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Growth and Wood Property Traits in Narrow Crowned Norway Spruce (*Picea abies* f. *pendula*) Clones Grown in Southern Finland

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We investigated the growth, yield, wood density traits and fibre properties in 13 narrow crowned Norway spruce (*Picea abies* f. *pendula*) clones grown at a spacing of 2 m × 1.5 m (about 3300 seedlings/ha) in a field trial established in 1988 in southern Finland on a forest soil. For comparison, we used 3 normal crowned Norway spruce (*Picea abies* (L.) Karst.) genetic entries grown as a mixture in the same trial representing southern Finnish breeding regions. We found that wood density traits and fibre properties showed, on average, lower phenotypic variation than growth and yield traits regardless of crown type. Narrow crowned clones also had, on average, lower stem volume and fibre length, but higher overall wood density. Moreover, the phenotypic correlations between studied growth and wood properties ranged, on average, from moderate (normal crown) to high (narrow crown). These results were opposite to previous findings for narrow and normal crowned genetic entries grown in narrower spacing (1 m × 1 m) in southern Finland. Thus, this indicates lower plasticity of narrow crowned clones to the increasing growing space compared to normal crowned ones, so, they should be grown at denser spacing in order to fully utilise its space efficiency capacity. However, this field trial was established as a mixture of normal and narrow crown trees, so that 90% of genetic entries were narrow crowned ones, and therefore the crown competition would be much higher for normal crowned trees when the whole trial would consist of that entry alone. In the latter case, we could expect significantly lower productivity of normal crowned genetic entries with this spacing.

Keywords diameter, earlywood, fibre length, height, latewood, stem volume, wood density

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1 Introduction

In the forest industry, and particularly in pulp and paper manufacturing, the quality of the final product is fundamentally related to the characteristics of tree species and their genetic entries as a raw material. Among the wood property traits, for example, wood density affects the pulp yield, while fibre properties affect the industrial processes and the final physical and optical properties of the paper products (Tyrväinen 1995, Karlsson 2006). Faced with this concern, the suitability of any genetic entry as a raw material for forest industry would depend on the quantity of wood produced, but also on its wood and fibre characteristics (Zobel and van Buijtenen 1989, Karlsson and Rosvall 1993, Zhang and Morgenstern 1995).

Norway spruce (*Picea abies* (L.) Karsten) is one of the most important commercial tree species in Finland and elsewhere in Scandinavia for the pulp and paper industry. But in Finnish climatic conditions, the growth and wood properties are especially affected by the length of growing season and prevailing temperature conditions (Peltola et al. 2002, Kilpeläinen et al. 2007). Additionally tree status in a stand (dominant, suppressed) and availability of water, nutrients and light, as controlled by silvicultural treatment, also affect the overall tree growth and consequently the properties of stem and wood (Herman et al. 1998, Bergh et al. 1999, Pape 1999a, 1999b, Mäkinen et al. 2002a, 2002b, Kellomäki et al. 2005, Jaakkola et al. 2007). As a consequence, stem wood production can be increased only by increasing either the overall growth rate of trees or the proportion of biomass allocated to the stem by proper silvicultural treatment, for example, by selection of proper spacing, thinning and fertilisation (e.g. Cannell et al. 1983, Ford 1985, Pulkkinen 1991a, 1991b, 1991c, Peltola et al. 2007). In this sense, tree breeding could be used to select genetic entries with desired properties, even in reasonably young ages because traits such as wood density and fibre morphology are usually moderately to highly inherited (Boyle et al. 1987, Zobel and van Buijtenen 1989, Hylen 1999) and show moderate genetic age-age correlations (Petty et al. 1990, Hannrup and Ekberg 1998, Hannrup et al. 1998).

In Finland, there exists a rare mutant of Norway spruce, the so called narrow crowned Norway spruce (*Picea abies* f. *pendula*), which shows significantly higher share of stem wood of total above ground dry mass production than normal crowned Norway spruce (Pulkkinen and Pöykkö 1990, Pulkkinen 1991a, 1991c). It is also expected to provide, at same age, significantly higher stem yield (total stem volume and mass) per occupied ground area than normal crowned Norway spruce trees with larger crowns, especially if grown in very dense spacing (see Zubizarreta Gerendiain et al. 2008b). This is because the narrow crowned Norway spruce is characterised by thin hanging branches and extremely narrow crown, which makes it less sensitive to competition from neighbouring trees than normal crowned Norway spruces. It is also considered as a future option for wood raw material source for pulp and paper production since it might be grown in significantly denser stands than normal crowned Norway spruce and even without any thinning and with short rotations (Pöykkö and Pulkkinen 1990, Pulkkinen 1991a, 1991b).

However, with the exception of the previous study by Zubizarreta Gerendiain et al. (2008b) with a very dense spacing in southern Finland, no concurrent studies exist on the growth and yield with impacts on wood density traits and fibre properties of narrow crowned Norway spruce. In their work, Zubizarreta Gerendiain et al. (2008b) reported that narrow crowned Norway spruce families with a very dense spacing, showed on average, both higher stem volume and longer fibre length and, despite of lower overall wood density, higher dry stem wood production than the normal crowned genetic entries of Norway spruce used in comparison. In addition, the phenotypic correlations between growth, yield,wood density traits and fibre properties, ranged, on average, from moderate (narrow crowned) to high (normal crowned). However, in the narrow crowned families, the growth rate of trees was, on average, negatively related with the overall wood density as was found in previous studies in normal crowned Norway spruce as well (e.g. Dutilleul et al. 1998, Hannrup et al. 2004, Jaakkola et al. 2005, Zubizarreta Gerendiain et al. 2007, 2008b).

On the other hand, even if narrow crowned Norway spruces would be more efficient in stem wood production per occupied ground area than the normal crowned ones in dense spacing, their total stem wood production may be significantly smaller than that of normal crowned Norway spruces if planted, for example, at the typical spacing used for this species in practical forestry, such as stand density range of 1600–2000 seedlings/ha (Pulkkinen and Pöykkö, 1990, Pulkkinen 1991a, 1991b). Moreover, the use of narrow crowned Norway spruce trees in practical forestry should also be based on vegetative propagation, because the progenies of open pollinated pendulous trees consist of only 18–50% pendulous seedlings since the inheritance of the pendulous crown form is predominantly controlled by a single dominant gene as modified by a number of minor genes (Lepistö 1985, Pulkkinen 1992). In this sense, it would be necessary to find a cost efficient planting density, which at the same time, provides the desired quantity and properties of wood.

In the above context, we investigated how the growth and yield traits (such as height, breast height diameter, stem volume, ring width, and earlywood and latewood width), wood density traits (overall wood density, latewood and earlywood density) and fibre properties (fibre length and width, cell wall thickness and fibre coarseness) differed in 13 narrow crowned Norway spruce clones grown as a mixture at the spacing of 2 m × 1.5 m (about 3300 seedlings/ha) compared to the three normal crowned genetic entries of Norway spruce grown in the same field trial, and representing southern Finnish breeding regions. We also aimed to compare our findings with corresponding work shown previously by Zubizarreta Gerendiain et al. (2008b) with much denser spacing.

2 Material and Methods

2.1 Experimental Data

The experimental sample tree data was collected from a clonal Norway spruce field trial established in 1988 in Karkkila (60°32′N, 24°12′E, 75 m above sea level), southern Finland by the Finnish Foundation for Forest Tree Breeding Station. The trial was located on a fertile forest soil (i.e. *Myrtillus–Oxalis-Myrtillus* type), with site fertility conditions typical for Norway spruce. The sample trees were grown at a spacing of 2 m × 1.5 m, with a corresponding stand density of 3300 seedlings/ha. Altogether, in the trial 98 genetic entries were replicated in 8 blocks (having 12 trees/clone/block), of which 90% were narrow crowned clones. In 2007, 13 narrow crowned Norway spruce clones were randomly chosen for this study from the 98 of the trial. Additionally, for comparison, material from three genetic entries representing normal crowned Norway spruce were harvested (Table 1). We collected 6 sample trees from each genetic entry, and each of these sample trees were taken from a different block.

The narrow crowned Norway spruce clones represented controlled crosses 1) between narrow crowned spruces from Mäntsälä stand, which were originally discovered in the 1950s (60°40′N, 25°15′E), or 2) between them and normal crowned spruces originated from southern or central Finland (60°45′N–64°58′N). The three normal crowned genetic entries used in comparison originated from seeds collected from typical commercial spruce forest stands grown in southern Finland (60°40′N–63°22′N). The age of the mother trees for the narrow crowned clones varied from 2 to 3 years at the time of cloning and this range was not expected to affect the results (Rautanen 1995).

No thinning had been carried out in the trial up to the time of harvesting of the sample trees. Tree height and stem diameters (at 1.3 and 6 m height from stem base) of the sample trees were measured, and used to calculate the stem volume for each tree according to volume functions developed by Laasasenaho (1982) for Norway spruce. Thereafter, one sample disc per sample tree was taken at a height of 1–1.3 m for laboratory analyses on growth.

2.2 Laboratory Measurements

The intra-ring wood densities were measured using a ITRAX X-ray microdensitometer (Cox Analytical Systems, Göteborg, Sweden) located

Table 1. Harvested normal (1C–3C) and narrow (4N24–6N76) crowned Norway spruce genetic entries and the geographical origin of their mother trees (C for normal crowned and N for narrow crowned)

Crown type	Genetic entry	Origin	Sample trees
Normal	1C	Breeding region: Loppi Haapastensyrjä (C)	6
Normal	2C	Breeding region: Eurajoki (C)	6
Normal	3C	Breeding region: Miehikkälä (C)	6
Narrow	4N24	K953 Pieksänmaa (C) × E480 Mäntsälä (N)	6
Narrow	4N25	K953 Pieksänmaa (C) × E480 Mäntsälä (N)	6
Narrow	4N28	K953 Pieksänmaa (C) × E480 Mäntsälä (N)	6
Narrow	4N29	K953 Pieksänmaa (C) × E480 Mäntsälä (N)	6
Narrow	5N43	E477 Mäntsälä (N) × K954 Pieksänmäen (C)	6
Narrow	5N44	E477 Mäntsälä (N) × K954 Pieksänmäen (C)	6
Narrow	5N45	E477 Mäntsälä (N) × K954 Pieksänmäen (C)	6
Narrow	5N46	E477 Mäntsälä (N) × K954 Pieksänmäen (C)	6
Narrow	6N70	E473 Mäntsälä (N)	6
Narrow	6N71	E473 Mäntsälä (N)	6
Narrow	6N72	E473 Mäntsälä (N)	6
Narrow	6N75	E473 Mäntsälä (N)	6
Narrow	6N76	E473 Mäntsälä (N)	6
Total	16		96

at the University of Joensuu, Faculty of Forest Sciences. For this purpose, rectangular wood specimens of 5 mm × 5 mm size (a radial segment from pith to bark) were first cut out, and thereafter stabilised for a few weeks to have a moisture content of 12% (air dry). The sample specimens were scanned with the ITRAX X-ray, which works with automatic collimator alignment (Bergsten et al. 2001) at a geometrical resolution of 40 measurements per mm. For the X-ray measurements, the standard X-ray intensity (30 kV, 35 mA) was used, with an exposure time of 20 ms (Bergsten et al. 2001, Peltola et al. 2007).

The X-ray images were examined with the Density software program (Bergsten et al. 2001) and excel macros to provide, based on ring density, the profiles following variables for each annual ring: ring width (RW, mm) and earlywood and latewood widths (EWW and LWW, mm), mean intra-ring wood density (WD, g/cm^3), minimum and maximum intra-ring wood densities (g/cm^3) and earlywood and latewood densities (EWD and LWD, g/cm^3). The average of the maximum and minimum intra-ring densities was used as the threshold for early and latewood in each ring (values above the average were defined as latewood, whereas the values below as earlywood).

For the intra-ring analyses of fibre properties, matchstick-sized wood specimens (each representing two annual rings) were chipped away next to corresponding wood specimens used for X-ray analysis and macerated in a boiling 1:1 (v/v) mixture of acetic acid and hydrogen peroxide. Thereafter, the fibre samples were diluted in 200 ml of water and measured with a L&W Fiber Tester (AB Lorentzen & Wettre, Kista, Sweden), which is a new measurement system based on two-dimensional image analyses, making it possible to determine the fibre length (FL, mm) and fibre width (FW, μm) for up to ten thousand fibres from each sample within a few minutes. The fibre coarseness (C, μg/m) was calculated based on dry weight of the sample and total length of fibres measured (see Karlsson 2006). Similarly, average of fibre wall thickness (FWT, μm) was determined as follows:

$$\mathrm{FWT} = \frac{\mathrm{FW}}{2} - \sqrt{\frac{\mathrm{FW}^2}{4} - \frac{\mathrm{C}}{\pi \times \mathrm{R}}} \qquad (1)$$

where FW is the average fibre width, C the average coarseness of the sample, and R is the expected density of fibre walls (for Norway spruce R of 1.5 g/cm^3 was used, see Kollman and Cõte 1968).

2.3 Data Analyses

Based on the intra-ring measurements from pith to bark, the weighted averages for wood density traits (WD, EWD and LWD) and fibre properties (FL, FW, FWT and C) for each sample tree was calculated by weighting each intra-ring value with its corresponding ring width. In addition, mean RW, EWW and LWW were also determined for each sample tree. The phenotypic coefficient of variation (CV_p) was calculated by normalising the standard deviation (σ) with the mean (μ) of the property for each genetic entry (i.e. $CV_p = \sigma \times 100/\mu$).

Statistical analyses were made using the SPSS statistical program package (SPSS for Windows, version 15.0, SPSS, Chicago, IL). Analysis of variance was performed for growth and yield traits (diameter, height, stem volume, EWW, LWW and RW), wood density traits (WD, EWD, LWD) and fibre properties (FL, FW, FWT and C) for the two crown types with the genetic entries nested within each crown type using the General Linear Model procedure. Block factor was tested as a random factor, but since it occurred not to be a significant variable, it was not included in the final model. Thus, the model applied to test the differences was as follows,

$$Y_{ijk} = \mu + C_i + GE_{j(i)} + e_{ijk} \qquad (2)$$

where Y_{ijk} is the value of the studied trait, μ is the general mean, C_i is the crown type fixed effect, $GE_{j(i)}$ is the random effect of the genetic entries within the crown type, and e_{ijk} is the residual effect.

Additionally relationships between different growth, yield, wood density traits and fibre properties were examined using phenotypic correlations, which have earlier been found to be generally comparable with genetic ones, especially if presented as an average over all the genetic entries (Haapanen and Pöykkö 1993, Zhang and Morgenstern 1995). The phenotypic correlations (r_p) between properties were computed using 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 properties 2, respectively. We reported correlations as significant at $p < 0.05$ level.

3 Results

3.1 Phenotypic Variation in Different Traits

Regarding the average phenotypic variation of the yield traits in the narrow crowned Norway spruce clones, the stem volume clearly showed the highest variation (average of 85%), followed by the breast height diameter and height (averages of 33 and 24%, respectively) (Table 2). As a comparison, in normal crowned genetic entries the phenotypic variation was, on average, considerably smaller especially for stem volume (average of 60%) (Table 2). Concerning the average yield traits, narrow crowned spruce clones and normal crowned genetic entries differed in respect to tree height, stem diameter and volume. On average, normal crowned genetic entries had 94% higher volume than narrow crowed clones (Fig. 1a), and 33% and 27% larger diameter and height, respectively (Table 2). Even if several narrow crowned clones, such as 4N29, 4N24 and 6N70, had, on average, a larger yield than the average of all narrow crowned clones, they were still lower than the most productive normal crowned genetic entries (Table 3). However, within the narrow crowned type, a large variability was found, especially for stem volume, i.e. the highest value was 52% larger than the average for the narrow crowned clones, while the lowest one was only 45% of the average. Nonetheless, no statistically significant differences were observed among the genetic entries regardless of the yield trait, neither within narrow crowned nor normal crowned types, due to large variation observed within genetic entries ($p > 0.05$) (table 2).

In comparison to the yield traits, the growth properties showed, on average, remarkably lower phenotypic variation ranging between 21 and 23% in narrow crowned clones, and between 16 and 25% in normal crowned genetic entries (Table 2). Moreover, on average, normal crowned genetic entries showed 12% wider earlywood widths and 10% wider annual rings, in addition to 2% wider latewood widths. Nevertheless, there were no statistically significant differences nor between both crown types neither within each crown type (among different genetic entries), despite of the growth trait (Table 2).

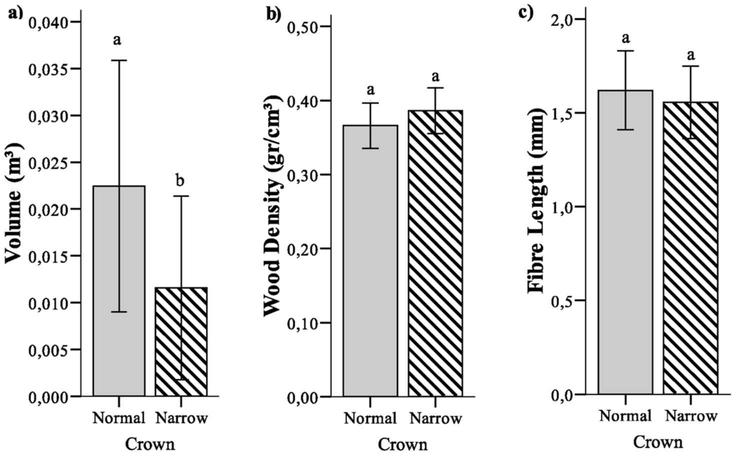

Fig. 1. Average stem volume, overall wood density and fibre length (with standard deviation) for the narrow and normal crowned genetic entries. Different letters above the bars indicate differences among two crown types ($p < 0.05$).

Table 2. Average statistics and phenotypic coefficient of variation ($CV_{p,\,\%}$) for narrow and normal crowned genetic entries, and analysis of variance (F-value and correspondent p[1]) for crown type and genetic entries within crown type for height, diameter (DBH), volume, early and latewood width (EWW, LWW), ring width (RW), early and latewood density (EWD, LWD), overall wood density (WD), fibre length and width (FL, FW), coarseness (C) and fibre wall thickness (FWT).

Trait	Narrow crowned		Normal crowned		Crown type		Genetic entry within crown type	
	Mean	CV_p	Mean	CV_p	F-ratio	P-value	F-ratio	P-value
Height (m)	5.7	23.6	7.3	17.1	**15.5**	**0.00**	1.37	0.19
DBH (cm)	6.0	32.7	8.0	25.8	**11.9**	**0.00**	1.30	0.23
Volume (m^3)	0.012	84.9	0.022	59.8	**14.8**	**0.00**	1.05	0.42
EWW (mm)	2.5	23.5	2.8	25.4	2.35	0.15	1.59	0.10
LWW (mm)	0.57	20.9	0.59	16.1	0.14	0.72	1.70	0.07
RW (mm)	3.1	20.7	3.4	21.6	2.32	0.15	1.54	0.12
EWD (gr/cm^3)	0.340	7.9	0.320	7.7	2.96	0.11	**3.95**	**0.00**
LWD (gr/cm^3)	0.585	6.0	0.575	6.6	0.42	0.53	**3.89**	**0.00**
WD (gr/cm^3)	0.386	8.0	0.366	8.4	2.30	0.15	**4.05**	**0.00**
FL (mm)	1.56	12.4	1.62	12.9	0.84	0.38	**2.14**	**0.02**
FW (µm)	25.2	5.8	26.4	6.3	4.30	0.06	**2.37**	**0.01**
C (µg/m)	122	10.8	133	11.2	**5.84**	**0.03**	**1.91**	**0.04**
FWT (µm)	1.07	5.9	1.12	5.4	**4.57**	**0.04**	**2.02**	**0.03**

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

Within the wood density traits, LWD had in narrow crowned clones, on average, the lowest phenotypic variation (average of 6%), followed by EWD (average of 7.9%) and overall WD (average of 8%). The normal crowned genetic entries used in comparison followed the same patterns as the narrow crowned clones. In both crown types, the wood density traits showed much lower phenotypic variation than the growth and yield traits (Table 2). Moreover, the narrow crowned clones showed, on average, higher wood density in spite of the wood density trait considered; both EWD and WD were 6% higher (Fig. 1b), and LWD 2% higher than the normal crowned genetic entries used in comparison, but these differences were not statistically significant ($p>0.05$) (Table 2).

Table 3. Average statistics and phenotypic coefficient of variation ($CV_{p,\ \%}$) for breast height diameter (cm), height (m), stem volume (m^3), earlywood width (EWW, mm), latewood width (LWW, mm) and ring width (RW, mm) for different normal crowned (1C–3C) and narrow crowned (4N24–6N76) genetic entries.

Genetic entry	Diameter		Height		Volume		EWW		LWW		RW	
	Mean±sd	CV_p	Mean±sd	CV_p	Mean±sd	CV_p	Mean±sd	CV_p	Mean±sd	CV_p	Mean±sd	CV_p
1C	7.4±1.7	22	7.6±1.2	15	0.020±0.010	50	2.5±0.7	27	0.52±0.04	8	3.0±0.68	23
2C	8.1±2.0	25	7.0±0.9	12	0.021±0.014	64	2.9±0.6	21	0.63±0.08	13	3.5±0.54	16
3C	8.6±2.6	31	7.2±1.7	24	0.026±0.017	67	3.1±0.9	28	0.61±0.12	20	3.7±0.88	24
4N24	7.2±2.7	37	6.4±1.7	26	0.018±0.019	103	2.8±0.4	13	0.63±0.10	16	3.5±0.57	16
4N25	5.1±1.1	22	5.2±0.8	15	0.007±0.004	57	2.1±0.6	26	0.57±0.04	7	2.7±0.54	20
4N28	5.0±1.9	38	5.0±0.9	18	0.007±0.006	77	2.2±0.7	31	0.61±0.11	18	2.8±0.76	27
4N29	7.2±2.4	34	6.4±1.5	24	0.018±0.015	87	2.8±0.8	28	0.61±0.13	22	3.4±0.87	26
5N43	6.5±1.6	25	5.8±1.0	17	0.012±0.008	67	2.7±0.6	23	0.57±0.19	34	3.2±0.64	20
5N44	4.5±1.1	25	4.7±0.9	19	0.005±0.003	56	2.1±0.3	14	0.55±0.05	10	2.7±0.33	12
5N45	4.9±1.2	24	4.8±1.2	25	0.006±0.004	63	2.2±0.2	10	0.50±0.03	5	2.7±0.22	8
5N46	5.7±1.4	25	5.6±1.2	19	0.009±0.005	50	2.5±0.4	17	0.53±0.05	10	3.1±0.44	14
6N70	7.1±2.2	31	6.7±1.5	23	0.017±0.011	63	2.8±0.7	24	0.61±0.09	15	3.4±0.73	22
6N71	7.2±2.5	35	5.6±1.7	28	0.017±0.012	74	3.1±0.7	23	0.47±0.06	12	3.6±0.77	22
6N72	6.0±2.0	33	5.9±1.6	27	0.012±0.009	74	2.5±0.4	15	0.58±0.16	28	3.1±0.51	17
6N75	6.2±1.7	27	6.4±1.3	21	0.012±0.009	71	2.4±0.4	16	0.55±0.10	18	2.9±0.47	16
6N76	5.8±1.9	34	5.5±1.3	24	0.010±0.006	59	2.4±0.8	31	0.60±0.06	10	3.0±0.71	24

Table 4. Average statistics and phenotypic coefficient of variation ($CV_{p,\ \%}$) for earlywood (EWD, gr/cm^3) and latewood densities (LWD, gr/cm^3) and overall wood density (WD, gr/cm^3) for different normal crowned (1C–3C) and narrow crowned (4N24–6N76) genetic entries.

Genetic entries	EWD		LWD		WD	
	Mean±sd	CV_p	Mean±sd	CV_p	Mean±sd	CV_p
1C	0.32±0.03	9.6	0.59±0.05	8.0	0.37±0.04	11.4
2C	0.31±0.02	5.9	0.55±0.03	5.6	0.35±0.03	7.6
3C	0.34±0.02	4.7	0.58±0.03	4.5	0.38±0.02	5.1
4N24	0.31±0.02	5.8	0.55±0.04	7.6	0.36±0.02	5.7
4N25	0.35±0.01	4.2	0.60±0.03	5.5	0.40±0.02	5.3
4N28	0.37±0.02	6.6	0.61±0.02	3.2	0.42±0.02	5.8
4N29	0.33±0.03	8.8	0.58±0.04	6.5	0.38±0.03	7.7
5N43	0.34±0.02	5.0	0.57±0.03	5.5	0.38±0.03	7.0
5N44	0.36±0.02	6.9	0.58±0.03	4.4	0.41±0.03	6.4
5N45	0.35±0.02	6.2	0.60±0.02	2.7	0.40±0.02	5.7
5N46	0.34±0.02	6.4	0.60±0.02	3.7	0.39±0.03	6.5
6N70	0.32±0.03	8.0	0.56±0.03	5.0	0.36±0.03	7.0
6N71	0.31±0.03	9.9	0.55±0.02	3.7	0.35±0.03	8.6
6N72	0.35±0.02	4.6	0.61±0.03	5.1	0.40±0.02	3.9
6N75	0.36±0.02	5.6	0.63±0.02	3.3	0.41±0.02	4.4
6N76	0.32±0.01	4.0	0.57±0.02	4.4	0.37±0.02	6.5

On the other hand, significant differences were observed among the genetic entries within each crown types in respect to different wood density traits ($p<0.05$) (Table 2). In this sense, within the narrow crowned clones, 4N28 and 6N75 showed the highest EWD (5.7–7.6% above the average), LWD and WD (4.2–7.7% and 6.2–8.7% above the average, respectively), while 4N24 and 6N71 represented the lowest (being 90–94% of the average) (Table 4).

Table 5. Average statistics and phenotypic coefficient of variation ($CV_{p,\,\%}$) for fibre length (FL), fibre width (FW), fibre wall thickness (FWT) and coarseness (C) for different normal crowned (1C–3C) and narrow crowned (4N24–6N76) genetic entries.

Genetic entry	FL (mm)		FW (µm)		FWT (µm)		C (µg/m)	
	Mean±sd	CV_p	Mean±sd	CV_p	Mean±sd	CV_p	Mean±sd	CV_p
1C	1.71±0.21	12.4	26.3±1.7	6.5	1.15±0.07	6.5	137±17	12.5
2C	1.56±0.17	11.1	26.1±1.3	4.9	1.10±0.04	3.8	130±11	8.5
3C	1.59±0.24	15.4	26.7±2.1	7.9	1.10±0.05	4.9	133±18	13.4
4N24	1.45±0.18	12.2	25.6±1.6	6.4	1.05±0.06	6.2	122±16	12.8
4N25	1.50±0.13	8.7	24.8±1.2	4.6	1.08±0.06	5.8	121±11	9.4
4N28	1.36±0.15	10.9	24.1±1.3	5.3	1.01±0.07	6.5	110±11	10.4
4N29	1.71±0.16	9.6	26.3±1.3	4.8	1.08±0.08	7.1	128±14	11.1
5N43	1.67±0.12	6.9	24.8±0.7	2.7	1.08±0.04	3.6	120±7	5.8
5N44	1.38±0.11	8.1	23.4±0.7	3.0	1.00±0.05	4.6	106±8	7.3
5N45	1.50±0.16	10.5	24.7±1.3	5.1	1.09±0.06	5.5	121±10	8.5
5N46	1.59±0.17	10.5	25.1±0.9	3.5	1.07±0.05	4.9	121±10	8.0
6N70	1.62±0.11	6.9	26.5±1.2	4.3	1.12±0.03	3.1	134±9	6.8
6N71	1.60±0.22	13.7	26.3±1.4	5.4	1.06±0.05	4.9	126±13	10.4
6N72	1.55±0.23	15.1	25.5±1.5	5.9	1.07±0.07	6.5	123±14	11.6
6N75	1.63±0.14	8.3	25.2±1.1	4.4	1.11±0.05	4.9	126±10	8.3
6N76	1.68±0.29	17.0	26.1±1.8	7.0	1.09±0.06	5.6	130±16	12.2

Regarding the fibre properties, FW and FWT showed, in narrow crowned clones, on average, the lowest phenotypic variation (averages of 5.8 and 5.9%), followed by C and FL (averages of 10.8 and 12.4%). In comparison, the variation observed in normal crowned genetic entries, were similar to that for narrow crowned clones. Among all the genetic entries, narrow crowned clones represented, in general, the lowest values for the fibre properties, while the normal crowned genetic entries the largest (Table 5). However, some narrow crowned clones such as 4N29 and 6N70 had, on average, as large values as the normal crowned genetic entries. Accordingly, the normal crowned genetic entries had on average 4% longer and 5% wider fibres than the narrow crowned clones (Fig. 1c), in addition to 4% larger FWT, and 9% larger C. Nonetheless, these differences between the narrow and normal crowned genetic entries were significant only for C and FWT, but not for FL and FW ($p<0.05$) (Table 2). Moreover, significant differences were found among the genetic entries within the crown types in respect to different fibre properties.

3.2 Phenotypic Correlations among Traits

In the narrow crowned Norway spruce clones, the phenotypic correlations between the yield properties (height, breast height diameter and stem volume) were positive and high (0.90–0.95, $p<0.05$). However, volume was calculated based on diameter and height. In addition, the correlations between yield and the growth traits (EWW, LWW and RW) were also positive, ranging from moderate to high (0.48–0.89, $p<0.05$) (Table 6). For comparison, in the normal crowned genetic entries, the phenotypic correlations generally followed similar patterns to the narrow crowned clones, excluding between LWW and the yield traits, which were very low and statistically not significant (Table 6).

Regarding wood density traits, the correlations among them were positive regardless of crown type, and ranged from moderate to high ($p<0.05$) (Table 6). Additionally, in narrow crowned clones, the correlations observed between EWD and WD, and yield and growth traits (excluding LWW) were negative and from moderate to high (from –0.42 to –0.65, $p<0.05$), while the correlations between LWD and the growth and yield traits were weak and statistically not significant

Table 6. Phenotypic correlations (r_p) between mean diameter at breast height (DBH), height (H), stem volume (V), earlywood width (EWW), latewood width (LWW), ring width (RW), earlywood density (EWD), latewood density (LWD), overall wood density (WD), fibre length (FL), fibre width (FW), coarseness (C) and fibre wall thickness (FWT) for narrow crowned (upper right) and normal crowned (lower left) genetic entries (Correlations at p < 0.05 marked in bold).

		Narrow crowned												
		DBH	H	V	EWW	LWW	RW	EWD	LWD	WD	FL	FW	FWT	C
Normal crowned	DBH		**0.94**	**0.95**	**0.86**	**0.50**	**0.89**	**–0.55**	–0.09	**–0.54**	**0.67**	**0.82**	**0.48**	**0.71**
	H	**0.82**		**0.90**	**0.76**	**0.48**	**0.80**	**–0.48**	0.00	**–0.45**	**0.70**	**0.83**	**0.57**	**0.77**
	V	**0.98**	**0.85**		**0.80**	**0.56**	**0.84**	**–0.44**	–0.08	**–0.42**	**0.56**	**0.76**	**0.46**	**0.67**
	EWW	**0.94**	**0.73**	**0.92**		**0.30**	**0.98**	**–0.59**	–0.10	**–0.65**	**0.52**	**0.71**	**0.31**	**0.57**
	LWW	0.14	0.16	0.07	0.16		**0.47**	–0.14	–0.19	0.01	0.13	**0.32**	0.10	**0.24**
	RW	**0.93**	**0.73**	**0.90**	**0.99**	0.29		**–0.57**	–0.13	**–0.60**	**0.51**	**0.72**	**0.31**	**0.57**
	EWD	**–0.48**	**–0.51**	–0.45	–0.46	–0.02	–0.45		**0.59**	**0.96**	**–0.43**	**–0.51**	**–0.26**	**–0.42**
	LWD	–0.30	–0.16	–0.20	–0.41	–0.43	–0.45	**0.60**		**0.61**	0.02	–0.06	0.14	0.04
	WD	**–0.65**	**–0.58**	**–0.60**	**–0.68**	–0.01	**–0.66**	**0.94**	**0.71**		**–0.43**	**–0.51**	–0.22	**–0.40**
	FL	0.09	0.32	0.14	0.00	–0.17	–0.02	–0.41	0.12	–0.29		**0.81**	**0.74**	**0.84**
	FW	0.33	**0.50**	0.36	0.31	0.22	0.32	–0.22	0.02	–0.23	**0.70**		**0.71**	**0.93**
	FWT	0.03	0.30	0.08	–0.12	–0.13	–0.13	–0.14	0.42	0.01	**0.76**	**0.75**		**0.91**
	C	0.22	0.44	0.25	0.13	0.07	0.14	–0.21	0.21	–0.13	**0.78**	**0.95**	**0.92**	

(Table 6). As a comparison, in the normal crowned genetic entries, WD, EWD and LWD followed similar patterns as the narrow crowned clones (Table 5, Fig. 2a). For instance, the correlation between WD and diameter in both crown types were negative and high ($p<0.05$) (Table 5, Fig. 2a).

All the phenotypic correlations observed between different fibre properties (FL, FW, C and FWT), in both the narrow crowned clones as well as in the normal crowned genetic entries, were strong and positive ($p < 0.05$), ranging from 0.70 to 0.95 (Table 6, Fig. 2b). In addition, the fibre properties showed, in the narrow crowned clones, from moderate to high positive correlation with all the yield traits (Fig. 2c, 2e), and from low to moderate, but also positive correlation with EWW and RW ($p<0.05$). Similarly, all the fibre properties had, in general, a negative and significant correlation with EWD and WD ($p<0.05$) (Fig. 2d, 2f), (excl. between FWT and WD), but no clear correlation with LWD. As a comparison, in regards to the correlations between fibre properties and all the other traits, differences could be observed between narrow and normal crowned genetic entries, since the only significant phenotypic correlation observed within the normal crowned ones was that found between height and FW, while all the others were very weak and not significant ($p>0.05$) (see Fig. 2 for comparison).

4 Discussion and Conclusions

In this study, yield traits (tree diameter, height and stem volume) clearly showed the highest phenotypic variation, and wood density traits and fibre properties the lowest variation. Similarly, several previous studies have showed considerably lower phenotypic variation for fibre properties and wood density traits than growth and yield traits in normal crowned Norway spruce (e.g. Hannrup et al. 2004, Zubizarreta Gerendiain et al. 2007, 2008a). In addition, in the present study the phenotypic variation was in some degree larger in narrow crowned Norway spruce clones in respect to the yield traits, and especially in the case of stem volume compared to normal crowned genetic entries.

Moreover, the normal crowned genetic entries showed, on average, significantly higher yield than the narrow crowned clones, when grown at a spacing of 2 m × 1.5 m (about 3300 seedlings/ha), which was the case of the present study. In fact,

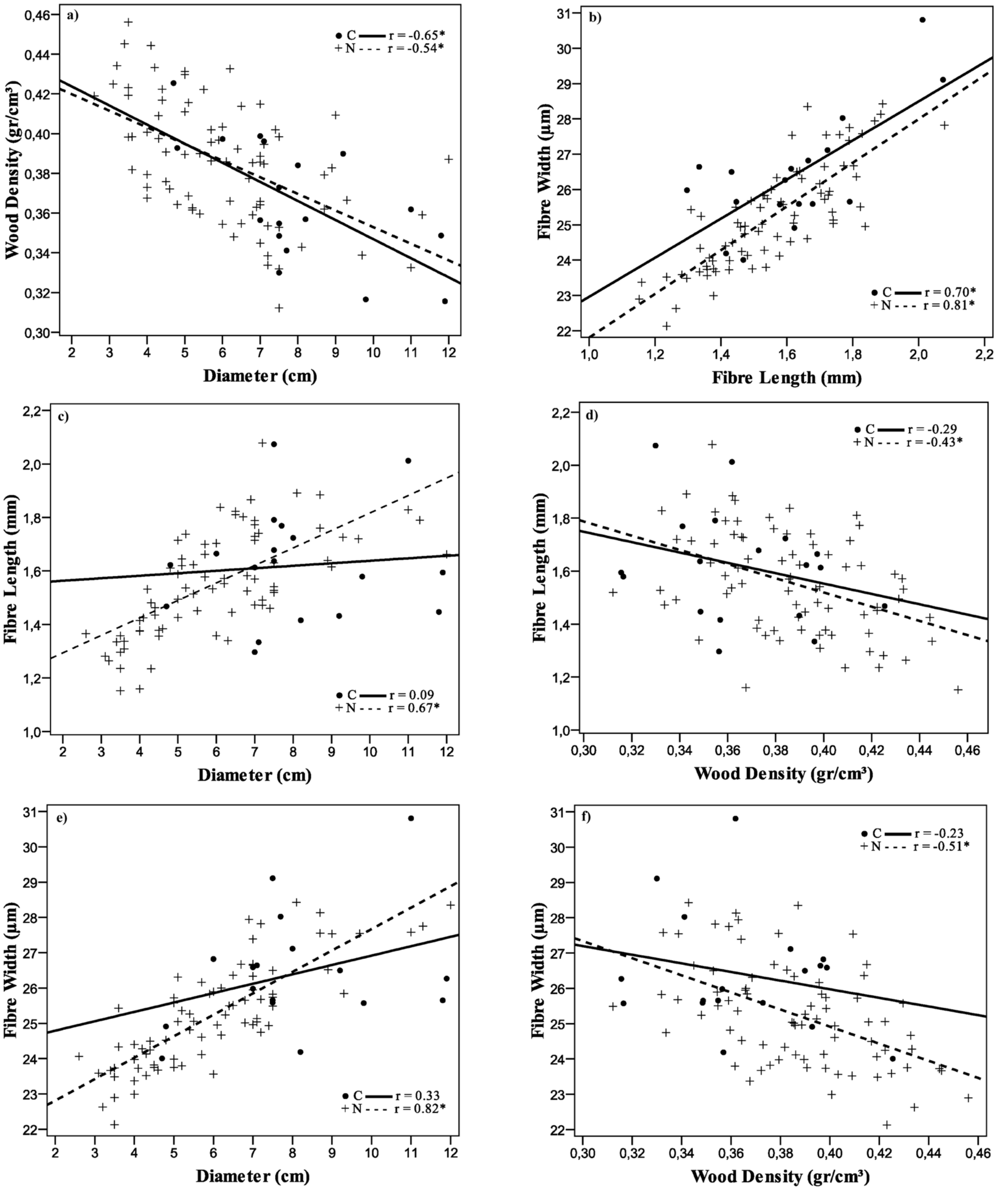

Fig. 2. Phenotypic correlations between breast height diameter, overall wood density, fibre length and fibre width for normal (C) and narrow crowned (N) genetic entries. Correlations significant at $p < 0.05$ are marked with *.

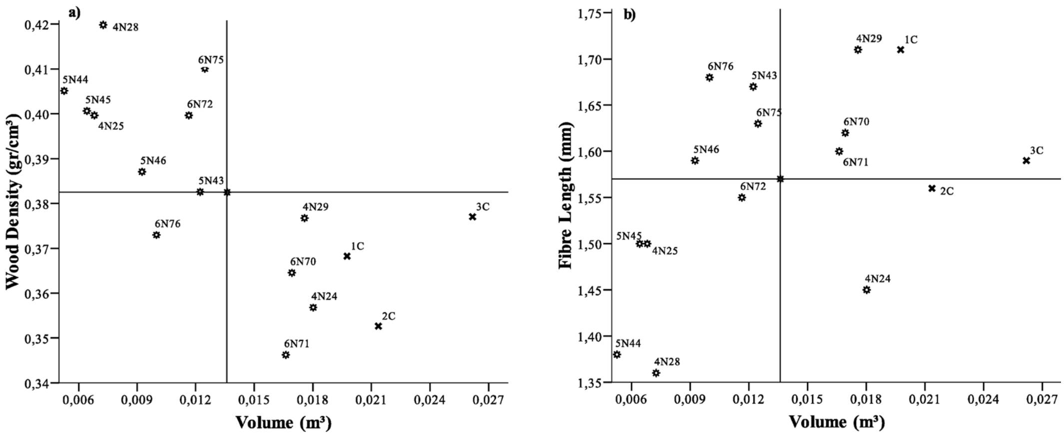

Fig. 3. Relationships between stem volume and overall wood density (a) and stem volume and fibre length (b) for the 16 genetic entries. The lines represent the average values over all the genetic entries for each trait.

on average, they were 27% taller, and had 33% larger breast height diameter and 94% higher stem volume. Our current findings are in concordance with previous studies in narrow crowned Norway spruce, where the normal crowned genetic entries had larger above ground dry biomass production than pendula trees, when grown at a spacing of 2 m×2 m (Pulkkinen and Pöykkö 1990, Pulkkinen 1991a, 1991c). In contrast, the present results are opposite to previous findings by Zubizarreta Gerendiain et al. (2008b), in which narrow crowned Norway spruce families showed, on average, lower phenotypic variation and higher yield traits than normal crowned genetic entries regardless of trait studied when grown at very dense spacing (of 1 m×1 m) on agricultural soil in southern Finland.

On the other hand, when comparing the findings of the narrow and normal crowned genetic entries in current study, we should keep in mind that they were grown as a mixture field trial where around 90% of the trees were narrow crowned ones. Thus, the crown competition between neighbouring trees at the current spacing (2 m×1.5 m) was in practice significantly lower for normal crowned genetic entries, compared to the situation in which the whole plantation would consist of only normal crowned genetic entries. Based on this, we could roughly estimate that the competition situation for narrow crowned clones would approximately correspond to a stand density of about 3900 trees/ha compared to that of about 1800 trees/ha for normal crowned genetic entries, if considering a crown size ratio of normal crowned tree to be about twice of that of narrow crowned one. Although, proper estimation of total stem wood production per occupied ground area would be difficult, we could approximately estimate it as a total average stem wood production of 45 m^3/ha for narrow crowned clones and 40 m^3/ha for normal crowned genetic entries when taking into account real competition situation in our field trial.

In terms of fibre characteristics, even if the normal crowned genetic entries, on average, showed longer and wider fibres, the differences were small. As a comparison, Zubizarreta Gerendiain et al. (2008b) found that at extremely narrow spacing, the narrow crowned Norway spruce concurrently produced significantly higher stem volume and longer fibres, but on average lower wood density, than the normal crowned genetic entries used as a comparison. Moreover, the overall wood density observed in the present work for narrow crowned clones was, in line with the previous findings in narrow crowned families grown in dense spacing (Zubizarreta Gerendiain et al. 2008b). Nonetheless, different narrow crowned clones showed variations in all the studied fibre properties and wood density traits in addition to growth and yield traits (see Fig. 3), making these results in agreement with previous studies in Norway spruce, where the different clones or families showed diversity in the studied properties (Zubizarreta Gerendiain et al. 2007, 2008a, 2008b).

The negative phenotypic correlation observed between stem growth and overall wood density for narrow crowned genetic entries agrees with corresponding findings in normal crowned Norway spruce by many authors (e.g. Lindström 1996, Hylen 1997, Dutilleul et al. 1998, Saranpää 2003) and in narrow crowned ones by Zubizarreta Gerendiain et al. (2008b). In addition, the positive phenotypic correlation between different fibre properties and between different wood density traits (ranging from moderate to high) also agree with the previous ones presented by Zubizarreta Gerendiain et al. (2007, 2008a, 2008b) for normal and narrow crowned genetic entries of Norway spruce. On the other hand, there are contradictory results regarding the correlation between fibre properties and growth rate; several previous investigations showed that increasing growth rate decreases fibre length and fibre wall thickness, and increases fibre width (e.g. Sirviö and Kärenlampi 2001, Jaakkola et al. 2005, Mäkinen et al. 2007). However, according to some other studies, no clear correlation, or even a positive correlation, between growth rate and fibre length could be found in some genetic entries of Norway spruce (Zobel and van Buijtenen 1989, Bergqvist et al. 2000, Zubizarreta Gerendiain et al. 2008a).

In the present study, in narrow crowned clones there was a clear positive phenotypic correlation between the growth and yield traits, and all the fibre properties, including fibre length. However, for normal crowned genetic entries those correlations were weak, and did not follow any general pattern. In this sense, narrow and normal crowned genetic entries differed, having the narrow crowned clones the highest phenotypic correlations. This was opposite to previous work by Zubizarreta Gerendiain et al. (2008b), in which the normal crowned genetic entries grown at very narrow spacing showed, on average, higher phenotypic correlations. In any case, although the phenotypic and genetic correlations could be taken as comparable, the phenotypic ones are usually higher than the genetic correlations (Haapanen and Pöykkö 1993, Zhang and Morgenstern 1995). Thus, our correlations could be expected, to some extent, to overestimate the latter ones.

To conclude, as it was demonstrated in this work as well as in a previous corresponding work by Zubizarreta Gerendiain et al. (2008b), narrow crowned Norway spruce is more efficient and superior in denser spacing compared to normal crowned one, but as having lower plasticity to the free growing space, it can not compete with the latter one in typical spacing used in practical forestry for Norway spruce in Finland. It is also clear, that narrow crowned spruce is not an outstanding tree as an individual, but, since it utilises the environmental resources in an efficient way, it could be grown in dense spacing even without thinning and with a relatively short rotation. However, in the follow-up investigations the response of growth, yield and wood density traits and fibre properties of narrow crowned genetic entries to a range of spacing and environmental conditions (climate, site), but also at older age, should still be studied in more detail. This is because our trees represented mainly juvenile phase (typically 10–15 inner rings in Norway spruce) and the properties of juvenile wood and mature wood may differ from each other. This suggested further work would allow the determination of the optimal management (and spacing), which would provide the desired stem dry mass quantity and quality in the most cost-efficient way.

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