GENOME SIZE, TRACHEID VOLUME, AND ENVIRONMENTAL FACTORS IN THE GENUS PINUS[1]

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Abstract.--Positive relationships have been reported between genome size and cell volume both in prokaryotes and eukaryotes. In six North American Pinus species, there appears to be a direct relationship between genome size and measured tracheid volume in greenhouse-grown seedlings. However, habitat precipitation seems to affect tracheid volume of trees grown in the field. Using genome size and habitat precipitation data of six Pinus species, tracheid volume in field-grown trees was estimated quantitatively. A theory is introduced for estimation of tracheid volume, and two terms, standard tracheid volume and tracheid volume change, are defined. Using an equation estimating tracheid volume derived from the six species, tracheid volume in field-grown trees was estimated in 15 North American Pinus species. Estimated tracheid volumes showed significant agreement with those calculated from tracheid dimensions obtained from the literature. Although this is a preliminary report, these results indicate that the theory might be effective for estimation of tracheid volume in North American Pinus species.

Keywords: genome size, Pinus species, estimation of tracheid volume, standard tracheid volume, tracheid volume change, environmental stress.

INTRODUCTION

Positive relationships between genome size and cell volume have been reported both in prokaryotes and eukaryotes (Price et al. 1973, Shuter et al. 1983, Cavalier-Smith 1985). Before examining the relationship between genome size and cell volume in the genus Pinus, a comprehensive data set of genome size was needed. Recently, genome size in 18 North American and one exotic Pinus species including two seed sources of P. taeda was measured by scanning Feulgen microspectrophotometry and laser flow cytometry (Wakamiya et al. 1993). The two methods showed a significant agreement with each other. In this paper, the relationship between genome size and tracheid volume is examined.

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Fiber dimension is an important characteristic of wood for the forestry industry. Factors affecting fiber dimensions have been studied, including types of indices related to the dimensions such as specific gravity (Zobel and van Buijtenen 1989). However, little interest has been given to the quantitative estimation for fiber dimensions. In this paper, one theory is introduced for estimation of tracheid volume, and is examined in North American Pinus species.

THEORY

According to Newton et al. (1993), tracheid dimensions from the literature appear to be directly related to genome size when a species is distributed in a region where the habitat lowest annual precipitation exceeds 800 mm. Habitat lowest annual precipitation (PRC) is the lowest annual precipitation within the natural distribution range of the species. Where PRC is less than 800 mm, tracheid dimension appears to decrease, compared with expected values from the relationship between genome size and tracheid dimensions. The decrease in tracheid dimension from expected values is negatively correlated to PRC. Therefore, it is hypothesized that the tracheid has an expected dimension if soil water is adequate. We used tracheid volume as a tracheid dimension in this study.

We introduce two terms, standard tracheid volume (V_t°) and tracheid volume change (ΔV_t). V_t° is defined as tracheid volume of pine trees grown under standard conditions (well-watered). ΔV_t is defined as the decrease in tracheid volume from V_t°. Therefore, tracheid volume (V_t) is defined as:

$$V_t = V_t^{\circ} + \Delta V_t. \tag{1}$$

In the genus Pinus, V_t° is hypothesized to be a function of genome size and ΔV_t to be a function of PRC (Newton et al. 1993).

MATERIALS AND METHODS

Tracheid volume

Assuming that tracheid shape is columnar, tracheid volume (V) was calculated as $V = \pi R^2 L$, where R and L are tracheid radius and length, respectively. In this paper, values of R were calculated from tracheid width (W) as $R = W / 2$.

Tracheid length is dependent upon age. Fibers appear to continue to grow for several decades (Zobel and van Buijtenen 1989). On the other hand, tracheid width can be assumed to be quite constant after one full growing season. There is a relationship between tracheid length and width which has been reported in the pulp sector of the forest industry, and tracheid length was estimated by that relationship (Newton et al. 1993). Tracheid width of stems for greenhouse-grown seedlings was measured and that for field-grown trees was obtained from the literature (Newton et al. 1993). Tracheid volume calculated from tracheid dimensions obtained from the literature is denoted as $V_{t,\text{field}}$.

Standard tracheid volume (V_t°)

Standard conditions for determination of V_t° are as follows. Seedlings were grown under well-watered conditions in a greenhouse equipped with an evaporative air conditioning system and shaded with 50% shadecloth. They were fertilized frequently and watered every other day. Fritted clay was used as the growth medium.

Two-year-old greenhouse-grown seedlings of six species (Table 1) were used for measurement of tracheid width. Using the measured tracheid width, tracheid volume (V) of the six species was calculated from the method previously described and was used as V_t°. Genome sizes were obtained from Wakamiya et al. (1993) and are shown in Table 1. Correlation and regression analyses were done to examine the relationship between genome size and V_t° in the six species.

Table 1. Genome size of six Pinus species used for determination of the standard tracheid volume (VC).

Range in U.S.	Species		Genome size [pg][1]
South-East	P. virginiana	Virginia pine	21.1
South-East	P. taeda	Loblolly pine	23.0
North-East	P. strobus	Eastern white pine	26.7
West	P. radiata	Monterey pine	24.3
West	P. lambertiana	Sugar pine	29.7
West	P. monophylla	Singleleaf pinyon pine	30.2

[1] Obtained from Wakamiya et al. (1993).

Tracheid volume change (ΔV_t)

Tracheid volume change (ΔV_t) was calculated as the difference between $V_{t,\ \mathrm{field}}$ and V_t°. Correlation and regression analyses were done to examine the relationship between PRC and ΔV_t in the six species. PRC was obtained from Wakamiya et al. (1993).

Estimation of tracheid volume

Tracheid volume for 15 North American Pinus species was estimated using Eq. 1. Estimates of V_t were compared with values of $V_{t,}$ field. Paired t-tests, correlation and regression analyses were used to substantiate the theory.

The 15 Pinus species used in the analysis were: P. virginiana, P. clausa, P. serotina, P. echinata, P. taeda, P. elliottii, P. strobus, P. radiata, P. attenuata, P. monticola, P. coulteri, P. torreyana, P. sabiniana, P. lambertiana, and P. monophylla.

RESULTS AND DISCUSSION

From the regression line where genome size was related to standard tracheid volume (Vt°) in the six Pinus species ($r^2 = 0.96$, $P < 0.1\%$), Vt° was described as

$$V_t = f(\text{genome size}) \tag{2}$$

where f denotes a function.

Figure 1 shows the relationship between PRC and AV_t. As previously suggested (Newton et al. 1993), $V_{t,}$ field decreased where PRC is less than 800 mm.

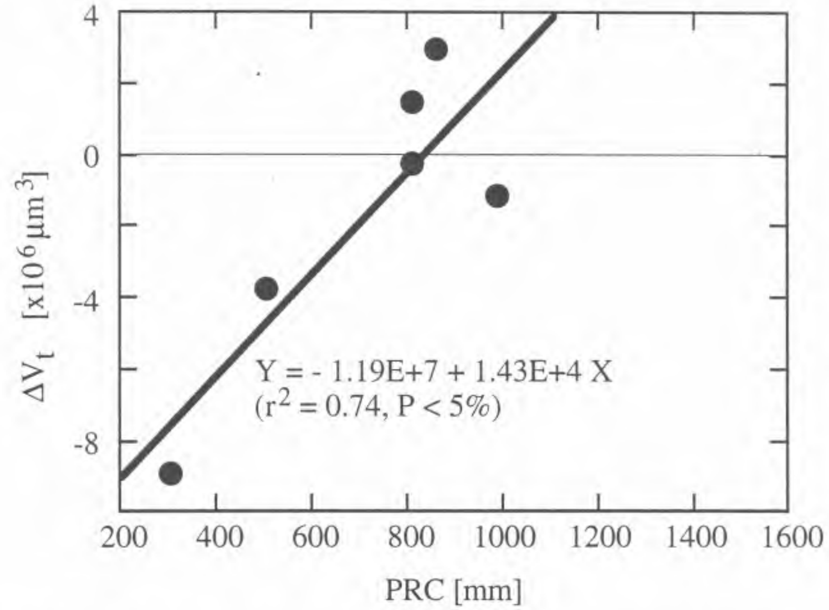

Figure 1. The relationship between the tracheid volume change (ΔV_t) and habitat lowest annual precipitation (PRC). At less than about 800 mm, tracheid volume decreases, compared with standard tracheid volume (V_t°). If tracheid volume calculated from tracheid dimensions obtained from the literature ($V_{t,\ field}$) is the same as V_t°, a plot is then shown by the thin line (Y = 0).

From the regression line describing the relationship of PRC to tracheid volume change(ΔV_t) ($r^2 = 0.74$, $P < 5\%$), ΔV_t was described as

$$\Delta V_t = f(\mathrm{PRC}). \tag{3}$$

V_t obtained using Eqs. 1,2, and 3 was compared with $Vt_{,}$ field. No significant differences between those values were shown by a paired t-test. Figure 2 shows the relationship between Vt and $Vt_{,}$ field. Both values were significantly correlated ($r^2 = 0.50$, $P < 1\%$) and showed significant agreement (intercept = - 0.95; slope = 1.12) (Fig. 2). These results indicate the effectiveness of this theory for estimation of tracheid volume, even though collected data used for substantiating this theory were from a small number of species.

CONCLUSIONS

In North American Pinus species, we were able to estimate tracheid volume of trees grown in the field using genome size and PRC. However, genome size and PRC are not the only factors related to tracheid volume. It is commonly known that several environmental factors such as air temperature and physiological characteristics such as age and genetic traits such as coding genes also alter cell volume. Also, precipitation data and values of tracheid dimensions used in this study are very general. Intraspecific variation needs to be studied, and standard environmental conditions should be determined and defined for standard tracheid volume (V_t). For more accurate estimation of tracheid volume, further investigations are needed.

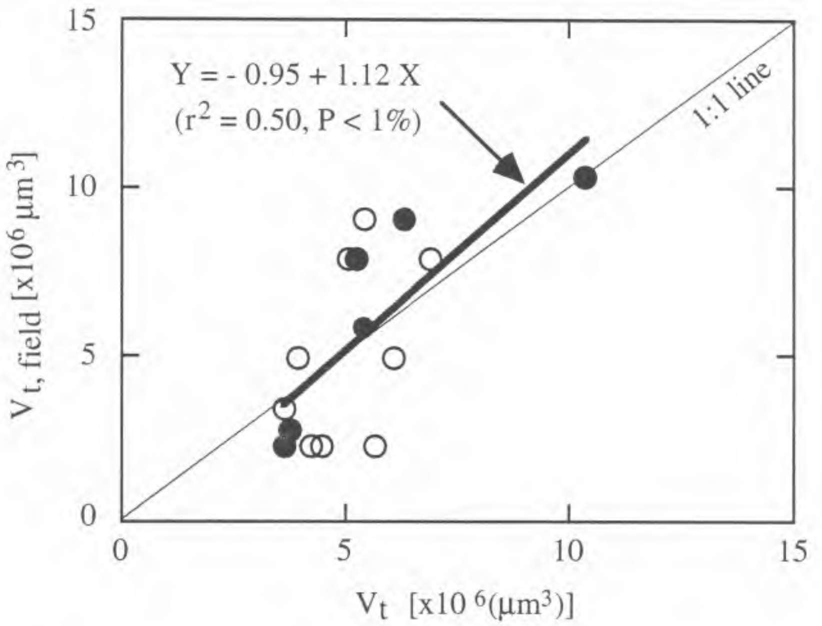

Figure 2. Comparison of estimated tracheid volume (V_t) and tracheid volume calculated from tracheid dimensions obtained from the literature ($V_{t,\ field}$) in 15 North American Pinus species. The solid line is a regression line for 15 species. The black circles show the six Pinus species used to determine ΔV_t listed in Table 1 and the white circles represent the remaining 9 of 15 species in the analysis.

LITERATURE CITED

Cavalier-Smith, T. 1985. Cell volume and the evolution of eukaryotic genome size. P.105-184. in The Evolution of Genome Size, T. Cavalier-Smith (ed.). John Wiley & Sons. London.

Newton, R.J., I. Wakamiya, and H.J. Price. 1993. Genome size and environmental stress in gymnosperm crops. P.321-345. in Handbook of Plant and Crop Stress, M. Pessarakli (ed.). Mercel Dekker. N.Y. (in press).

Price, H.J., A.H. Sparrow, and A.F. Nauman. 1973. Evolutionary and developmental considerations of variability of nuclear parameters in higher plants. I. Genome volume, interphase chromosome volume and estimated DNA content of 236 gymnosperms. Brookhaven Symposia in Biology. 25:390-421.

Shuter, B.J., J.E. Thomas, W.D. Taylor, and A.M. Zimmerman. 1983. Phenotypic correlates to genomic DNA content in unicellular eukaryotes and other cells. Amer. Nat. 122:26-44.

Wakamiya, I., R.J. Newton, J.S. Johnston, and H.J. Price. 1993. Genome size, growth indices, and environmental factors in the genus Pinus. Am. J. Bot. (in press).

Zobel, B.J., and J.P. van Buijtenen. 1989. Wood variation - Its causes and control. Springer-Verlag. Berlin. 363p.