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Differences in Growth and Wood Density Traits in Scots Pine (*Pinus sylvestris* L.) Genetic Entries Grown at Different Spacing and Sites

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In forest breeding, stem volume has typically taken as the most important selection trait, whereas less attention has been given to wood density traits. In this work, we investigated the effects of spacing and genetic entry on the growth, yield and wood density traits in 20 year old Scots pines (Pinus sylvestris L.) based on 10 genetic entries harvested from a spacing trial (stand density range 2000–4000 trees/ha) in central Finland. In order to study also the site effects, we harvested additional material from a trial located in southern Finland (stand density of 2000 trees/ha). Compared to growth and yield properties, wood density traits showed a lower phenotypic variation. Phenotypic correlations among different traits were negative, and mostly moderate to high, suggesting that selection for one trait would simultaneously affect the others. In addition, moderate to strong phenotypic correlations were found among different wood density traits. Stem volume (V) and breast height diameter (DBH) were the largest in widest spacing, whereas in the densest one tree height (H) and latewood percentage were the highest. Genetic entry affected H and wood density traits regardless of spacing. When comparing two sites (with same stand density), genetic entry affected H, whereas site affected DBH and wood density traits. Ranking between genetic entries changed depending on the trait, spacing or site considered. Therefore, no overall ranking was possible. However, we could identify genetic entries having a high V and a relatively high wood density, showing potential for future forest regeneration material.

Keywords genetic entry, stem volume, height, diameter, wood property traits, phenotypic correlation

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1 Introduction

Both quantity and properties of stem wood, such as wood density and fibre length, affects the suitability of tree species and their genetic entries as a raw material for mechanical wood processing and pulp and paper production. Despite this, in long-term breeding programmes for Scots pine (*Pinus sylvestris* L.), stem volume growth and sawn timber quality (branch characteristics and stem straightness) have typically been considered as selection traits of primary importance, whereas other wood properties, such as overall wood density or fibre properties, have been considered as secondary traits (Ståhl 1988, Haapanen and Pöykkö 1993). However, wood density and fibre length are moderately to highly inherited and show moderate genetic age-age correlations between juvenile and mature wood for Scots pine, like in other conifers (Hannrup and Ekberg 1998, Hylen 1999). Therefore, tree selection could be successful even in reasonably young trees (Zobel and van Buijtenen 1989, Hannrup et al. 1998, 2001, Fries and Eriksson 2006).

In Scandinavia, Scots pine is an important source of raw material especially for the sawn timber industry, but also for the pulp and paper industry. In these circumstances, the interaction of the prevailing temperature conditions during the growing season and its length, availability of water, nutrients and light has an effect on the overall growth of trees, and the properties of stem and wood in tree stands (Linder 1987, Allen et al. 1990, Albaugh et al. 1998, Svensson et al. 1999). On the other hand, silvicultural management, such as selection of proper genetic entries and species, spacing, thinning, fertilisation and rotation length, can be used to modify the growth of trees within stands and, thus, affect stem wood production in tree stands.

In pine species, overall wood density is affected by genetic entry, growth rate and ageing of cambium (e.g. Hakkila 1966, Campbell et al. 1986, Björklund and Walfridsson 1993, Persson et al. 1995, Ridoutt et al. 1998, Mörling 2002, Kang et al. 2004). Particularly, in Scots pine, an increase in growth has, in general, been thought to decrease, at least slightly, the overall wood density (Atmer and Thörnqvist 1982, Persson and Persson 1997, Wilhelmsson et al. 2002). However, a non-significant or a weak positive relationship between wood density and growth has also been observed previously in Scots pine (Mörling 2002), and in other tree species such as lodgepole pine (*Pinus contorta*) (Wang et al. 2000), black spruce (*Picea mariana*) (Zhang and Morgenstern 1995, Zhang et al. 1996), and Norway spruce (*Picea abies*) (Bujold et al. 1996, Zubizarreta Gerendiain et al. 2007). Moreover, in Scots pine, overall wood density generally correlates strongly with latewood percentage (Hannrup et al. 2001), which is significantly affected by tree age and growth rate (Hakkila 1966, 1968, Tyrväinen 1995).

Interest to shorten the rotation of Scots pine, as for other production tree species, by increasing the intensity of management (e.g. thinning intensity), can be expected to increase the proportion of juvenile wood (first 10 to 15 annual rings from pith to bark), which has lower overall wood density and different mechanical properties than mature wood (Zobel and van Buijtenen 1989, Thörnqvist 1990, Persson et al. 1995). Thus, genetic entries which have, on average, higher overall wood density also in the juvenile phase would be desirable. In addition to genetic entry, initial stand density also considerably affects the growth and yield (such as height, diameter, stem volume, ring width and earlywood percentage), the properties of the stem (e.g. branches on stem and knots in wood) and wood characteristics such as wood density and fibre length in the early phase of a rotation. This was earlier found, for example, in genetically unimproved Scots pine (Persson 1975, 1976, Ståhl 1988) and jack pine (*Pinus banksiana*) (Kang et al. 2004). It has also been found that in the juvenile phase the overall wood density and ring width do not necessarily correlate negatively in Scots pine (Haapanen et al. 1997, Hannrup et al. 2000). The response of different genetic entries may also be affected by the environmental conditions of the site (e.g. Zobel and Talbert 1984), and therefore, the potential of different genetic entries as future regeneration material should be studied with sufficient spacing variation and different site conditions as well.

Little is known about the interaction between genetic entries and spacing, in respect to simultaneous effects on growth, yield and wood density traits in Scots pine in Finland because few experiments have been designed for this purpose. In the above context, we investigated the effects of genetic entry (mainly full-sib families) and spacing, as well as site, on the growth and yield (such as height, breast height diameter, stem volume and early and late wood width and percentage) and wood density traits (such as mean intra-ring wood density, earlywood and latewood density) in Scots pine (*Pinus sylvestris* L.). The main objective was to find if there exist genetic entries having, simultaneously, a high growth rate and relatively high overall wood density.

2 Material and Methods

2.1 Experimental Data

The material used in this study 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.)). This trial is located on agricultural soil and it consists of three different spacing treatments with initial stand densities of 2000, 4000 and 8000–8200 seedlings/ha. When in autumn 2000, the tending of the seedling stand was carried out, the widest spacing was left unmanaged (referred later as site 1, spacing 1), 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). From this trial, we selected 10 of 20 genetic entries (mainly full-sib families) representing 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 it was not overestimated the effect of one of the parent in the material (plus tree S1101, so called Kanerva pine, was parent tree for 13 of 20 genetic entries). Due to its thin and short branches, Kanerva pine is expected to behave, at least to some degree, in a different way than other genetic entries of Scots pine, especially in denser spacing.

In addition, we harvested material from another trial 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.). It was located on a forest soil (with relatively poor site fertility, *Vaccinium* type), which typically is regenerated with Scots pine in practical forestry in Finland. In this trial (referred later as site 2), the seedlings were planted with an initial stand density of about 2000 seedlings/ha; no pre-commercial thinning was done before harvesting. When selecting genetic entries on this site, we aimed to harvest same ones, which were harvested on site 1. However, only four same genetic entries could be found on these sites and therefore, only 7 genetic entries out of 44 were finally harvested from this site (see Table 1).

Altogether, we randomly harvested, from each site and spacing, five trees per genetic entry (Table 1). Thus, in site 1, in autumn 2006, we harvested a total of 145 sample trees, and in site 2 a total of 35 trees (in autumn 2007). We also measured the height and stem diameters (at 1.3 and 6 m from stem base) for each sample tree, and calculated their stem volume based on volume functions developed by Laasasenaho (1982) for Scots pine. Moreover, 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.

The intra-ring growth and wood densities were measured by the ITRAX X-ray microdensitometer (Cox Analytical Systems, Göteborg, Sweden) at the University of Joensuu, Faculty of Forest Sciences (see Peltola et al. 2007). For this purpose, rectangular wood specimens of 5 mm × 5 mm size (a radial segment from pith to bark) were cut out of the stem discs (at 1 m above ground) and then stabilised for a few weeks to have 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. Based on these density profiles, and with the help of Excel macros, we determined the following intra-ring variables: ring width (RW, mm) and 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

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

Genetic entry no	Crossing type	Site	Entry type	Site origins of mother trees
1	StandardS12	Site 1	Open pollinated forest stand seed	Central: Lieksa (mother)
2	StandardS13	Site 1	Open pollinated forest stand seed	Central: Pihtipudas (mother)
3	C205×S1101	Site 1&2	Controlled crosses seed	Central: Multia (mother), South: Punkaharju (father)
4	C214B×S1101	Site 1&2	Controlled crosses seed	Central: Äänekoski (mother), South: Punkaharju (father)
5	S2582×S1101	Site 1&2	Controlled crosses seed	South: Kuru (mother), South: Punkaharju (father)
6	S104×S1101	Site 1&2	Controlled crosses seed	South: Tammela (mother), South: Punkaharju (father)
7	S104×C205	Site 1	Controlled crosses seed	South: Tammela (mother), Central: Multia (father)
8	C205×S80	Site 1	Controlled crosses seed	Central: Multia (mother), South: Heinola (father)
9	C214B×C205	Site 1	Controlled crosses seed	Central: Äänekoski (mother), Central: Multia (father)
10	SeedOrchardC97	Site 1	Open pollinated orchard seed	Central: Varkaus Kuvansi (mother)
11	C205×S710D	Site 2	Controlled crosses seed	Central: Multia (mother), South: Ruokolahti (father)
12	StandardSPM	Site 2	Open pollinated forest stand seed	South: Pieksämäki (mother)
13	StandardS17	Site 2	Open pollinated forest stand seed	South: Padasjoki (mother)

mean of the maximum and minimum intra-ring densities were used as the threshold for earlywood and latewood in each ring (see Peltola et al. 2007, Helama et al. 2008).

2.2 Data Analyses

Based on intra-ring measurements from pith to bark, we determined the weighted cross-sectional averages for overall wood density (WD), earlywood density (EWD) and latewood density (LWD) for each sample tree by weighting each ring value with its corresponding ring width, as was done previously by, for example, Zubizarreta Gerendiain et al. (2007, 2008a, b). In addition, mean widths of the annual ring (RW), earlywood (EWW) and latewood width (LWW), as well as latewood width percentage (LWW%), were also calculated for each sample tree. Thereafter, statistical analyses were made using the SPSS statistical program package 15.0 (SPSS for Windows, version 15.0, SPSS, Chicago, IL). Differences in growth and yield (diameter, height, stem volume, EWW, LWW, RW, LWW%) and wood density traits (WD, EWD, LWD) between genetic entries in each spacing were tested with a one-way ANOVA, by applying a pairwise analysis (with a 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.

To test the simultaneous effects of genetic entry, spacing and site we applied two-way ANOVA.

We also calculated the phenotypic coefficient of variation (CV%) for each genetic entry (and separately for each spacing and site) by normalising the standard deviation (σ) by the mean (μ) of the property (i.e. $CV\% = \sigma * 100 / \mu$). Relationships between growth and yield and wood density traits were also examined in different genetic entries using phenotypic correlations, which 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 deviations for properties 1 and properties 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.

Similar to our previous work in Norway spruce (see Zubizarreta Gerendiain et al. 2007, 2008a, b), we calculated phenotypic correlations instead of genetic ones because of 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). Previously, Haapanen and Pöykkö (1993) have also suggested that genetic and phenotypic correlations appeared to be considerably analogous in Scots pine, especially when the latter were computed on the genetic entry-mean level (see also e.g. Zhang and Morgenstern 1995). On the other hand, because the genetic correlations estimate the degree of relationship between two traits due to genetic causes and the phenotypic correlations measure the closeness of the relationship between two observed traits, combining, thus, genetic and environmental causes (Hannrup et al. 2000), these correlations would not be fully comparable to each other (see e.g. Hannrup et al. 2000). In our work, we also ranked different genetic entries according to their growth and yield and wood density traits in order to summarise our findings.

3 Results

3.1 Phenotypic Variation in Growth, Yield and Wood Density Traits

3.1.1 Yield Traits

Regardless of the spacing, the height (H) and breast height diameter (D) showed on site 1, on average, the smallest phenotypic variation among the different genetic entries (average of 8–10%), while stem volume (V) showed a larger variation (average of 19–24%). The corresponding average variation observed on site 2 was 8% for H and D and 22% for V. Furthermore, relatively large phenotypic variation was found for yield traits within genetic entries in each of the spacing and site.

On site 1, with spacing 1 (with stand density of 2000 trees/ha), the average D, H and V were 12.2 cm, 10.2 m and 0.067 m^3, respectively (see Table 2). In comparison, in spacing 2 (with stand density of 2000–2500 trees/ha) the average D and V were 4–5% smaller than in spacing 1, while H was 3% higher. In spacing 3 (with stand density of 4000 trees/ha) the average D and V were 17

Table 2. Mean and standard deviation (sd) for the breast height diameter, height, stem volume, latewood percentage (LWW%) and ring width (RW) in spacing 1 to 3 on site 1 (Siilinjärvi trial) and on site 2 (Loppi trial) with stand density of 2000 trees/ha.

Site	Spacing	Diameter (cm) Mean ± sd	Height (m) Mean ± sd	Volume (m^3) Mean ± sd	LWW% Mean ± sd	RW (mm) Mean ± sd
Site 1	2000 trees/ha	12.2 ± 1.1	10.2 ± 1.0*	0.067 ± 0.20*	24 ± 1.7	3.6 ± 0.2
	2000–2500 trees/ha	11.7 ± 1.0	10.5 ± 0.9*	0.064 ± 0.01	26 ± 2.1	3.5 ± 0.3
	4000 trees/ha	10.1 ± 0.8	11.0 ± 1.0*	0.051 ± 0.01	28 ± 1.9	3.0 ± 0.3
Site 2	2000 trees/ha	12.6 ± 1.0	10.2 ± 0.8	0.070 ± 0.02	26 ± 1.5	3.6 ± 0.3

* Differences between genetic entries ($p < 0.05$)

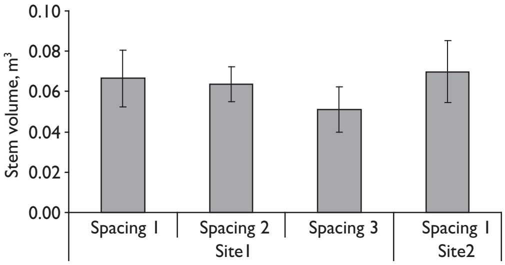

Fig. 1. Average stem volume (V, m^3) for different genetic entries on site 1 with different spacing 1 to 3 (from widest to densest spacing) and on site 2.

and 24% smaller and H was 8% higher compared to spacing 1 (see Table 2). Those differences between spacings were significant for all the three yield traits ($p<0.05$) (Table 3). Moreover, in site 1, regardless of spacing, only the genetic entries with the highest and lowest H and V differed from each other ($p<0.05$) (Fig. 1). Regarding individual genetic entries, genetic entry 9 had the largest D and V in spacing 1 (D 12% and V 37% above the average) and genetic entry 6 in spacing 2 (D 12% and V 31% above the average). Whereas in spacing 3 genetic entry 4 had the largest D (12% above the average) and genetic entry 8 largest V (32% above the average) (see Fig. 3). Thus, the ranking between genetic entries changed depending on the yield trait considered and spacing (see Table 5). In addition the interaction between spacing and genetic entries were not significant for any of the traits ($p>0.05$) (Table 3).

On site 2, the average D, H and V were comparable to those observed in similar spacing (with stand density of 2000 trees/ha) on site 1 (see Table 2), i.e. 12.6 cm, 10.2 m, and 0.070 m^3, respectively. On site 2, genetic entry 4 had clearly the largest D, H and V (12, 13 and 38% above the average). Despite of this, we did not find any significant differences between genetic entries in any of the studied yield traits. However, when comparing the same four genetic entries grown on both sites, we found that site significantly affected D, but not H or V. In addition, genetic entry affected H, but not D or V. Furthermore, no site × genetic entry interaction was observed (Table 3). Thus, the ranking between genetic entries was affected by the site, in addition to the yield trait considered. As a result, no overall ranking between genetic entries was possible (see Table 5).

3.1.2 Growth Traits

On site 1, regardless of the spacing, the earlywood width (EWW) showed, on average, the largest phenotypic variation among the different genetic entries (average of 7–13%), followed by ring width (RW, average of 6–10%) and latewood width and percentage (LWW and LWW%, average of 6–9%). The corresponding average variation observed on site 2, for the different genetic entries, was 10% for EWW and 17, 20 and 13% for RW, LWW and LWW%, respectively. However, similar to yield traits, there existed relatively large phenotypic variation in growth traits within genetic entries in each spacing and site.

On site 1, with spacing 1, the average RW was 3.6 mm while LWW% was 24% (Table 2). In spacing 2 the average RW was 6% lower and LWW% was 8% higher, while in spacing 3 RW was 17% lower and LWW % 17% higher than in spacing 1. In this sense, spacing significantly affected RW (and EWW), which was clearly higher in the two widest spacing compared to the densest one, where LWW% was larger ($p<0.05$). Among the individual genetic entries, genetic entry 10 had the largest RW (9% larger than average) in spacing 1, whereas the lowest LWW% (90% of average) was observed in genetic entry 7. As a comparison, in spacing 2 genetic entry 5 had both the largest RW (10% above average) and the lowest LWW% (87% of average). Whereas in spacing 3, genetic entry 1 had clearly the largest RW (17% above the average) while genetic entry 6 the lowest LWW% (92% of average). Nonetheless, no differences ($p<0.05$) were found between genetic entries in respect to any growth traits, regardless of spacing (Table 3). Thus, similar to yield traits, the ranking between genetic entries changed depending on the growth trait considered and spacing (see Table 5).

As a comparison, on site 2 the average RW and LWW% were very similar to those observed in similar spacing on site 1 (average of 3.6 mm and 26%) (Table 2). On site 2, genetic entry 4 had the largest RW (10% higher), whereas genetic entry 3 had the lowest LWW% (92% of average).

Table 3. Analysis of variance (F-value and probability*) on the effects of spacing and genetic entry and their interaction (spacing × genetic entry) for the growth and yield and wood density traits on site 1 (A), and on the effects of site and genetic entry and their interaction (site × genetic entry) on site 1 versus site 2 (B).

A. Site 1

	Spacing		Genetic entry		Spacing × genetic entry	
	F-ratio	P-value	F-ratio	P-value	F-ratio	P-value
D	**19.05**	**0.00**	1.52	0.15	1.39	0.15
H	**7.97**	**0.00**	**17.40**	**0.00**	1.03	0.43
V	**9.22**	**0.00**	**3.31**	**0.00**	1.31	0.20
EWW	**16.69**	**0.00**	0.73	0.68	1.41	0.14
LWW	1.92	0.15	1.74	0.09	1.48	0.11
RW	**15.31**	**0.00**	0.75	0.66	1.43	0.14
EWD	1.99	0.14	**2.95**	**0.00**	**2.02**	**0.02**
LWD	1.35	0.26	**3.62**	**0.00**	1.00	0.46
WD	0.42	0.66	**2.99**	**0.00**	1.67	0.06

B. Site 1 vs. site 2

	Site		Genetic entry		Site × genetic entry	
	F-ratio	P-value	F-ratio	P-value	F-ratio	P-value
D	**835.62**	**0.00**	1.06	0.38	1.05	0.39
H	1.34	0.26	**2.99**	**0.05**	0.64	0.59
V	0.01	0.91	1.51	0.23	0.92	0.44
EWW	0.09	0.77	1.11	0.36	0.95	0.43
LWW	3.88	0.06	0.78	0.52	0.63	0.60
RW	0.14	0.71	1.05	0.39	0.95	0.43
EWD	**4.81**	**0.04**	1.02	0.40	1.15	0.34
LWD	2.88	0.10	2.33	0.09	0.63	0.60
WD	**8.12**	**0.01**	1.79	0.17	0.48	0.70

* Significance of F-ratio with $p<0.05$ is given in bold.

Regardless of site, no statistically significant differences were found between genetic entries in respect to any growth traits (see Table 3). When comparing the same genetic entries grown on both sites, we also found no genetic entry or site effect on the growth traits considered. Thus, the ranking between genetic entries was also affected by the site in addition to the growth trait considered (see Table 5).

3.1.3 Wood Density Traits

On site 1, regardless of the spacing, wood density traits showed, on average, smaller phenotypic variation among different genetic entries (average of 3–5%) compared to the growth or yield traits. On site 2, the corresponding average variation for different genetic entries was even less (only 1%). However, differences in phenotypic variation still existed between genetic entries in each spacing and site. On average, the overall WD, EWD and LWD were not affected by spacing on site 1 ($p>0.05$). The average of overall WD for different genetic entries was 0.362 g/cm^3 in spacing 1 and 2, while in comparison, the overall WD was only 1% higher in spacing 3 (see Table 4, Fig. 2).

Among the individual genetic entries, genetic entry 2 had, on average, the highest overall WD (about 7% higher than average of all genetic entries) in spacing 1 (see Fig. 3). Moreover, genetic entry 4 had the highest overall WD in

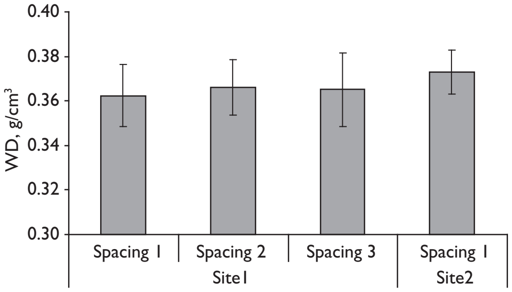

Fig. 2. Overall wood density (WD, g/cm^3) for different genetic entries on site 1 with different spacing 1 to 3 (from widest to densest spacing) and on site 2.

spacing 2, whereas genetic entry 3 had clearly the highest overall WD (about 7% higher than average) in spacing 3 (see Fig. 3). However, only the genetic entries having the highest and lowest EWD in spacing 1, and corresponding EWD and overall WD in spacing 3, differed significantly from each other. Moreover, on site 1, genetic entry significantly affected all the wood density traits ($p < 0.05$), while spacing × genetic entry interaction only affected the EWD (see Table 3). Thus, the ranking between genetic entries changed also depending on the wood density trait considered and spacing (see Table 5).

On site 2, the overall WD was slightly higher (average of 0.373 g/cm^3) compared to the corresponding spacing 1 on site 1, as were EWD and LWD (average of 0.305 and 0.567 g/cm^3, respectively). However, very little variation in the overall WD between genetic entries existed ($p > 0.05$). Genetic entries 3 and 11, with the highest overall WD, had only 2% higher WD than the average for all genetic entries. When comparing the same four genetic entries grown on both sites, we found that site significantly affected EWD and overall WD. However, the ranking between different genetic entries changed significantly depending on the wood density trait considered and site (see Table 5).

3.2 Phenotypic Correlations between Growth, Yield and Wood Density Traits

Regardless of spacing, the phenotypic correlation between different yield traits (D, H and V) was on both sites, on average, a positive and strong between D and V and between H and V, and moderate and positive between D and H ($p < 0.05$) (see Table 6). Nonetheless, V is correlated with D and H, since it was calculated based on those two variables. V and D also showed a strong positive phenotypic correlation with EWW and moderate (site 1) to strong (site 2) positive correlation with LWW ($p < 0.05$). On site 1, V and D had a weak negative correlation with overall WD and EWD, but not with LWD ($p < 0.05$). Unlike on site 2, LWW% correlated moderately and negatively with V and D on site 1 ($p < 0.05$).

RW correlated strongly with EWW and LWW on both sites ($p < 0.05$). On site 1, RW also correlated negatively and moderately with overall WD and weakly (negative correlation) with EWD and LWD ($p < 0.05$). Additionally, a negative moderate phenotypic correlation between overall WD and EWW and between EWW and EWD ($p < 0.05$) was observed on site 1. Furthermore, LWW%

Table 4. Mean and standard deviation (sd) for the early and latewood density (EWD and LWD) and overall wood density (WD) for spacing 1 to 3 on site 1 and on site 2.

Site	Spacing	EWD (g cm^{-3}) Mean ± sd	LWD (g cm^{-3}) Mean ± sd	WD (g cm^{-3}) Mean ± sd
Site 1	2000 trees/ha	0.302 ± 0.01	0.551 ± 0.03*	0.362 ± 0.01
	2000–2500 trees/ha	0.301 ± 0.01	0.550 ± 0.03	0.366 ± 0.01
	4000 trees/ha	0.295 ± 0.01*	0.545 ± 0.02	0.365 ± 0.02*
Site 2	2000 trees/ha	0.305 ± 0.00	0.567 ± 0.01	0.373 ± 0.01

* Differences between genetic entries ($p < 0.05$)

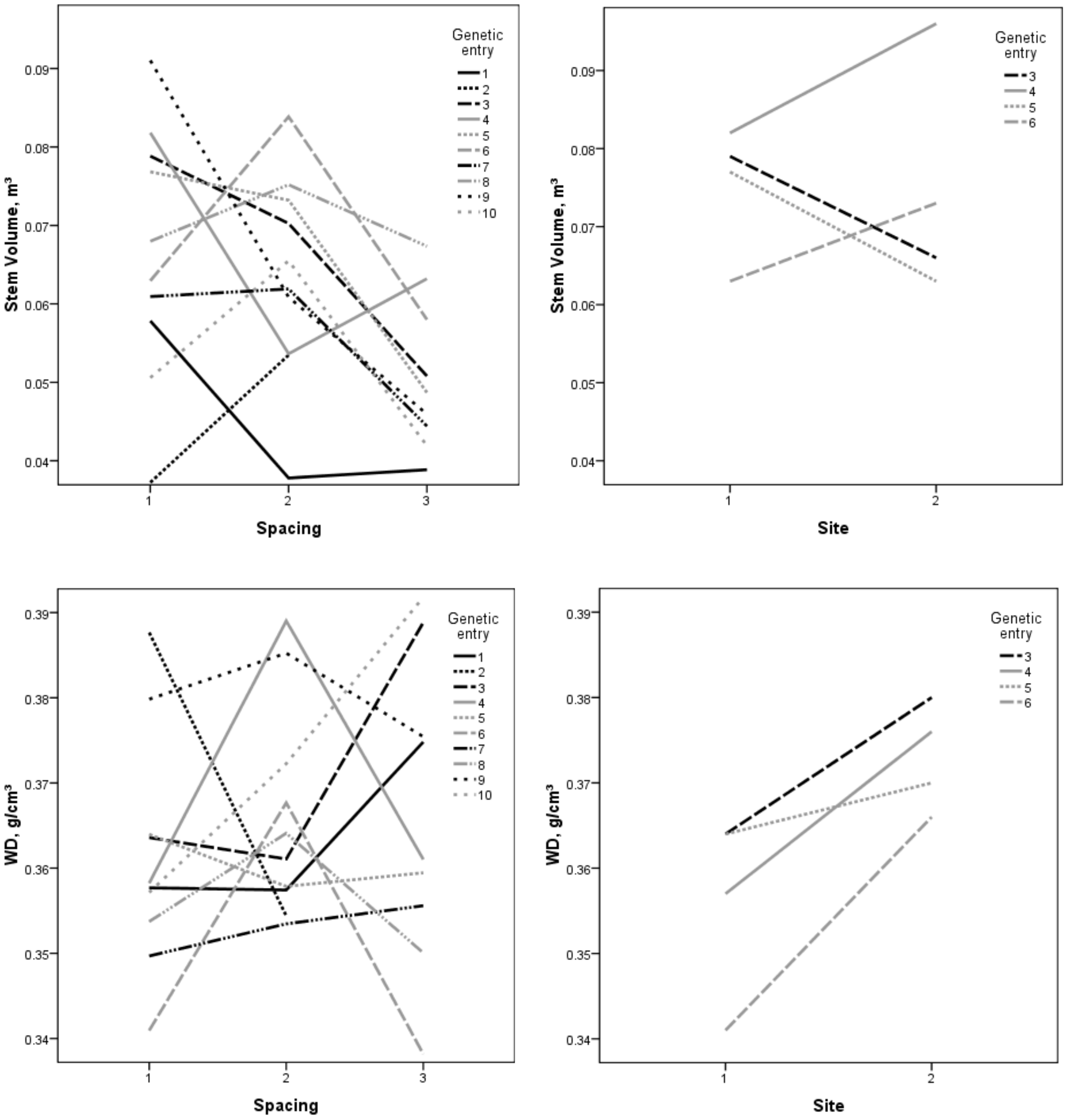

Fig. 3. Effect of spacing on average stem volume (V, m^3) and overall wood density (WD, g/cm^3) for different genetic entries on site 1 (left) and for selected entries grown on both sites 1 and 2 (right).

had a moderate negative correlation with EWW on site 2, whereas it was negative and strong ($p < 0.05$) on site 1. Moreover, strong positive phenotypic correlations were observed among wood density traits on both sites. The correlation was highest between overall WD and EWD, but also strong between overall WD and LWD and moderate between EWD and LWD ($p < 0.05$). However, the average phenotypic correlations observed between overall WD and different growth and yield traits and other wood density traits varied significantly among the genetic entries and sites (see Table 7).

Table 5. Ranking of genetic entries for the growth and yield traits (H, D, V, LWW%) and overall WD, on site 1 for spacing 1 to 3 and site 2. The ranking of genetic entries is done so that highest value gets number 1 and lowest one 10 regardless of trait.

Genetic entries	H				D				V				LWW%				WD			
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		6	10	4		8	10	9		1	9	8		3	8	3	
2. StandardS13*	9	9	-		10	7	-		10	9	-		2	7	-		1	9	-	
3. C205×S1101	1	1	1	2	4	5	6	4	3	4	4	4	4	5	1	1	5	6	1	1
4. C214B×S1101	3	4	4	1	3	9	1	1	2	8	2	1	6	2	3	2	7	1	5	3
5. S2582×S1101	7	8	6	5	2	2	5	5	4	3	5	5	5	10	4	5	4	7	6	5
6. S104×S1101	6	3	2	6	9	1	3	3	6	1	3	3	8	6	9	6	10	4	9	7
7. S104×C205	4	6	7		8	6	9		7	6	7		10	8	5		9	10	7	
8. C205×S80	5	2	3		5	3	2		5	2	1		9	4	7		8	5	8	
9. C214B×C205	2	5	5		1	8	8		1	7	6		3	1	6		2	2	4	
10. SeedOrchardC97	10	7	8		7	4	7		9	5	8		7	3	2		6	3	2	
11. C205×S710D				3				7				6				4				2
12. StandardSPM				4				2				2				3				4
13. StandardS17				7				6				7				7				6

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

Table 6. Phenotypic correlations (r_p) between different growth and yield (D, H, V, EWW, LWW, RW, LWW%) and wood density traits (WD, EWD, LWD) on average for different genetic entries grown on site 1 (regardless of spacing) and 2 (bold means statistically significant correlation, $p < 0.05$). Upper right is shown correlations on site 1 and on lower left for site 2, respectively.

Site 1 Site 2	D	H	V	EWD	LWD	WD	EWW	LWW	RW	LWW%
D		**0.55**	**0.95**	**–0.26**	0.03	**–0.25**	**0.79**	**0.57**	**0.83**	**–0.45**
H	**0.44**		**0.72**	–0.15	0.12	–0.02	**0.17**	**0.29**	**0.22**	0.13
V	**0.93**	**0.65**		**–0.23**	0.07	**–0.19**	**0.67**	**0.54**	**0.71**	**–0.33**
EWD	–0.01	–0.03	–0.06		**0.51**	**0.85**	**–0.34**	**0.02**	**–0.29**	**0.29**
LWD	0.11	**0.40**	0.18	**0.45**		**0.75**	**–0.21**	–0.00	**–0.19**	**0.19**
WD	0.01	0.28	0.07	**0.79**	**0.66**		**–0.52**	0.15	**–0.42**	**0.64**
EWW	**0.85**	**0.19**	**0.74**	–0.01	–0.03	–0.22		**0.42**	**0.98**	**–0.72**
LWW	**0.71**	**0.37**	**0.70**	0.27	0.05	**0.43**	**0.56**		**0.60**	**0.29**
RW	**0.89**	0.26	**0.80**	0.07	–0.01	–0.05	**0.97**	**0.75**		**–0.57**
LWW%	–0.05	0.24	0.06	0.26	0.09	**0.68**	**–0.37**	**0.55**	–0.13	

Table 7. Means for the phenotypic correlations between overall WD and different growth and yield traits and other wood density traits for different genetic entries on site 1 (regardless of spacing) and site 2, latter ones are shown in parenthesis. Bold text means statistically significant correlation ($p<0.05$).

Genetic entry	Phenotypic correlation between WD and						
	EWW	LWW	RW	EWD	LWD	D	V
1. StandardS12	–0.71	0.16	–0.61	0.92	0.82	–0.29	–0.28
2. StandardS13	–0.70	–0.05	–0.62	0.89	0.79	–0.56	–0.54
3. C205×S1101	**–0.70** (0.28)	0.17 **(0.97)**	**–0.60** (0.58)	**0.74** (0.58)	0.71 (0.91)	–0.48 (0.44)	–0.43 (0.65)
4. C214B×S1101	**–0.59** (–0.51)	0.18 (0.33)	–0.50 (–0.30)	**0.91** (0.77)	0.67 (0.90)	–0.47 (0.19)	–0.36 (0.41)
5. S2582×S1101	–0.38 (–0.18)	–0.12 (0.61)	–0.36 (0.06)	**0.87** (0.87)	**0.76** (0.73)	–0.17 (–0.43)	–0.06 (–0.30)
6. S104×S1101	–0.04 (0.33)	0.02 (0.47)	–0.03 (0.41)	**0.94** (0.82)	**0.91** (0.42)	0.26 (0.55)	0.31 (0.74)
7. S104×C205	–0.29	0.01	–0.25	0.71	0.79	0.01	0.09
8. C205×S80	–0.63	–0.25	–0.62	0.61	0.56	–0.51	–0.51
9. C214B×C205	–0.10	0.16	–0.03	0.83	0.95	–0.07	–0.11
10. SeedOrchardC97	–0.60	0.56	–0.49	0.78	0.29	–0.27	–0.02
11. C205×S710D	(0.29)	(0.42)	(0.334)	(0.62)	(0.33)	(0.42)	(0.52)
12. StandardSPM	(–0.72)	(0.62)	(–0.55)	(0.96)	(0.40)	(–0.59)	(–0.64)
13. StandardS17	(0.66)	0.78	(0.69)	(0.86)	(0.98)	(0.82)	(0.91)

4 Discussion and Conclusions

Compared to the growth and yield traits of different genetic entries, the wood density traits generally showed, in Scots pine, significantly lower phenotypic variation regardless of spacing or site, which is in agreement with the previous findings for this species (Persson 1972, Velling 1974) and other species like Norway spruce (*Picea abies*) (e.g. Hannrup et al. 2004, Zubizarreta Gerendiain et al. 2007). The higher variability in growth and yield traits implies that these traits are under poor genetic control, and are affected by the environment and competition between trees (Zhang and Morgenstern 1995, Hannrup et al. 2000).

We also observed that the phenotypic correlations between different growth and yield traits showed moderate to strong positive correlations on both sites, on average. However, they varied between the genetic entries and sites, which is also 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, we found 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 and Morgenstern 1995).

In general, overall wood density showed a weak negative correlation with growth and yield traits. Previously, Haapanen et al. (1997) and Hannrup et al. (2000) have also reported, in Scots pine, weak negative phenotypic and genetic correlations between wood density of juvenile wood and breast height diameter. Contrary to our findings, even a non-significant or a weak positive relationship between wood density and growth has been observed previously in Scots pine (Mörling 2002), in addition to other species such as lodgepole pine (*Pinus contorta*) (Wang et al. 2000). However, especially if significant genetic correlations among various growth, yield and wood density traits exist, selection for one trait would simultaneously affect the other traits.

In our study, spacing affected all yield traits on site 1. The average stem diameter and volume were significantly higher in the two widest spacing compared to the densest one, in which the

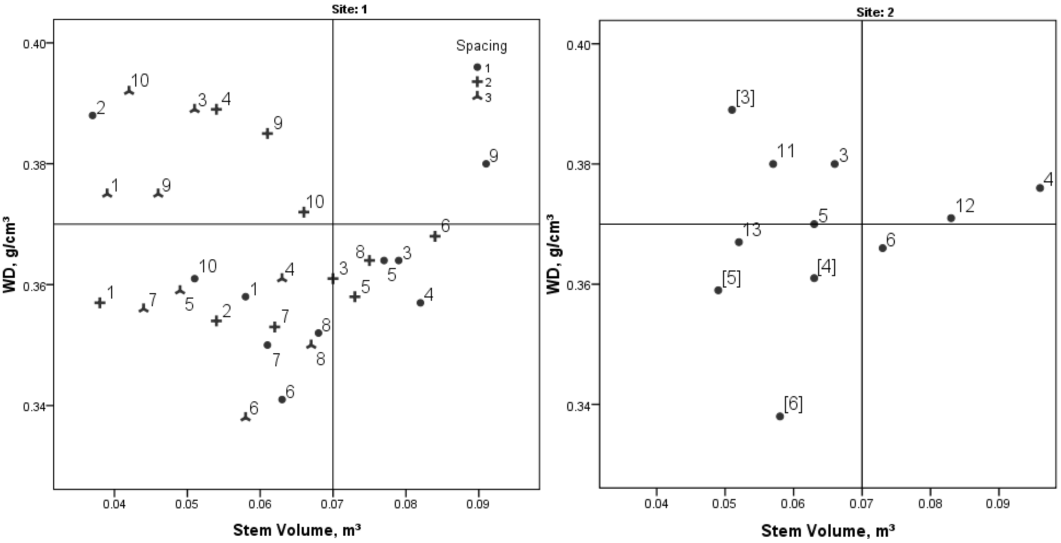

Fig. 4. Relationships between average stem volume (V, m^3) and overall wood density (WD, g/cm^3) for different genetic entries on site 1 with different spacing 1 to 3 (left) and on site 2 (right), respectively. However, in the right, it is also shown in parenthesis the corresponding values for same four genetic entries grown on site 1 for comparison.

average height was highest. However, only the genetic entries with the highest and lowest height differed statistically significantly from each other. Similar to our work, Persson et al. (1995) reported earlier that an increase in spacing increased stem diameter and volume growth at the cost of height growth in Scots pine. In addition, Ståhl (1988) earlier found that average ring width was larger for wider spacing in Scots pine, as a result of relatively larger earlywood percentage in wider spacing. When analysing the concurrent effects of site and genetic entry on yield traits, we found that site significantly affected stem diameter, whereas genetic entry affected height, but not any effect was observed on site × genetic entry interaction. Unlike in this study, Persson et al. (1995) observed differences in volume in different genetic entries.

On average, the overall WD of different genetic entries was not affected statistically significantly by spacing on site 1 (only 1% difference was observed between spacing 1 and 3), despite of differences observed in the growth rate of trees (and LWW% as well). The fact that both the average EWD and LWD were, to some degree, lower, but LWW% higher, in the densest spacing, explains the non-significant differences of overall WD between spacings. Similar to our work, in some previous studies the overall WD was not affected in Scots pine by the growth rate at a relatively young age (Persson et al 1995), although in Scots pine, in general, overall WD correlates strongly with LWW% (Hannrup et al. 2001). In our work, genetic entry significantly affected the wood density traits on both sites, unlike spacing. In comparison, Persson et al. (1995) also found differences among genetic entries for wood density traits, but opposite to our results, spacing also affected them. In radiata pine (*Pinus radiata*) (Donaldson et al. 1995) and black spruce (Zhang and Morgenstern 1995) EWD has affected the overall WD the most (followed by LWW% and LWD), whereas in Loblolly Pine (*Pinus taeda*) and Norway spruce LWW% has affected the overall WD the most (Hodge and Purnell 1993, Lindström 1997).

We also found that, in general, the ranking between genetic entries changed significantly depending on the growth, yield, wood density trait considered and spacing or site. Thus, no overall ranking was possible in this respect (see Table 5). However, we could still find some genetic entries which had high stem volume, but also relatively dense wood and thus, high dry stem mass production at the same time (see Fig. 4). For example, on site 1 in this sense genetic entry 9 was superior in the widest spacing, whereas in spacing 2 and 3, genetic entries 6 and 8 were ranked first. Genetic entry 4, which was ranked first on site 2, had also a high ranking on site 1. In addition, the response of genetic entries with Kanerva pine as one of the parents (genetic entries 3 to 6) did not differ from other genetic entries even in dense spacing. This was, to some degree, unexpected, based on its higher harvest index compared to other genetic entries in Scots pine (see e.g. Kärki 1985, Pöykkö 1993).

Differences observed in the property traits for the same genetic entries grown on different sites may be related, in our study, to the differences in the fertility of the sites, but also to the differences in climatic conditions. In contrast to the findings of Bujold et al. (1996), we did not observe systematic differences in any property traits at a geographical origin level. Similarly, the differences observed in various genetic entries in different spacing may be due to their different capacity to react to competition caused by neighbour trees. However, in the present study we did not have the opportunity to study the competition effect (but it will be done in the future work). Moreover, due to the lack of calculation of genetic correlations and the relatively low number of sample trees per genetic entry, it is not possible to draw very detailed conclusions on our results. However, site 1, with its relatively high site fertility (and range of spacing treatments), could be expected to be highly suitable for these kinds of studies in the future (see e.g. Haapanen 1996).

The unique field experiments established in Finland in the recent decades for Scots pine are very suitable for studies on effects of genetic entry, management and site, on the quantity and quality of properties. These studies should, however, also include calculation of genetic correlations between properties (also for branch characteristics) and should be based on a larger number of genetic entries and sample trees. These studies could make it possible to find genetic entries, which have, for example, relatively high overall wood density, but also maintains higher growth rate, even after canopy closure as a result of higher light interception and/or stem wood production per unit of light intercepted (see e.g. Svensson et al. 1999). In the future, it may also be necessary to balance the gain or loss, for example, in overall wood density and stem volume, depending on the final target of wood production (e.g. pulp wood or sawn timber products). By doing so, it may even be possible to identify some genetic entries that could be the most suited to particular product types or processes (Ridoutt et al. 1998).

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Appendix 1. Means and standard deviation for diameter, height, stem volume, latewood percentage (LWW%) and overall wood density (WD) for different genetic entries in spacing 1 to 3 on site 1 (Siilinjärvi trial) and on site 2 (Loppi trial). Different letters indicate differences among genetic entries (Tukey $p < 0.05$).

Genetic entry	Diameter (cm)	Height (m)	Volume (m^3)	LWW%	WD ($g\ cm^{-3}$)
	Mean ± sd	Mean ± sd	Mean ± sd	Mean ± sd	Mean ± sd
Site 1, spacing 1					
1. StandardS12	12.0 ± 2.9a	9.0 ± 1.0a	0.058 ± 0.03ab	28 ± 5.5a	0.358 ± 0.03a
2. StandardS13	10.0 ± 1.0a	8.7 ± 0.8a	0.037 ± 0.01a	26 ± 5.2a	0.388 ± 0.04a
3. C205×S1101	12.9 ± 1.4a	11.2 ± 0.8b	0.079 ± 0.02ab	24 ± 2.5a	0.364 ± 0.01a
4 .C214B×S1101	13.2 ± 1.5a	11.0 ± 1.2b	0.082 ± 0.02ab	24 ± 2.9a	0.357 ± 0.03a
5. S2582×S1101	13.3 ± 1.5a	10.3 ± 1.0ab	0.077 ± 0.02ab	24 ± 2.5a	0.364 ± 0.03a
6. S104×S1101	11.6 ± 2.5a	10.4 ± 1.1ab	0.063 ± 0.03ab	24 ± 2.1a	0.341 ± 0.01a
7. S104×C205	11.6 ± 1.0a	10.6 ± 1.1ab	0.061 ± 0.02ab	22 ± 2.6a	0.350 ± 0.02a
8. C205×S80	12.3 ± 2.1a	10.6 ± 0.8ab	0.068 ± 0.03ab	23 ± 2.5a	0.352 ± 0.02a
9. C214B×C205	13.7 ± 2.3a	11.1 ± 0.8b	0.091 ± 0.03b	25 ± 2.4a	0.380 ± 0.03a
10. SeedOrchardC97	11.9 ± 1.6a	8.6 ± 0.6a	0.051 ± 0.01ab	24 ± 4.0a	0.361 ± 0.01a
Site 1, spacing 2					
1. StandardS12	9.8 ± 1.6a	8.9 ± 0.8a	0.038 ± 0.01a	24 ± 2.5a	0.357 ± 0.02a
2. StandardS13	11.6 ± 2.6a	9.0 ± 1.1ab	0.054 ± 0.02a	24 ± 2.0a	0.354 ± 0.01a
3. C205×S1101	11.7 ± 1.2a	11.4 ± 0.7c	0.070 ± 0.02a	26 ± 3.0a	0.361 ± 0.02a
4. C214B×S1101	10.6 ± 1.8a	11.2 ± 0.3c	0.054 ± 0.02a	28 ± 3.6a	0.389 ± 0.02a
5. S2582×S1101	12.7 ± 1.5a	10.2 ± 1.1abc	0.073 ± 0.02a	22 ± 1.9a	0.358 ± 0.01a
6. S104×S1101	13.2 ± 2.1a	11.2 ± 0.6c	0.084 ± 0.03a	25 ± 1.3a	0.368 ± 0.02a
7. S104×C205	11.7 ± 2.3a	10.5 ± 1.0bc	0.062 ± 0.02a	24 ± 2.6a	0.353 ± 0.02a
8. C205×S80	12.3 ± 2.7a	11.2 ± 0.4c	0.075 ± 0.04a	26 ± 6.1a	0.364 ± 0.02a
9. C214B×C205	11.2 ± 1.5a	10.9 ± 0.9c	0.061 ± 0.02a	29 ± 1.3a	0.385 ± 0.03a
10. SeedOrchardC97	12.0 ± 0.8a	10.4 ± 0.4abc	0.066 ± 0.01a	26 ± 4.4a	0.372 ± 0.02a
Site 1, spacing 3					
1. StandardS12	10.0 ± 2.5a	8.7 ± 0.8a	0.039 ± 0.02a	26 ± 7.2a	0.375 ± 0.04ab
2. StandardS13*	-	-	-	-	-
3. C205×S1101	9.7 ± 1.1a	11.9 ± 1.1c	0.051 ± 0.01a	32 ± 2.2a	0.389 ± 0.03b
4. C214B×S1101	11.3 ± 1.3a	11.4 ± 0.7bc	0.063 ± 0.02a	28 ± 2.6a	0.361 ± 0.02ab
5. S2582×S1101	9.9 ± 1.4a	11.3 ± 0.4bc	0.049 ± 0.01a	28 ± 1.5a	0.359 ± 0.02ab
6. S104×S1101	10.8 ± 0.8a	11.7 ± 0.5c	0.058 ± 0.01a	26 ± 2.4a	0.338 ± 0.02a
7. S104×C205	9.1 ± 2.1a	11.3 ± 0.9bc	0.044 ± 0.02a	27 ± 2.2a	0.356 ± 0.01ab
8. C205×S80	11.2 ± 2.0a	11.6 ± 1.2bc	0.067 ± 0.03a	27 ± 5.4a	0.350 ± 0.02ab
9. C214B×C205	9.5 ± 1.0a	11.3 ± 0.8bc	0.046 ± 0.01a	27 ± 2.9a	0.375 ± 0.02ab
10. SeedOrchardC97	9.6 ± 1.1a	10.0 ± 0.7ab	0.042 ± 0.01a	29 ± 4.4a	0.392 ± 0.02b
Site 2					
3. C205×S1101	12.6 ± 2.1a	10.6 ± 1.0a	0.066 ± 0.02a	24 ± 1.3a	0.380 ± 0.02a
4. C214B×S1101	14.1 ± 1.5a	11.5 ± 1.2a	0.096 ± 0.03a	27 ± 5.5a	0.376 ± 0.02a
5. S2582×S1101	12.2 ± 1.6a	9.7 ± 0.6a	0.063 ± 0.02a	25 ± 4.4a	0.370 ± 0.02a
6. S104×S1101	12.9 ± 2.6a	9.4 ± 2.2a	0.073 ± 0.04a	25 ± 3.1a	0.366 ± 0.01a
11. C205×S710D	11.1 ± 2.5a	10.3 ± 1.4a	0.057 ± 0.03a	26 ± 1.7a	0.380 ± 0.01a
12. StandardSPM	13.3 ± 3.0a	10.3 ± 1.2a	0.083 ± 0.04a	28 ± 4.4a	0.371 ± 0.03a
13. StandardS17	11.9 ± 1.1a	9.3 ± 1.9a	0.052 ± 0.01a	27 ± 2.5a	0.367 ± 0.02a

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