Annals of Warsaw University of Life Sciences – SGGW
Forestry and Wood Technology No 74, 2011: 170-173
(Ann. WULS-SGGW, Forestry and Wood Technology 74, 2011

Genetic correlations between tracheid biometric traits in European Larch

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Abstract: *Genetic correlations between tracheid biometric traits in European Larch.* Genetic correlations between tracheid biometric traits were estimated in 25-year-old trees of 161 full-sib families of European larch growing in seed orchard from northern Poland. The tracheid length for juvenile-wood increment core were obtained from optical fibre-analyser. All genetic correlations calculated between tracheid biometric traits were strong and positive. Tracheid length weighted showed the strongest positive correlation with tracheid wall thickness (0,90). These results for European larch are consistent with those from studies in Norway spruce [8].

Keywords: European Larch, tracheid biometric traits, genetic correlations, phenotypic correlations

INTRODUCTION

Wood and paper are basically constituted of the same type of fibres, but they are organized in different ways. Tracheid in wood are arranged in the same direction, while fibres in paper are randomly organized, bonded together at the contact points between them [2]. The most important aspects for pulping process are tracheid dimensions: length of tracheid and cell wall thickness. Tracheid length highly correlated with bending and strength properties. Thin-walled cells provide a low bending stiffness but good tensile strength. Thicker-walled cells contribute higher bending stiffness, tear strength and breaking length but provide weak paper [10]. The value of tear strength, tensile strength, and breaking length and degree of bonding in the paper are the most important characteristics of high quality paper product [4]. Investigations of genetic correlations between tracheid biometric traits seems to be important for improving knowledge about paper quality.

MATERIAL AND METHODS

Wood material used in study was European larch (*Larix decidua* Mill.), coming from seed orchard established in 1985 in the Forest Ranges Mlynary in northern Poland. The tracheid biometric traits were estimated in 161 trees of full-sib families. The five-millimeter juvenile-wood increment cores from each sample-tree were collected at 1,3 height. Tracheid traits samples were soften in 1:1 solution of hydrogen peroxide (H_2O_2) diluted to 25% and acetic acid (CH_3COOH) at 90-100°C for about 20-24 hours [6]. Thereafter samples were manually squeezed in a tube until a homogenous tracheid was formed. The fibre parameters were measured using a Kajaani FiberLab 3.5 optical fibre-analyser with three runs per sample [11]. Because the Kajaani FiberLab is an optical method without the ability to separate tracheids from other particals or unbroken from broken tracheids [3] the images were defined manually in a web database, whether the fibres were unbroken, cut, joined or measured incorrectly. All tracheid shorter than 0.5mm were excluded from the data because of a high potential error in correct definition at this size. The tracheid were classified into six length classes following Nilsson [12]. During analyzing process four biometric traits were measured as follows [9]:

trachied length: $TL = \Sigma n_i l_i / \Sigma n_i$

tracheid length weighted: $TLW = \Sigma n_i l^2_i / \Sigma n_i$

tracheid diameter: $TD = \Sigma n_i w_i / \Sigma n_i$

cell wall thickness: $CWT = \Sigma n_i cwt_i / \Sigma n_i$

where:
l_i – mid-class length in class *i*,
w_i – mid-class width in class *i*,
cwt_i – mid-class cell wall thickness in class *i*,
n_i – tracheid count in class *i*.

Length-square-weighted mean lengths were used to minimize the influence on the mean of the large number of small fragments that are inevitable in 5 mm core samples and not distinguished from intact tracheids by the analyser. Variance components for each traits were estimated using method of the SAS 9.2 Pl VARCOMP procedure, and estimated of the covariance between different traits were obtained from the MANOVA statement [13]. The genetic correlation was calculated as follows [14]:

$r_{gxy} = Cov_{Fxy} / (\sigma_{Fx}^2 \sigma_{Fy}^2)^{1/2}$

where:
σ_{Fx}^2 – family variance components for traits X and Y, respectively,
Cov_{Fxy} – family covariance components for traits X and Y.

RESULTS

The genetic correlation between tracheid biometric traits were calculated (Fig. 1). Strong and positive genetic correlations exist between all tracheid biometric traits. Correlation between tracheid length weighted and cell wall thickness reached the highest value of correlation (0,95), while correlation between tracheid length weighted and tracheid diameter was high but not so strong (0,74). Furthermore correlations tracheid length with tracheid diameter and with cell wall thickness were strong and positive (respectively: 0,90 and 0,89). Additionally strong positive correlation was observed between tracheid length and tracheid length weighted (0,88).

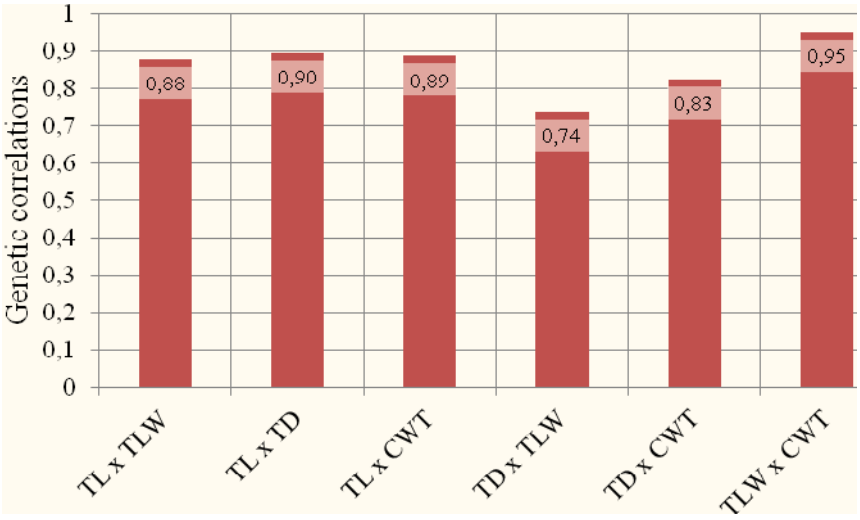

Fig 1 Genetic correlation between tracheid biometric traits.
Tracheid length (TL), tracheid length weighted (TLW), tracheid diameter (TD), cell wall thickness (CWT).

CONCLUSIONS

Genetic correlation between tracheid biometric traits were all strongly positive and significant. Positive genetic correlation between tracheid diameter and tracheid length has been reported for Norway spruce [8]. In contrast to the results in the present study Ericsson and Fries [5] state that "there was a strong negative genetic correlation between fibre length and fibre width in Scotch pine". The explanation may be hidden by differences in the width if annual rings in Scotch pine and European larch which influence tracheid formation [1]. Published genetic correlation estimates for tracheid width and double wall thickness in Loblolly pine are high ranging from 0,31 to 0,59 [7]. The estimated in present study genetic correlation for tracheid diameter and cell wall thickness in European larch were 0,89. In conclusion, the result of the present investigation shows the genetic background for the relations between tracheid biometric traits.

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Streszczenie: *Korelacje genetyczne pomiędzy cechami biometrycznymi cewek modrzewia europejskiego.* Dla 25-letnich pół-rodów modrzewia europejskiego z plantacyjnej uprawy nasiennej z północnej Polski obliczono współczynniki korelacji genetycznych pomiędzy cechami składowymi gęstości drewna długością cewek. Cechy gęstości drewna i słoja rocznego określono z wykorzystaniem rentgenograficznej metody obrazowania struktury drewna. Długość cewek określono z wykorzystaniem optycznego analizatora włókien. Współczynniki korelacji genetycznych cech słoja rocznego i długości cewek były umiarkowanie negatywne, natomiast korelacje z cechami gęstości drewna były pozytywne. Jedynie dla gęstości drewna wczesnego otrzymano przeciwstawne wyniki.

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