Dissertationes Forestales 110

Effects of genetic entry and spacing on growth and wood properties in Scots pine

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Academic dissertation

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ABSTRACT

In forest breeding, stem volume and sawn timber quality have typically been used as the most important selection traits. Less attention has been paid to wood density and fibre properties. This study investigates the effects of genetic entry and spacing on the growth and yield traits, branch characteristics, wood density traits and fibre properties in 20-year-old Scots pines (*Pinus sylvestris* L.). Additionally, the phenotypic variation within, and correlations between, different traits and the effects of cambial age, spacing, genetic entry and climatic variables on the ring width and ring density development from pith to bark are studied. Kanerva pine (Finnish plus tree S1101) was the father tree for most of the genetic entries included in this study, whereas the mother trees represented Finnish plus trees with a relatively wide geographical range from northern to southern Finland. The effects of genetic entry (mainly full-sib families) and spacing on the growth and yield traits, wood density traits and fibre properties were analysed (Papers I-II) based on materials, harvested in 2006, from 10 genetic entries grown in a spacing trial in central Finland, with a current stand density range of 2000-4000 trees/ha. Furthermore, additional material was harvested from the same trial in 2008 to study the effects of genetic entry and spacing on the branch characteristics (Paper III) and the effects of cambial age, spacing, genetic entry and climatic variables on the ring width and ring density development from pith to bark (Paper IV).

In this study wood density traits show lower phenotypic variation compared to growth and yield traits, regardless of spacing. Wood density traits present from moderate to strong phenotypic correlations among them (Paper I). Spacing affects significantly ($p<0.05$) all the yield traits, wood density traits and fibre properties (Papers I-II). Furthermore, spacing affects living branch characteristics such as relative average branch diameter and relative cumulative branch area (Paper III). Genetic entry affects tree height, wood density traits and fibre length (Papers I-II). When grouping the Kanerva tree crossings into different geographical origins based on their mother trees, the northern ones have, on average, the largest diameter at breast height and the highest mean wood density, while the central ones have the tallest trees (Paper III). Branch diameter along the stem is affected by branch age, geographical origin group and spacing, while branch angle is affected by branch age and genetic entry ($p<0.05$). Radial growth and ring density development are both affected by cambial age and spacing, and the latter is also affected by origin group and several climatic variables. The phenotypic correlations between various growth, yield and wood density traits are negative, which suggests that selection for one trait would simultaneously affect the other traits. The phenotypic correlations between different fibre properties are strong, but not well correlated with growth, yield and wood density traits. This kind of information is currently needed for breeders for considering different traits as selection criteria for tree breeding in Scots pine.

Keywords: spacing, genetic entry, origin group, phenotypic correlation, growth and yield, branch characteristics, wood density, fibre properties.

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LIST OF ORIGINAL ARTICLES

This thesis is a summary of the following papers, which are referred to in the text by the Roman numerals I-IV.

I Peltola, H., Gort, J., Pulkkinen, P., Zubizarreta-Gerendiain, A., Karppinen, J. & Ikonen, V-P. 2009. Differences in growth and wood density traits in Scots pine (*Pinus sylvestris* L.) genetic entries grown at different spacing and sites. Silva Fennica 43(3): 339–354. www.metla.fi/silvafennica/full/sf43/sf433339.pdf

II Gort, J., Zubizarreta-Gerendiain, A., Peltola, H., Pulkkinen, P., Routa, J. & Jaatinen, R. 2009. Differences in fibre properties in Scots pine (*Pinus sylvestris* L.) genetic entries grown at different spacing and sites. Silva Fennica 43(3): 355–368. www.metla.fi/silvafennica/full/sf43/sf433355.pdf

III Gort, J., Zubizarreta-Gerendiain, A., Peltola, H., Kilpeläinen, A., Pulkkinen, P., Jaatinen, R. & Kellomäki, S. 2010. Differences in branch characteristics of Scots pine (*Pinus sylvestris* L.) genetic entries grown at different spacing. Annals of Forest Science. 67 (2010) 705.

IV Gort, J., Mehtätalo, L., Peltola, H., Zubizarreta-Gerendiain, A., Pulkkinen, P., & Venäläinen, A. 2010. Effects of spacing and genetic entry on radial growth and ring density development of Scots pine (*Pinus sylvestris* L.). Manuscript.

Jaume Gort-Oromi had the main responsibility for all the work done in Papers I-IV. Co-authors of separate papers (I-IV) have participated in the work mainly by commenting on the manuscripts and supporting the data analyses. Paper I was written jointly by Heli Peltola and Jaume Gort-Oromi.

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ABBREVIATIONS

Short name of variables	Variables and their units
DBH	Diameter at breast height, cm
H	Tree height, m
V	Stem volume, m^3
WD	Mean wood density, g/cm^3
RD	Ring density, g/cm^3
EWD	Earlywood density, g/cm^3
LWD	Latewood density, g/cm^3
RW	Ring width, mm
EWW	Earlywood width, mm
LWW	Latewood width, mm
LWW%	Latewood percentage
RW	Ring width, mm
FL	Fibre length, mm
FW	Fibre width, µm
C	Coarseness, µg/m
BA	Branch angle, degrees
CBH	Crown base height, m
RCBH	Relative crown base height
NLB	Number of living branches
BD	Branch diameter, mm
ABD	Average branch diameter, mm
RCBA	Relative cumulated branch area
RABD	Relative average branch diameter
ABA	Average branch angle, degrees

1 INTRODUCTION

1.1 Background

In Scandinavia, Scots pine (*Pinus sylvestris* L.) is an important source of raw material especially for the sawn timber industry, but also for the pulp and paper industry. The quantity and properties of stem wood, such as stem volume, stem straightness, knot characteristics, wood density and fibre properties, affect the suitability of tree species and their genetic entries as a raw material for mechanical wood processing and pulp and paper production. Additionally, wood density affects the pulp yield, and wood density and fibre properties have also a large influence on the energy needed in the pulp and paper manufacturing processes (Tyrväinen 1995, Chambers & Borralho 1999). Relatively small variations in wood properties affect the sustainability of the processes and the properties of the final products.

Despite this, in long-term breeding programmes for Scots pine, stem volume and sawn timber quality (i.e. knot/branch characteristics and stem straightness) have usually been considered as selection traits of primary importance (Ståhl 1988, Haapanen et al. 1997, Hannrup et al., 2000). Other traits, such as wood density or fibre properties, have been considered as secondary selection traits (Ståhl 1988, Haapanen & Pöykkö 1993). However, wood density and fibre properties such as fibre length are from moderately to highly inherited properties and show a moderate genetic age-age correlation between juvenile and mature wood for Scots pine (Hannrup & Ekberg 1998). Therefore, tree selection could be successful even for reasonably young trees (Zobel & van Buijtenen 1989, Hannrup et al. 1998, Hannrup et al. 2001, Fries & Eriksson 2006).

The interaction of the prevailing temperature conditions during the growing season, its length, the availability of water, nutrients and light affect the overall tree growth and stem and wood properties (Linder 1987, Allen et al. 1990, Albaugh et al. 1998, Fries et al. 1998, Svensson et al. 1999, Miina 2000). For example, in central Finland, the radial growth of Scots pine lasts from May to August (Kanninen et al. 1982, Peltola et al. 2002, Henttonen et al. 2009). To date, the observed variation in precipitation has been found to have only minor or no effect on growth and wood properties for Scots pine in Finnish conditions (Miina 2000, Mäkinen et al. 2000).

Silvicultural management, such as initial spacing and thinning offer a means to affect the growing conditions of trees, and thus, also the stem wood production. In Scots pine, initial spacing (stand density) most clearly affects the growth and yield traits such as diameter at breast height and stem volume (Fries 1984, Persson et al. 1995). Initial spacing also affects the stem properties such as branch characteristics (especially in lower tree canopy) and wood properties such as wood density, particularly during the early phase of a rotation (Persson 1975, Persson 1976, Ståhl 1988, Persson et al. 1995, Hannrup et al. 1998). Similar results have been found for Jack pine (*Pinus banksiana*) (Kang et al. 2004). Nonetheless, there exist contradictory results about the effects of spacing on the fibre properties in Scots pine (e.g. Persson 1975). The effect of stand density on different wood properties is also larger in relatively young trees compared to older ones (Björklund & Walfridsson 1993). This could be explained by the fact that wood properties, such as wood density and fibre length, increase most rapidly in juvenile wood, i.e. within the 10-20 first annual rings from the pith (Hakkila 1966, Björklund & Walfridsson 1993, Persson et al. 1995, Zobel & Jett 1995, Hannrup & Ekberg 1998, Ridoutt et al. 1998, Hannrup et al. 2001, Hannrup et al. 2004).

In Scots pine, an increase in growth has, in general, been thought to decrease at least slightly the mean wood density (Atmer & Thörnqvist 1982, Persson & Persson 1997, Wilhelmsson et al. 2002). On the other hand, a non-significant or a weak positive relationship between wood density and growth has been observed previously for the species (Mörling 2002) and in other tree species such as Lodgepole pine (*Pinus contorta*) (Wang et al. 2000), Black spruce (*Picea mariana*) (Zhang & Morgenstern 1995, Zhang et al. 1996), and Norway spruce (*Picea abies*) (Bujold et al. 1996, Zubizarreta-Gerendiain et al. 2007). Moreover, in Scots pine, mean wood density generally correlates strongly with latewood percentage (Hannrup et al. 2001), which is significantly affected by tree age and growth rate (Hakkila 1966, Hakkila 1968, Tyrväinen 1995).

Interest to shorten the rotation, by more intense management, can increase the proportion of juvenile wood, which has lower mean wood density and different mechanical properties than mature wood (Zobel & van Buijtenen 1989, Thörnqvist 1990, Persson et al. 1995). On the other hand, it has been found that during the juvenile phase the mean wood density and ring width do not necessarily correlate negatively in Scots pine (Haapanen et al. 1997, Hannrup et al. 2000). Therefore, it would be desirable to identify genetic entries with a higher mean wood density during the juvenile phase for use as a regeneration material.

A strong correlation exists between the growth of the stem and branches in Scots pine, with implications also on the mortality and self-pruning of branches along the stem, as well as on the properties of the sawn timber (Ikonen et al. 2009, Högberg et al. 2010). In Scots pine, the reduction of branch size has been found possible, in general, only at the expense of total tree growth (Mäkinen & Colin 1998, Mäkinen 1999a). Furthermore, in Scots pine, like in other coniferous species, the average size of living branches normally increases along the stem from the stem apex to the living crown base (Kellomäki et al. 1999, Mäkinen et al. 1999b). However, it is possible to control the growth of the stem and branches in the middle and lower crown by controlling the light competition, especially in the early phase of the rotation. This can be done by the appropriate choice of initial spacing, timing and intensity of tending of the seedling stand and/or first thinning. As a result, the quality of the most valuable lower part of the stem can be improved (Kellomäki et al. 1999, Ikonen et al. 2009).

In Scots pine, a significant correlation among several wood properties, growth and yield traits has been found, for example, between fibre length and tree height (a moderate correlation) and between fibre length and tree diameter at breast height (a weak correlation) (Ståhl 1988). On the other hand, only a few studies exist on the phenotypic or genetic correlations between growth and yield, stem quality traits (e.g. stem straightness, branch characteristics) and mean wood density in Scots pine (Haapanen et al. 1997; Hannrup et al. 2000). In these studies, weak negative or no genetic/phenotypic correlations have been reported between traits such as branch angle, branch thickness, number of branches, stem straightness and mean wood density. According to Hannrup et al. (2000), the relative branch diameter also correlates positively with wood density in Scots pine. Previously, Velling (1988) suggested that if there is a preference for narrow-crowned Scots pine trees with fine branches and large branch angle, this might lead to lower mean wood density.

In recent decades Finnish tree breeders have paid special attention to a genetic entry called Kanerva pine (S1101). This individual tree was originally found in Punkaharju, in south-eastern Finland (lat. 61°43′ N, long. 28°25′E, alt. 85 m). About 50 % of its offspring are characterised by a high stem wood productivity, reduced stem tapering, narrow crown and short thin branches with an insertion angle close to 90 degrees (Kärki 1985, Pöykkö 1993, Pöykkö & Velling 1993). However, poor stem straightness is typically observed in Kanerva pine, although this characteristic can be avoided by crossing Kanerva pine with other genetic entries possessing superior stem straightness. Different genetic entries may show different responses to silvicultural treatments (Velling 1988, Haapanen et al. 1997) depending on the environmental conditions of the site (Zobel & Talbert 1984). Therefore, the potential of different genetic entries, such as crossings of Kanerva pine with other genetic entries, as future regeneration material should be studied with sufficient spacing variation and under different site conditions.

1.2 Aims of the study

Relatively little is known about the simultaneous effects of genetic entry and spacing on the growth and yield traits, branch characteristics, wood density traits and fibre properties for Scots pine in Finnish conditions, because few experiments have been designed for this purpose. In the above context, this study investigated the effects of genetic entry (mainly full-sib families) and spacing on the growth and yield traits (e.g. tree height, breast height diameter, stem volume), branch characteristics (e.g. mean relative branch diameter, mean relative basal area of branches), wood density traits (e.g. mean wood density) and fibre properties (fibre length, fibre width and coarseness) in 20-year-old Scots pines. Additionally, the phenotypic variation within, and correlations between, different traits were studied, as well as the effects of cambial age, spacing, genetic entry and climatic variables, on the ring width and ring density development. Kanerva pine (Finnish plus tree S1101) was a father tree for the majority of the genetic entries included in this study, whereas their mother trees represented Finnish plus trees with a relatively wide geographical range from northern to southern Finland. More specifically, the main research tasks of the different papers were as follows:

i) Differences in growth and wood density traits of Scots pine genetic entries grown at different spacing and sites (Paper I).

ii) Differences in fibre properties of Scots pine genetic entries grown at different spacing and sites (Paper II).

iii) Differences in branch characteristics of Scots pine genetic entries grown at different spacing (Paper III).

iv) Radial growth and ring density development of Scots pine genetic entries under varying spacing treatments (Paper IV).

2 MATERIAL AND METHODS

2.1 Experimental data

The material used in this work was mainly based on a Scots pine spacing trial established in 1987 at Siilinjärvi (trial 1216/01) in central Finland (63°06’N, 27°41’E, 1100 degree days (d.d.), 85 m above sea level (a.s.l.)). The trial is located on agricultural soil and consists of three different spacings, with initial stand densities of 2000, 4000 and 8000-8200 seedlings/ha (referred later as site 1). When, in autumn 2000, the tending of the seedling stand was carried out, the widest spacing was left unmanaged (referred as spacing 1), the medium spacing was thinned to a stand density of 2000-2500 seedlings/ha (spacing 2) and the densest one to 4000 seedlings/ha (spacing 3).

In autumn 2006, 10 of 20 genetic entries (mainly full-sib families) were harvested from this trial for the study material for Papers I-II. They mainly represented different types of crossings of selected Finnish plus trees with a relatively wide geographical range in southern and central Finland. The selection of genetic entries was done so that the effect of one of the parents in the material (plus tree S1101, also called Kanerva pine, which was parent tree for 13 of 20 genetic entries) was not overestimated. In autumn 2008, additional material was harvested from this trial for Papers III-IV, including sample trees from 6 genetic entries, of which all had Kanerva pine (Finnish plus tree S1101) as a father tree, whereas the mother trees represented Finnish plus trees with a relatively wide geographical range from northern to southern Finland (Figure 1, Table 1).

Table 1. Genetic entries (GE) used in each study (Papers I-IV); trial sites 1 and 2, with their crossing type and the origin of the mother trees.

GE	Crossed trees	Papers	Trial	Crossing type	Origin of mother trees
1	StandardS12	I&II	1	Open pollination in forest stand	Central: Lieksa
2	StandardS13	I&II	1	Open pollination in forest stand	Central: Pihtipudas
3	C205xS1101	I&II	1&2	Controlled crossing	Central: Multia
4	C214BxS1101	I&II	1&2	Controlled crossing	Central: Äänekoski
5	S2582xS1101	I&II	1&2	Controlled crossing	South: Kuru
6	S104xS1101	I&II	1&2	Controlled crossing	South: Tammela
7	S104xC205	I&II	1	Controlled crossing	South: Tammela
8	C205xS80	I&II	1	Controlled crossing	Central: Multia
9	C214BxC205	I&II	1	Controlled crossing	Central: Äänekoski
10	SeedOrchardC97	I&II	1	Open pollination in seed orchard	Central: Varkaus Kuvansi
11	C205xS710D	I&II	2	Controlled crossing	Central: Multia
12	StandardSPM	I&II	2	Open pollination in forest stand	South: Pieksämäki
13	StandardS17	I&II	2	Open pollination in forest stand	South: Padasjoki
5 (3)*	C205 x S1101	III&IV	1	Controlled crossing	Central: Multia
6 (4)*	C214B x S1101	III&IV	1	Controlled crossing	Central: Äänekoski
9 (5)*	S2582 x S1101	III&IV	1	Controlled crossing	South: Kuru
10 (6)*	S104 x S1101	III&IV	1	Controlled crossing	South: Tammela
15	N1924 x S1101	III&IV	1	Controlled crossing	North: Taivalkoski
16	N334 x S1101	III&IV	1	Controlled crossing	North: Kemijärvi

*in parenthesis, it is shown the corresponding genetic entry numbers used in Papers I & II

Due to its thin and short branches, Kanerva pine was expected to behave, at least to some degree, in a different way than the other genetic entries of Scots pine, especially in narrow spacing. Altogether, five trees per genetic entry in each spacing were harvested in 2006 and 2008, i.e. a total of 145 and 90 sample trees, respectively.

In addition, material was harvested from another trial site established in 1988 at Loppi (trial 1241/2) in southern Finland (60°35'N, 24°27'E, 1250 (d.d.), 140 m a.s.l.) as additional study material for Papers I-II. This trial is located on a forest soil with relatively poor site fertility, Vaccinium type according to Cajander (1926). This type of forest in Finland typically is regenerated with Scots pine. In this trial (referred later as site 2), the seedlings were planted with an initial stand density of 2000 seedlings/ha. No pre-commercial thinning was done before the sample trees were harvested. When selecting the genetic entries on this site, the aim was to harvest the same ones that were harvested on site 1. However, only four of the same genetic entries could be found on these sites. Therefore only 7 genetic entries out of 44 were finally harvested from this site in autumn 2007 (Table 1). Meanwhile in site 2, five trees per genetic entry were harvested, i.e. a total of 35 trees (autumn 2007).

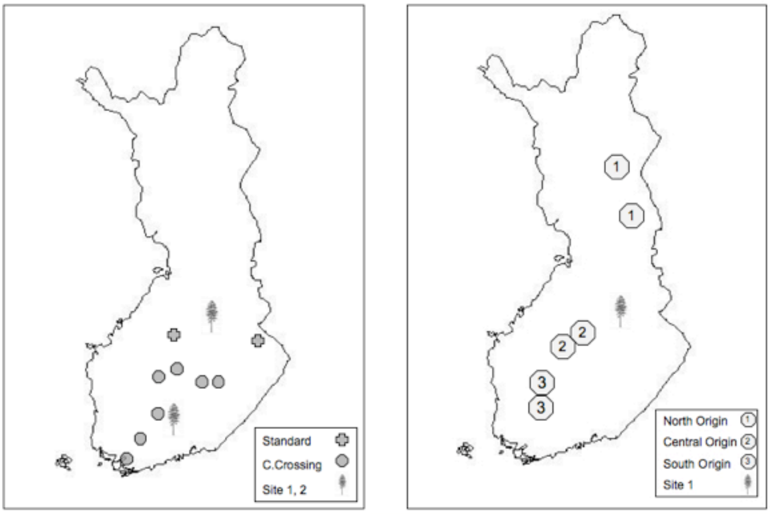

Figure 1. Location of all mother trees (Standard and controlled crossings) of the study material from site 1 for papers I-II (see left map, upper tree figure) and corresponding location of the mother trees crossed with Kanerva pine of the study material from site 1 for papers III-IV as grouped into different geographical origin groups 1-3 (see right map).

2.2 Field measurements

In the field, tree height and stem diameters (at 1.3 and 6 m from stem base) were measured for each sample tree (Papers I-IV). Stem volume was calculated based on volume functions developed by Laasasenaho (1982) for Scots pine. The branch measurements (Paper III) were taken every third whorl (i.e. whorls 2, 5 and 8 from top) and in each whorl only the main living branches were measured. The distance of each whorl from the tree top was determined. Altogether, the following branch characteristics were measured: i) branch diameter at one centimetre distance from stem insertion point (BD, mm); ii) branch length (BL, cm) and iii) branch insertion angle (BA, degrees) with an accuracy of 10º (i.e. 0º for vertical and 90º for perpendicular angle with the tree stem). Crown base height (CBH, cm) was defined as the lowest whorl having at least one living branch (green needles). Above the lowest living whorl all the main branches should be alive. Only living branches were considered, because pruning of dead branches had been carried out in the trial in winter 2005-2006, i.e. before harvesting this study material. Sample discs were cut at 1 m height from the stem base in each sample tree for detailed measurements of intra-ring growth and wood density traits and fibre properties (Papers I-IV).

2.3 Laboratory measurements

The intra-ring growth and wood densities were measured (Papers I-IV) using the ITRAX X-ray microdensitometer (Cox Analytical Systems, Göteborg, Sweden) at the University of Eastern Finland, Faculty of Science and Forestry, School of Forest Sciences (see Peltola et al. 2007). For this purpose, rectangular wood specimens of 5 mm x 5 mm size (radial segment from pith to bark, northern direction) were cut out of the stem discs (at 1 m above ground) and then stabilised for a few weeks until they had a moisture content of 12 % (air dry). Thereafter, they were scanned in batches using the ITRAX (with standard X-ray intensity 30 kV, 35 mA, exposure time of 20 ms) to produce X-ray images with a geometrical resolution of 40 measurements per mm.

The X-ray images were analysed with the Density software program (Bergsten et al. 2001) to determine intra-ring density profiles for each wood specimen from pith to bark (see Figure 2). Based on these density profiles and with the help of Excel macros, the following intra-ring variables were determined: ring width (RW, mm), earlywood and latewood width (EWW and LWW, mm), mean wood density (WD, g/cm^3), minimum and maximum wood densities (g/cm^3) as well as earlywood and latewood density (EWD and LWD, g/cm^3). Similar to previous work on Scots pine, the mean of the maximum and minimum intra-ring densities were used as the threshold between earlywood and latewood for each ring (see Peltola et al., 2007; Helama et al. 2008). Based on intra-ring measurements from pith to bark, the cross-sectional averages for growth and wood density traits for each sample tree was determined.

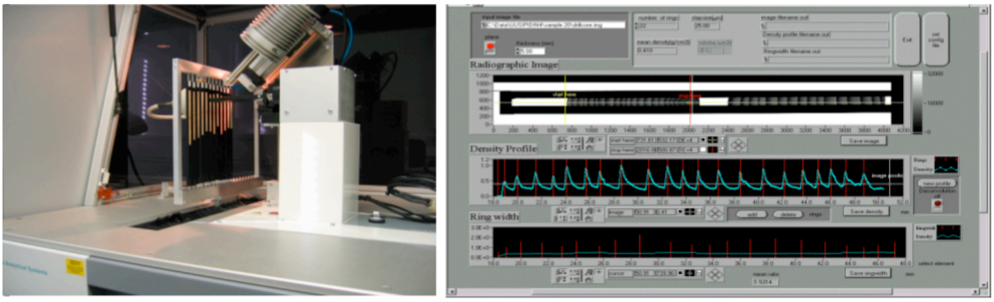

Figure 2. ITRAX microdensitometer (left) and Density software program (right).

For the intra-ring analysis of fibre properties (Paper II), matchstick-sized wood specimens (for 2 annual ring pairs) were chipped away from the stem discs (taken at 1 m above the stem base) and then macerated in a boiling 1:1 (v/v) mixture of acetic acid and hydrogen peroxide. Thereafter, fibre length (FL, mm) and fibre width (FW, μm) were measured using the L&W Fibre Tester (AB Lorentzen & Wettre, Kista, Sweden) based on image analysis (see Figure 3).

In the fibre measurements, the highly diluted suspension flows between the narrow space of two glass plates, which limits the possibility of the fibres moving in one direction, but allows them to move freely in the other two directions. The two-dimensional images permit the measurement of fibre length and deformations separately. The use of the L&W Fibre Tester makes it possible to observe a large number of fibres for each sample in a few minutes (i.e. up to tens of thousands of fibres). It provides, in addition to mean values, the distributions of fibre properties as classified in different fibre length classes (e.g. <0.2 mm, 0.2-0.5 mm, 0.5-1.0 mm, etc.). Based on dry weight of the sample and total length of fibres measured, coarseness (C, μg/m) could also be calculated as a fibre mass per unit fibre length of the sample (see Karlsson, 2006). Based on intra-ring measurements from pith to bark for different fibre properties, cross-sectional averages were also determined for each sample tree.

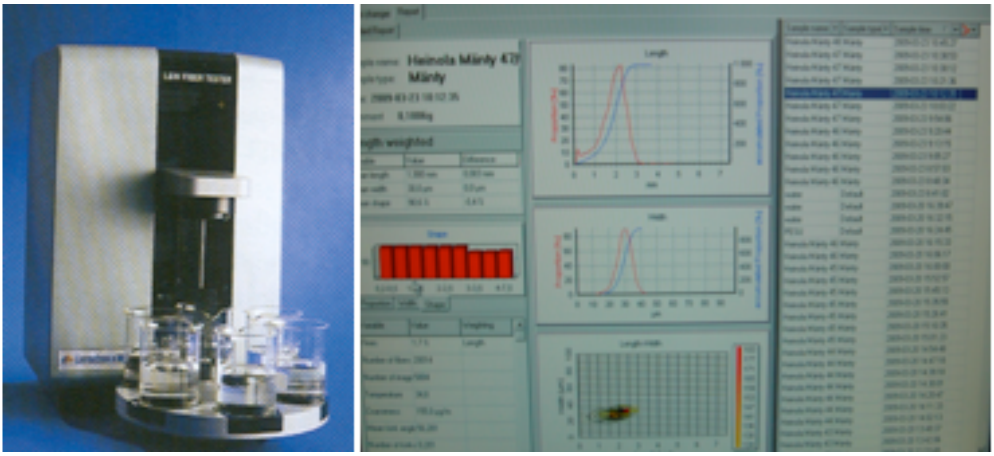

Figure 3. L&W Fibre Tester (left) and software output (right).

2.4 Data Analysis

Differences in growth and yield traits (Papers I, III), branch characteristics (Paper III), wood density traits (Paper I) and fibre properties (Paper II) between genetic entries / origin groups (Kanerva pine crossings grouped into southern, central and northern ones) were tested in each spacing with a one-way ANOVA (with a Tukey pairwise test, $p<0.05$). To test the simultaneous effects of genetic entry/origin group and spacing (also site effects in Papers I-II), a two-way ANOVA was applied.

The phenotypic coefficient of variation (CV %) was calculated for each variable, separately for each genetic entry and as an average, for each spacing and site. Relationships between the different traits (see Table 2) were examined using phenotypic correlations (Pearson's correlation method, $p<0.05$). The phenotypic correlations were calculated instead of genetic ones, because the relatively small number of genetic entries and replicates (sample trees) available for each spacing (and site) did not support the calculation of genetic correlations (see e.g. Klein et al. 1973, Hannrup et al. 2000). All these statistical analyses were made using the SPSS (SPSS for Windows, versions 15.0 and 16.0, SPSS, Chicago, IL).

Table 2. Different traits and variables used in different statistical analyses. Short names of variables are explained in Abbreviations.

Traits	Variables	Statistical analyses
Yield	H, DBH, Volume	Phenotypic variation within/between genetic entries (Paper I)
		Phenotypic correlations between yield traits and other traits (Papers I & III)
		Effects of genetic entry, spacing and site (Paper I)
Growth	RW, EWW, LWW, LWW%	Phenotypic variation within/between genetic entries (Paper I)
		Phenotypic correlations between growth traits and other traits (Paper I)
		Effects of genetic entry, spacing and site (Paper I)
		Effects of cambial age, genetic entry/origin group, spacing and climatic variables on RW development (Paper IV)
Branch characteristics	NLB, RCBA,RABD	Phenotypic variation within/between genetic entries (Paper III)
		Phenotypic correlations between branch characteristics and other traits (Paper III)
		Effects of branch age, genetic entry/origin group and spacing (Paper III)
Wood density	RD, EWD, LWD	Phenotypic variation within/between genetic entries (Paper I)
		Phenotypic correlations between wood density traits and other traits (Paper I)
		Effects of genetic entry, spacing and site (Paper I)
		Effects of cambial age, genetic entry/origin group and spacing on RD development (Paper IV)
Fibre properties	FL, FW, C	Phenotypic variation within/between genetic entries (Paper II)
		Phenotypic correlations between fibre properties and other traits (Paper II)
		Effects of genetic entry, spacing and site (Paper II)

Mixed modelling was applied to study the effects of spacing, genetic entry/origin group and branch age on the average branch diameter and branch angle (Paper III). This approach allowed taking into account the hierarchical structure of the measurements (Mäkinen & Colin 1998) controlling the source of variation inside clusters (whorls of individual trees) and between them (spacing and genetic entry or origin group). A mixed model was also fitted to the RW and RD data in order to determine which factors (e.g. cambial age, genetic entry/origin group, spacing and climatic variables) could best explain the annual variability in RW and RD and their development from pith to bark (Paper IV). The full model for observed RW or RD of tree i in stand k in a given year t consists of the following components, $R_{kit}=A_{kit}+S_k + OG_k + a_t + b_{ki} + e_{kit}$, where R_{kit} is the observed response for tree i in origin group k at year t, A_{kit} is the trend related to the (cambial) age of the tree, S_k is the fixed spacing effect, OG_k is the fixed effect of the origin group, a_t is the random effect of calendar year, b_{ki} is the random tree effect and e_{kit} is the unexplained residual variation. The age trend was modelled using a restricted cubic spline regression (Harrell 2001). The mixed model was first used to test the statistical significance of the fixed effects of spacing and origin group on the response. Secondly, it was used to extract the year effects in order to study their correlation with climatic variables. The climatic variables tested were average temperatures for the months January to December, monthly precipitation sums from January to December and temperature sum (i.e. sum of temperatures over +5°C) during the current growing season (for May-September). A one-way ANOVA was used to determine which climatic variables (provided by the Finnish Meteorological Institute, for the nearby Kuopio meteorological station) reveals statistically significant differences between the years 1991-2007 (i.e. for years with ring data available).

3 RESULTS

3.1 Effects of genetic entry/origin group and spacing on different growth and yield traits

A relatively large phenotypic variation is observed for the yield traits over the 10 genetic entries representing either open pollinated forest stand seed, orchard seed material or controlled crossings, regardless of spacing and site (Paper I). Spacing significantly ($p<0.05$) affects all the yield traits (H, DBH and V) and mean ring width (RW) on site 1 (see Table 3 below, Paper I). In spacing 3 (with current stand density of 4000 trees/ha), DBH and V are, on average, 15-16 % and 20 % smaller, respectively, but H is 5-7 % higher compared to spacing 1 and 2 (with current stand densities of 2000 and 2000-2500 trees/ha, Paper I). H is also affected, regardless of spacing, by the genetic entry and/or origin group (Paper I and III). The central origin group shows the highest H on average (for spacing 1 and 2, $p<0.05$) (Paper III). Site affects also DBH ($p<0.05$) for the four genetic entries grown on both sites (Paper I).

Genetic entry 10 has the largest RW (9 % larger than average) on site 1 in spacing 1 (Paper I). In spacing 2, genetic entry 5 has the largest RW (10 % above average), whereas, in spacing 3, genetic entry 1 has the largest RW (17 % above average). Genetic entry 4 has the largest RW (10 % higher than the average) on site 2 (Paper I). On site 2, the average RW is similar as in the same spacing on site 1.

Since the year 1995, spacing affects ($p<0.05$) mean RW development on site 1, i.e., mean RW is thereafter, on average, lower ($p<0.05$) for the narrowest spacing 3 (current stand density of 4000 trees/ha) compared to others (spacing 1 and 2 with current stand density of 2000-2500 trees/ha) (Paper IV). The pre-commercial thinning in the year 2000 in spacing 2 and 3 and the pruning of branches in the lower stem height, regardless of spacing, (in winter 2005-2006) are increasing ring width (the most in spacing 2). In general, the mean RW decreases as cambial age increases regardless of spacing and origin group. However, it starts slightly earlier in the densest spacing. In the year 2002, an increase in the mean RW can be observed regardless of spacing and origin group. In this work, RW development could be explained, in general, by the linear mixed model with cambial age, spacing, and random "Tree" and "Year" effects as explanatory variables (Paper IV). However, the year effects (residuals) of RW did not correlate well with any of the climatic variables considered.

3.2 Effects of genetic entry/origin group and spacing on different branch characteristics, wood density traits and fibre properties

Opposite to genetic entry, spacing does not affect ($p<0.05$), in general, wood density traits (Paper I, see also Table 3 below). However, when only considering Kanerva pine crossings (Paper III), the mean wood density (WD) is affected by spacing and origin group. The southern origin group shows, on average, the lowest mean WD, regardless of spacing. Additionally, spacing affects all the fibre properties (Paper II).

On site 1, genetic entry 2 has, on average, the highest mean WD (7 % higher than average of all genetic entries) in spacing 1 (Paper I). Genetic entry 4 has the highest mean WD in spacing 2 (6 % higher than average) and genetic entry 3 (7 % higher than average) in spacing 3. Site also affects the earlywood density (EWD) and WD ($p<0.05$) for the four genetic entries grown on both sites (Paper I). Thus, the ranking between genetic entries changes, depending on the trait, spacing or site considered.

Several branch characteristics, such as the total number of living branches (NLB), relative living crown base height (RCBH) and relative cumulative cross-sectional branch area (RCBA) are significantly ($p<0.05$) affected by spacing (Paper III, see Table 3 below). In spacing 2, the NLB is, on average, 9 and 17 % higher than in spacing 1 and 3, respectively. Furthermore, RCBA is, on average, 23-46 % lower and RCBH 5-8 % higher in spacing 3 than in spacing 1 and 2. Average branch characteristics such as NLB, relative average branch diameter (RABD) and RCBA are also affected by the origin group (Paper III). The average branch diameter (ABD) along the stem is also affected by the spacing, branch age (whorl) and origin group (Paper III). As a comparison, the average branch angle (ABA) along the stem is affected by the branch age (whorl) and genetic entry or origin group. The southern origin group has the lowest RABD, regardless of spacing. For ABD and ABA, the northern origin group differs significantly from the southern one. Furthermore, the spacing x genetic entry interaction affects EWD, whereas site x genetic entry interaction and spacing x origin group interaction affects the fibre length (FL) and NLB, respectively.

In this work, RD development could be explained, in general, by the linear mixed model with cambial age, spacing, origin group (OG) and random "Tree" and "Year" effects, as explanatory variables. However, only the mean temperature for June and the degree days correlated with the year effect (residuals) of the model for RD ($p<0.05$).

Table 3. Analysis of variance on the effects of genetic entry (GE), origin group (OG) and spacing (S), and their interaction (spacing x genetic entry and spacing x origin group) on different growth and yield and wood density traits, fibre properties and branch characteristics on site 1. Statistically significant effect ($p<0.05$) is shown by X, no effect by O and not studied by (-).

Variables	Dataset 1 (Papers I & II); site1			Dataset 2 (Papers III & IV); site1				
	S	GE	S x GE	S	GE	OG	S x GE	S x OG
DBH	X	O	O	X	O	O	O	O
H	X	X	O	X	X	X	O	O
V	X	X	O	X	O	O	O	O
WD	O	X	O	X	O	X	X	O
EWD	O	X	X	-	-	-	-	-
LWD	O	X	O	-	-	-	-	-
EWW	X	O	O	-	-	-	-	-
LWW	O	O	O	-	-	-	-	-
RW	X	O	O	-	-	-	-	-
FL	X	O	X	-	-	-	-	-
FW	X	O	O	-	-	-	-	-
C	X	O	O	-	-	-	-	-
NLB	-	-	-	X	O	X	O	X
RCBA	-	-	-	X	O	X	O	O
RABD	-	-	-	O	O	X	O	O
ABA	-	-	-	O	O	O	O	O

3.3 Phenotypic correlations between different traits

DBH does not correlate significantly ($p<0.05$) with H (Paper I, II). However, V and DBH show a strong correlation ($p<0.05$) with earlywood width (EWW) and moderate to strong (from site 1 to 2) correlation with latewood width (LWW) (all positive). On site 1, V and DBH have a weak negative correlation with mean WD and EWD ($p<0.05$). The correlations between DBH and V with fibre width (FW) are also positive on both sites ($p<0.05$), while the correlation (also positive) between DBH and coarseness (C) is significant only on site 1 (Paper II). WD also shows a low positive correlation on site 1 with FW and C ($p<0.05$) (Paper I). DBH and V correlate also with all branch characteristics (excluding V with average branch angle, ABA). On the contrary, H correlates only with the relative average branch diameter (RABD). Furthermore, the correlation between DBH with number of living branches (NLB) is moderate and positive, whereas between DBH and relative crown base height (RCBH) it is moderate, but negative ($p<0.05$).

RW correlates positively with EWW and LWW ($p<0.05$) and negatively and moderately with mean WD and weakly (negative correlation) with EWD and LWD (Paper I). Additionally, a negative moderate phenotypic correlation exists between mean WD and EWW and between EWW and EWD ($p<0.05$). Moderate to strong and positive correlations are also observed among all wood density traits (Paper I). When considering only the Kanerva pine crossings, the correlations between WD and DBH and V are negative ($p<0.05$) (Paper III). The correlations observed between different fibre properties (FL, FW and C), show, on average, also strong and positive correlation ($p< 0.05$) on both sites (Paper II).

Table 4. Phenotypic correlations (positive: **+**; negative: **-**; no significant correlation: 0, significance p<0.05) between different growth and yield traits (H, DBH, V, EWW, LWW, LWW%, RW), wood density traits (WD, EWD, LWD), fibre properties (FL, FW, C) and branch characteristics (NLB, RABD, RCAB) over all genetic entries. Dataset 1 (Papers 1 and 2) is shown bottom left (site 1) and dataset 2 (Papers 3 and 4) top right.

	H	DBH	V	NLB	RABD	RCBA	ABA	RW	EWW	LWW	LWW%	WD	EWD	LWD	FL	FW	C
H	x	0	+	0	-	0	0					0					
DBH	+	x	+	+	-	+	+					-					
V	+	+	x	+	-	+	0					-					
NLB				x	-	+	+					0					
RABD					x	+	-					0					
RCBA						x	-					0					
ABA							x					0					
RW	+	+	+					x									
EWW	+	+	+					+	x								
LWW	+	+	+					+	+	x							
LWW%	0	0	0					0	-	+	x						
WD	0	0	0					-	-	+	+	x					
EWD	0	0	0					-	-	0	0	+	x				
LWD	+	0	0					-	-	0	0	+	+	x			
FL		0	0									0			x		
FW		+	0									0			+	x	
C		+	0									+			+	+	x

Among the branch characteristics, number of living branches (NLB) correlates negatively with relative crown base height (RCBH) and positively with average branch angle (ABA) (Paper III). Relative average branch diameter (RABD) and relative cumulated branch area (RCBA) also correlate negatively with ABA (p<0.05). RABD correlates negatively with H, DBH and V. Furthermore, RCBA is positively correlated with DBH and V. However, most of these correlations are moderate or low.

4 DISCUSSION AND CONCLUSIONS

4.1 Effects of genetic entry/origin group and spacing on growth and yield traits

In this work, the growth and yield traits of different genetic entries of Scots pine showed, in general, significantly higher phenotypic variation than the wood density traits and fibre properties regardless of spacing or site (Papers I and II). This is in agreement with previous corresponding findings for Scots pine and Norway spruce (e.g. Persson 1972, Velling 1974, Hannrup et al. 2004, Fries & Ericsson 2006, Zubizarreta-Gerendiain et al. 2007, 2008, Fries & Ericsson, 2009). The higher variability in growth and yield traits implies that these traits are under poorer genetic control compared to wood density and fibre properties. They are also strongly affected by the environmental conditions and competition between trees (Zhang & Morgenstern 1995, Hannrup et al., 2000). Similar to this work (Paper I), Persson et al. (1995) and Hannrup et al. (1998) reported that wider spacing increased DBH and stem volume at the cost of height growth in Scots pine. In addition, Ståhl (1988) found that average ring width was larger for wider spacing in Scots pine, as a result of relatively larger earlywood percentage. In this work, site significantly affected DBH and genetic entry affected tree height (Paper I).

Initial spacing, tending of the seedling stand and thinning can be used to control the growth, mortality and self-pruning of branches, especially in the most valuable lower part of the stem in tree species like Scots pine (Kellomäki et al. 1999). However, because the growth of the stem and branches correlates strongly (and positively) in Scots pine, branch size could usually be reduced at the expense of total tree growth (e.g. Mäkinen & Colin 1998, Mäkinen 1999a). On the other hand, different genetic entries may show differences in their stem growth and branch characteristics, which was found previously in Scots pine (e.g. Velling 1988, Haapanen et al. 1997). Also in this work, it was expected, in general, that both spacing and genetic entry / origin group affect different traits, and that there may exist differences between individual Kanerva pine crossings. However, in this work only spacing affects all the yield traits ($p<0.05$), not genetic entry or origin group (Papers I and III).

Contradictory to this work, Persson et al. (1995) found differences in stem volume between different genetic entries of Scots pine (5 genetic entries were compared). In this work, the diameter at breast height (DBH) and stem volume (V) are, on average, the highest in the two widest spacings (1 and 2) on site 1 (having practically the same stand density after the tending of seedling stand). As a comparison, the average tree height (H) is the highest in the narrowest spacing (Paper I). Regardless of spacing, the central origin group shows the highest H (Paper III), which might be because they were growing in a field experiment with similar climatic conditions compared to where they originated.

In this work, it was observed that in the year 2002, which had the highest temperature sum over the growing season (from May to September), an increase in the mean RW can be seen regardless of spacing and origin group (Paper IV). Furthermore, May 2002 was the warmest month over all these years studied. Despite this, the climatic variables considered did not significantly explain RW variation during the study period as cambial age, spacing and origin group did (Paper IV). However, this result may be due to a too short time period used for such analyses. Fries et al. (1998) found that the climatic variables had stronger effect on growth on less fertile sites than that represented by site 1 in this work (being a more fertile former agricultural site).

4.2 Effects of genetic entry/origin group and spacing on branch characteristics and wood properties

In this work, the mean WD of the 10 genetic entries, representing either open pollinated forest stand seed, orchard seed material or controlled crossings, is not affected significantly ($p<0.05$) by spacing (Papers I and III). However, the fact that EWD and LWD are, to some degree, lower, and LWW % higher in the densest spacing, could explain this result. In previous studies for Scots pine, the mean WD was not affected by the growth rate at a relatively young age (Persson et al. 1995). This was despite the fact that in Scots pine, in general, WD correlates strongly with LWW % (Hannrup et al. 2001). In this work, genetic entry significantly affects the wood density traits on both sites, unlike spacing (Papers I and II). Persson et al. (1995) found differences among genetic entries for wood density traits, but opposite to this work (Paper I) also spacing affected those traits. However, when considering only Kanerva pine crossings, in this work spacing significantly affected mean WD in addition to origin group (Paper III). The northern origin group has, on average, the highest WD, regardless of the spacing. This result is in line with previous findings where northern provenances when transferred to the south had, on average, higher WD than the local ones (Ståhl & Ericson 1991). Likewise, Zubizarreta-Gerendiain et al. (2007, 2009) observed differences for WD among origin groups and/or genetic entries in Norway spruce grown in southern Finland.

Similar to this work Persson et al. (1995) observed that spacing affected the fibre length (see Paper II). However, they found, contrary to this work (for site 1) (Paper II), that genetic entry also affected FL. In this work, on site 2, the average fibre properties are comparable to those observed on site 1 with similar spacing 1 (Paper II). In this work site also affects all fibre properties ($p<0.05$), while genetic entry affects FL (Paper II, table 4). In accordance with these results, Ståhl (1988) found that, for Scots pine, site significantly affects both FL and tree height. Additionally, Persson et al. (1995) found that FL and FW increased with increasing spacing. However, this tendency is not found in the present study even though spacing affects both FL and FW.

The relative values for living crown base height (RCBH), cumulative cross-sectional branch area (RCBA) and number of living branches (i.e. NLB) are affected by spacing ($p<0.05$) (Paper III), opposite to RABD as DBH and branch size will change simultaneously. In the narrowest spacing, RCBA (in whorls 2, 5 and 8) is lower than in the two widest ones. This is in line with the findings of Kellomäki and Tuimala (1981), i.e. the branch cross sectional area per stem unit is negatively correlated with the stand density. This result could be explained by the fact that the dynamics of crown development (and thus, branches) depends on the light available in the lower canopy (Kellomäki et al. 1999). Branch characteristics, such as relative average branch diameter (RABD) and relative cumulative cross-sectional branch area (RCBA), are important factors from the point of view of timber quality. In this work, they are both affected by the origin group (Paper III); for example the northern origin group has, on average, the highest RABD, RCBA and DBH.

The differences observed in the average diameter of living branches (ABD) along the stem (between whorls 2 and 8) could be explained by the branch age, spacing and origin group (Paper III). The narrowest spacing has less light interception especially in the lower crown, reducing the growth rate of the lowest branches, compared to the wider spacing (e.g. Kellomäki & Oker-Blom 1983). Average branch angle (ABA) could be explained by the branch age and genetic entry/origin group (Paper III). The ABD and ABA from the northern origin group differ clearly from the others. In previous studies for Scots pine (Haapanen et al. 1997, Hannrup et al. 2000), the heritability estimates have also been considerably lower for branch characteristics. Thus, they are more influenced by the environmental conditions (e.g. availability of light) and silvicultural management such as spacing, being, thus under poor genetic control like growth and yield traits. In this work, spacing affected, in general, more clearly the yield traits, fibre properties and branch characteristics than genetic entry did. Furthermore, in general, no genetic entry-spacing interaction was observed (excluding some variables, see Table 3). These results are in line with previous findings observed by Fries (1984) for Scots pine at the same age.

4.3 Phenotypic correlations between different studied traits

In this work, it was found that the phenotypic correlations between different growth and yield traits show moderate to strong positive correlations on both sites, on average (Paper I). However, they vary between sites. These findings are in line with previous findings for different coniferous species, based on the calculation of either phenotypic or genetic correlations (Campbell et al. 1986, Zhang et al. 1996, Hannrup et al. 2004). Similarly, this work found from moderate to strong positive phenotypic correlations among different wood density traits, which reveals limited opportunity for the improvement of intra-ring uniformity for wood density (see e.g. Donaldson et al. 1995, Zhang & Morgenstern 1995). In this study, mean wood density showed a weak negative correlation ($p<0.05$) with growth and yield traits (DBH and V), when considering only the Kanerva pine crossings (Paper III). Previously, Haapanen et al. (1997) and Hannrup et al. (2000) have reported, in Scots pine, weak negative phenotypic and genetic correlations between wood density of juvenile wood and DBH. Fries and Ericsson (2006, 2009) have recently reported also negative genetic correlation between wood density and DBH in Scots pine. However, even a non-significant or a weak positive relationship between wood density and growth has been observed previously in Scots pine (Mörling 2002) and lodgepole pine (Wang et al. 2000), for example. This was found to be the case, in general, for all materials used in Papers I and II, in which genetic entries ranged from open pollinated forest stand seed to orchard seed material and controlled crossings. However, if significant genetic correlations among various growth, yield and wood density traits exist, selection for one trait would simultaneously affect the other traits.

Compared to other fibre properties, fibre width (FW) generally shows, in this work, significantly lower phenotypic variation regardless of spacing or site, which is in agreement with the previous findings for Scots pine (Hannrup et al. 2001) and other coniferous species like Norway spruce (Hannrup et al. 2004; Zubizarreta-Gerendiain et al. 2007). The moderate to low variability in fibre properties indicates that these traits are under a moderate genetic control and are, therefore, less affected by the environment and competition between trees (Hannrup & Ekberg 1998, Ståhl 1988, Hannrup et al. 2001). In this work, phenotypic correlations among the fibre properties (as an average of all genetic entries) are, on both sites, positive and from moderate to strong, with the strongest correlation being between FW and C (Paper II). These results suggest that the same sets of genes are likely to be responsible for controlling the different fibre properties (Zobel & Jett 1995). These results are in agreement with previous studies for other pine species such as Maritime pine (*Pinus pinaster*) (Pot et al. 2002), as well as other coniferous species such as Norway spruce (Zubizarreta-Gerendiain et al. 2008).

On the contrary, in this work no clear phenotypic correlation is obtained between fibre properties and V or between fibre properties and DBH. Ericsson and Fries (2004) also did not find any positive correlation between H or DBH and FL in Scots pine. In previous work on Scots pine, a positive correlation was obtained between FL, H and DBH (Ståhl 1988, Hannrup & Ekberg 1998, Hannrup et al. 2000). In general, in this study, a weak positive, but not consistent correlation is obtained between FL and WD. As a comparison, Hannrup et al. (2001) observed for Scots pine a positive weak correlation between WD and FL for juvenile wood, but a negative or even non-existent correlation in mature wood. In other pine species, such as Maritime pine or Radiata pine (*Pinus radiata*) negative genetic correlations have been observed between WD and FL (Nyakuengama 1999, Pot 2002).

Furthermore, in this work WD correlates negatively with DBH and V, which agrees with previous studies in Scots pine, as well as other coniferous species (e.g. Hannrup et al. 2000, Kang et al. 2004, Zubizarreta-Gerendiain et al. 2007). RABD correlates negatively with H, DBH and V, whereas RCBA correlates positively with DBH and V, but not with H. In the same way, Haapanen et al. (1997) found that DBH and average branch diameter showed a reasonably high positive correlation. However, many of the correlations of yield traits with branch characteristics and among branch characteristics are from low to moderate, although they are significant in this work ($p<0.05$). The phenotypic correlations between WD and branch characteristics are close to zero, and in many cases non-significant in this work, which is in agreement with previous findings, for example, by Hannrup et al. (2000). In general, only a few studies are available that examine the phenotypic or genetic correlations between yield and stem quality traits and average wood density in Scots pine (Haapanen et al. 1997, Hannrup et al. 2000). These studies have also reported no, or weak negative, genetic/phenotypic correlations between traits such as branch angle, branch thickness, number of branches, stem straightness and average wood density.

Compared to the previous work reported by Zubizarreta-Gerendiain et al. (2007, 2008, 2009) for different Norway spruce clones grown in southern and central Finland, in this work it was observed, on average, less variation in different traits between different genetic entries in Scots pine (for same spacing and site). This result may, at least partly, be explained firstly because Scots pine and Norway spruce have differences in their responses to environmental conditions and secondly Kanerva pine was father of about 80 % of this study material (consisting also of mainly full-sib families). The latter limits, to some degree, the generalization of findings.

4.4. Conclusions

A future challenge for forestry is to identify the most suitable tree species / genetic entries and their site-specific management in order to supply, both in a sustainable and economic way, a large quantity of uniform raw material for different products by the forest industry. In the future, Scots pine may also be preferred on those less fertile sites currently occupied by Norway spruce, if latter suffers drought in southern Finland under the changing climate (Kellomäki et al. 2005). Therefore, identification of the potential offered by different genetic entries of Scots pine, including Kanerva pine crossings, as future regeneration material is of primary importance.

This work is the first attempt to provide such detailed information on the simultaneous effects of genetic entry and spacing on growth, yield and wood density traits and fibre properties of Scots pine in Finnish conditions. As a result, it was found that spacing especially affects, in general, yield and wood density traits and fibre properties as well as branch characteristics, while genetic entry and origin group affect several traits. However, contrary to expectations, significant differences did not exist for different traits between other genetic entries and Kanerva pine (plus tree S1101) crossings. It was also observed that growth and yield traits are, in general, positively correlated to each other. Similarly, the branch growth could be limited only at expense of DBH growth. Furthermore, all wood density traits are positively correlated with each other as well as fibre properties with each other. However, negative phenotypic correlations observed between growth, yield and wood density traits suggest that selection for one trait would simultaneously affect the other traits.

It would have been interesting to also consider the effects of spacing and genetic entry/origin group on characteristics of dead branches and their presence in the lower crown, but unfortunately this was not possible due to an earlier pruning of dead branches. One other limitation of this work is that despite the large amount of wood samples that were measured they only represented one relatively low height along the stem due to the relatively young age of the experimental trials. Additionally, the number of replicates for each genetic entry, as well as the number of genetic entries (and sites) used in comparison were limited in this work, which restricts the generalization of findings.

In the future, it may become necessary to balance the gain / loss between the quantity and quality of raw material, considering the final target of wood production (e.g. pulp wood or sawn timber products). It may be possible to identify some genetic entries that could be suited to particular product types or processes (Ridoutt et al. 1998). However, giving preference, for example, to the fibre characteristics probably will not be a first option in the future, if considering long term breeding goals (Ericsson & Fries 2004). Breeding for high biomass production or yield and quality of pulp and wood products definitely requires detailed knowledge of the genetic parameters for different wood properties in the breeding population before including these traits in the breeding programs (Fries & Ericsson 2006). This provides that, for example, genetic correlations should be calculated between different traits interested and based on enough large number of genetic entries and replicates.

In this work, the ranking of genetic entries varied depending on trait, but also depending on spacing for the same trait. As it may also change over time (e.g. related to canopy closure), the genetic entry x spacing and genetic entry x site interactions should be studied over a sufficiently long time period. Furthermore, other important wood properties such as microfibril angle and wood stiffness, should be considered in future research as well as how different properties change along the tree stem. Such information is crucial for breeders considering different traits as possible additional selection criteria for tree breeding. Such material is also useful for comparison with open pollinated stand material. This kind of information is also urgently needed in order to move towards a more intensive management (and value-added wood utilization), but still considering the ecological, economical and socio-economical dimensions of sustainable management.

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