SILVA FENNICA

Silva Fennica 43(3) research articles

www.metla.fi/silvafennica · ISSN 0037-5330
The Finnish Society of Forest Science · The Finnish Forest Research Institute

Differences in Fibre Properties in Scots Pine (*Pinus sylvestris* L.) Genetic Entries Grown at Different Spacing and Sites

Jaume Gort, Ane Zubizarreta Gerendiain, Heli Peltola, Pertti Pulkkinen, Johanna Routa and Raimo Jaatinen

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.

In forest breeding, stem volume growth and sawn timber quality indicators have been used as the most important selection traits for Scots pine, whereas less attention has been given to characteristics such as fibre properties. In the above context, we investigated the differences in fibre properties (i.e. fibre length, fibre width and coarseness) in 20 year old Scots pine (*Pinus sylvestris* L.) genetic entries as affected by spacing and site, but also the phenotypic correlations between fibre properties, yield and wood density. The study was based on materials harvested from 10 genetic entries grown in a spacing trial (site 1) in central Finland, with a current stand density of 2000 (spacing 1), 2000–2500 (spacing 2) and 4000 trees/ha (spacing 3). In order to study the effects of site, we harvested additional material (4 of 7 genetic entries same as on site 1) from a trial located in southern Finland with a corresponding stand density of 2000 trees/ha (site 2). On site 1, spacing 1 and 3, all average values for analysed fibre properties were similar. In spacing 2 average values were slightly higher. On site 2, the average values for different fibre properties were similar compared to the corresponding spacing 1 on site 1. Spacing affected ($p<0.05$) all average fibre properties on site 1; as did also site, when comparing same genetic entries grown on both sites. Regardless of spacing and site, the phenotypic correlations between average fibre length, fibre width and coarseness showed, on average, moderate to strong correlation ($p<0.05$). Fibre width showed, in general, low and positive phenotypic correlation with diameter at breast height, stem volume and wood density on site 1. However, as a whole, the ranking of genetic entries changed depending on the trait and spacing considered. Thus, no overall ranking between genetic entries was possible.

Keywords genetic entry, growth, wood density, fibre length, fibre width, coarseness, spacing
Addresses *Gort, Zubizarreta Gerendiain, Peltola* and *Routa*, University of Joensuu, Faculty of Forest Sciences, FI-80101 Joensuu, Finland; *Pulkkinen* and *Jaatinen*, Finnish Forest Research Institute, Haapastensyrjä Breeding Station, Karkkilantie 247, FI-12600 Läyliäinen, Finland
E-mail jaume.gort@joensuu.fi
Received 2 June 2008 **Revised** 10 December 2008 **Accepted** 2 June 2009
Available at http://www.metla.fi/silvafennica/full/sf43/sf433355.pdf

1 Introduction

Both quantity and properties of stem wood affect the suitability of trees as a raw material for the pulp and paper industry. For example, wood density affects the pulp yield, while many pulp properties are largely determined by the properties of the fibres (Zobel and Buijtenen 1989, Karlsson 2006). Relatively small variations in these properties affect also the sustainability of the pulp and paper manufacturing processes (e.g. energy needed) and the properties of the final products (Tyrväinen 1995, Chambers and Borralho 1999). Despite of this, stem volume production and sawn timber quality have typically been used as the most important selection traits in long-term breeding programmes in tree species like Scots pine (*Pinus sylvestris* L.) grown in Scandinavia, whereas other property traits such as wood density and fibre properties have been considered as secondary traits (Haapanen and Pöykkö 1993, Hannrup et al. 2000). On the other hand, this could be partly explained by the fact that Scots pine has been in the past the most important raw material for sawn timber industry, while its use for the pulp and paper industry has been increasing recently.

In general, the fibre properties and wood density of Scots pine, like in other conifers, are affected both by the growth rate and ageing of the cambium (Hannrup et al. 2000, 2004). The effects of the growth rate on these properties are also higher in relatively young trees, i.e. at juvenile phase and within first 10–15 annual rings from pith, where the values of these properties change most rapidly from the pith to bark (Björklund and Walfridsson 1993, Zobel and Jett 1995, Hannrup and Ekberg 1998). Therefore, by controlling the growth rate of trees within tree stands in the early phase of the rotation by, for instance, initial stand density and pre-commercial thinning, it could be affected the properties of trees as well (Persson et al. 1995). In fact, wider spacing has previously shown to considerably accelerate the growth of trees, and consequently affect the properties of wood in tree species such as Scots pine (see e.g. Persson et al. 1995), jack pine (*Pinus baksiana*) (Kang et al. 2004) and Norway spruce (*Picea abies*) (Pfister et al. 2007). For example, Persson et al. (1995) observed that among genetic entries in Scots pine, the fibre length increases with increasing spacing along with increase in growth of trees. Contradictorily, Persson (1975) and Ståhl (1988) did not found any spacing effect on fibre length in Scots pine. On the other hand, the fact that fibre characteristics are affected simultaneously both by the cambium aging and the distance from pith to bark (as affected by radial growth), could partly explain these contradictory findings (see Ikonen et al. 2008).

In addition to silvicultural treatments, tree breeding could offer means to affect the growth, yield and properties of trees as well. Furthermore, tree selection could be successful even in reasonably young trees (Zobel and Buijtenen 1989, Hannrup et al. 1998, 2001, Fries and Eriksson 2006) since wood properties such as wood density and fibre length are moderately (even highly) inherited and show also moderate genetic age-age correlations between juvenile and mature wood. This has been previously observed in Scots pine but also in other conifers such as Norway spruce, slash pine (*Pinus elliottii*) and black spruce (*Picea mariana*) (Zobel and Buijtenen 1989, Hannrup and Ekberg 1998, Hannrup et al. 1998, Zhang 1998). However, for example in loblolly pine (*Pinus taeda*) the corresponding findings have been contradictory (Loo-Dinkins et al. 1984), and in maritime pine (*Pinus pinaster*) only a weak heritability of fibre length has been observed previously (Keller 1973).

Nowadays, in Scots pine the simultaneous effect of genetic entries and spacing on the growth, yield, wood density traits and fibre properties is largely unknown in Finland because few experiments have been designed so far for this purpose. In the above context, we investigated especially the differences in fibre properties (i.e. fibre length, fibre width and coarseness) in 20 year old Scots pine genetic entries (mainly full-sib families) as affected by spacing and site, but also the phenotypic correlations between fibre properties and yield and wood density traits. This work was done to find out if some genetic entries could have simultaneously a high growth rate (e.g. stem volume) and relatively long fibres, for example. The present research is a continuous work for that reported by Peltola et al. (2009), in which based on the same study material, it was investigated the effects of spacing, genetic entry and site on the

phenotypic variation of growth, yield and wood density traits in Scots pine.

2 Material and Methods

2.1 Experimental Data

The main material used in this study was harvested from a Scots pine spacing trial established in 1987 on agricultural soil 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.)). This trial consists of three different spacing treatments with initial stand densities of 2000, 4000 and 8000 seedlings/ha. In autumn 2000, a pre-commercial thinning (i.e. tending of seedlings stand) was carried out, in which the widest spacing (referred later as site 1, spacing 1) was left unmanaged, while the medium spacing was thinned to 2000–2500 seedlings/ha (spacing 2) and the densest one to 4000 seedlings/ha (spacing 3). In autumn 2006, we harvested from this trial 10 genetic entries (mainly full-sib families) of total of 20 available, representing different types of crossings of selected Finnish plus trees with a relatively wide geographical range in southern and central Finland (Table 1). The selection of genetic entries was done so that it was not overestimated the effect of one of the parent in the material (i.e. plus tree S1101, so called Kanerva pine), which was parent tree for 13 of 20 genetic entries.

Additional material was harvested in autumn 2007 from another trial established in 1988 at Loppi in southern Finland (60°35´N, 24°27´E, 1250 d.d., 140 a.s.l.). This trial was located on a forest soil with relatively poor site fertility, *Vaccinium* type (see Cajander 1926), which is typically regenerated with Scots pine in practical forestry in Finland. In this trial (referred later as site 2), the seedlings were planted with an

Table 1. Genetic entries and geographical origins of the crossings in trials located on site 1 (Siilinjärvi trial) and site 2 (Loppi trial).

Genetic entry	Crossing type	Site	Entry type	Site origins of mother trees
1	StandardS12	1	Open pollinated forest stand seed	Central: Lieksa (mother)
2	StandardS13	1	Open pollinated forest stand seed	Central: Pihtipudas (mother)
3	C205×S1101	1 & 2	Controlled crosses seed	Central: Multia (mother), South: Punkaharju (father)
4	C214B×S1101	1 & 2	Controlled crosses seed	Central: Äänekoski (mother), South: Punkaharju (father)
5	S2582×S1101	1 & 2	Controlled crosses seed	South: Kuru (mother), South: Punkaharju (father)
6	S104×S1101	1 & 2	Controlled crosses seed	South: Tammela (mother), South: Punkaharju (father)
7	S104×C205	1	Controlled crosses seed	South: Tammela (mother), Central: Multia (father)
8	C205×S80	1	Controlled crosses seed	Central: Multia (mother), South: Heinola (father)
9	C214B×C205	1	Controlled crosses seed	Central: Äänekoski (mother), Central: Multia (father)
10	SeedOrchardC97	1	Open pollinated seed orchard seed	Central: Varkaus Kuvansi (mother)
11	C205×S710D	2	Controlled crosses seed	Central: Multia (mother), South: Ruokolahti (father)
12	StandardSPM	2	Open pollinated forest stand seed	South: Pieksämäki (mother)
13	StandardS17	2	Open pollinated forest stand seed	South: Padasjoki (mother)

initial stand density of about 2000 seedlings/ha and no pre-commercial thinning was done before harvesting the sample trees. We harvested finally only 7 genetic entries out of 44 available from this site, because only four same genetic entries could be found on both sites (original plan was to harvest the same genetic entries on both sites) (see Table 1).

Altogether, we randomly harvested 5 trees per genetic entry from both trials (sites 1 and 2), and all spacing. Thus, in total 145 sample trees from site 1 and 35 trees from site 2 were harvested. The height and stem diameters were measured for each sample tree (at 1.3 and 6 m from stem base), and thereafter, based on those measurements stem volume was calculated based on stem volume function for Scots pine developed by Laasasenaho (1982). In addition, one sample disc was cut at 1 m height from the stem base in each sample tree for detailed measurements of intra-ring wood properties.

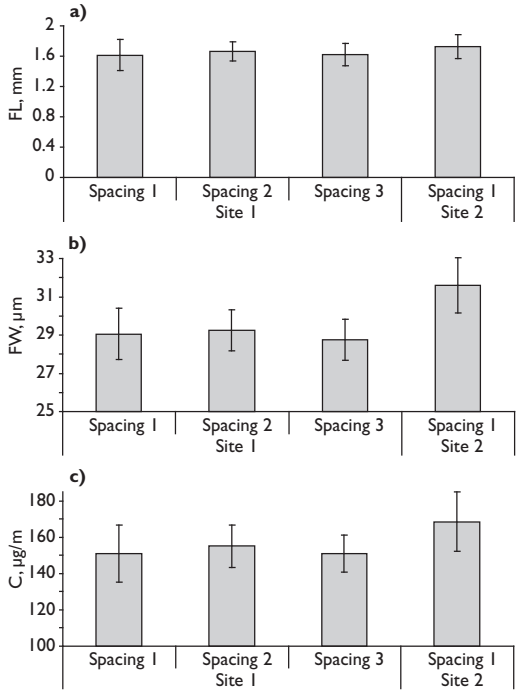

Fig. 1. Averages of different genetic entries for a) fibre length (FL), b) fibre width (FW) and c) coarseness (C) on site 1 for spacing 1, 2 and 3 with current stand densities of 2000, 2000–2500 and 4000 trees/ha and site 2 with stand density of 2000 trees/ha, respectively.

For intra-ring analysis of fibre properties, matchstick-sized wood specimens from pith to bark, each of them representing two annual ring pairs, were first 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) and fibre width (FW) were measured for each ring pair using the L&W Fibre Tester (AB Lorentzen & Wettre, Kista, Sweden) based on image analysis. In the fibre measurements, the highly diluted suspension flows between the narrow space of two glass plates, i.e. limiting the possibility of the fibres moving in one direction, but allowing them to move freely in the other two directions. The two-dimensional image permits 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 fibres per sample), and thus provide, 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 measured fibres, coarseness (C) for each ring pairs could also be calculated (see Karlsson 2006).

We also determined for each annual ring its wood density (WD) and ring width based on measured intra-ring density profiles from pith to bark, using a direct scanning ITRAX X-ray microdensitometer (Cox Analytical Systems, Göteborg, Sweden, see Bergsten et al. 2001). For this purpose, we used air dry small rectangular wood specimens (size of 5 mm × 5 mm) cut side by side with the specimens used for fibre measurements (at 1 m height). Further details for the X-ray measurements of these samples can be found from the work shown by Peltola et al. (2009).

2.2 Data Analyses

Based on intra-ring measurements from pith to bark, we first determined the weighted cross-sectional averages for fibre length (FL), fibre

width (FW), coarseness (C) and overall wood density (WD) for each sample tree by weighting each ring value with its corresponding ring width, as was done previously by Peltola et al. (2009). Thereafter, statistical analyses were made using the SPSS statistical program package 15.0 (SPSS for Windows, version 15.0, SPSS, Chicago, IL). Differences in fibre properties between genetic

Table 2. Average statistics and phenotypic coefficient of variation (CV%) for fibre length (FL), fibre width (FW), coarseness (C) and diameter at breast height (DBH) for different genetic entries in spacing 1 to 3 on site 1 (Siilinjärvi trial). Different letters indicate differences among genetic entries within each spacing (Tukey $p<0.05$).

Genetic entry	FL (mm)		FW (μm)		C (μg/m)		DBH (cm)	
Spacing 1: 2000 trees/ha	Mean ± sd	CV %	Mean ± sd	CV %	Mean ± sd	CV %	Mean ± sd	CV %
1. StandardS12	1.58 ± 0.2^{abcd}	9	28.8 ± 1^{ab}	5	147 ± 17^{ab}	11	12.0 ± 2.9^{a}	25
2. StandardS13	1.82 ± 0.2^{ad}	12	29.9 ± 2^{ab}	5	163 ± 20^{a}	12	10.0 ± 1.0^{a}	10
3. C205 × S1101	1.45 ± 0.2^{bc}	13	28.8 ± 1^{ab}	5	151 ± 15^{ab}	10	12.9 ± 1.4^{a}	10
4. C214B × S1101	1.58 ± 0.1^{abcd}	7	29.0 ± 1^{ab}	4	155 ± 10^{ab}	7	13.2 ± 1.5^{a}	11
5. S2582 × S1101	1.75 ± 0.1^{acd}	3	30.0 ± 1^{ab}	3	160 ± 12^{ab}	7	13.3 ± 1.5^{a}	11
6. S104 × S1101	1.75 ± 0.1^{acd}	6	29.3 ± 1^{ab}	3	152 ± 9^{ab}	6	11.6 ± 2.5^{a}	22
7. S104 × C205	1.40 ± 0.1^{b}	10	27.7 ± 1^{b}	3	134 ± 8^{b}	6	11.6 ± 1.0^{a}	9
8. C205 × S80	1.49 ± 0.3^{bc}	15	28.3 ± 2^{ab}	6	141 ± 18^{ab}	13	12.3 ± 2.1^{a}	17
9. C214B × C205	1.50 ± 0.1^{bcd}	9	28.2 ± 1^{ab}	4	142 ± 14^{ab}	10	13.7 ± 2.3^{a}	17
10. SeedOrchardC97	1.82 ± 0.1^{a}	7	30.3 ± 1^{a}	3	165 ± 8^{a}	5	11.9 ± 1.6^{a}	14
Average	1.61 ± 0.2	10	29.1 ± 1	3	151 ± 10	7	12.2 ± 1.1	9
Spacing 2: 2000–2500 trees/ha								
1. StandardS12	1.75 ± 0.1^{a}	7	29.1 ± 1^{a}	3	151 ± 13^{a}	9	9.8 ± 1.6^{a}	17
2. StandardS13	1.55 ± 0.2^{a}	13	28.9 ± 2^{a}	7	150 ± 18^{a}	12	11.6 ± 2.6^{a}	22
3. C205 × S1101	1.63 ± 0.1^{a}	6	29.1 ± 1^{a}	2	154 ± 9^{a}	6	11.7 ± 1.2^{a}	10
4. C214B × S1101	1.67 ± 0.1^{a}	6	29.3 ± 1^{a}	2	156 ± 7^{a}	5	10.6 ± 1.8^{a}	17
5. S2582 × S1101	1.68 ± 0.1^{a}	7	29.5 ± 1^{a}	2	159 ± 7^{a}	5	12.7 ± 1.5^{a}	12
6. S104 × S1101	1.69 ± 0.2^{a}	9	29.0 ± 1^{a}	3	149 ± 6^{a}	4	13.2 ± 2.1^{a}	16
7. S104 × C205	1.63 ± 0.0^{a}	3	28.6 ± 1^{a}	4	146 ± 13^{a}	9	11.7 ± 2.3^{a}	19
8. C205 × S80	1.70 ± 0.1^{a}	6	29.4 ± 1^{a}	3	161 ± 10^{a}	6	12.3 ± 2.7^{a}	22
9. C214B × C205	1.67 ± 0.1^{a}	6	29.6 ± 1^{a}	4	159 ± 12^{a}	8	11.2 ± 1.5^{a}	14
10. SeedOrchardC97	1.71 ± 0.1^{a}	8	30.0 ± 1^{a}	4	166 ± 13^{a}	8	12.0 ± 0.8^{a}	7
Average	1.67 ± 0.1	3	29.2 ± 1	1	155 ± 6	4	11.7 ± 1.0	8
Spacing 3: 4000 trees/ha								
1. StandardS12	1.62 ± 0.2^{a}	14	29.6 ± 1^{a}	2	156 ± 6^{ab}	4	10.0 ± 2.5^{a}	25
2. StandardS13 *	-	-	-	-	-	-	-	-
3. C205 × S1101	1.65 ± 0.2^{a}	9	29.0 ± 1^{a}	3	157 ± 10^{ab}	6	9.7 ± 1.1^{a}	11
4. C214B × S1101	1.67 ± 0.0^{a}	3	29.3 ± 1^{a}	2	155 ± 8^{ab}	5	11.3 ± 1.3^{a}	12
5. S2582 × S1101	1.68 ± 0.1^{a}	8	29.3 ± 1^{a}	3	161 ± 9^{a}	5	9.9 ± 1.4^{a}	14
6. S104 × S1101	1.58 ± 0.0^{a}	3	28.1 ± 1^{a}	4	144 ± 4^{ab}	3	10.8 ± 0.8^{a}	8
7. S104 × C205	1.56 ± 0.2^{a}	12	27.9 ± 1^{a}	4	141 ± 10^{b}	7	9.1 ± 2.1^{a}	23
8. C205 × S80	1.63 ± 0.2^{a}	9	28.5 ± 1^{a}	4	150 ± 7^{ab}	5	11.2 ± 2.0^{a}	17
9. C214B × C205	1.57 ± 0.1^{a}	9	28.3 ± 2^{a}	6	150 ± 16^{ab}	11	9.5 ± 1.0^{a}	10
10. SeedOrchardC97	1.62 ± 0.2^{a}	13	28.9 ± 1^{a}	3	146 ± 8^{ab}	5	9.6 ± 1.1^{a}	11
Average	1.62 ± 0.04	2	28.8 ± 1	2	151 ± 6	4	10.1 ± 0.8	8

*Data not available for genetic entry 2 in spacing 3.

Table 3. Average statistics and phenotypic coefficient of variation (CV%) for fibre length (FL), fibre width (FW), coarseness (C) and diameter at breast height (DBH) for different genetic entries on site 2 (Loppi trial). Different letters indicate differences among genetic entries (Tukey $p<0.05$).

Genetic entry	FL (mm)		FW (μm)		C (μg/m)		DBH (cm)	
	Mean ± sd	CV%	Mean ± sd	CV%	Mean ± sd	CV%	Mean ± sd	CV%
3. C205 × S1101	1.64 ± 0.2[a]	10	31.2 ± 2[a]	7	167 ± 18[a]	11	12.6 ± 2.14[a]	17
4. C214B × S1101	1.77 ± 0.2[a]	10	31.4 ± 1[a]	3	167 ± 19[a]	11	14.1 ± 1.47[a]	10
5. S2582 × S1101	1.82 ± 0.1[a]	4	31.4 ± 1[a]	3	173 ± 12[a]	7	12.2 ± 1.59[a]	13
6. S104 × S1101	1.64 ± 0.1[a]	5	31.2 ± 1[a]	4	158 ± 7[a]	4	12.9 ± 2.59[a]	20
11. C205 × S710D	1.82 ± 0.1[a]	6	32.3 ± 2[a]	5	181 ± 20[a]	11	11.1 ± 2.53[a]	23
12. StandardSPM	1.67 ± 0.1[a]	5	32.8 ± 1[a]	3	172 ± 11[a]	6	13.3 ± 2.95[a]	22
13. StandardS17	1.74 ± 0.3[a]	15	30.7 ± 2[a]	5	163 ± 22[a]	13	11.9 ± 1.09[a]	9
Average	1.73 ± 0.1	5	31.6 ± 1	2	169 ± 8	4	12.6 ± 1.0	8

entries (as well as for diameter at breast height, DBH) in each spacing and site were tested with a one-way ANOVA, by applying a pairwise analysis (Tukey pairwise test, $p<0.05$). In this context, the homogeneity of the variance (Levene's test of equality of error variances) and normality of the data (Kolmogorov-Smirnov test) were also tested. In addition, we applied a two-way ANOVA to test the simultaneous effects of genetic entry and spacing or the effects of genetic entry and site.

Additionally, we calculated the phenotypic coefficient of variation (CV%) by normalising the standard deviation (σ) by the mean (μ) of the property for each genetic entry (i.e. CV% = σ*100/μ), spacing by spacing and site by site. Relationships between average fibre properties (cross-sectional averages), yield traits and overall wood density were also examined in different genetic entries using phenotypic correlations (r_p) computed based on the Pearson's correlation method; $r_p = \sigma_{p1p2} / \sigma_{p1}\,\sigma_{p2}$, where σ_{p1p2} is the phenotypic covariance between properties 1 and 2, while σ_{p1} and σ_{p2} are the phenotypic standard deviation for properties 1 and 2, respectively. Correlations were expected to be significant at $p<0.05$ level. The CV% and r_p were computed both for individual genetic entries and as an average for all of them.

We only calculated phenotypic correlations, because of the relatively small number of genetic entries (and replicates) available for each spacing and site did not support the calculation of genetic correlations as the estimation errors of the genetic correlations in such cases are large (see e.g. Cheverud 1988, Roff 1995). On the other hand, phenotypic correlations have been suggested to be quite comparable with genetic ones, for example, in Scots pine if presented as an average over all the genetic entries (e.g. Haapanen and Pöykkö 1993), but naturally they would not be fully comparable to each other because in reality phenotypic correlations combine genetic and environmental causes (see e.g. Hannrup et al. 2000). In our work, we also ranked different genetic entries according to their average fibre properties, overall wood density and yield traits (i.e. stem volume and dry stem mass, the latter is estimated based on stem volume and overall wood density) in order to summarise our findings.

3 Results

3.1 Phenotypic Variation in Fibre Properties

Regardless of the spacing on site 1, fibre width (FW) showed, on average, the smallest phenotypic variation among the different genetic entries (average of 1–3% for spacing 1, 2 and 3), while fibre length (FL) and coarseness (C) showed clearly larger phenotypic variation (averages of 2–10% and 4–7%) (Table 2). On site 2, the corresponding phenotypic variation observed among

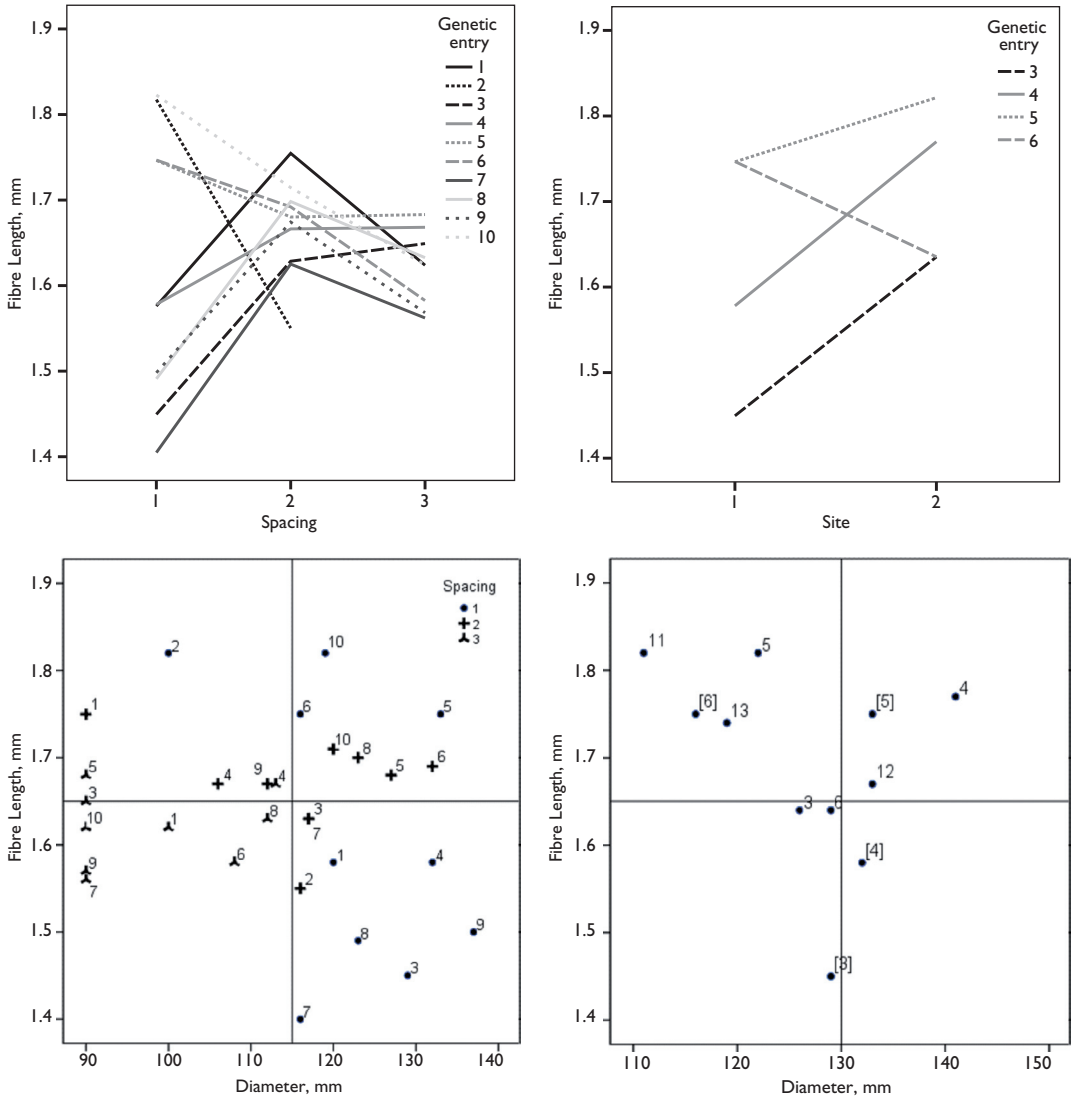

Fig. 2. Effect of spacing on average fibre length (FL) for different genetic entries on site 1 with spacing 1, 2 and 3 with current stand densities of 2000, 2000–2500 and 4000 trees/ha (above left) and for selected genetic entries grown on both sites 1 and 2 (above right), and relationships between average diameter at breast height and FL for different genetic entries on site 1 (below left) and on site 2 with stand density of 2000 trees/ha (below right), respectively. However, in the below left it is also shown in parenthesis the corresponding values for same four genetic entries grown on site 1 with spacing 1 for comparison.

the different genetic entries was, on average, in line with site 1, being 2% for FW, 5% for FL and 4% for C (see Table 3).

On site 1, with spacing 1 (current stand density of 2000 trees/ha), the average FL, FW and C were 1.61 mm, 29.1 μm and 151 μg/m, respectively. Regarding individual genetic entries, genetic entry 10 had the largest FW and C (13 and 10% above the average), and showed together with genetic entry 2 the largest FL (13% above the average) (Table 2). In spacing 2 (current stand density of 2000–2500 trees/ha), the average FL,

Table 4. Analysis of variance (F-value and probability [1]) on the effects of spacing, genetic entry and their interaction for fibre length (FL), fibre width (FW) and coarseness (C) on site 1 (A), and on the effects of site, genetic entry and their interaction on site 1 versus site 2 (B) for same genetic entries in both sites.

A. Site 1	Spacing		Genetic entry		Spacing × Genetic entry	
	F-ratio	P-value	F-ratio	P-value	F-ratio	P-value
FL	**2.27**	**0.02**	2.27	0.11	**2.36**	**0.00**
FW	**2.48**	**0.01**	2.56	0.08	1.22	0.26
C	**3.58**	**0.00**	2.03	0.14	1.55	0.09
B. Site 1 vs. site2	Site		Genetic entry		Site × Genetic entry	
	F-ratio	P-value	F-ratio	P-value	F-ratio	P-value
FL	**4.47**	**0.04**	**6.08**	**0.00**	**3.08**	**0.04**
FW	**28.17**	**0.00**	0.57	0.64	0.45	0.72
C	**8.03**	**0.01**	1.40	0.26	0.27	0.85

[1] Significance of F-ratio with $p<0.05$ in bold.

FW and C were 1.67 mm, 29.2 μm and 155 μg/m, respectively. In this spacing, genetic entry 1 had the largest FL (5% above the average), whereas genetic entry 10 had the highest FW and C (3 and 7% above the average) (Table 2). In spacing 3 (current stand density of 4000 trees/ha), the average FL, FW and C were similar to spacing 1, being 1.62 mm, 28.8 μm and 151 μg/m, respectively. In this spacing, genetic entry 5 had the highest FL and C (4 and 7% above the average), while genetic entry 1 showed the largest FW (3% above the average) (Table 2). Nonetheless, differences observed among the genetic entries in each of the spacing were not, in general, statistically significant.

On site 2 (with stand density of 2000 seedlings/ha), the average FL was 1.7 mm, similar to the same spacing on site 1. As a comparison, FW and

Table 5. Ranking of different genetic entries for stem volume (V), overall wood density (WD), stem dry mass (SM, i.e. stem volume × overall wood density), fibre length (FL) and fibre width (FW) on site 1 for spacing 1, 2 and 3 (with current stand density of 2000, 2000-2500 and 4000 trees/ha) and site 2 (stand density of 2000 trees/ha). The ranking of genetic entries is done so that the highest value gets number 1 and the lowest gets 10 regardless of trait.

Genetic entry	V				WD				SM				FL				FW			
Site	S1			S2	S1			S2	S1			S2	S1			S2	S1			S2
Spacing	1	2	3	1	1	2	3	1	1	2	3	1	1	2	3	1	1	2	3	1
1. StandardS12	8	10	9		3	8	3		8	10	9		6	1	6		6	6	1	
2. StandardS13 *	10	9	-		1	9	-		10	9	-		2	10	-		3	9	-	
3. C205×S1101	3	4	4	4	5	6	1	1	3	4	3	4	9	8	3	7	7	7	4	5
4. C214B×S1101	2	8	2	1	7	1	5	3	2	8	2	1	5	7	2	3	5	5	3	3
5. S2582×S1101	4	3	5	5	4	7	6	5	4	3	5	5	4	5	1	2	2	3	2	4
6. S104×S1101	6	1	3	3	10	4	9	7	6	1	4	3	3	4	7	6	4	8	8	6
7. S104×C205	7	6	7		9	10	7		7	7	8		10	9	9		10	10	9	
8. C205×S80	5	2	1		8	5	8		5	2	1		8	3	4		8	4	6	
9. C214B×C205	1	7	6		2	2	4		1	6	6		7	6	8		9	2	7	
10.SeedOrchardC97	9	5	8		6	3	2		9	5	7		1	2	5		1	1	5	
11. C205×S710D				6				2				6				1				2
12. StandardSPM				2				4				2				5				1
13. StandardS17				7				6				7				4				7

*Data not available for genetic entry 2 in spacing 3

C (32 μm and 169 μg/m), were to some degree higher than on site 1 (for same spacing). On this site, genetic entries 5 and 11 showed the highest FL (6% above the average), and the latter one had also the highest C (7% above the average), while genetic entry 12 had the largest FW (5% above the average) (Table 3, Fig. 1). Nonetheless, differences observed among the genetic entries on this site were not statistically significant.

Despite the fact that on site 1 the trees were, on average, larger in spacing 1 (average diameter of 12.2 cm) than in spacing 2 and 3 (averages of 11.7 and 10.1 cm), the average FL was slightly higher in spacing 2 compared to spacing 1 and 3 (see Table 2, Fig. 2). Spacing had a statistically significant effect ($p<0.05$) on all the studied fibre properties (FL, FW and C), while genetic entry in interaction with spacing affected significantly the FL, but not FW and C (Table 4). Moreover, site affected significantly FL, FW and C when comparing the same genetic entries grown on both sites. Similarly, in this case genetic entry affected also FL as did site × genetic entry interaction (Table 4). In order to have an integrated picture of the overall results, we also ranked the genetic entries in regard to different traits. Nevertheless, we found that the ranking changed, to some degree, depending on the trait and spacing considered. Therefore, no overall ranking between genetic entries was possible in this respect (see Fig. 2, Table 5).

We also found that the average fibre length distribution among the genetic entries (i.e. percentage of fibres in different fibre length classes such as 0.2–0.5, 0.5–1.0, 1.0–1.5 mm, etc.) differed, to some degree, depending on spacing on site 1 (see Fig. 3). The fibre length distribution moved slightly to the right towards longer fibres and the distribution was slightly narrower when moving from spacing 1 to spacing 3 with higher stand density.

3.2 Phenotypic Correlation between Fibre Properties, Yield and Wood Density Traits

Regardless of spacing and site, the phenotypic correlations observed between different fibre properties (FL, FW and C) showed, on average, strong positive correlation, being moderate only between FW and FL on site 2 ($p<0.05$) (see Table 6). However, FL and C were partly correlated, because C was calculated based on FL. All the individual genetic entries also followed these general patterns regarding the correlations between FL and FW/C on site 1, unlike on site 2 (see Appendix 1). The diameter at breast height (DBH) showed, on average, a low phenotypic correlation with FL on both sites, being positive

Table 6. Phenotypic correlations between fibre length (FL), fibre width (FW), coarseness (C), diameter at breast height (DBH), stem volume (V) and overall wood density (WD), on average, for different genetic entries grown on site 1 (regardless of spacing) (upper right) and on site 2 (lower left).

Traits	FL	FW	C	DBH	V	WD
FL	1	**0.72**	**0.73**	0.10	0.07	0.14
FW	**0.40**	1	**0.88**	**0.28**	0.21	0.20
C	**0.67**	**0.77**	1	**0.17**	0.15	**0.32**
D	-0.09	**0.46**	0.14	1	**0.95**	**-0.25**
V	0.03	**0.54**	0.23	**0.93**	1	**-0.19**
WD	-0.06	0.21	0.18	0.01	0.07	1

[1]Significance $p<0.05$ in bold.

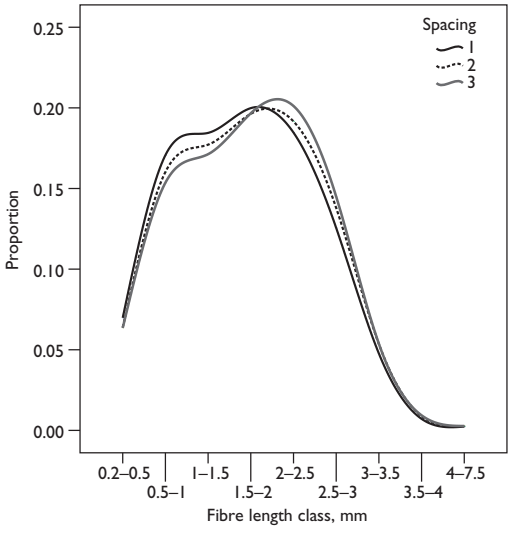

Fig. 3. Average fibre length distribution over all genetic entries on site 1 for spacing 1, 2 and 3 with current stand densities of 2000, 2000–2500 and 4000 trees/ha.

on site 1, but negative on site 2. In any case, none of these correlations were statistically significant. On the contrary, the phenotypic correlation between DBH and FW was positive and significant on both sites ($p < 0.05$), while between DBH and C it was also positive but significant only on site 1. Additionally, stem volume showed moderate and positive correlation with FW on both sites. Regarding overall wood density (WD), on site 1 it showed a low positive correlation with FW and C ($p < 0.05$), unlike on site 2. When looking at the correlations between FL and DBH or WD for individual genetic entries there was no general patterns observed, since the correlations ranged from slightly negative to moderately positive, being in all the cases, not significant (see Appendix 1).

4 Discussion and Conclusions

Compared to fibre length (FL) and coarseness (C), in this study, fibre width (FW) showed, in general, lower phenotypic variation regardless of spacing or site, which is in agreement with previous findings in Scots pine (Hannrup et al. 2001), but also in other coniferous species like Norway spruce (Hannrup et al. 2004, Zubizarreta Gerendiain et al. 2008). In general, the moderate to low variability in fibre properties indicates that these traits might be under a moderate genetic control and are, therefore, less affected by the environment and competition between trees than the growth and yield traits, for example (see e.g. Ståhl et al. 1988, Hannrup and Ekberg 1998).

In our work, we also found that phenotypic correlation among fibre properties, as an average of all entries, and regardless of the site, was positive and ranged from moderate to strong, with the strongest correlation being observed between FW and C. These results are in agreement with previous findings in Maritime pine (*Pinus pinaster*) (Pot et al. 2002) and Norway spruce, for example (Zubizarreta Gerendiain et al. 2008). These findings may suggest that the same sets of genes are likely to be responsible for controlling the different fibre properties, and if so, selection for a single fibre trait would simultaneously affect the others (Zobel and Jett 1995).

On the contrary, we did not observe, as expected, any significant phenotypic correlation between fibre properties such as fibre length and yield traits (e.g. stem volume and diameter at breast height; not analysed in respect to tree height) in Scots pine. However, previously it has been found also in Scots pine, as well as in loblolly pine (*Pinus taeda*), Maritime pine and Norway spruce a week to moderate positive phenotypic or genetic correlation between fibre length and stem diameter and/or tree height, for example (see e.g. Loo-Dinkins et al. 1984, Ståhl 1988, Hannrup and Ekberg 1998, Hannrup et al. 2000, Pot et al. 2002, Zubizarreta Gerendiain et al. 2008). Nonetheless, in Norway spruce, also a negative correlation between fibre length and growth rate has been observed (see e.g. Lindström 1997, Dutilleul et al. 1998).

Additionally, we found a weak positive correlation between different fibre properties and overall wood density (but it was not statistically significant for FL). Similarly, Hannrup et al. (2001) previously observed in Scots pine a positive weak correlation between wood density and fibre length for juvenile wood, but not in mature wood, where it was negative or even non-existent. In other pine species such as Maritime pine or radiata pine (*Pinus radiata*), negative correlations have also been observed previously between wood density and fibre length or width, for example (Nyakuengama et al. 1999, 2003, Pot et al. 2002).

On site 1, the average FL, FW and C were very similar to each other in spacing 1 and 3, but slightly lower compared to spacing 2 (differences were also statistically significant). On the other hand, genetic entry did not significantly affect the fibre traits on site 1 regardless of spacing considered. In contrast to our findings, Persson et al. (1995) observed that increase in spacing increased clearly both tree growth (height and DBH) and FL and FW in different genetic entries of Scots pine, and genetic entries also affected those fibre properties. However, also in our study material an increase in spacing increased average diameter at breast height and stem volume at a cost of height growth (see in details from Peltola et al. 2009), as was found by Persson et al. (1995). Regarding site 2, the average fibre traits were comparable to those observed on site 1 with similar spacing in our work. On the other hand, site affected sig-

nificantly all fibre properties, but genetic entry affected only FL, when comparing same genetic entries grown on both sites. In accordance with our results, Ståhl (1988) also reported in Scots pine, that site affected FL.

In addition to average fibre dimensions, spacing had an effect on the frequency distribution of fibre length. In our case, the narrowest spacing had a slightly more uniform fibre length distribution than the widest spacing. Furthermore, in the narrowest spacing a higher percentage of long fibres was observed compared to the widest spacing and vice versa. These changes in the fibre length distribution as a result of changing spacing were gradual, however. The studies regarding fibre length distribution are very scarce, since fibre dimension measurements are laborious especially if based on microscopy analyses. Nevertheless, Zubizarreta Gerendiain et al. (2008) found in a previous work in Norway spruce that this distribution may change among the different genetic entries, thus, the improved knowledge regarding property distribution in addition to mean values could facilitate a better understanding of raw material characteristics (Herman et al. 1998, Mäkinen et al. 2002).

As a whole, it would be desirable to find such genetic entries which, at the same time, have desired fibre properties as well as provide a high yield and a fairly high overall wood density, which implies high stem mass production as well. The most productive genetic entries should also maintain a higher growth rate even after the stand canopy had closed, resulting from a higher light interception and/or more stem wood produced per unit of light intercepted (see e.g. Svensson et al. 1999). In our work, the ranking between different genetic entries changed significantly depending on the trait, spacing or site considered, and therefore, no overall ranking was possible in this respect. However, we could find some genetic entries, which at the same time had a fairly high FL and FW as well as moderate to high stem volume and overall wood density as well (indicating also relatively high stem dry mass production). For example, on site 1, the genetic entry 5 in spacing 1 and 2, and genetic entry 8 in spacing 2 and 3 showed those characteristics (also genetic entry 3 in spacing 3). On the other hand, previously it has been thought that the Kanerva pine (with thin and short branches) may be superior in terms of yield because of its high harvest index especially in denser spacing (Kärki 1985, Pöykkö 1993), but we could not observe it. In this sense, opposite to what it was expected beforehand, genetic entries with Kanerva pine as one of the parents seemed to behave in a similar way than the other entries and even in narrow spacing.

To conclude, in this work, we demonstrated that ranking of genetic entries based on fibre properties may be different compared to the ranking by stem volume or overall wood density and it may also change in Scots pine depending on silvicultural management (e.g. spacing) or site conditions. However, we should point out that the differences observed in this study for various genetic entries with different spacing and sites may be partly due to their varying capacity to react in different environmental conditions (e.g. neighbours' competition, site). On the other hand, the relatively low number of sample trees per genetic entry (in each trial and spacing) may also affect these results. However, we believe the trial 1 (with relative fertile agricultural soil) with quite a large range of stand density treatments could be expected to suit well for these kinds of studies (see e.g. Haapanen 1996). Anyway, further work is still needed based on larger study material to understand in details, how silvicultural management, such as the control of spacing, in addition to site conditions (and microclimate), affects the growth, yield and properties of different genetic entries in order to provide integrated picture of their raw material properties and, thus, suitability for the final target of wood production (e.g. pulp wood or sawn timber products). Based on such information, it may be possible to identify some genetic entries and their site-specific management that could be suited to particular product types or processes (Ridoutt et al. 1998).

Acknowledgements

This work is related to the research carried out at the Centre of Excellence for Boreal Forest Management Research led by Prof. Seppo Kellomäki at the Faculty of Forest Sciences, University of Joensuu. The authors would like to thank the

Finnish Forest Research Institute (FFRI) for providing the material for this study. Moreover, Mr. Jyrki Airaksinen and Ms. Pirita Lohela from FFRI and Mr. Jarmo Pennala and Ms. Marja Kuskelin, from the University of Joensuu, Faculty of Forest Sciences, are thanked for harvesting the sample trees for this work. Mr. Jarmo Pennala and Ms. Maini Mononen are also thanked for assistance with X-ray and fibre properties measurements. Dr. David Gritten is thanked for the English revision of the manuscript. The scholarship obtained by M.Sc. Jaume Gort for his PhD thesis from Fundación Caja Madrid, Spain, is also gratefully acknowledged. The support provided by the University of Joensuu, Faculty of Forest Sciences and the Finnish Forest Research Institute are gratefully acknowledged.

References

Bergsten, U., Lindeberg, J., Rindby, A. & Evans, R. 2001. Batch measurements of wood density on intact or prepared drill cores using x-ray microdensitometry. Wood Science and Technology 35: 435–452.

Björklund, L. & Walfridsson, E. 1993. Properties of Scots pine wood in Sweden. – Basic density, heartwood, moisture and bark content. Sveriges Lantbruksuniversitet, Institutionen for virkeslära, Rapport 234: 1–67.

Cajander A.K. 1926. The theory of forest types, Acta Forest. Fennica 29, p. 1–108.

Chambers P.G.S. & Borralho N.M. 1999. A simple model to examine the impact of changes in wood traits on the costs of thermomechanical pulping and high-brightness newsprint production with radiata pine. Canadian Journal of Forest Research 29: 1615–1626.

Cheverud, J.H. 1988. A comparison of genetic and phenotypic correlations. Evolution 42: 958–968.

Fries, A. & Eriksson, T. 2006. Estimating genetic parameters for wood density of Scots pine (Pinus sylvestris L.). Silvae Genetica 55: 84–92.

Haapanen, M. 1996. Impact of family-by-trial interaction on the utility of progeny testing methods for Scots pine. Silvae Genetica 45: 130–135.

— & Pöykkö, T. 1993. Genetic relationship between growth and quality traits in an 8-year old half-sib progeny trial of Pinus sylvestris. Scandinavian Journal of Forest Research 8: 305–318.

Hannrup, B & Ekberg, I. 1998. Age-age correlations for tracheid length and wood density in Pinus sylvestris. Canadian Journal of Forest Research 28: 1373–1379.

—, Wilhelmsson, L. & Danell, Ö. 1998. Time trends for genetic parameters of wood density and growth traits in Pinus sylvestris. Silvae Genetica 47(4): 214–219.

—, Ekberg, I. & Persson, A. 2000. Genetic correlations among wood, growth capacity and stem traits in Pinus silvestris. Scandinavian Journal of Forest Research 15: 161–170.

—, Danell, Ö., Ekberg, I. & Moëll, M. 2001. Relationships between wood density and tracheid dimensions in Pinus sylvestris L. Wood and Fiber Science 33(2): 173–181.

—, Calahan, C., Chantre, G., Grabner, M., Kalrlsson, B., Le Bayon, I., Lloyd Jones G., Müller, U., Pereira, H., Rodriques, J.C., Rosner, S., Rozenberg, P., Wilhelmsson, L. & Wimmer, R. 2004. Genetic parameters of growth and wood quality traits in Picea abies. Scandinavian Journal of Forest Research 19: 14–29.

Herman, M., Dutilleul, P & Avella-Shaw, T. 1998. Growth rate effects on temporal trajectories of ring width, wood density, and mean tracheid length in Norway spruce (Picea abies (L.) Karst.). Wood and Fiber Science 30(1): 6–17.

Ikonen, V-P., Peltola, H., Wilhelmsson, L., Kilpeläinen, A., Väisänen, H., Nuutinen, T., & Kellomäki, S. 2008. Modelling the distribution of wood properties along the stems of Scots pine (Pinus sylvestris L.) and Norway spruce (Picea abies (L.) Karst.) as affected by silvicultural management. Forest Ecology and Management 256: 1356–1371.

Kang, K., Zhang, S & Mansfield, S. 2004. The effects of initial spacing on wood density, fiber and pulp properties in jack pine (Pinus banksiana Lamb.) Holzforschung 58: 455–468.

Kärki, L. 1985. Crop tree ideotypes and harvest index should be the basis of selection in cultivated trees. Foundation of Forest Tree Breeding in Finland, Annual report 1984. p. 20–23.

Karlsson, H. 2006. Fibre guide – fibre analysis and process applications in the pulp and paper industry. A handbook. Published by AB Lorentzen & Wettre, Kista, Sweden. 120 p.

Keller, R. 1973. Caractéristiques du bois du pin

maritime. Variabilité et transmission héréditaire. Annales des Sciences Forestières 30: 31–62.

Laasasenaho. J. 1982. Taper curve and volume functions for pine, spruce and birch. Communicationes Instituti Forestalia Fenniae 108. 74 p.

Lindström, H. 1997. Fiber length, tracheid diameter and latewood percentage in Norway spruce: development from pith to outwards. Wood and Fiber Science 29: 21–34.

Loo-Dinkins, J.A., Tauder, C.G. & van Buijtenen, J.P. 1984. Juvenile-mature relationships and heritability estimates of several traits in loblolly pine (Pinus taeda). Canadian Journal of Forest Research 14: 822–825.

Mäkinen, H., Saranpää, P. & Linder, S. 2002. Effect of growth rate on fibre characteristics in Norway spruce (Picea abies (L.) Karst.). Holzforschung 56: 449–460.

Nyakuengama, J.G., Downes, G.M. & Ng, J. 2003. Changes caused by mid-rotation fertilizer application to the fibre anatomy of Pinus radiata. IAWA Journal 24: 397–409.

—, Evans, R.. Matheson, C., Spencer, D. & Vinden, P. 1999. Wood quality and quantitative genetics of Pinus radiata D. Don: fiber traits and wood density. Appita Journal 52: 348–350.

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).

Persson, A. 1975. Wood and pulp of Norway spruce and Scots pine at various spacings. Research Notes 37. Department of Forest Yield Research, Royal College of Forestry, Stockholm. p. 1–145.

Persson, B., Persson, A., Ståhl, E.G. & Karlmats, U. 1995. Wood quality of Pinus sylvestris progenies at various spacings. Forest Ecology and Management 76: 127–138.

Pfister, O., Wallentin, C., Nilsson U. & Eko, P.M. 2007. Effects of wide spacing and thinning strategies on wood quality Norway spruce (Picea abies) stands in southern Sweden. Scandinavian Journal of Forest Research 22: 333–343.

Pot, D., Chantre, G., Rozenberg, P., Rodrigues, J.C., Jones, G.L., Pereira, H., Hannrup, B., Cahalan, C. & Plomion, C. 2002. Genetic control of pulp and timber properties in maritime pine (Pinus pinaster Ait.). Annales des Sciences Forestières 59: 563–575.

Pöykkö, T. 1993. Selection criteria in Scots pine breeding with special reference to ideotype. The Foundation for Forest Tree Breeding in Finland, Report 6. 66 p.

Ridoutt, B., Sorensson, C. & Lausberg, M. 1998. Wood properties of twenty highly ranked Radiata pine seed production parents selected for growth and form. Wood and Fiber Science 30(2): 128–137.

Roff, D.A. 1995. The estimation of genetic correlations from phenotypic correlations: a test of Cheverud's conjecture. Heredity 74: 481–490.

Ståhl, E.G., 1988. Transfer effect and variations in basic density and tracheid length of Pinus sylvestris L. populations. Studia Forestalia Suecica 180. 15 p.

Svensson, J., Mckeand, S., Allen, H. & Campbell, R. 1999. Genetic variation in height and volume of Loblolly pine open-pollinated families during canopy closure. Silvae Genetica 48: 204–207.

Tyrväinen, J. 1995. Wood and fiber properties of Norway spruce and its suitability for thermomechanical pulping. Acta Forestalia Fennica 249. 155 p.

Zhang, S.Y. 1998. Effect of age on the variation, correlations and inheritance of selected wood characteristics in black spruce (Picea mariana). Wood Science and Technology 32: 197–204.

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

— & Jett J.B. 1995. Genetics of Wood Production. Springer-Verlag, Berlin, Germany. 352 p.

Zubizarreta Gerendiain, A., Peltola, H., Pulkkinen, P., Jaatinen, R. & Pappinen, A. 2008. Differences in fibre properties in cloned Norway spruce (Picea abies). Canadian Journal of Forest Research 38: 1071–1082.

Total of 40 references

Table A1. Phenotypic correlations of fibre length (FL) with fibre width (FW), coarseness (C), diameter at breast height (DBH), stem volume (V) and wood density (WD) for different genetic entries on site 1 (regardless of spacing) and site 2 (in parenthesis). Bold text means statistically significant correlation ($p<0.05$).

Genetic entry	Phenotypic correlation between FL and				
	FW	C	DBH	V	WD
1. StandardS12	0.31	**0.54**	-0.07	0.00	0.42
2. StandardS13	**0.82**	**0.81**	-0.02	-0.13	0.13
3. C205×S1101	**0.72** (0.51)	**0.80** (0.64)	-0.16 (0.29)	-0.13 (0.57)	0.43 (0.82)
4. C214B×S1101	**0.67** (0.61)	**0.72** (0.78)	-0.17 (-0.37)	-0.03 (0.04)	0.33 (-0.07)
5. S2582×S1101	**0.52** (-0.03)	**0.50** (0.06)	0.49 (-0.19)	0.44 (-0.34)	-0.20 (-0.71)
6. S104×S1101	**0.54** (-0.20)	**0.57** (-0.11)	0.13 (-0.01)	0.13 (0.00)	-0.10 (-0.14)
7. S104×C205	**0.67**	**0.65**	0.23	0.22	0.17
8. C205×S80	**0.91**	**0.93**	0.37	0.40	0.14
9. C214B×C205	**0.92**	**0.92**	-0.01	0.00	0.17
10.SeedOrchardC97	**0.74**	**0.65**	0.14	0.05	-0.21
11. C205×S710D	(0.22)	**(0.88)**	(0.47)	(0.46)	(0.04)
12. StandardSPM	(0.27)	(0.78)	(0.03)	(0.17)	(-0.71)
13. StandardS17	**(0.92)**	(0.84)	(-0.54)	(0.02)	(-0.06)