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**60. © Genetic parameters for bud flushing and growth characteristics of white spruce seedlings.** Rweyongeza, D. M., Yeh, F. C., and Dhir, N. K. *Silvae Genetica* 59(4):151-158. 2010.

# Genetic Parameters for Bud Flushing and Growth Characteristics of White Spruce Seedlings<sup>1)</sup>

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## Abstract

We estimated heritabilities and correlations for bud flushing and growth traits of white spruce seedlings, and the correlations of seedling traits with 10- and 11-year height of the same families in the field. The seedling greenhouse experiment had a randomized complete block design with 30 replications, 58 open-pollinated families and single-tree plots. Individual tree heritability ( $h_i^2$ ) was 0.78 and 0.54 for 18 (H18) and 36 (H36)-week total height, respectively. The corresponding heritabilities for family means ( $h_f^2$ ) were 0.91 and 0.82. For root collar diameter,  $h_i^2$  were respectively, 0.61 and 0.22 at 24 and 54 weeks from germination. The corresponding  $h_f^2$  were 0.87 and 0.55. Heritability for bud flushing ranged from 0.13 to 0.46 ( $h_i^2$ ) and 0.44 to 0.83 ( $h_f^2$ ). The genetic correlation ( $r_a$ ) between H18 and H36 was 0.70 and that of D24 and D54 was 0.89, indicating a substantial change in family ranking in one growing season. The type B genetic correlation for H18 with field heights ranged from 0.22 to 0.30. Type B genetic correlations of field height with all other seedling traits were very low and largely negative. It can be concluded that: (1) age-age correlation of seedling height can be expected to decline drastically even in a stable environment of the greenhouse, (2) heritability for growth potential is meaningful when estimated on cumulative growth not on individual annual growth increments that are susceptible to short-term environmental variation, (3) dates of bud flushing did not influence variation in height and root collar diameter, and (4) field growth potential is better predicted by greenhouse growth potential than other morphological and shoot phenological traits.

**Key words:** Heritability; genetic correlation; early selection; bud flushing; progeny test.

## Introduction

Genetic studies of tree seedlings in controlled environments provide an opportunity for assessing the genetic variation of growth and phenological traits with limited environmental noises. In these experiments, many morphological, growth, and growth rhythm-related traits can be measured or scored at short regular intervals than would be possible in field progeny and provenance trials. Serial measurements of height and diameter growth allow us to develop growth trajectories of indi-

vidual families and predict their possible effect on future growth of older trees (e.g., RWEYONGEZA *et al.*, 2003). Heritability and genetic correlation from serial measurements show an extent with which genetic variation in quantitative traits is affected by tree age/size (e.g., NIENSTAEDT and RIEMENSCHNEIDER, 1985; YING and MORGENSTERN, 1979) and how this could affect decisions on early selection. Variation in the timing of bud flushing and budset has implications on susceptibility of genotypes to frost damage and could also influence variation in annual height growth (e.g., WILKINSON, 1977; LI *et al.*, 1997; O'REILLY and PARKER, 1982).

White spruce (*Picea glauca* [Moench] Voss) is the most important conifer tree species in Alberta, which makes up 45.9% by volume of all conifers (AFLW, 1985). Genetic improvement activities in Alberta are centered around improving growth and yield of white spruce and lodgepole pine (*Pinus contorta* Dougl) as the two major conifers. Thus, understanding the genetics of white spruce at all levels of tree growth and development is essential for the management of the species in the province. This article is part of the large retrospective genetic study of white spruce from the northwest boreal forest in Alberta, which is designed to study genetic variation in juvenile traits in the greenhouse and their possible use as genetic indicators of late growth potential in field experiments.

## Materials and Methods

### *Families and Experimental Procedures*

The 58 families involved in the greenhouse study were collected as open-pollinated seedlots from the Peace River region in central and northwestern Alberta, Canada (54°31' – 58°03' N, 117°35' – 119°22' W, and 365–945 metres above sea level). They were earlier included in the field progeny trial at Chinchaga (57°50' N, 118°12' W and 470 metres above sea level) and Saddle Hills (55°31' N, 119°40' W and 914 metres). These field trials have a randomised complete block design with 6 replications and 6-tree row plots at 2.5 x 2.5-metre spacing. Both trials were measured for height growth at age ten and eleven years from seeds.

The greenhouse retrospective progeny test was conducted from 1996 to 2000 at the University of Alberta in Edmonton, Canada, to estimate genetic parameters of seedling traits and genetic correlations of seedling traits with advanced age growth of the same families in the field. The greenhouse-field correlations would show the extent with which seedling growth and shoot phenology assessed in controlled environment corresponded with height growth potential in the field. This would in turn reveal the merits of early selection for white spruce in

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