S	2	M	4	14.76	97.7	
validation	SA2	T	2	M	8	14.89	113.51	
validation	SA2	T	2	L	1	15.08	135.39	
validation	SA2	T	2	L	7	18.88	213.91	
selection	NM6	S	1	M	6	3.81	3.34	265
selection	NM6	S	1	L	4	3.82	2.42	285
selection	NM6	T	1	S	3	5.54	5.96	220
selection	NM6	T	1	S	2	5.64	6.95	220
selection	NM6	S	1	L	1	6.42	11.85	285
selection	NM6	S	1	S	3	7.34	15.23	220
selection	NM6	T	2	L	2	8.81	20.74	
selection	NM6	T	2	M	8	10.75	24.17	
selection	NM6	S	1	S	2	10.85	44.48	220
selection	NM6	T	1	L	4	11.71	51.39	300
selection	NM6	T	2	M	4	12.4	62.8	
selection	NM6	S	1	L	5	12.76	86.3	285
selection	NM6	T	2	L	6	13.01	49.12	
selection	NM6	T	2	L	4	13.81	69.94	
selection	NM6	S	1	L	8	14.66	86.85	285
selection	NM6	S	1	L	7	16.37	117.98	285
selection	NM6	S	1	M	2	17.64	102.95	265
selection	NM6	T	1	M	1	19.03	188.95	300
selection	NM6	T	1	M	5	19.48	205.32	300
selection	NM6	S	1	L	6	20.51	240.41	285
selection	NM6	S	2	M	2	20.73	241.1	
selection	NM6	T	1	L	1	26.41	385.82	300
selection	NM6	T	2	L	5	29.66	678.9	

Appendix 3 (cont.)

SPLIT‡	CLONE	SITE†	AGE (yr)	STOOL SIZE§	STEM NO.	DIAMETER (mm)	DRY WT (g)	HT (cm)
selection	NM6	T	2	M	1	36.59	1084.8	
validation	NM6	S	1	L	2	3.93	3.04	285
validation	NM6	S	1	M	7	3.98	3.09	265
validation	NM6	S	1	M	3	4.71	5.11	265
validation	NM6	T	1	M	9	4.96	6.55	300
validation	NM6	T	1	M	7	5.6	7.32	300
validation	NM6	T	1	M	8	5.94	7.7	300
validation	NM6	S	1	S	5	6.5	11.96	220
validation	NM6	S	1	S	1	7.08	12.62	220
validation	NM6	T	1	M	2	7.3	14.03	300
validation	NM6	T	2	L	3	7.49	12	
validation	NM6	T	1	M	6	8	21.09	300
validation	NM6	S	1	M	1	8.03	20.01	265
validation	NM6	T	1	L	2	8.06	18.43	300
validation	NM6	T	2	S	3	8.27	15.02	
validation	NM6	T	1	M	4	8.44	21.09	300
validation	NM6	T	2	L	7	8.82	15.48	
validation	NM6	T	2	M	6	8.87	21.58	
validation	NM6	T	1	L	5	10.36	38.32	300
validation	NM6	T	2	S	2	11.53	36.48	
validation	NM6	T	2	M	5	11.9	56.81	
validation	NM6	T	1	M	3	12.87	68.03	300
validation	NM6	T	1	L	3	13.72	82.51	300
validation	NM6	T	1	S	1	13.88	85.69	220
validation	NM6	S	2	M	1	16.51	132.33	
validation	NM6	T	2	M	3	16.54	128.8	
validation	NM6	S	1	L	3	16.56	129.32	285
validation	NM6	S	1	M	5	17.23	96.94	265
validation	NM6	T	2	M	2	17.78	172.4	
validation	NM6	S	1	S	4	20.48	206.41	220
validation	NM6	S	1	M	4	25.13	306.8	265
validation	NM6	T	2	S	1	27.36	534.21	
validation	NM6	T	2	L	1	36.11	1055.5	
validation	NM6	S	2	M	3	43.41	1572.7	

‡ Split refers to the model-selection and validation data sets; these data were randomly divided in to approximately equal halves by clone.

† Sites: King Ferry (KF), Somerset (S), and Tully (T), New York

§ Stool sizes are relative categories by clone: Small (S), Medium (M), and Large (L).

Appendix 4. Survival adjusted (SADJ) and unadjusted tree biomass yields (oven-dry Mg/ha) for individual fertilization treatment plots derived from logarithmic regression equations.

CLONE	SITE†	FERTILIZER TRT (kg N/ha)	BLOCK	SADJ YIELD 1996 (Mg/ha)	UNADJUSTED YIELD 1996 (Mg/ha)	SADJ YIELD 1997 (Mg/ha)	UNADJUSTED YIELD 1997 (Mg/ha)
NM6	KF	0		2.13	1.21	5.62	3.81
NM6	KF	100		5.38	4.03	17.31	12.98
NM6	KF	200		4.36	1.71	17.35	8.68
NM6	KF	300		11.53	11.53	26.09	26.09
NM6	S	0		4.53	4.53	11.83	11.83
NM6	S	100		8.53	6.98	21.93	17.87
NM6	S	200		4.61	3.56	14.28	11.03
NM6	S	300		10.63	10.63	19.10	19.10
NM6	T	0		8.42	8.04	18.73	17.88
NM6	T	100		10.35	10.35	21.12	21.12
NM6	T	200		9.98	9.98	19.20	19.20
NM6	T	300		12.00	12.00	23.46	23.46
S25	KF	0		0.68	0.29	3.81	2.18
S25	KF	100		3.58	2.43	13.36	8.59
S25	KF	200		1.00	0.25	6.48	1.62
S25	KF	300		2.77	1.39	12.37	7.07
S25	S	0		1.52	1.52	5.91	5.91
S25	S	100		1.00	0.91	5.16	4.46
S25	S	200		3.42	3.42	9.64	9.64
S25	S	300		1.32	1.08	6.06	4.96
S25	T	0		3.72	2.87	12.07	8.78
S25	T	100		8.50	8.12	18.34	15.84
S25	T	200		10.96	10.96	21.05	21.05
S25	T	300		7.80	7.09	17.69	16.08
S301	KF	0		0.19	0.03	2.01	0.36
S301	KF	100		0.52	0.09	7.39	1.58
S301	KF	200		0.69	0.17	3.28	1.05
S301	KF	300		2.02	0.51	7.50	2.95
S301	S	0		1.17	0.96	4.85	3.97
S301	S	100		1.08	0.98	4.18	3.99
S301	S	200		1.34	1.22	5.36	4.87
S301	S	300		0.18	0.14	1.10	0.85
S301	T	0		3.07	3.07	9.70	9.26
S301	T	100		5.45	5.45	13.93	13.93
S301	T	200		6.53	6.53	15.23	15.23
S301	T	300		3.00	3.00	8.70	8.70

Appendix 4 (cont.)

CLONE	SITE†	FERTILIZER TRT (kg N/ha)	BLOCK	SADJ YIELD 1996 (Mg/ha)	UNADJUSTED YIELD 1996 (Mg/ha)	SADJ YIELD 1997 (Mg/ha)	UNADJUSTED YIELD 1997 (Mg/ha)
S546	KF	0		0.46	0.30	2.99	1.92
S546	KF	100		2.19	0.63	8.49	2.12
S546	KF	200		1.38	0.49	8.21	2.93
S546	KF	300		4.39	2.66	14.53	8.82
S546	S	0		1.84	1.76	7.05	6.73
S546	S	100		0.55	0.52	3.24	3.10
S546	S	200		2.47	1.91	8.59	6.64
S546	S	300		2.09	1.90	6.46	5.58
S546	T	0		5.54	4.79	13.40	10.96
S546	T	100		8.49	7.33	15.27	12.50
S546	T	200		9.14	8.30	15.08	13.02
S546	T	300		5.72	4.68	13.88	10.10
SA2	KF	0		0.20	0.04	0.60	0.21
SA2	KF	100		0.16	0.05	1.58	0.39
SA2	KF	200		0.00	0.00	1.34	0.10
SA2	KF	300		0.74	0.11	4.12	0.87
SA2	S	0		0.34	0.33	1.72	1.71
SA2	S	100		0.21	0.15	1.18	0.86
SA2	S	200		1.67	1.60	6.07	6.00
SA2	S	300		0.99	0.90	4.67	4.39
SA2	T	0		3.02	2.89	5.32	4.55
SA2	T	100		4.13	4.13	10.02	9.43
SA2	T	200		7.50	6.77	15.84	15.33
SA2	T	300		7.01	6.95	13.19	12.89
SV1	KF	0		0.81	0.52	4.65	3.16
SV1	KF	100		2.98	2.35	10.95	8.91
SV1	KF	200		0.82	0.15	14.39	3.92
SV1	KF	300		6.56	3.75	24.36	14.26
SV1	S	0		3.90	3.90	14.44	14.44
SV1	S	100		4.81	4.38	19.27	17.52
SV1	S	200		8.64	8.24	16.47	15.72
SV1	S	300		3.86	3.33	15.30	13.09
SV1	T	0		6.12	5.84	15.88	14.91
SV1	T	100		10.05	10.05	22.69	21.34
SV1	T	200		11.05	10.05	20.63	18.50
SV1	T	300		6.37	6.37	15.80	14.56

Appendix 4 (cont.)

CLONE	SITE†	FERTILIZER TRT (kg N/ha)	BLOCK	SADJ YIELD 1996 (Mg/ha)	UNADJUSTED YIELD 1996 (Mg/ha)	SADJ YIELD 1997 (Mg/ha)	UNADJUSTED YIELD 1997 (Mg/ha)
SV1	T	0	1	5.06	4.90	11.28	10.93
SV1	T	0	2	6.41	6.21	16.03	15.53
SV1	T	0	3	5.60	5.60	13.52	13.52
SV1	T	100	1	12.35	11.58	22.83	21.40
SV1	T	100	2	7.75	7.75	16.77	16.25
SV1	T	100	3	12.47	12.47	19.85	19.85
SV1	T	200	1	8.12	8.12	17.36	16.82
SV1	T	200	2	8.69	8.42	18.08	17.52
SV1	T	200	3	11.99	11.61	19.60	19.60
SV1	T	300	1	12.75	11.15	22.16	19.39
SV1	T	300	2	14.21	14.21	26.01	25.19
SV1	T	300	3	12.69	12.69	23.44	23.44

† Sites: King Ferry (KF), Somerset (S), and Tully (T), New York

Appendix 5. Proportion of replanted cuttings, frost heaved[‡] cuttings, and survival, and weed biomass for individual fertilization treatment plots.

CLONE	SITE[†]	FERTILIZER TRT (kg N/ha)	BLOCK	REPLANTS	NO FROST HEAVE[‡]	FROST HEAVE 0 - 7.6 cm	FROST HEAVE > 7.6 cm	SURVIVAL 1995	SURVIVAL 1996	SURVIVAL 1997	WEED BIOMASS 1996 (Mg/ha)	WEED BIOMASS 1997 (Mg/ha)
NM6	KF	0		0.00	0.08	0.63	0.29	0.86	0.68	0.68	0.69	3.48
NM6	KF	100		0.00	0.00	0.83	0.17	0.82	0.75	0.75	1.15	0.53
NM6	KF	200		0.00	0.00	0.60	0.40	0.71	0.50	0.50	1.12	0.19
NM6	KF	300		0.00	0.00	1.00	0.00	1.00	1.00	1.00	0.00	0.01
NM6	S	0		0.00	0.23	0.77	0.00	1.00	1.00	1.00	1.02	0.01
NM6	S	100		0.09	0.81	0.05	0.14	0.95	0.86	0.86	3.11	0.01
NM6	S	200		0.05	0.06	0.41	0.53	0.77	0.77	0.77	2.26	0.01
NM6	S	300		0.00	0.91	0.09	0.00	1.00	1.00	1.00	2.44	0.00
NM6	T	0		0.05	1.00	0.00	0.00	1.00	0.95	0.95	0.00	0.00
NM6	T	100		0.00	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
NM6	T	200		0.00	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
NM6	T	300		0.00	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
S25	KF	0		0.00	0.00	0.84	0.16	0.68	0.57	0.57	0.98	1.88
S25	KF	100		0.00	0.00	0.83	0.17	0.82	0.68	0.64	0.13	0.48
S25	KF	200		0.00	0.00	0.69	0.31	0.57	0.25	0.25	2.45	2.16
S25	KF	300		0.00	0.00	0.94	0.06	0.57	0.57	0.57	0.44	1.43
S25	S	0		0.00	0.95	0.00	0.05	1.00	1.00	1.00	1.03	0.03
S25	S	100		0.14	0.00	0.82	0.18	1.00	0.91	0.86	3.06	0.04
S25	S	200		0.00	1.00	0.00	0.00	1.00	1.00	1.00	2.65	0.01
S25	S	300		0.14	0.42	0.26	0.32	0.86	0.82	0.82	4.39	0.06
S25	T	0		0.36	1.00	0.00	0.00	1.00	0.77	0.73	0.00	0.00
S25	T	100		0.14	1.00	0.00	0.00	1.00	0.95	0.86	0.00	0.00
S25	T	200		0.00	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
S25	T	300		0.14	1.00	0.00	0.00	1.00	0.91	0.91	0.00	0.00

Appendix 5 (cont.)

CLONE	SITE†	FERTILIZER TRT (kg N/ha)	BLOCK	REPLANTS	NO FROST HEAVE‡	FROST HEAVE 0 - 7.6 cm	FROST HEAVE > 7.6 cm	SURVIVAL 1995	SURVIVAL 1996	SURVIVAL 1997	WEED BIOMASS 1996 (Mg/ha)	WEED BIOMASS 1997 (Mg/ha)
S301	KF	0		0.00	0.50	0.50	0.00	0.18	0.18	0.18	2.30	2.05
S301	KF	100		0.00	0.17	0.83	0.00	0.21	0.21	0.21	1.13	1.31
S301	KF	200		0.00	0.00	0.59	0.41	0.61	0.32	0.32	0.69	7.09
S301	KF	300		0.00	0.00	0.85	0.15	0.46	0.39	0.39	1.56	3.60
S301	S	0		0.00	0.36	0.45	0.18	1.00	0.82	0.82	0.33	0.02
S301	S	100		0.00	1.00	0.00	0.00	0.95	0.95	0.95	2.86	0.04
S301	S	200		0.00	0.40	0.60	0.00	0.91	0.91	0.91	3.16	0.03
S301	S	300		0.27	0.20	0.05	0.75	0.91	0.77	0.77	3.76	0.06
S301	T	0		0.14	1.00	0.00	0.00	1.00	1.00	0.95	0.00	0.00
S301	T	100		0.09	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
S301	T	200		0.00	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
S301	T	300		0.14	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
S546	KF	0		0.00	0.00	1.00	0.00	0.71	0.64	0.64	2.20	1.93
S546	KF	100		0.00	0.00	1.00	0.00	0.29	0.29	0.25	2.80	1.80
S546	KF	200		0.00	0.00	1.00	0.00	0.39	0.36	0.36	3.43	1.17
S546	KF	300		0.00	0.00	0.50	0.50	0.71	0.61	0.61	2.03	0.34
S546	S	0		0.00	0.86	0.09	0.05	1.00	0.95	0.95	0.87	0.36
S546	S	100		0.18	0.00	0.82	0.18	1.00	0.95	0.95	2.81	0.93
S546	S	200		0.14	0.82	0.09	0.09	1.00	0.77	0.77	3.58	0.58
S546	S	300		0.18	0.85	0.05	0.10	0.91	0.91	0.86	4.91	0.92
S546	T	0		0.00	1.00	0.00	0.00	0.91	0.86	0.82	0.00	0.00
S546	T	100		0.23	1.00	0.00	0.00	1.00	0.86	0.82	0.00	0.00
S546	T	200		0.14	1.00	0.00	0.00	0.95	0.91	0.86	0.00	0.00
S546	T	300		0.45	1.00	0.00	0.00	0.86	0.82	0.73	0.00	0.00

Appendix 5 (cont.)

CLONE	SITE†	FERTILIZER TRT (kg N/ha)	BLOCK	REPLANTS	NO FROST HEAVE‡	FROST HEAVE 0 - 7.6 cm	FROST HEAVE > 7.6 cm	SURVIVAL 1995	SURVIVAL 1996	SURVIVAL 1997	WEED BIOMASS 1996 (Mg/ha)	WEED BIOMASS 1997 (Mg/ha)
SA2	KF	0		0.00	0.68	0.32	0.00	0.68	0.36	0.36	2.24	2.37
SA2	KF	100		0.00	0.00	0.52	0.48	0.75	0.29	0.25	0.31	2.62
SA2	KF	200		0.00	0.00	0.00	1.00	0.57	0.07	0.07	1.83	6.79
SA2	KF	300		0.00	0.00	0.25	0.75	0.29	0.21	0.21	1.31	1.72
SA2	S	0		0.00	0.09	0.59	0.32	1.00	1.00	1.00	0.89	0.03
SA2	S	100		0.09	0.00	0.80	0.20	0.91	0.73	0.73	1.52	0.05
SA2	S	200		0.00	0.23	0.41	0.36	1.00	1.00	1.00	2.60	0.03
SA2	S	300		0.00	0.73	0.23	0.05	1.00	0.95	0.95	3.63	0.03
SA2	T	0		0.27	1.00	0.00	0.00	0.95	0.95	0.86	0.60	0.00
SA2	T	100		0.05	1.00	0.00	0.00	1.00	1.00	0.95	0.00	0.00
SA2	T	200		0.00	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
SA2	T	300		0.00	1.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00
SV1	KF	0		0.00	0.05	0.57	0.38	0.75	0.68	0.68	1.66	0.78
SV1	KF	100		0.00	0.47	0.42	0.11	0.82	0.82	0.82	2.28	0.78
SV1	KF	200		0.00	0.00	0.11	0.89	0.64	0.27	0.27	1.94	6.73
SV1	KF	300		0.00	0.00	0.93	0.07	0.61	0.61	0.61	4.40	0.00
SV1	S	0		0.00	1.00	0.00	0.00	1.00	1.00	1.00	0.77	0.32
SV1	S	100		0.00	0.00	1.00	0.00	0.91	0.91	0.91	3.08	0.21
SV1	S	200		0.00	0.68	0.23	0.09	1.00	0.95	0.95	3.13	0.14
SV1	S	300		0.00	0.89	0.00	0.11	0.86	0.86	0.86	4.56	0.79
SV1	T	0		0.14	1.00	0.00	0.00	1.00	0.95	0.95	0.00	0.00
SV1	T	100		0.14	1.00	0.00	0.00	1.00	1.00	0.95	0.00	0.00
SV1	T	200		0.05	1.00	0.00	0.00	1.00	0.91	0.91	0.00	0.00
SV1	T	300		0.18	1.00	0.00	0.00	1.00	1.00	0.95	0.00	0.00

Appendix 5 (cont.)

CLONE	SITE†	FERTILIZER TRT (kg N/ha)	BLOCK	REPLANTS	NO FROST HEAVE‡	FROST HEAVE 0 - 7.6 cm	FROST HEAVE > 7.6 cm	SURVIVAL 1995	SURVIVAL 1996	SURVIVAL 1997	WEED BIOMASS 1996 (Mg/ha)	WEED BIOMASS 1997 (Mg/ha)
SV1	T	0	1						0.97	0.97	0.00	0.00
SV1	T	0	2						0.97	0.97	0.00	0.00
SV1	T	0	3						1.00	1.00	0.00	0.00
SV1	T	100	1						0.94	0.94	0.00	0.00
SV1	T	100	2						1.00	0.97	0.00	0.00
SV1	T	100	3						1.00	1.00	0.00	0.00
SV1	T	200	1						1.00	0.97	0.00	0.00
SV1	T	200	2						0.97	0.97	0.00	0.00
SV1	T	200	3						1.00	1.00	0.00	0.00
SV1	T	300	1						0.88	0.88	0.00	0.00
SV1	T	300	2						1.00	0.97	0.00	0.00
SV1	T	300	3						1.00	1.00	0.00	0.00

† Sites: King Ferry (KF), Somerset (S), and Tully (T), New York.

‡ Frost heave: proportion of total cuttings that heaved 0, 0 - 7.6, and >7.6 cm out of the ground the winter after planting (1995-96).

Appendix 6. Foliar nutrient concentration (and N content, 1997) and foliar and woody stem biomass‡ for individual fertilization treatment plots.

CLONE	SITE†	FERT. TRT. (kg N/ha)	BLOCK	N 1996 (g/kg)	P 1996 (g/kg)	K 1996 (g/kg)	Ca 1996 (g/kg)	Mg 1996 (g/kg)	FOLIAR BIOMASS 1997 (Mg/ha)	WOODY BIOMASS‡ 1997 (Mg/ha)	N 1997 (g/kg)	FOLIAR N CONTENT 1997 (kg N/ha)	P 1997 (g/kg)	K 1997 (g/kg)	Ca 1997 (g/kg)	Mg 1997 (g/kg)
NM6	KF	0		18.9	2.1	16.3	13.1	2.4	2.77	32.84	14.8	40.95	2.7	16.8	24.8	2.9
NM6	KF	100		30.9	2.6	13.8	14	2.4	2.09	29.04	18.2	37.97	1.5	17.5	28.4	3.1
NM6	KF	200		25.9	1.9	11.8	14.6	2.4	1.59	15.47	17.6	27.98	1.5	13.4	24.4	3.0
NM6	KF	300		29.4	2.3	13.4	18.6	2.6	2.22	39.77	21.6	47.99	1.5	16.0	24.7	3.6
NM6	S	0		19.1	2.6	15.2	19.8	3.2	1.25	12.07	16.9	21.19	4.8	9.4	17.0	3.3
NM6	S	100		15.8	2.1	14.1	24.6	3	1.16	14.35	16.5	19.13	3.9	8.7	20.6	3.2
NM6	S	200		22	2.2	11.5	13	2.7	1.69	16.41	16.7	28.19	2.9	14.0	25.0	2.8
NM6	S	300		33.5	2.1	12.6	17	2.5	0.88	18.03	24.9	21.86	1.6	16.6	25.5	3.3
NM6	T	0		29.3	2.6	16.4	14.7	2.2	1.17	16.28	18.4	21.52	3.6	14.5	22.0	2.2
NM6	T	100		33.2	2.5	13.6	13.8	2.3	0.87	13.21	20.2	17.67	2.5	14.1	21.1	3.0
NM6	T	200		36.2	2.4	15.6	15.6	2	1.81	26.27	22.9	41.40	1.6	15.4	23.0	2.2
NM6	T	300		35.4	2.3	18.3	13.5	1.7	1.22	19.20	23.5	28.62	1.6	16.5	20.3	2.1
S25	KF	0		16.1	1.7	11.8	27.6	2.9	0.75	4.43	14.6	10.97	1.7	18.4	27.0	3.4
S25	KF	100		27.7	1.7	10.3	23.2	2.6	2.14	21.41	20.0	42.76	1.3	15.7	22.0	3.2
S25	KF	200		25.6	1.5	10.9	26.3	4	0.76	5.69	16.8	12.75	1.7	12.0	27.7	4.0
S25	KF	300		28.2	1.7	11.5	24.3	2.9	1.34	16.10	19.0	25.40	1.4	15.8	29.6	3.7
S25	S	0		19.5	2.4	9.9	13.8	4.1	0.71	5.65	20.0	14.32	2.6	11.3	23.1	4.6
S25	S	100		20.2	2.4	10.3	23.3	3.9	0.68	4.44	19.9	13.54	3.7	10.1	22.9	3.6
S25	S	200		24.7	2.1	10.3	22.4	3.9	1.10	9.08	20.5	22.51	1.8	11.2	19.3	3.4
S25	S	300		25.9	2	10	18.5	3.1	0.90	5.65	19.3	17.44	3.5	13.3	24.9	3.9
S25	T	0		28.4	3.1	10.5	24.7	3.9	0.87	13.15	19.7	17.20	2.1	13.0	18.2	3.8
S25	T	100		32.7	2.8	12.3	25.7	3.9	0.79	11.61	20.9	16.47	1.7	11.8	18.8	3.1
S25	T	200		32.9	2.6	12.5	26.3	3.5	0.83	16.13	26.5	21.97	2.6	15.6	22.2	3.5
S25	T	300		36.7	3	12.1	21.6	3.4	0.31	5.13	23.0	7.13	1.7	9.5	13.8	3.5

Appendix 6 (cont.)

CLONE	SITE†	FERT. TRT. (kg N/ha)	BLOCK	N 1996 (g/kg)	P 1996 (g/kg)	K 1996 (g/kg)	Ca 1996 (g/kg)	Mg 1996 (g/kg)	FOLIAR BIOMASS 1997 (Mg/ha)	WOODY BIOMASS‡ 1997 (Mg/ha)	N 1997 (g/kg)	FOLIAR N CONTENT 1997 (kg N/ha)	P 1997 (g/kg)	K 1997 (g/kg)	Ca 1997 (g/kg)	Mg 1997 (g/kg)
S301	KF	0		16.7	1.8	14.1	26.6	16.7	0.95	5.66	15.2	14.53	2.3	15.1	24.8	3.4
S301	KF	100		26.0	1.4	13.2	19.3	26.0	0.85	12.22	17.2	14.62	1.4	13.6	20.2	2.4
S301	KF	200		24.5	1.3	10.6	16.7	24.5	1.06	9.44	19.7	20.90	1.7	13.7	24.6	2.7
S301	KF	300		23.2	1.6	12.5	18.3	23.2	1.47	16.17	18.8	27.64	1.5	12.8	20.3	2.7
S301	S	0		15.7	1.9	12.1	24.2	15.7	0.89	5.63	17.9	15.98	2.2	9.9	27.1	2.9
S301	S	100		17.4	1.7	11.8	18.4	17.4	0.94	5.83	17.5	16.40	1.6	14.9	24.7	3.2
S301	S	200		18.0	1.8	10.9	20.4	18.0	0.61	3.55	15.7	9.53	1.7	10.4	26.3	4.0
S301	S	300		20.7	1.4	9.1	18.3	20.7	0.60	2.82	15.3	9.21	1.4	9.1	27.2	3.1
S301	T	0		27.5	2.5	16.0	16.1	27.5	0.86	8.61	18.0	15.44	1.7	22.3	14.5	2.2
S301	T	100		33.8	3.0	15.9	14.4	33.8	1.36	16.70	19.5	26.58	2.4	18.4	16.0	2.5
S301	T	200		33.2	3.0	15.6	15.4	33.2	0.88	12.29	22.7	19.97	1.7	21.1	17.0	2.1
S301	T	300		33.3	2.7	14.4	12.3	33.3	1.47	20.17	21.3	31.24	1.6	18.7	21.0	2.1
S546	KF	0		17.6	2.0	9.8	20.9	17.6	0.41	5.03	20.8	8.59	5.5	8.5	29.1	4.5
S546	KF	100		22.9	1.7	9.8	24.3	22.9	1.24	9.30	17.8	22.14	2.4	10.5	26.0	4.1
S546	KF	200		24.6	1.8	8.3	22.1	24.6	1.05	8.36	21.5	22.59	1.7	13.6	16.8	2.6
S546	KF	300		24.9	1.7	11.8	18.2	24.9	1.30	14.68	23.8	31.04	1.7	9.6	25.9	4.2
S546	S	0		19.9	2.7	9.4	30.3	19.9	1.52	12.79	23.2	35.20	4.5	10.0	18.6	4.6
S546	S	100		15.1	2.5	11.4	25.4	15.1	0.41	2.21	16.8	6.85	2.5	7.4	27.8	5.2
S546	S	200		26.0	2.3	9.0	19.1	26.0	1.13	10.25	22.7	25.67	2.7	11.0	23.9	3.6
S546	S	300		29.0	1.9	9.2	19.0	29.0	0.59	4.79	22.1	13.12	1.5	8.7	24.1	4.9
S546	T	0		22.6	2.7	10.8	15.2	22.6	1.08	14.00	23.6	25.42	5.7	9.2	23.3	3.9
S546	T	100		28.7	2.3	11.8	21.8	28.7	0.94	16.07	22.5	21.01	4.6	8.2	21.0	4.1
S546	T	200		30.3	2.2	14.5	23.2	30.3	0.78	19.64	26.4	20.60	3.6	11.5	23.9	3.6
S546	T	300		33.7	2.5	12.8	15.5	33.7	1.26	21.47	24.4	30.73	1.8	12.4	21.2	4.1

Appendix 6 (cont.)

CLONE	SITE†	FERT. TRT. (kg N/ha)	BLOCK	N 1996 (g/kg)	P 1996 (g/kg)	K 1996 (g/kg)	Ca 1996 (g/kg)	Mg 1996 (g/kg)	FOLIAR BIOMASS 1997 (Mg/ha)	WOODY BIOMASS‡ 1997 (Mg/ha)	N 1997 (g/kg)	FOLIAR N CONTENT 1997 (kg N/ha)	P 1997 (g/kg)	K 1997 (g/kg)	Ca 1997 (g/kg)	Mg 1997 (g/kg)
SA2	KF	0		17.5	1.3	11.0	17.5	2.9	0.15	0.81	17.2	2.56	1.8	11.9	15.2	3.6
SA2	KF	100		25.1	1.3	12.8	13.0	2.1	1.38	17.55	25.5	35.03	1.5	9.2	19.6	3.1
SA2	KF	200		22.3	1.3	9.2	17.9	3.9	0.21	2.37	18.1	3.88	1.5	12.0	18.7	3.1
SA2	KF	300		21.7	1.4	13.8	14.6	2.2	0.51	4.20	18.5	9.43	1.9	12.1	18.5	3.6
SA2	S	0		15.2	1.8	10.8	19.7	4.4	0.27	1.05	14.7	3.94	1.5	8.4	19.5	4.5
SA2	S	100		15.7	1.7	9.7	21.1	3.6	0.17	1.05	16.1	2.68	1.7	9.8	28.8	4.1
SA2	S	200		20.5	1.7	9.6	16.8	3.9	0.47	3.80	15.6	7.40	1.4	12.8	19.0	3.2
SA2	S	300		22.8	1.7	8.9	18.3	3.9	0.24	1.47	15.2	3.70	1.3	7.9	17.5	4.7
SA2	T	0		24.1	2.0	12.6	15.6	3.8	0.29	7.89	21.6	6.32	2.6	8.9	23.4	3.7
SA2	T	100		27.7	2.4	14.1	16.1	3.5	0.47	14.84	22.3	10.45	1.8	10.7	20.3	3.7
SA2	T	200		34.2	2.5	13.4	19.2	2.7	0.58	22.93	26.7	15.49	1.7	10.7	21.8	3.4
SA2	T	300		33.9	2.4	12.9	17.3	3.8	0.63	22.50	23.7	14.90	1.7	11.7	22.1	2.6
SV1	KF	0		22.1	2.4	12.2	18.9	3.1	0.38	4.05	20.4	7.77	5.6	11.5	23.5	3.5
SV1	KF	100		27.8	2.0	11.8	16.2	2.5	1.32	25.92	24.1	31.82	2.9	9.8	26.5	3.8
SV1	KF	200		29.6	1.7	10.5	20.9	2.6	1.11	16.11	26.2	29.05	1.6	9.6	26.0	3.5
SV1	KF	300		30.6	2.2	14.4	17.0	2.4	0.99	27.84	27.0	26.74	4.0	11.0	25.3	3.4
SV1	S	0		19.1	2.8	9.6	21.8	4.8	1.02	14.11	24.2	24.72	5.2	11.0	19.3	2.8
SV1	S	100		23.6	3.0	14.0	19.2	2.5	0.77	10.36	24.3	18.72	5.5	13.3	19.9	2.6
SV1	S	200		30.7	2.3	15.6	15.6	2.7	0.57	8.82	28.0	15.84	4.6	12.5	23.1	2.9
SV1	S	300		31.0	2.2	11.7	14.9	3.2	0.54	8.65	28.1	15.25	4.5	11.7	24.8	2.5
SV1	T	0		29.8	3.2	15.9	20.8	2.2	0.54	24.12	23.6	12.66	5.7	12.9	25.4	2.0
SV1	T	100		30.8	2.6	14.3	20.1	2.0	0.37	12.21	26.1	9.78	5.7	12.4	23.4	2.6
SV1	T	200		36.5	2.5	16.5	22.1	2.0	0.48	32.64	26.7	12.86	4.7	9.3	25.2	2.7
SV1	T	300		38.3	2.8	14.3	18.1	2.5	0.33	21.66	27.5	9.01	4.3	7.1	22.9	4.3

Appendix 6 (cont.)

CLONE	SITE†	FERT. TRT. (kg N/ha)	BLOCK	N 1996 (g/kg)	P 1996 (g/kg)	K 1996 (g/kg)	Ca 1996 (g/kg)	Mg 1996 (g/kg)	FOLIAR BIOMASS 1997 (Mg/ha)	WOODY BIOMASS‡ 1997 (Mg/ha)	N 1997 (g/kg)	FOLIAR N CONTENT 1997 (kg N/ha)	P 1997 (g/kg)	K 1997 (g/kg)	Ca 1997 (g/kg)	Mg 1997 (g/kg)
SV1	T	0	1	23.3	2.8	11.5	20.9	2.7			29.2		5.0	10.9	18.2	2.1
SV1	T	0	2	31.0	3.2	14.3	17.4	2.2			30.7		4.8	12.2	19.8	2.0
SV1	T	0	3	28.8	3.4	13.5	17.5	2.7			25.1		3.8	10.7	18.4	2.2
SV1	T	100	1	32.3	2.6	17.0	16.2	2.4			26.8		3.0	9.4	23.8	2.2
SV1	T	100	2	33.9	2.3	12.6	17.1	2.9			25.2		2.6	10.2	19.5	2.4
SV1	T	100	3	34.6	2.6	16.2	18.7	2.5			22.5		2.8	9.8	22.4	2.2
SV1	T	200	1	36.0	2.7	15.6	14.3	2.7			24.9		2.6	8.5	19.4	2.8
SV1	T	200	2	37.0	2.5	13.9	15.0	2.7			25.8		2.4	10.4	18.9	2.7
SV1	T	200	3	35.3	2.4	14.9	13.7	2.5			26.1		2.4	9.2	20.4	2.9
SV1	T	300	1	35.9	0.0	13.5	18.1	3.0			23.2		2.4	8.3	22.1	3.0
SV1	T	300	2	38.1	2.6	15.1	15.1	2.5			25.8		2.2	9.4	16.2	2.5
SV1	T	300	3	35.9	2.5	13.3	15.8	2.8			26.4		1.9	6.7	20.9	2.9

† Sites: King Ferry (KF), Somerset (S), and Tully (T), New York.

‡ Foliar and woody stem biomass: stools sampled for foliage (nutrients and biomass) were also measured for woody stem biomass in 1997.

Appendix 7. Soil laboratory and field data: pH, OM, CEC, texture, nutrients, and moisture for individual fertilization treatment plots in 1995.

CLONE	SITE†	FERT. TRT. (kg N/ha)	pH	OM (g/kg)	CEC ($cmol_c$/kg)	SAND (%)	CLAY (%)	SILT (%)	N (g/kg)	K (mg/kg)	Ca (mg/kg)	Mg (mg/kg)	Na (mg/kg)	P (mg/kg)	SOIL MOISTURE (m^3/m^3)
NM6	KF	0	6.2	45.7	15.12	37.00	47.40	15.60	1.6	68.57	2644.7	256.37	34.03	26.62	0.329
NM6	KF	100	6.2	41.2	14.74	44.80	40.60	14.60	1.6	64.97	2506.2	223.89	19.04	26.90	0.359
NM6	KF	200	5.5	41.7	12.98	46.40	40.80	12.80	1.5	73.26	1462.8	160.92	9.50	27.59	0.294
NM6	KF	300	6.7	46.0	18.14	40.40	44.80	14.80	1.7	67.45	2650.5	300.00	12.35	26.58	0.357
NM6	S	0	6.6	36.8	13.38	37.60	50.00	12.40	1.2	94.15	1355.5	299.50	11.10	34.60	0.331
NM6	S	100	6.1	38.6	12.50	37.60	52.00	10.40	1.2	75.90	1103.0	264.50	12.85	31.65	0.348
NM6	S	200	6.6	36.8	13.38	37.60	50.00	12.40	1.2	94.15	1355.5	299.50	11.10	34.60	0.361
NM6	S	300	5.7	34.0	10.58	43.20	46.40	10.40	1.2	98.40	1961.5	228.00	11.50	24.17	0.298
NM6	T	0	na	0.0											0.346
NM6	T	100	na	0.0											0.363
NM6	T	200	na	0.0											0.364
NM6	T	300	na	0.0											0.357
S25	KF	0	6.4	48.4	9.98	40.40	43.80	15.80	1.7	84.75	2805.0	356.50	10.05	24.16	0.372
S25	KF	100	6.3	46.9	15.90	38.60	44.80	16.60	1.5	188.91	2960.0	273.86	15.64	23.86	0.346
S25	KF	200	6.2	49.5	15.04	40.40	45.80	13.80	1.7	75.51	2691.2	324.34	11.94	23.19	0.365
S25	KF	300	6.8	48.9	17.08	42.40	42.80	14.80	1.7	66.97	3121.9	386.31	12.19	17.88	0.346
S25	S	0	5.7	37.3	13.22	41.20	48.40	10.40	1.2	93.45	1004.0	153.50	5.95	21.73	0.258
S25	S	100	6.2	36.8	9.50	39.20	48.40	12.40	1.2	93.65	1219.4	255.37	8.45	35.41	0.327
S25	S	200	5.7	37.3	13.22	41.20	48.40	10.40	1.2	93.45	1004.0	153.50	5.95	21.73	0.302
S25	S	300	6.3	38.1	14.66	31.60	56.00	12.40	1.2	133.10	1535.0	236.00	15.30	34.07	0.331
S25	T	0	na												0.349
S25	T	100	na												0.365
S25	T	200	na												0.369
S25	T	300	na												0.351

Appendix 7 (cont.)

CLONE	SITE†	FERT. TRT. (kg N/ha)	pH	OM (g/kg)	CEC ($cmol_c$/kg)	SAND (%)	CLAY (%)	SILT (%)	N (g/kg)	K (mg/kg)	Ca (mg/kg)	Mg (mg/kg)	Na (mg/kg)	P (mg/kg)	SOIL MOISTURE (m^3/m^3)
S301	KF	0	6.4	47.6	14.62	42.40	42.80	14.80	1.6	82.26	2831.6	339.83	11.74	24.45	0.362
S301	KF	100	5.6	46.8	13.98	42.80	41.60	15.60	1.5	98.00	1816.5	197.00	18.85	18.88	0.313
S301	KF	200	5.9	41.0	13.00	42.80	41.60	15.60	1.5	144.80	1970.0	225.00	11.20	24.29	0.294
S301	KF	300	5.7	40.2	13.28	44.40	41.80	13.80	1.5	109.10	1135.5	187.50	15.65	24.98	0.321
S301	S	0	6.5	33.5	13.16	35.20	54.40	10.40	1.1	86.50	1431.0	202.00	10.25	35.50	0.329
S301	S	100	5.9	38.1	13.14	33.20	55.40	11.40	1.3	99.00	1171.0	153.00	12.25	36.03	0.338
S301	S	200	6.5	33.5	13.16	35.20	54.40	10.40	1.1	86.50	1431.0	202.00	10.25	35.50	0.341
S301	S	300	6.2	34.6	15.10	33.20	54.40	12.40	1.1	86.50	1234.0	189.00	10.00	31.87	0.351
S301	T	0	na												0.342
S301	T	100	na												0.378
S301	T	200	na												0.365
S301	T	300	na												0.344
S546	KF	0	5.9	46.0	13.88	38.40	46.80	14.80	1.6	78.60	1557.0	298.00	7.25	17.88	0.310
S546	KF	100	6.4	46.2	15.08	42.80	41.50	15.70	1.6	105.20	2887.6	298.35	31.63	31.72	0.391
S546	KF	200	5.2	37.8	12.42	48.40	37.80	13.80	1.4	132.05	1364.0	170.00	10.00	26.62	0.289
S546	KF	300	6.0	44.2	17.18	36.40	47.80	15.80	1.6	91.05	2335.5	295.00	10.40	24.69	0.341
S546	S	0	5.6	41.6	13.28	33.20	55.40	11.40	1.3	130.58	1162.9	161.92	6.80	29.75	0.309
S546	S	100	6.8	42.0	15.14	40.40	48.80	10.80	1.4	106.20	1622.5	241.50	10.35	40.84	0.325
S546	S	200	5.6	41.6	13.28	33.20	55.40	11.40	1.3	130.58	1162.9	161.92	6.80	29.75	0.298
S546	S	300	6.0	36.4	11.88	43.20	45.40	11.40	1.1	102.65	957.5	257.00	8.65	21.73	0.300
S546	T	0	na												0.370
S546	T	100	na												0.369
S546	T	200	na												0.366
S546	T	300	na												0.332

Appendix 7 (cont.)

CLONE	SITE†	FERT. TRT. (kg N/ha)	pH	OM (g/kg)	CEC ($cmol_c$/kg)	SAND (%)	CLAY (%)	SILT (%)	N (g/kg)	K (mg/kg)	Ca (mg/kg)	Mg (mg/kg)	Na (mg/kg)	P (mg/kg)	SOIL MOISTURE (m^3/m^3)
SA2	KF	0	6.1	45.1	15.00	41.20	43.30	15.50	1.7	74.70	2387.0	262.50	34.90	22.91	0.343
SA2	KF	100	5.7	38.5	11.68	40.40	44.90	14.70	1.3	338.83	1436.8	140.93	13.14	26.07	0.311
SA2	KF	200	6.0	45.1	14.86	42.40	43.80	13.80	1.6	87.46	2590.7	237.88	12.24	24.56	0.344
SA2	KF	300	5.9	41.4	15.58	42.40	43.80	13.80	1.6	99.90	1798.1	253.87	9.95	17.79	0.339
SA2	S	0	6.0	36.2	11.82	40.40	49.80	9.80	1.1	94.25	1163.0	138.00	4.40	21.89	0.343
SA2	S	100	6.8	39.6	14.32	35.60	52.00	12.40	1.3	92.80	1542.0	328.50	12.60	48.55	0.322
SA2	S	200	6.0	36.2	11.82	40.40	49.80	9.80	1.1	94.25	1163.0	138.00	4.40	21.89	0.301
SA2	S	300	6.0	37.1	12.60	31.20	56.40	12.40	1.1	74.96	1159.4	170.91	8.25	30.43	0.356
SA2	T	0	na												0.337
SA2	T	100	na												0.341
SA2	T	200	na												0.356
SA2	T	300	na												0.366
SV1	KF	0	na	50.4	17.16	36.40	48.80	14.80	1.9	77.40	3165.0	392.50	26.80	25.54	0.394
SV1	KF	100	6.3	45.5	14.92	40.80	43.40	15.80	1.5	91.50	2669.5	245.00	18.90	26.21	0.346
SV1	KF	200	6.1	42.1	15.44	36.80	47.60	15.60	1.7	79.05	2713.5	252.00	10.95	23.86	0.329
SV1	KF	300	6.1	42.9	15.30	40.40	45.80	13.80	1.7	88.65	1951.5	266.50	8.10	24.30	0.370
SV1	S	0	5.4	37.5	11.90	42.40	48.80	8.80	1.3	112.75	1089.0	133.50	4.90	23.11	0.331
SV1	S	100	6.1	41.2	12.76	37.20	52.40	10.40	1.3	127.60	1385.5	155.00	12.05	35.14	0.325
SV1	S	200	5.4	37.5	11.90	42.40	48.80	8.80	1.3	112.75	1089.0	133.50	4.90	23.11	0.325
SV1	S	300	5.6	34.6	12.10	37.20	52.40	10.40	1.2	126.44	1635.2	237.38	5.55	22.26	0.332
SV1	T	0	na												0.366
SV1	T	100	na												0.385
SV1	T	200	na												0.366
SV1	T	300	na												0.365

† Sites: King Ferry (KF), Somerset (S), and Tully (T), New York.

Appendix 8. Soil laboratory data: pH, OM, CEC, texture, and nutrients for individual fertilization treatment plots of clone SV1 and NM6 in 1997.

CLONE	SITE†	FERT. TRT. (kg N/ha)	pH	OM (g/kg)	CEC ($cmol_c$/kg)	SAND (%)	CLAY (%)	SILT (%)	N (g/kg)	K (mg/kg)	Ca (mg/kg)	Mg (mg/kg)	P (mg/kg)
NM6	KF	0	6.6	38.8	13.80	48.51	26.59	24.89	1.2	68.60	2008.8	243.68	17.09
NM6	KF	100	6.3	51.2	18.24	46.41	27.00	26.60	1.7	82.83	1645.5	183.98	19.77
NM6	KF	200	6.1	36.0	14.16	49.21	26.00	24.80	1.2	77.88	1575.8	202.80	14.98
NM6	KF	300	6.3	48.8	17.77	38.80	29.40	31.80	1.6	71.58	2578.0	265.35	16.24
NM6	S	0	6.6	40.7	13.47	42.40	21.80	35.80	1.2	81.78	1290.5	150.93	22.69
NM6	S	100	6.7	35.2	11.86	43.50	18.00	38.50	1.1	65.06	1755.0	190.87	14.72
NM6	S	200	6.7	37.1	14.24	43.81	22.30	33.90	1.2	98.35	2288.0	264.10	27.91
NM6	S	300	5.9	38.4	11.27	50.60	18.50	30.90	1.2	73.48	1216.2	152.64	15.30
NM6	T	0	5.2	51.8	15.22	36.21	26.90	36.90	1.7	70.03	679.5	51.18	8.17
NM6	T	100	5.2	50.2	15.75	37.50	22.70	39.80	1.8	130.90	690.5	62.80	15.95
NM6	T	200	5.4	60.8	17.50	33.41	25.69	40.89	2.2	106.80	1469.3	114.10	9.87
NM6	T	300	5.1	58.6	17.30	37.11	23.00	39.90	2.0	107.28	722.5	51.45	4.66
SV1	KF	0	6.9	50.0	17.03	36.62	30.39	32.99	1.5	83.48	2488.6	279.17	19.33
SV1	KF	100	6.7	44.8	15.87	45.80	28.60	25.60	1.5	87.00	2217.3	255.15	20.48
SV1	KF	200	6.1	43.0	14.23	43.61	29.40	27.00	1.5	76.75	1761.1	180.96	17.83
SV1	KF	300	6.2	51.5	17.35	41.41	28.69	29.89	1.7	106.40	2135.5	237.79	20.22
SV1	S	0	5.9	40.3	12.45	50.61	18.60	30.79	1.3	93.55	1323.5	145.68	13.54
SV1	S	100	6.7	39.6	12.71	40.81	24.50	34.69	1.1	95.40	1745.8	178.80	22.01
SV1	S	200	5.6	39.0	13.06	38.51	22.80	38.69	1.1	85.20	1059.0	141.73	12.02
SV1	S	300	6.0	42.7	15.38	42.61	22.70	34.69	1.3	186.48	1330.3	182.35	19.77
SV1	T	0	5.2	64.0	16.94	36.30	24.90	38.80	2.1	85.45	853.3	70.53	6.89
SV1	T	100	5.5	53.8	17.55	34.20	24.90	40.90	1.9	50.55	982.8	56.75	4.66
SV1	T	200	5.5	67.0	20.08	36.11	25.00	38.90	2.3	153.35	1352.3	114.45	7.16
SV1	T	300	5.2	55.3	15.45	35.41	24.80	39.79	1.8	78.25	700.8	38.01	5.51

† Sites: King Ferry (KF), Somerset (S), and Tully (T), New York.

Appendix 9. Standard Operating Procedures for sampling willow foliage for nutrient measurements (ESF Willow Bioenergy Program, 1998).

Purpose: to diagnose nutrition status of plantations as a basis for: (1) prescribing fertilizer amendments, and (2) relating nutrient status to wood production.

Sampling dates: sampling should occur late in the growing season, preferably between August 15 and September 15. Late season foliage should be green (photosynthetically active). If foliage has started to senesce, as indicated by a change in color (green to yellow), it should not be collected.

Sample location--programmatic: All research, demonstration, and commercial plantings will be sampled for foliage nutrient analysis at various times in plantation development. Demonstration and commercial plantings will be sampled the summer before dormant season harvest, e.g., at the end of the first growing season (before cut back), at the end of the fourth growing season (3-yr-old plants on 4-yr-old root systems), etc. All research plantings will, at minimum, be sampled using this schedule with additional samples taken as dictated by the study.

Sample location--within area (NOTE--an area may be a single rep in the case of a clone site trial, or a large planting block in the case of a commercial planting): A number of trees should be sampled across the area from as many trees as possible. For example, 10 leaves from each of ten "trees" of a single clone would be adequate for large-leaved clones. NOTE that the sample size of 10 trees is a minimum. Sampling of more trees, perhaps up to 30 per area, would be better.

Sample location--with a tree crown: Ten to 20 leaves from the top one third of a crown (sun-exposed portion of crown).

Sample quantity: Depends on the clone. A total of 200 leaves (10 leaves from 10 trees) of small-leaved clones (e.g., *Salix purpurea*) or 100 leaves from large-leaved clones (e.g., Salix dasyclados). The purpose here is to produce enough dry tissue to perform various nutrient analyses, including a reserve amount of material for reanalysis if necessary, perhaps as part of the Quality Assurance Program.

Sample quality: mature, "normal" leaves are to be collected. Mature connotes fully formed, normal sized leaves. Normal is a clone-specific, year-to-year condition defined by the general quality of foliage for all of the trees in the area. It may be that foliage is normally discolored by nutrient stress or disease, or partially missing due to insects. The description of "normal" condition should be included with sample information (see below), particularly if it deviates from green, whole, healthy tissue.

Sample information: each sample should be uniquely identified by date of sampling, sample I.D. number, area location, clone, rep, and any miscellaneous notes about condition. This information should be recorded with the field sample collection (brown bag) and study notebook.

Field and laboratory techniques: follow Bickelhaupt and White (1982). In particular, care should be given to either cooling (ice packs, refrigerator) or drying (preferable) samples the same day as collected.