

Genetic Control of Foliar Nutrient Concentration in Loblolly Pine (*Pinus taeda* L.)

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Overview of SSIGNS

The Site Specific Interactions of Genetics and Nutrition Study (SSIGNS) is a factorial study that considers the performance of loblolly pine (*Pinus taeda* L.) genotypes treated with five different fertilization regimes across a range of environments. SSIGNS explores the causative factors underlying genotype-by-environment interactions, genetic differences in nutrient uptake and retention, and the relationship between soil type and productivity.

This study was established by the Forest Biology Research Cooperative (FBRC) at the University of Florida starting in the winter of 2013. Each site is laid out in a randomized factorial design with complete treatment blocks. Each of five treatment levels is replicated three times at each site. Within each plot, 30 full-sib families are replicated twice. In all, each site would have $30 \times 2 \times 5 \times 3 = 900$ individuals. The five fertilization treatments are none (control), N+P, N+P + Macros, N+P + Micros, and N+P + Micros + Macros. For further context, see Figure 1.

The oldest trials are in the 4th growing season and are beginning to exhibit stratification of diameter at breast height (DBH) between levels of fertilization. This separation is expected, and observable differences associated with genotype are expected to be observed in a few years.

Motivation for Pilot Study

Assessing foliar nutrient concentration incurs a substantial cost of time and money, and is known to be difficult to quantify. This is especially true for elements such as boron and molybdenum, where concentrations can be <1ppm. An important research question is whether nutrient uptake and retention are under genetic control. Here we performed a pilot study to assess the genetic control of nutrient concentration in a subsample of plots in order to motivate sampling on a much larger scale.

Experiment Design and Analysis

The control and full fertilization treatment plots were sampled for a single replication at the installation in Gainesville, FL. Needles were taken from the center 3rd of the stem and placed in envelopes, then dried in a climate controlled heating chamber. Each sample was ground using a GenoGrinder, then analyzed for nutrient content by MMI Labs. For elements analyzed, see Table 1.

For each element, a linear mixed model (LMM) was fit with plot as a fixed effect, row within plot as a random effect associated with spatial relationships, and genotype as a random effect. These models were evaluated with genotype evaluated as a family effect and the animal model using the pedigree associated with the site.

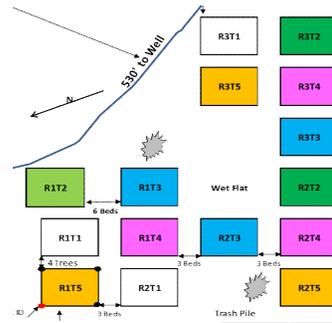


Figure 1: A site map for the Gainesville SSIGNS site. Each site has three replications of five levels of fertilizer treatment.

Table 1: Elements sampled in the pilot study, whether or not they were in the fertilizer treatment, effect of difference in plot (treatment), and heritability.

Element	In Fertilizer Mix	Plot P-Value	h^2_{Family}	$h^2_{Additive}$
S	Yes	0.998	0.01	0.03
Cu	Yes	0.788	0.00	0.00
Ca	Yes	0.511	0.00	0.01
Mo	Yes	0.218	0.00	0.00
Fe	Yes	0.214	0.01	0.09
B	Yes	0.020	0.02	0.00
P	Yes	0.003	0.07	0.04
N	Yes	0.000	0.00	0.00
Mg	Yes	0.000	0.14	0.12
K	Yes	0.000	0.00	0.00
Mn	Yes	0.000	0.07	0.07
Zn	No	0.880	0.25	0.25
Si	No	0.276	0.08	0.13
Al	No	0.000	0.22	0.20
Na	No	0.000	0.07	0.04

Results and Discussion

Plot effect was statistically significant as a source of variance for eight of the fifteen macro- and micronutrients. However, it is important to note that treatment and plot (i.e. random blocking) effects are confounded.

Additive heritability estimates for concentration were non zero for 5 elements (Table 1). Greater replication of treatments and genotypes is needed to estimate standard error.

Pertaining to our broad objectives for the pilot study, these results suggest that heritability is non zero for multiple element concentrations, indicating that there is likely a genetic basis for differences in needle concentration, even in very young trees.

Conclusions

While the sample size is too small for solid inference, it is still plausible that a genetic control exists and justifies expanded replication, especially as trees age and begin to stratify with growth phenotypes. Loblolly pine is typically phenotyped between 4 to 7 years for genetic analysis of growth traits, so more time and added degrees of freedom may enable secondary analyses including genetic correlation, age-age correlations, and analysis of retained nutrient content in senescing foliage.