1	Genetic control of transition from juvenile to mature wood with respect to
2	microfibril angle (MFA) in Norway spruce (Picea abies) and lodgepole pine
3	(Pinus contorta)
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## 15 Abstract

Genetic control of microfibril angle (MFA) transition from juvenile to mature was evaluated 16 in Norway spruce and lodgepole pine. Increment cores were collected at breast height from 17 18 5,618 trees in two 21-year-old Norway spruce progeny trials in southern Sweden, and from 19 823 trees in two 34-35 – year-old lodgepole pine progeny trials in northern Sweden. Radial 20 variations in MFA from pith to bark were measured for each core using SilviScan. To estimate 21 MFA transition from juvenile to mature, a threshold level of MFA 20° was considered and six 22 different regression functions were fitted to the MFA profile of each tree after exclusion of outliers, following three steps. The narrow-sense heritability estimates  $(h^2)$  obtained for MFA 23 24 transition were highest based on the slope function, ranging from 0.21 to 0.23 for Norway spruce and from 0.34 to 0.53 for lodgepole pine, while  $h^2$  were mostly non-significant based 25 26 on the logistic function, under all exclusion methods. Results of this study indicate that it is 27 possible to select for an earlier MFA transition from juvenile to mature in Norway spruce and 28 lodgepole pine selective breeding programs, as the genetic gains ( $\Delta_G$ ) obtained in direct 29 selection of this trait were very high in both species.

30

### 31 Introduction

Wood properties have become an important focus in advanced tree breeding programs, along with growth, vitality and form traits (Bouffier et al. 2009; Isik et al. 2008). The variability in wood properties within a tree is very large (Larson 1967), owing to the within-ring differences, the changes along a radius from pith to bark, and the differences associated with different heights in the tree (Zobel and Van Buijtenen 1989).

37 Differences between juvenile and mature wood are the major sources of variation in wood

38 quality, both among and within trees (Zobel and Sprague, 1998). Such differences occur in

39 various wood characteristics, including specific gravity, mechanical properties (Bendtsen and

- 40 Senft, 1984), cell length (Shiokura, 1982, Yang et al., 1986), and pulp yields (Zobel and
- 41 Sprague, 1998).

42 The usual pattern for conifers is that wood density and MOE increase and MFA decreases as

43 trees become older (Dungey et al. 2006). As such, juvenile wood is mostly undesirable due to

44 its low density, low strength, high content of compression wood, high cellulose microfibril

45 angle (MFA, the angle between the prevailing cellulose orientation and the long cell axis),

46 low crystallinity and general high variability, as compared to mature wood (Barnett and

47 Jeronimidis 2009; Mellerowicz et all., 2001; Zobel and van Buijtenen 1989).

48 MFA, is one of the key determinants of solid-wood quality due to its strong influence on the

49 stiffness, strength, shrinkage properties and dimensional stability of structural lumber

50 (Bendtsen and Senft 2007; Cave and Walker 1994). Several studies in conifers have shown

that very large angles of MFA (about  $45^{\circ}$ ) are common in the first 5 to 10 growth rings near

52 the pith and MFA values decline gradually until they stabilize towards the bark (Zobel and

- 53 Jett 1995). Furthermore, it has been shown that in conifers, the average MFA of the S2 layer
- 54 lies between 5°- 20° in mature wood (BOWYER and SHMULSKY 2007; Donaldson 2008).

The radial pith-to-bark variation of MFA is also altered by other environmental factors, whereby MFA values increase in compression wood, decrease in tension wood, and mostly increase following fertilization and thinning (Donaldson 2008).

58 In recent decades, most forest industries moved their attention towards usage of fast-growing 59 tree plantations (Gräns et al. 2009), which implies that trees are harvested at younger ages 60 than before and subsequently have greater proportion of juvenile wood (Larson 2001; Zobel 61 and Van Buijtenen 1989). However, the negative impact of using fast-growing plantations can 62 be reduced by changing the proportion of juvenile wood through breeding (Abdel-Gadir and 63 Krahmer 1993; Gapare et al. 2006; Zobel and Jett 1995). In addition to selecting for trees with 64 improved juvenile wood, it is also possible to select for an earlier transition from juvenile to 65 mature wood in breeding programs (Gapare et al. 2006).

66 Transition from juvenile to mature wood usually occurs over two to five growth rings, 67 depending on the wood property (Alteyrac et al. 2006; Mutz et al. 2004). The point at which 68 this transition occurs is of great importance for forest managers and tree breeders as it 69 determines the quality and value of end-use products. However, it is difficult to estimate this 70 boundary with adequate reliability as there is usually no clear demarcation line between 71 juvenile wood and mature wood in a tree stem (Mutz et al. 2004; Zobel and Sprague 1998). 72 The distinction between juvenile wood and mature wood has mostly been determined by 73 analyzing trends of radial variation (from pith to bark) for different wood properties such as 74 density (Alteyrac et al. 2006; Mansfield et al. 2007), MOE (Wang and Stewart 2013), fiber 75 length, and MFA (Bhat et al. 2001; Mansfield et al. 2009; Wang and Stewart 2012). This 76 method is so-called threshold or graphic method whereby plots of each wood property are 77 visually evaluated to locate a ring number or cambial age when the property reaches the 78 threshold value for mature wood (Clark et al. 2007). An alternative approach is to use 79 mathematical methods such as segmented regression (Abdel-Gadir and Krahmer 1993;

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Gapare et al. 2006; Szymanski and Tauer 1991) and segmented non-linear models (Alteyrac
et al. 2006; Koubaa et al. 2007; Mutz et al. 2004).

It is well recognized that the proportion of juvenile wood and timing of transition in a tree is influenced by both genetic and environmental factors (Abdel-Gadir and Krahmer 1993; Mansfield et al. 2007). For instance, high heritabilities have been reported for age of transition and juvenile-wood proportion in loblolly pine (*Pinus taeda L.*) specific gravity and tracheid length (Loo et al. 1985; Stonecypher and Zobel 1966). Similarly, genetic control of time of transition has been reported to be high in slash pine (*Pinus elliottii* Engelm.) (Hodge and Purnell 1993).

89 The genetic control of MFA as a function of cambial age in two progeny trials of Norway 90 spruce (*Picea abies* L.) (Chen et al. 2014) and two progeny trials of lodgepole pine (*Pinus* 91 contorta Dougl.) (Hayatgheibi et al. 2017) have been recently investigated in Sweden. 92 Estimated heritabilities fluctuated near the pith and then stabilized after the cambial age of 10 93 years in both species (Chen et al. 2014; Hayatgheibi et al. 2017). However, genetic control of 94 MFA transition from juvenile to mature was not considered in those studies. The main 95 objective of this study was therefore to quantify genetic variation of transition between 96 juvenile and mature MFA based on application of different regression functions in these 97 species, using similar progeny trials to those used by Chen et al. (2014) and Hayatgheibi et al. 98 (2017).

99

### 100 Material and Methods

# 101 Study materials and trial design

This study utilized data from two large open-pollinated progeny trials of Norway spruce,
located in southern Sweden, and two genetically unrelated open-pollinated progeny trials of
lodgepole pine, located in northern Sweden (Table 1). Trials of Norway spruce, S21F9021146

aka F1146 (trial 1) and S21F9021147 aka F1147 (trial 2), comprised of 1,373 and 1,375 halfsib families, respectively, were established in 1990. Both trials were planted as randomized incomplete blocks with single-tree plots at spacing of  $1.4 \times 1.4$  m. A set of 524 families within 112 sampling provenances were selected for this study. More detailed information about trial characteristics can be found in (Chen et al. 2014).

Furthermore, two trials of lodgepole pine, Övra (Skogforsk S23F8060373) with 178 families, and Lagfors with 214 families (Skogforsk S23F7960), were established in 1980 and 1979, respectively. These families at both trials were planted in a randomized complete block (RCB) design. Each family was represented by 10 trees planted in a row with five replicates (blocks), resulting in 50 planted trees per family. Tree spacing was 2 m between rows and 1.5 m within rows. More details about trials characteristics have been further described in (Hayatgheibi et

116 al. 2017).

#### 117 Sampling and SilviScan measurement

118 Increment cores (12-mm in diameter) were collected at breast height (1.3 m) from a total of 119 5618 Norway spruce, aged 21 years, and 823 lodgepole pine trees, aged 34-35 years, and 120 assessed by a SilviScan instrument (Innventia, now part of RISE, Stockholm, Sweden). 121 Before the SilviScan measurement, each increment core was sawn into a 7 mm high  $\times$  2 mm 122 thick radial strip from the pith to the bark. The SilviScan system combines image analysis 123 with X-ray absorption and X-ray diffraction to determine high-resolution pith-to-bark radial 124 variations for several important wood properties, including wood density, MFA and MOE 125 (Evans 2006; Evans and Ilic 2001). The variations in MFA from pith to bark of each core was 126 measured as averages across consecutive 2 mm wide intervals. The annual rings were 127 identified from the corresponding variations in wood density, and the average MFA for all 128 rings were calculated. The number of annual rings ranged from 6 to 19 for Norway spruce and 129 from 20 to 32 for lodgepole pine.

### 130 Model fitting and determination of MFA transition

### 131 Data exclusion

The radial patterns for MFA of all 5618 Norway spruce and 823 lodgepole pine individual trees were plotted against the cambial age. However, there were some individuals for which the general MFA decreasing trend from pith to the bark had been changed, due to some disturbances such as compression wood. Therefore, such outliers were identified and excluded prior to data analysis. Following removal of such outliers, the remaining Norway spruce and lodgepole pine individuals having fewer than 12 and 20 annual rings, respectively, were also excluded from data analysis. The three applied exclusion methods are as follows:

139 1) Exclusion\_1 or basic method: exclusion of those individuals for which MFA values
140 increased with cambial age (abnormal curves). This was the baseline of data treatment and
141 thus the first step of exclusion methods 2 and 3. This first exclusion step resulted in exclusion
142 of about 2.8 % and 5.1 % of Norway spruce (Höreda and Erikstorp, respectively) and 0.2 %
143 and 1.7 % of lodgepole pine individuals (Lagfors and Övra, respectively)

2) Exclusion\_2 or shape-based method: following the baseline method, annual rings of the individuals for which average MFA values were greater than their three previous rings average MFA, were removed. Based on this method, about 480 and 959 annual rings in Norway spruce (Höreda and Erikstorp, respectively) and about 613 and 398 annual rings in lodgepole pine (Lagfors and Övra, respectively) were removed. This resulted in removal of about 4.0 % and 7.5 % of Norway spruce (Höreda and Erikstorp, respectively) and 0.9 % and 7.3 % of lodgepole pine individuals (Lagfors and Övra, respectively).

3) Exclusion\_3 or family-based method: the data after exclusion with the baseline method were exposed to another method of data exclusion. Annual rings, which had average MFA values deviating from their corresponding family-mean MFA values by more than  $1.96 \times SD$ , were excluded from data analysis. Based on this method, about 838 and 665 annual rings in

- 155 Norway spruce (Höreda and Erikstorp, respectively) and about 177 and 159 annual rings in
- 156 lodgepole pine (Lagfors and Övra, respectively) were removed. This method resulted in the
- removal of about 3.4 % and 5.2 % of Norway spruce (Höreda and Erikstorp, respectively) and
- 158 0.2 % and 1.5 % of lodgepole pine individuals (Lagfors and Övra, respectively).
- 159 **Regression functions and MFA transition**
- 160 After removal of outliers, six different regression functions were fitted to the pith-to-bark
- 161 MFA profiles of the individual trees. A threshold value of  $20^{\circ}$  was considered for MFA and
- 162 when the parameter of the fitted functions fell below the threshold, the estimated parameter
- 163 was defined as MFA transition.
- 164 All data analysis was carried out using the R statistical programming environment (R
- 165 Development Core).
- 166 The fitted models were as follow:
- 167 1. *Slope function*

$$Y_i = \beta_0 + \beta_1 C A + \varepsilon_i$$

- where  $\beta_0$  is the intercept and  $\beta_1$  is the slope. In all equations,  $Y_i$  is the MFA value of the tree *i* , *CA* is the cambial age, and  $\varepsilon_i$  is the random error.
- 170 2. Logistic function

171 
$$Y_i = \beta_0 + \frac{\beta_1 - \beta_0}{1 + e^{\beta_3(\beta_2 - CA)}} + \varepsilon_i$$

- 172 where  $\beta_0$  is the upper asymptote MFA,  $\beta_1$  is the lower asymptote MFA,  $\beta_2$  is the inflection
- 173 point, and  $\beta_3$  is the sharpness.
- 174 3. Central peak

$$Y_i = \frac{\beta_0}{1 + \beta_1 \times CA^2} + \beta_2 + \varepsilon_i$$

175 where  $\beta_0 + \beta_2$  is the upper asymptote MFA,  $\sqrt{\frac{1}{\beta_1}}$  is the inflection point, and  $\beta_2$  is the lower

asymptote MFA.

#### 177 4. Polynomial

- 178 The radial profile of MFA from each tree was plotted with respect to cambial age and fitted
- 179 with a third-order polynomial regression as below:

$$Y_i = \beta_0 + \beta_1 CA + \beta_2 CA^2 + \beta_3 CA^3 + \varepsilon_i$$

180 5. Arctangent

$$Y_i = \frac{\beta_0 + \beta_1}{2} + \frac{(\beta_0 - \beta_1) \times \arctan\left((\beta_2 - CA) \times \beta_3\right)}{\pi} + \varepsilon_i$$

181 where  $\beta_0$  is the upper asymptote MFA,  $\beta_1$  is the lower asymptote MFA,  $\beta_2$  is the inflection

182 point, and  $\beta_3$  is the slope.

183 6. Negative exponential

$$Y_i = (\beta_0 - \beta_1) \times e^{(-\beta_2 \times CA)} + \beta_1 + \varepsilon_i$$

184 where  $\beta_0$  is the MFA at cambial age zero,  $\beta_1$  is the lower asymptote MFA, and  $\beta_2$  is the slope 185 at cambial age zero.

### 186 Genetic analysis

187 Variance components for genetic analysis were estimated using ASReml 3.0 (Gilmour et al.

2009) based on linear mixed-effects model using joint-site analysis for Norway spruce and
single-site analysis for lodgepole pine as follows:

190 Norway spruce  $y_{ijklm} = \mu + S_i + B_{j(i)} + P_k + F_{l(k)} + SF_{il(k)} + e_{ijklm}$ 

where  $y_{ijklm}$  is the observation on the *m*th tree from the *l*th family within the *k*th provenance in the *j*th block within the *i*th site.  $\mu$  is the overall mean;  $S_i$  is the fixed effect of the *i*th site;  $B_{j(i)}$  is the fixed effect of the *j*th block within the *i*th site;  $P_k$  is the fixed effect of the *k*th provenance;  $F_{l(k)}$  is the random effect of the *l*th family within the *k*th provenance;  $SF_{il(k)}$  is the random interaction effect of the *i*th site and the *l*th family within the *k*th provenance; and  $e_{ijklm}$  is the random residual effect.

197 Lodgepole pine 
$$y_{jklm} = \mu + P_k + B_j + F_{l(k)} + BF_{jl(k)} + e_{jklm}$$

where  $y_{jklm}$  is the vector of observation on the *m*th tree from the *l*th family within the *k*th provenance in the *j*th block.  $\mu$  is the overall mean;  $P_k$  and  $B_j$  are the fixed effects of the *k*th provenance and the *j*th block, respectively;  $F_{l(k)}$  is the random effect of the *l*th family within the *k*th provenance;  $BF_{jl(k)}$  is the random interactive effect of the *j*th block and the *l*th family within the *k*th provenance and  $e_{jklm}$  is the random residual effect.

Estimates of heritability were obtained using variance components from the univariate joinsite (for Norway spruce) and single-site (for lodgepole pine) analysis. Approximate standard errors were estimated using the Taylor series expansion method (Gilmour et al. 2009). Individual-tree narrow-sense heritability  $(h_i^2)$  for MFA of each mathematical model was calculated using the following equations assuming these open-pollinated family are half-sib families (Falconer and Mackay 1996):

209 Norway spruce 
$$h_i^2 = \frac{\hat{\sigma}_A^2}{\hat{\sigma}_P^2} = \frac{4 \times \hat{\sigma}_f^2}{\hat{\sigma}_f^2 + \hat{\sigma}_{sf}^2 + \hat{\sigma}_e^2}$$

210 Lodgepole pine 
$$h_i^2 = \frac{\hat{\sigma}_A^2}{\hat{\sigma}_P^2} = \frac{4 \times \hat{\sigma}_f^2}{\hat{\sigma}_f^2 + \hat{\sigma}_{bf}^2 + \hat{\sigma}_e^2}$$

211 where  $\hat{\sigma}_A^2$  is the additive genetic variance;  $\hat{\sigma}_f^2$  is among family variance;  $\hat{\sigma}_{sf}^2$  is the site by 212 family variance;  $\hat{\sigma}_{bf}^2$  is the family by block variance; and  $\hat{\sigma}_e^2$  is the residual variance.

Pooled-site analysis genetic gain ( $\Delta G_t$ ), expressed as percentage in direct selection of MFA transition-age was estimated as:

$$\Delta G_t = i \times h_t^2 \times CV_t$$

- 216 where *i* is the selection intensity of 1% (*i*=2.67),  $h_t^2$  is the narrow-sense heritability of MFA
- 217 transition and CV is the coefficient of variation of the phenotypic effect (calculated as the
- 218 phenotypic standard deviation divided by the mean of the trait).
- 219 **Results**

# 220 MFA transition and model fitting in Norway spruce and lodgepole pine

## 221 MFA radial variation

For both species, the MFA average profiles decreased from high values close to the pith towards stable levels close to the bark (Fig. 1). In Norway spruce, mean MFA profile decreased from about  $30^{\circ}$  at the pith and then stabilized after reaching a cambial age of 10 years at about  $10^{\circ}$  in Höreda and about  $12^{\circ}$  in Erikstorp. The mean MFA profile for lodgepole pine started at  $40^{\circ}$  followed by a rapid decrease to about  $30^{\circ}$  after 3 years, after which the shape of the development was similar to that for Norway spruce but slower, stabilizing after cambial age of 15 years at about  $12^{\circ}$  in Övra and about  $10^{\circ}$  in Lagfors.

#### 229 Model fitting and MFA transition

For each fitted regression function, different threshold values were tested to define the best model fit for individual trees transition from juvenile to mature MFA. Although the threshold value of  $20^{\circ}$  gave the best model fit, there were still some individuals for which the MFA profile never passed the threshold, thus, they remained constantly above or below the threshold. Figures 2 to 5 show the proportion of Norway spruce and lodgepole pine individuals for which the MFA transition was estimated based on the applied six different regression functions, under the threshold of  $20^{\circ}$ .

# 237 Heritability estimates

Narrow-sense heritability estimates were obtained for combined-site Norway spruce andsingle-site lodgepole pine MFA transition.

### 240 Norway spruce

Estimated heritabilities were mostly stable following data exclusions. However, heritabilities were slightly higher after shape-based exclusion (exclusion\_2), while they were slightly lower after the family-based exclusion (exclusion\_3), particularly for arctangent, polynomial and negative-exponential functions (Table 1). In general,  $h^2$  ranged from 0.08 to 0.23 with the highest estimate obtained based on the slope function and the lowest estimate obtained based on the logistic function, under all exclusion methods.

#### 247 Lodgepole pine

In general,  $h^2$  estimates observed for lodgepole pine were higher than those for Norway 248 249 spruce (Table 1). Heritabilities in Övra increased significantly after exclusion\_2 and 250 exclusion\_3, particularly after exclusion\_2, while they slightly decreased after exclusion\_3 in 251 Lagfors. As similarly observed for Norway spruce, heritability estimates were lowest based 252 on the logistic function, while they were highest based on the slope function. In general, 253 heritabilities ranged from 0.15 to 0.53 in Övra and from 0.22 to 0.43 in Lagfors (logistic 254 function was excluded). In addition to the slope function, high heritabilities obtained based on 255 the central peak (ranging from 0.33 to 0.38) and negative exponential functions (ranging from 256 0.26 to 0.34) in Övra, and based on the arctangent (ranging from 0.41 to 0.43) and polynomial 257 (ranging from 0.36 to 0.38) in Lagfors.

## 258 Genetic gain

As was observed for heritability estimates, genetic gains obtained based on the slope function were highest, while those obtained based on the logistic function were lowest, regardless of which exclusion method was applied (Table 2). High genetic gains were also obtained based on the negative-exponential function for both species when using exclusion-1. Similarly, application of exclusion-2 and exclusion-3 led to high genetic gains when MFA was modelled by negative-exponential and central peak functions in Norway spruce and by arctangent and

265 negative-exponential functions in lodgepole pine (Table 2).

### 266 Discussion and conclusion

267 Several investigations in various conifers have determined the age for MFA transition from 268 juvenile to mature, using different linear and non-linear models (Clark et al. 2007; Mansfield 269 et al. 2009; Wang and Stewart 2012). However, no study to date has examined genetic 270 variation of MFA transition and its possible genetic gain based on employing different 271 regression functions. Few studies have investigated the genetic control of transition age in fast 272 growing pines (Gapare et al. 2006). As such, a family heritability estimate of 0.36 and 273 moderate genetic gains in selection of early age of transition for specific gravity in loblolly 274 pine has been reported (Loo et al. 1985). Similarly, moderate genetic gains were reported for 275 latewood density transition age in radiata pine (Pinus radiata D. Don) (Gapare et al. 2006).

One of the central goals in forest tree breeding is to reduce costs and time of breeding cycles by making genetic gains as early as possible. Additionally, due to the increased demand in fast-grown plantations, which contain more juvenile wood, it is of vital importance to breed for more uniform wood, or a wood with lower proportion of juvenile wood.

Therefore, the main focus of this study was to evaluate the degree of genetic control in MFA transition from juvenile to mature in Norway spruce and lodgepole pine to ensure that future end-use products obtained from these species have desirable wood characteristics.

Although the MFA average profiles started to stabilize at about 15° in both species (Fig. 1), the chosen threshold value of 20° resulted in the best model fit for estimation of individual trees MFA transition from juvenile to mature. Furthermore, as the wood of conifers having MFA of 20° is considered as mature (Bowyer and Shmulsky 2007; Donaldson 2008), such a high transition degree for MFA will enables incorporation of wood quality traits into selective breeding programs of Norway spruce and lodgepole pine as early as possible. Most of the narrow-sense heritability estimates obtained in this study were statistically significant, except for those obtained based on the logistic function under all exclusion models. This might be driven by the inability of this function to estimate MFA transition under the selected threshold, particularly in lodgepole pine.

293 Overall, heritability estimates obtained for lodgepole pine were generally greater than those 294 obtained for Norway spruce. This is in line with results of the studies by Chen et al. (2014) 295 and Hayatgheibi et al. (2017), as  $h^2$  obtained for area-weighted MFA in two progeny trials of 296 lodgepole pine were greater than that obtained for Norway spruce. Similarly, heritability 297 estimates obtained based on the slope function were highest in both species across all exclusion methods. However,  $h^2$  obtained for Norway spruce based on negative exponential 298 299 and central peak, were also high. Similarly, high  $h^2$  were observed based on the negative 300 exponential and central peak functions in Övra, and based on the arctangent and polynomial 301 functions in Lagfors.

Results of this study, which made use of large genetic data sets of two important coniferous species, revealed that there is a possibility to breed for earlier MFA transition from juvenile to mature as genetic gains achieved for this trait were very high.

305 In general, genetic gains obtained for MFA transition, except for those obtained based on the 306 logistic function, were higher in lodgepole pine due to the higher narrow-sense heritability 307 estimates obtained for this trait in lodgepole pine. Further, in addition to the slope function, 308 highest genetic gains were achieved based on the negative exponential and central peak 309 functions in Norway spruce when data trimming by exclusion-2 was applied, and based on the 310 negative exponential and arctangent functions in lodgepole pine after applying exclusion-3. 311 Findings of this study indicate that there is a possibility to select for a reduction in MFA 312 transition age, and therefore, a decrease in proportion of the log containing juvenile wood in 313 Norway spruce and lodgepole pine selective breeding programs.

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Table 1. Narrow-sense heritability estimates of Norway spruce (combined-trial) and lodgepole pine (Övra and Lagfors)
MFA transition from juvenile to mature wood obtained from six different regression functions applying three different exclusion methods.
Standard errors of the heritabilities are in parenthesis.

	I	Narrow-sense heritability estimates				
Modelling method	Norway s	Norway spruce		Lodgepole pine		
			Övra		Lagfors	
		Exclusion	_1			
1) slope	0.21 (0.0	5)	0.34 (0.21)		0.42 (0.19)	
2) log	0.09 (0.0)	3)	0		0.13 (0.19)	
3) peak	0.18 (0.0	5)	0.33 (0.21)		0.28 (0.19)	
4) atan	0.19 (0.04	4)	0.15 (0.21)		0.43 (0.19)	
5) poly	0.19 (0.0	5)	0.19 (0.20)		0.36 (0.18)	
6) nexp	0.19 (0.04	4)	0.26 (0.21)		0.29 (0.18)	
		Exclusion	_2			
1) slope	0.23 (0.0	5)	0.53 (0.23)		0.41 (0.19)	
2) log	0.09 (0.04	4)	0		0	
3) peak	0.21 (0.0	5)	0.35 (0.21)		0.22 (0.19)	
4) atan	0.17 (0.0	5)	0.31 (0.22)		0.43 (0.19)	
5) poly	0.19 (0.0	5)	0.19 (0.20)		0.36 (0.18)	
6) nexp	0.20 (0.0	5)	0.34 (0.21)		0.32 (0.18)	
		Exclusion	_3			
1) slope	0.21 (0.0	5)	0.46 (0.20)		0.39 (0.19)	
2) log	0.08 (0.04	4)	0		0	
3) peak	0.20 (0.0	5)	0.38 (0.22)		0.27 (0.18)	
4) atan	0.15 (0.04	4)	0.31 (0.22)		0.41 (0.19)	
5) poly	0.17 (0.0	5)	0.28 (0.21)		0.38 (0.18)	
6) nexp	0.18 (0.0	5)	0.34 (0.21)		0.29 (0.18)	
: log= logistic,	peak= central	peak,	poly=polynomial,	atan=	arctangent,	n.e

negative exponential

		Norway spruce						
Model		$\Delta G_t$ (%)						
	exclusion-1	exclusion-2	exclusion-3					
Slope	27.4	29.4	27.1					
Log	13.3	13.0	11.1					
Peak	20.9	24.1	23.2					
Atan	23.2	20.2	17.1					
Poly	23.3	23.0	21.6					
N. ex	25.0	25.7	20.1					
lodgepole pine								
Model	$\Delta G_{t}(\%)$							
	exclusion-1	exclusion-2	exclusion-3					
Slope	40.2	48.4	45					
Log	0	3.7	11					
Peak	32.8	30.2	35.7					
Atan	29.4	39.5	39.9					
Poly	29.6	29.7	35.6					
N. ex	33.4	38.2	38.9					

Table 2. Genetic gains ( $\Delta G_t$ %) obtained for transition age in combined-site Norway spruce and combined-site lodgepole pine using the selection intensity of 1%

Note: Log= logistic, Peak= Central peak, Poly=polynomial, Atan= arctangent, N.exp= negative exponential

Fig. 1. Radial trends for MFA of *Picea abies* at two trials (Höreda and Erikstorp) from cambial age 1 to 20 and for *Pinus contorta* at two trials (Övra and Lagfors) from cambial age









Fig. 3. Proportion of Norway spruce (Erikstorp) transition age under the mean (raw data) and six different regression functions using the threshold level of 20 degrees for MFA



Fig. 4. Proportion of lodgepole pine (Övra) transition age under the mean (raw data) and six different regression functions using the threshold level of 20 degrees for MFA



Fig. 5. Proportion of lodgepole pine (Lagfors) transition age under the mean (raw data) and six different regression functions using the threshold level of 20 degrees for MFA

