

Prediction of Breeding Values and Expected Genetic Gains in Diameter Growth, Wood Density and Spiral Grain from Parental Selection in *Picea abies* (L.) KARST.

By J. COSTA E SILVA¹), H. WELLENDORF¹) and N. M. G. BORRALHO²)

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Abstract

Parental breeding values were predicted for diameter growth, pilodyn penetration, basic density and spiral grain in Norway spruce (*Picea abies* (L.) KARST.). Cross- and open-pollinated progenies, tested across a range of sites, were evaluated under univariate and multivariate individual tree mixed models. Best Linear Unbiased Predictions (BLUP) of breeding values were obtained by linking data from different mating designs, in order to evaluate parents present as both females (open-pollinated progenies) and males (controlled crosses). The BLUP analysis of diameter followed a multivariate approach that combined correlated information across two different planting environments in Denmark. For selection targeting one of the planting zones, the analysis took simultaneously into account the data available on different characters, and the BLUP solutions of the parent effects were then applied to construct an index for genetic improvement of multiple traits. In this context, the evaluations used pilodyn as a selection criterion, basic density as a goal trait, and spiral grain and diameter as both selection criteria and goal traits. The single and multiple trait evaluations served as a basis to discuss strategies and associated genetic gains from parental selection.

Key words: *Picea abies*, open-pollination, controlled crosses, REML, BLUP, heritability, genetic correlation, genotype by environment interaction, genetic gain, sawn timber production.

Introduction

The breeding programme of Norway spruce (*Picea abies* (L.) KARST.) in Denmark is structured in one multiple purpose central population and a number of small elite populations with alternative selection goals: growth rate, wood quality, health or a multi-trait breeding objective (WELLENDORF *et al.*, 1994). In the early 1980s, two clonal seed orchards were established with the same set of 100 plus trees, from 1st generation selections in mature Danish stands of German origin. These orchards are expected to be culled based on progeny testing results and supply improved seed for two planting environments, the eastern and western regions of Denmark, contrasting in silvicultural treatments and in some edaphic and climatic factors.

Short-rotation forestry has been common in the eastern region, where sites are in general more productive and the mean annual increment reaches its maximum early, being then followed by a rapid decline. Marketable timber dimensions under short rotations have been obtained by enhancing diameter growth rate, through intense early thinnings. This has also been practised to promote root development which, in combination with lower thinning intensities at later stages, is expected

to reduce the risk of windthrow (NIELSEN, 1990). However, the increase in diameter growth rate, associated with high site fertility and more intense silvicultural practices, has decreased key quality properties (stability, visual grading outcome, strength) for sawn timber (DANBORG, 1996). Wider annual rings in early years and short rotations result in a larger amount of juvenile wood present in the harvested log, which also contributes to a drop in quality of the sawn timber: juvenile wood in itself has poorer properties when compared with the mature wood (BRAZIER, 1985; SENFT, 1986; DANBORG, 1996). Therefore, while the intended use of Norway spruce plantations in both regions is structural timber, a much greater emphasis on wood quality is required in the eastern zone, in order to improve the end-product value. In the western region, sites are generally less fertile, and resistance to needle cast and increasing growth rate could be targeted without affecting significantly wood quality.

Wood density and spiral grain are two important basic properties influencing the quality of structural timber. Strength properties of spruce boards are reduced by decreasing wood density and increasing knot size (DANBORG, 1996), with other factors such as spiral grain and microfibrillar angle being also involved (BRAZIER, 1985). Among the stability properties studied in Norway spruce boards, twist was found to be the most serious downgrading parameter, and it is induced by higher incidence of spiral grain (DANBORG, 1996).

As with other conifers, in Norway spruce, large annual rings will contribute to lower wood density in both juvenile and mature wood (OLESEN, 1976, 1977; DANBORG, 1994; ROZENBERG and CAHALAN, 1997). Moreover, faster diameter growth in young wood will increase the average grain angle in the tree, because the incidence of spiral grain is higher in the juvenile wood (BRAZIER, 1985; SENFT, 1986; HARRIS, 1989; DANBORG, 1996). Thus, particularly for spruce plantations growing in productive environments, attempts to decrease the amount of juvenile wood in the stem and/or improve its quality (as by selecting material with higher wood density and reduced grain angle) may improve the value of timber for structural purposes.

The aim of this study was to predict parental breeding values and associated genetic gains for diameter growth, wood density and spiral grain. Additive genetic (co)variance estimates were pooled across sites and then used to derive Best Linear Unbiased Predictions (BLUP) of breeding values (HENDERSON, 1984; WHITE and HODGE, 1989; BORRALHO, 1995), under univariate and multivariate analyses. Results concerning site estimates of (co)variance components and genetic parameters have been reported previously for the cross- and open-pollinated progenies used in the evaluations (COSTA E SILVA *et al.*, 2000). The BLUP analysis allowed for heterogeneous residual variances across sites and used pedigree information to link data from different mating designs. The evaluations served as a basis to develop strategies and related genetic gains from parental selection.

¹) Department of Economics and Natural Resources, Royal Veterinary and Agricultural University, Arboretum, Kirkegårdsvej 3A, DK-2970 Hørsholm, Denmark.

²) RAIZ Forest and Paper Research Institute, Herdade da Torre Bela, Apartado 15, P-2065 Alcoentre, Portugal.

Table 1. – Estimates for additive genetic variances (diagonal) and covariances (off-diagonal) used in single and multiple trait parental evaluations. DM – diameter (in the western and eastern regions); SG – spiral grain; WD – wood density (raw measures and values adjusted for differences in ring width); PL – pilodyn (raw measures and values adjusted for differences in DM).

	DM _w	DM _E	SG	WD _{raw}	WD _{adj.}	PL _{raw}	PL _{adj.}
DM _w	48,0 ^{1j}	38,9 ^{2j}	-	-	-	-	-
DM _E		132,6 ^{3j}	3,30 ^{4j}	-109,0 ^{4j}	-	12,01 ^{4j}	-
SG			0,8 ^{5j}	-1,63 ^{9j}	-1,42 ^{10j}	0,36 ^{6j}	0,18 ^{6j}
WD _{raw}				331,4 ^{7j}	-	-20,65 ^{11j}	-
WD _{adj.}					250,9 ^{7j}	-	-18,70 ^{12j}
PL _{raw}						1,7 ^{5j}	-
PL _{adj.}							1,8 ^{5j}

1) Pooled estimate from F226, F243, F244

2) $(48.0)^{1/2} \times (132.6)^{1/2} \times$ weighted average of genetic correlations from the pairs F226/F228, F226/F229, F241/F243, F241/F244

3) Pooled estimate from F228, F229, F241

4) Genetic correlations from F228 multiplied by square roots of pooled genetic variances

5) Pooled estimates from F228, F241, F243

6) Weighted average of genetic correlations from F228, F241, F243 multiplied by square roots of pooled genetic variances

7) Estimates from F168

8) $-0.52 \times (331.4)^{1/2} \times (132.6)^{1/2}$

9) $-0.1 \times (331.4)^{1/2} \times (0.8)^{1/2}$

10) $-0.1 \times (250.9)^{1/2} \times (0.8)^{1/2}$

11) $-0.87 \times (331.4)^{1/2} \times (1.7)^{1/2}$

12) $-0.88 \times (250.9)^{1/2} \times (1.8)^{1/2}$

Material and Methods

Details about the plant material, mating schemes, field experimental design and characters used in this study have been described previously (COSTA E SILVA *et al.*, 2000). Briefly, the data are from three groups of 15 to 18-year-old progeny tests, comprising cross- and open-pollinated families (for summary information, see Table 1 of COSTA E SILVA *et al.*, 2000). The progeny test data refer to 90 out of 100 parents represented in the seed orchards, plus a parent that belongs to the general breeding population. The remaining 10 parents will be evaluated in the near future, following collection of data in other progeny tests.

BLUPs of breeding values (and their standard errors) were obtained for male parents used in the controlled crosses (group I) and female parents of open-pollinated families (groups II and III), under the following general mixed linear model:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{s} + \mathbf{W}_1\mathbf{m} + \mathbf{W}_2\mathbf{p} + \mathbf{e}$$

where \mathbf{y} is the vector of individual tree observations; \mathbf{b} is the vector of fixed effects; \mathbf{a} is the vector of random additive genetic effects of individual trees; \mathbf{s} is the vector of random non-additive genetic effects due to the specific combinations of males with females; \mathbf{m} is the vector of random main plot effects; \mathbf{p} is the vector of random subplot effects; \mathbf{e} is the vector of random residual deviations of individual trees; \mathbf{X} , \mathbf{Z}_1 , \mathbf{Z}_2 , \mathbf{W}_1 and \mathbf{W}_2 are incidence matrices relating the observations to the model effects. It is assumed that the random terms are jointly normal with zero mean and (co)variance matrix:

$$\text{VAR} \begin{bmatrix} \mathbf{a} \\ \mathbf{s} \\ \mathbf{m} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G} \otimes \mathbf{A} & 0 & 0 & 0 & 0 \\ 0 & \mathbf{S} \otimes \mathbf{I} & 0 & 0 & 0 \\ 0 & 0 & \mathbf{M} \otimes \mathbf{I} & 0 & 0 \\ 0 & 0 & 0 & \mathbf{P} \otimes \mathbf{I} & 0 \\ 0 & 0 & 0 & 0 & \mathbf{R} \otimes \mathbf{I} \end{bmatrix}$$

where \mathbf{G} is the additive genetic (co)variance matrix, \mathbf{S} is the (co)variance matrix due to the specific combinations of males with females, \mathbf{M} is the (co)variance matrix with main plot effects, \mathbf{P} is the (co)variance matrix with subplot effects, \mathbf{R} is the residual (co)variance matrix, \mathbf{A} is the additive genetic relationship matrix between trees, \mathbf{I} is an identity matrix and \otimes denotes the Kronecker product.

The progeny groups I and II were combined in the BLUP analysis, as there were eleven common parents between them. Data of group III were analysed separately because, apart from a common reference population, the group has no connections with series I and II. As in previous analyses (COSTA E SILVA *et al.*, 2000), the bulked stand seedlots in groups II and III and the common reference seedlot were not used in the evaluations.

Single trait evaluations were first carried out to identify superior parents for the allocation to elite breeding populations, aiming to improve growth rate or wood quality. A multivariate BLUP analysis was also applied to construct indices for genetic improvement of multiple traits, and an important objective here was parental selection for roguing the seed

orchard (known locally as FP241) which targets the eastern region.

Table 1 shows the additive genetic (co)variance estimates applied in single and multiple trait BLUP analyses. REML (Restricted Maximum Likelihood) estimates of (co)variance components have been reported previously (COSTA E SILVA *et al.*, 2000) for diameter growth (DM), pilodyn penetration (PL) and spiral grain (SG). For these traits, the additive genetic (co)variances were pooled across trials (Table 1), assuming that true genotype by environment interactions were not serious for the wood properties, as well as for DM within defined planting zones in Denmark (COSTA E SILVA *et al.*, 2000). Basic density (usually termed here as wood density) determinations were absent in the studied progeny trials. Therefore, external information (see Discussion) was used to get estimates for the genetic variance of wood density (WD) and its genetic covariance with DM, PL and SG. For WD and PL, the genetic (co)variance estimates were derived (Table 1) with raw measures and with values adjusted for differences in radial growth by means of covariance analysis, using ring width and DM as covariates (respectively).

The pooled estimates of additive genetic (co)variances used in the evaluations (Table 1) were constrained to remain fixed at their initial values when iterating to obtain solutions for the model effects. Heterogeneous (co)variances across sites were allowed for non-additive genetic (i.e. the s effects in group I only), main plot, subplot and residual terms. Previous analyses provided starting values for these (co)variances, and indicated significant main plot and subplot effects to be fitted.

The ASREML programme (GILMOUR *et al.*, 1999) was used in the BLUP evaluations. Details concerning the analysis are described below.

Single trait evaluations

To reduce the risk of genotype by environment interactions for DM, the field trials across the three groups were allocated to the eastern and western regions (COSTA E SILVA *et al.*, 2000). This allocation of sites refers to an adjusted version of a previous proposal for environmental zonation of the breeding programme (WELLENDORF *et al.*, 1999). No division in different planting zones was made for the wood quality traits. Given the heterogeneous additive genetic variances between sites for all traits (COSTA E SILVA *et al.*, 2000), the data was adjusted to a common estimate within a region for DM, or overall for PL and SG, as follows:

$$y_{j(adj)} = y_j \frac{\hat{\sigma}_a}{\hat{\sigma}_{a_j}}$$

where $y_{j(adj)}$ and y_j are the adjusted and original records (respectively) in site j ; $\hat{\sigma}_{a_j}$ is the additive genetic standard deviation for the trait, estimated in site j ; $\hat{\sigma}_a$ is a prior estimate for the additive genetic standard deviation of the population at the specified environment and age (i.e. in the range from 15 to 18 years). The $\hat{\sigma}_a$ was obtained as the average of individual site estimates, but excluding trials F245 and F246 (as the variances here were estimated from a small set of male parents) and F242 (because the heritability was too low here for DM).

For DM, and using correlation estimates involving pairs of representative trials from the two regions, a weighted genetic correlation was calculated as:

$$\hat{r}_a = \sum_{j=1}^n w_j \hat{r}_{a_j}$$

with

$$w_j = \frac{1/\text{VAR}(\hat{r}_{a_j})}{\sum_{j=1}^n 1/\text{VAR}(\hat{r}_{a_j})}$$

where w_j is a weighting factor and $\text{VAR}(\hat{r}_{a_j})$ is the variance of the correlation estimate \hat{r}_{a_j} for the j th site pair. A common additive genetic covariance across the two regions was calculated by multiplying \hat{r}_a by the product of the within-region $\hat{\sigma}_a$ estimates.

The BLUP analysis of DM followed a multivariate approach that considered the performance of the same trait in the two regions as two different traits, and took into account the additive genetic covariance (estimated as described above) across regions. The analysis combining groups I and II included four trials in the eastern region and one trial in the western region (see Table 1 of COSTA E SILVA *et al.*, 2000). The estimators and predictors of model terms were obtained by solving the mixed model equations (MME) which, for the full model, are represented in the form of partitioned matrices as:

$$\begin{bmatrix} \mathbf{D}_{11} & \mathbf{D}_{12} \\ \mathbf{D}_{21} & \mathbf{D}_{22} \end{bmatrix} \begin{bmatrix} \mathbf{E}_{11} \\ \mathbf{E}_{21} \end{bmatrix} = \begin{bmatrix} \mathbf{F}_{11} \\ \mathbf{F}_{21} \end{bmatrix}$$

where the submatrix \mathbf{D}_{11} , referring to data adjusted to a common genetic scale in the eastern region (denoted as k), is defined as

$$\begin{bmatrix} \mathbf{X}'_k \mathbf{R}_k^{-1} \mathbf{X}_k & \mathbf{X}'_k \mathbf{R}_k^{-1} \mathbf{Z}_{1k} & \mathbf{X}'_k \mathbf{R}_k^{-1} \mathbf{Z}_{2k} & \mathbf{X}'_k \mathbf{R}_k^{-1} \mathbf{W}_{1k} & \mathbf{X}'_k \mathbf{R}_k^{-1} \mathbf{W}_{2k} \\ \mathbf{Z}'_{1k} \mathbf{R}_k^{-1} \mathbf{X}_k & \mathbf{Z}'_{1k} \mathbf{R}_k^{-1} \mathbf{Z}_{1k} + \mathbf{g}^{kk} & \mathbf{Z}'_{1k} \mathbf{R}_k^{-1} \mathbf{Z}_{2k} & \mathbf{Z}'_{1k} \mathbf{R}_k^{-1} \mathbf{W}_{1k} & \mathbf{Z}'_{1k} \mathbf{R}_k^{-1} \mathbf{W}_{2k} \\ \mathbf{Z}'_{2k} \mathbf{R}_k^{-1} \mathbf{X}_k & \mathbf{Z}'_{2k} \mathbf{R}_k^{-1} \mathbf{Z}_{1k} & \mathbf{Z}'_{2k} \mathbf{R}_k^{-1} \mathbf{Z}_{2k} + \mathbf{S}_k^{-1} & \mathbf{Z}'_{2k} \mathbf{R}_k^{-1} \mathbf{W}_{1k} & \mathbf{Z}'_{2k} \mathbf{R}_k^{-1} \mathbf{W}_{2k} \\ \mathbf{W}'_{1k} \mathbf{R}_k^{-1} \mathbf{X}_k & \mathbf{W}'_{1k} \mathbf{R}_k^{-1} \mathbf{Z}_{1k} & \mathbf{W}'_{1k} \mathbf{R}_k^{-1} \mathbf{Z}_{2k} & \mathbf{W}'_{1k} \mathbf{R}_k^{-1} \mathbf{W}_{1k} + \mathbf{M}_k^{-1} & \mathbf{W}'_{1k} \mathbf{R}_k^{-1} \mathbf{W}_{2k} \\ \mathbf{W}'_{2k} \mathbf{R}_k^{-1} \mathbf{X}_k & \mathbf{W}'_{2k} \mathbf{R}_k^{-1} \mathbf{Z}_{1k} & \mathbf{W}'_{2k} \mathbf{R}_k^{-1} \mathbf{Z}_{2k} & \mathbf{W}'_{2k} \mathbf{R}_k^{-1} \mathbf{W}_{1k} & \mathbf{W}'_{2k} \mathbf{R}_k^{-1} \mathbf{W}_{2k} + \mathbf{P}_k^{-1} \end{bmatrix}$$

\mathbf{D}_{22} , pertaining to data adjusted to a common genetic scale in the western region (denoted as l), is defined as

$$\begin{bmatrix} \mathbf{X}'_l \mathbf{R}_l^{-1} \mathbf{X}_l & \mathbf{X}'_l \mathbf{R}_l^{-1} \mathbf{Z}_l & \mathbf{X}'_l \mathbf{R}_l^{-1} \mathbf{W}_{1l} & \mathbf{X}'_l \mathbf{R}_l^{-1} \mathbf{W}_{2l} \\ \mathbf{Z}'_l \mathbf{R}_l^{-1} \mathbf{X}_l & \mathbf{Z}'_l \mathbf{R}_l^{-1} \mathbf{Z}_l + \mathbf{g}^{ll} & \mathbf{Z}'_l \mathbf{R}_l^{-1} \mathbf{W}_{1l} & \mathbf{Z}'_l \mathbf{R}_l^{-1} \mathbf{W}_{2l} \\ \mathbf{W}'_{1l} \mathbf{R}_l^{-1} \mathbf{X}_l & \mathbf{W}'_{1l} \mathbf{R}_l^{-1} \mathbf{Z}_l & \mathbf{W}'_{1l} \mathbf{R}_l^{-1} \mathbf{W}_{1l} + \mathbf{M}_l^{-1} & \mathbf{W}'_{1l} \mathbf{R}_l^{-1} \mathbf{W}_{2l} \\ \mathbf{W}'_{2l} \mathbf{R}_l^{-1} \mathbf{X}_l & \mathbf{W}'_{2l} \mathbf{R}_l^{-1} \mathbf{Z}_l & \mathbf{W}'_{2l} \mathbf{R}_l^{-1} \mathbf{W}_{1l} & \mathbf{W}'_{2l} \mathbf{R}_l^{-1} \mathbf{W}_{2l} + \mathbf{P}_l^{-1} \end{bmatrix}$$

\mathbf{D}_{12} , concerning correlated information between the two regions, is defined as

$$\begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & \mathbf{g}^{kl} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$\mathbf{D}_{21} = \mathbf{D}_{12}'$ (with $'$ denoting transpose), and

$$\mathbf{E}_{11} = \begin{bmatrix} \hat{\mathbf{b}}_k \\ \hat{\mathbf{a}}_k \\ \hat{\mathbf{s}}_k \\ \hat{\mathbf{m}}_k \\ \hat{\mathbf{p}}_k \end{bmatrix} \quad \mathbf{E}_{21} = \begin{bmatrix} \hat{\mathbf{b}}_l \\ \hat{\mathbf{a}}_l \\ \hat{\mathbf{m}}_l \\ \hat{\mathbf{p}}_l \end{bmatrix} \quad \mathbf{F}_{11} = \begin{bmatrix} \mathbf{X}'_k \mathbf{R}_k^{-1} \mathbf{y}_k \\ \mathbf{Z}'_{1k} \mathbf{R}_k^{-1} \mathbf{y}_k \\ \mathbf{Z}'_{2k} \mathbf{R}_k^{-1} \mathbf{y}_k \\ \mathbf{W}'_{1k} \mathbf{R}_k^{-1} \mathbf{y}_k \\ \mathbf{W}'_{2k} \mathbf{R}_k^{-1} \mathbf{y}_k \end{bmatrix} \quad \mathbf{F}_{21} = \begin{bmatrix} \mathbf{X}'_l \mathbf{R}_l^{-1} \mathbf{y}_l \\ \mathbf{Z}'_l \mathbf{R}_l^{-1} \mathbf{y}_l \\ \mathbf{W}'_{1l} \mathbf{R}_l^{-1} \mathbf{y}_l \\ \mathbf{W}'_{2l} \mathbf{R}_l^{-1} \mathbf{y}_l \end{bmatrix}$$

where \mathbf{y}_k and \mathbf{y}_l are the observations in regions k and l (respectively); g^{kk} , g^{ll} and g^{kl} are the elements of

$$\begin{bmatrix} g^{kk} & g^{kl} \\ g^{kl} & g^{ll} \end{bmatrix} = \mathbf{G}^{-1} \otimes \mathbf{A}^{-1} = \begin{bmatrix} \hat{\sigma}_{a_{kk}}^2 & \hat{\sigma}_{a_{kl}} \\ \hat{\sigma}_{a_{kl}} & \hat{\sigma}_{a_{ll}}^2 \end{bmatrix}^{-1} \otimes \mathbf{A}^{-1}$$

where \mathbf{G} is the additive genetic variance-covariance matrix with elements $\hat{\sigma}_{a_{kk}}^2$, $\hat{\sigma}_{a_{ll}}^2$ and $\hat{\sigma}_{a_{kl}}$ pertaining to the common estimates for variances within k and l and the covariance between k and l (respectively); \mathbf{S}_k^{-1} is the inverse of $\mathbf{S}_k \otimes \mathbf{I}$, where \mathbf{S}_k is the variance-covariance matrix due to the specific combinations of males with females (for the two sites from group I within k); \mathbf{M}_k^{-1} is the inverse of the block diagonal matrix $\mathbf{M}_k = \bigoplus_{j=1}^4 \mathbf{M}_j$, where $\mathbf{M}_j = \hat{\sigma}_{m_j}^2 \mathbf{I}$; \mathbf{P}_k^{-1} is the inverse of the block diagonal matrix $\mathbf{P}_k = \bigoplus_{j=1}^4 \mathbf{P}_j$, where $\mathbf{P}_j = \hat{\sigma}_{p_j}^2 \mathbf{I}$; \mathbf{R}_k^{-1} is the inverse of the block diagonal matrix $\mathbf{R}_k = \bigoplus_{j=1}^4 \mathbf{R}_j$, where $\mathbf{R}_j = \hat{\sigma}_{e_j}^2 \mathbf{I}$; $\hat{\sigma}_{m_j}^2$, $\hat{\sigma}_{p_j}^2$ and $\hat{\sigma}_{e_j}^2$ are variances for main plot, subplot and residual effects (respectively) in site j within region k , and \bigoplus denotes the direct sum; $\mathbf{M}_l^{-1} = \frac{1}{\hat{\sigma}_{m_l}^2} \mathbf{I}$, $\mathbf{P}_l^{-1} = \frac{1}{\hat{\sigma}_{p_l}^2} \mathbf{I}$ and $\mathbf{R}_l^{-1} = \frac{1}{\hat{\sigma}_{e_l}^2} \mathbf{I}$ refer to main plot, subplot and residual effects in

the site from region l ; the matrix \mathbf{A} is as defined before; \mathbf{I} is an identity matrix of an appropriate order (i.e. equal to the number of full-sib families to fit the \mathbf{s} term, or equal to the number of main plots, subplots or trees for the given site in the \mathbf{M} , \mathbf{P} and \mathbf{R} matrices); \mathbf{X} , \mathbf{Z} , \mathbf{Z}_1 , \mathbf{Z}_2 , \mathbf{W}_1 , \mathbf{W}_2 are design matrices. The estimators of fixed effects (regions, sites within regions, blocks within regions and sites) are given in $\hat{\mathbf{b}}$. The vector $\hat{\mathbf{a}}$ has predictions of breeding values for parents, as well as for individual trees in each region. Correlated information across regions makes it possible to obtain predictions for all parents in k and l , even if parents are only represented at one region.

As zonation was not taken into account for SG and PL, the BLUP analysis followed a univariate approach combining the trials F246 (group I) and F228 (group II). The set-up of the MME was simplified to $\mathbf{D}_{11} \mathbf{E}_{11} = \mathbf{F}_{11}$, where the submatrix elements (without a subscript denoting the region) were defined in a similar form and g^{kk} was replaced by $\frac{1}{\hat{\sigma}_a^2} \mathbf{A}^{-1}$ where $\hat{\sigma}_a^2$ is

the pooled additive genetic variance for the character.

The progeny group III refers to open-pollinated data only, and thus the \mathbf{s} term was not fitted. In the BLUP analysis, the MME were set up as in the other series, accommodating the correlated information across the two regions for DM and accounting for differences of heritability amongst sites in all cases. The evaluations used one trial in region k and three trials in region l for DM, and two trials were combined in the analysis of SG and PL.

For WD, the predictions of breeding values were obtained by (after FALCONER and MACKAY, 1996):

$$\hat{\mathbf{a}}_{\text{wd}i} = \frac{\hat{\sigma}_{a(\text{wd,pl})}}{\hat{\sigma}_{a(\text{pl})}^2} \cdot \hat{\mathbf{a}}_{\text{pl}i}$$

where $\hat{\mathbf{a}}_{\text{wd}i}$ and $\hat{\mathbf{a}}_{\text{pl}i}$ are breeding values for WD and PL, predicted for the i th parent; $\hat{\sigma}_{a(\text{pl})}^2$ and $\hat{\sigma}_{a(\text{wd,pl})}$ are genetic estimates for the variance of PL and covariance between WD and PL (respectively).

Multiple trait evaluations

A multiple trait BLUP analysis was applied to take simultaneously into account the information available on different characters. The BLUP solutions of parent effects were then used to construct an index for genetic improvement of multiple traits.

To predict parental breeding values for roguing the seed orchard FP241, the evaluations used the DM records from the target (i.e. eastern) region only and all data for SG and raw PL measures (as no zonation was made for the wood properties). The analysis combined groups I and II as previously, including DM records from three tests (F246, F228, F229) and observations from two tests (F246, F228) for SG and PL. Trial F245 was excluded from this analysis: the heritability was low for DM and data was missing for the wood properties, which suggested that the penalty from discarding this information would have a marginal effect on gain in accuracy. The analysis of group III involved measures of SG and PL from two trials (F241, F243) and DM observations from the eastern site only (F241).

In the multivariate BLUP analysis, the data vector \mathbf{y} contained adjusted (to a common genetic scale) records on up to three characters per individual. The analysis combining groups I and II used a structure $\mathbf{S} \otimes \mathbf{I}$, where \mathbf{S} is a variance-covariance matrix for relationships between traits that are due to the combinations of males with females (for F246 in group I only). In all cases, the structure $\mathbf{G} \otimes \mathbf{A}$ was applied to fit the additive genetic effects, with \mathbf{G} defining the corresponding variance-covariance matrix of traits. A common estimate for the additive genetic covariance between SG and PL at age 18 was obtained by multiplying a weighted genetic correlation (using individual estimates from F228, F241 and F243) by the product of the pooled genetic standard deviations. The genetic covariances between DM and the wood properties at age 18 were derived in a similar form, but using individual correlations (from F228) estimated in the eastern region only. Different variance-covariance structures (Σ) of traits were allowed across sites for main plot, subplot and residual effects: for the j th site, $\mathbf{M}_j = \Sigma_{m_j} \otimes \mathbf{I}$, $\mathbf{P}_j = \Sigma_{p_j} \otimes \mathbf{I}$ and $\mathbf{R}_j = \Sigma_{e_j} \otimes \mathbf{I}$.

A general aggregate objective for genetic improvement was defined as:

$$\hat{H}_i = v_{\text{sg}} \hat{\mathbf{a}}_{i_{\text{sg}}} + v_{\text{wd}} \hat{\mathbf{a}}_{i_{\text{wd}}} + v_{\text{dm}} \hat{\mathbf{a}}_{i_{\text{dm}}}$$

where \hat{H}_i is the aggregate breeding objective predicted for the i th parent; $\hat{\mathbf{a}}_{i_{\text{sg}}}$, $\hat{\mathbf{a}}_{i_{\text{wd}}}$ and $\hat{\mathbf{a}}_{i_{\text{dm}}}$ are breeding values for the target traits – SG, WD and DM (respectively) – predicted for the i th parent; v_{sg} , v_{wd} and v_{dm} are the relative economic values of the target traits. For WD, the breeding values were predicted by (after SCHNEEBERGER *et al.*, 1992):

$$\hat{\mathbf{a}}_{i_{\text{wd}}} = \hat{\mathbf{c}} \hat{\mathbf{G}}^{-1} \hat{\mathbf{a}}_i$$

where $\hat{\mathbf{c}}$ is a (1x3) vector of estimated additive genetic covariances between WD and SG, PL and DM; $\hat{\mathbf{G}}$ is a (3x3) variance-covariance matrix with additive genetic estimates for SG, PL and DM; $\hat{\mathbf{a}}_i$ is a (3x1) vector of breeding values for SG, PL and DM, predicted for the i th parent.

Expected genetic gains from parental selection

The top 20 parents (i.e. about the top 22% of all parents) were selected following ranks of breeding values or index scores, and genetic responses (expected at an age within the range from 15 to 18 years for DM, or at 17 to 18 years for the wood properties) were estimated for each trait by averaging the breeding value predictions of the selected individuals.

Under multiple trait selection, the index scores were calculated with arbitrary "economic" weights set to the target traits. Estimates of expected genetic responses based on the index were used to evaluate alternative options, produced by modifying iteratively the arbitrary weights (COTTERILL and DEAN, 1990). To overcome scale effects due to different measurement units, the searching procedure applied weighting coefficients that were pre-multiplied by the reciprocal of the additive genetic standard deviation of the traits. This amounts to specify the relative importance of different traits on the basis of changes in genetic standard deviation units. Ultimately, the aim was to use biological and end-product information (as outlined in *Introduction*) for choosing combinations of trait responses which may contribute to increase (or, at least, not degrade) the value of Norway spruce young wood for structural timber.

Results

The expected genetic responses in goal traits (SG, WD and DM) are presented in *tables 2* and *3* for single and multiple trait selections, respectively, using SG, PL and DM as selection criteria. The overall trait means are also shown in *table 2*; for SG and DM, they were estimated by averaging the individual means of representative sites (i.e. trials used for pooling the additive genetic variances); for WD, the estimate is based on 17-year-old basic density determinations at breast-height (see *Discussion*), and is taken as an approximate average value for the density of young Norway spruce wood produced under fast growing conditions. The multiple trait selection options in *table 3* refer to indices constructed to select parents for the elite population aiming to improve wood quality (option 1) or for roguing the seed orchard FP241 targeting the eastern region (options 2).

Table 2. – Expected genetic responses in spiral grain (SG), wood density (WD) and diameter (DM) from single trait selections. For DM, the responses are given for the eastern (E) and western (W) regions.

trait	mean	expected genetic response
SG (degrees)	2.2	-1.0
WD (Kg/m ³)	325	14.5
DM _E (mm)	104	11.4
DM _W (mm)	76	7.1

The expected genetic gains from single trait selection (*Table 2*) were 11.5 mm and 7.1 mm for DM in the eastern and western regions, respectively. This difference in predicted responses reflects partly a scale effect associated with larger

Table 3. – Expected genetic responses in spiral grain (SG), wood density (WD) and diameter (DM) from multiple trait selections. For DM, the responses refer to the eastern region. The weighting coefficients were pre-multiplied by the reciprocal of the additive genetic standard deviation of the traits.

selection options	weighting coefficients			expected genetic responses		
	SG	WD	DM	SG (degrees)	WD (kg/m ³)	DM (mm)
1	-1	1	-	-0.8	9.3	-
2a	-1	1	1	-0.7	7.1	-0.8
2b	-0.8	1	1	-0.6	7.3	0.3
2c	-0.7	1	1	-0.5	8.3	0.3
2d	-0.3	0.6	1	0.06	0.4	7.9
2e	-0.5	0.8	1	-0.3	5.2	3.7

stem diameters (and thus larger additive genetic variances) in the eastern zone. Expressing the results in percentage of the overall trait means, the predicted relative gains were 11.1% and 9.3% in the eastern and western regions, respectively. For wood properties, the expected gains in SG and WD were -1.0° and 14.5 kg/m³, respectively.

An index combining wood properties only (*Table 3*, option 1), resulted in improvements of -0.8° and 9.3 kg/m³ for SG and WD, by giving equal weighting per genetic standard deviation change in each trait. For an aggregate breeding objective combining all traits (*Table 3*, options 2), improvements of -0.7° and 7.1 kg/m³ and a slight loss of -0.8 mm were predicted for SG, WD and DM, following selection on an index giving equal importance to each trait (option 2a). Decreasing only the weight placed on SG led to predicted responses ranging from -0.5° to -0.6° for SG and from 7.3 kg/m³ to 8.3 kg/m³ for WD, while the expected changes were close to zero for DM (options 2b and 2c). Optimizing selection for growth rate over wood quality, but keeping the responses in SG and WD near by zero, gave a gain of 7.9 mm in DM (option 2d). For a selection option approaching maximum simultaneous improvements (KING *et al.*, 1988; MAGNUSSEN, 1990), the predicted responses were modest for all traits (i.e. -0.3°, 5.2 kg/m³ and 3.7 mm for SG, WD and DM, option 2e).

The correlation between the true and predicted breeding value (r_{aa}) was calculated for each parent and trait, and *table 4* lists mean estimates for the analysed groups of progeny trials. The correlation r_{aa} is an indicator of the precision of the predicted breeding values for a given trait, and may be affected by several factors as the number of parents and progeny per parent, the relationships in the data, the heritability of the observations and the importance of correlated information. As shown in *table 4*, for DM evaluations, r_{aa} was lower in the western region for parents of the set 1 ($r_{aa} = 0.70$), as well as in the eastern region for parents of the set 2 ($r_{aa} = 0.68$). These results probably reflect predictions of breeding values that are based on direct observations from one trial only: F226 in set 1 and F241 in set 2. Although the heritability was lower for DM in F226 when compared with F241, the accuracy of the estimate was higher in F226 (COSTA E SILVA *et al.*, 2000). The larger number of parents and trees per parent in F226 contributed to this result, and also influenced the accuracy of the predicted breeding values for DM (i.e. 0.70 versus 0.68,

table 4). Within each set of parents, the amount of information available for evaluation was similar for PL and SG, and the trends in r_{aa} values (Table 4) are comparable to the heritability estimates (COSTA E SILVA *et al.*, 2000).

Discussion

Genetic variances and covariances

Estimates for the genetic variance of WD and its genetic covariance with SG, PL and DM (Table 1) were based on heritability and genetic correlation estimates taken from external data.

Basic density, PL and DM were measured in the same trees of a 17-year-old clonal trial (F168), established on a fertile soil in the eastern part of Denmark. If it can be assumed that the total genetic variation in WD reflects mainly additive effects, then the additive genetic variance may be approximated by clonal variance estimates. The same applies to clonal correlations estimated for WD and the other traits. A random sample of 21 clones from trial F168 provided individual heritabilities for WD, being 0.62 (s.e = 0.12) and 0.76 (s.e = 0.08) for raw measures and for values adjusted for differences in ring width, respectively (data not shown). Heritabilities based on clone means were reported previously for adjusted WD measures (LARSEN *et al.*, 1997). The genetic correlations were -0.52 (s.e = 0.21) and -0.87 (s.e = 0.07) for raw WD observations with DM and raw PL measures (respectively), and -0.88 (s.e = 0.07) between WD adjusted for ring width and PL adjusted for DM (data not shown).

The (co)variance estimates based on adjusted values were used only for selection aiming to improve WD alone (Table 2) or combining WD and SG in an index (Table 3, option 1). As reported by COSTA E SILVA *et al.* (2000), adjusting raw PL readings to a common DM, reduced substantially the variance due to residual deviations of individual trees; this usually increased the magnitude and accuracy of the heritability estimates of the indirect measure of WD. Moreover, the adjustment by covariance analysis always improved the accuracy of the predicted breeding values for PL (Table 4). Therefore, if selection is targeting wood quality only, DM may be applied as a covariate to increase the precision of the PL measure used as a selection criterion. A similar adjustment may be applied to WD, the goal trait. In this context, methods to adjust basic density variation for differences in ring width have been described elsewhere (OLESEN, 1976, 1977; COSTA E SILVA *et al.*, 1994; DANBORG, 1994; LARSEN *et al.*, 1997). However, for the aggregate breeding objective targeting both growth rate and wood quality (Table 3, options 2), the multiple trait BLUP analysis used parameter estimates based on raw measures of PL and WD, in order to take simultaneously into account genetic and residual relationships between DM and the wood properties.

Table 4. – Average accuracy of breeding value estimates, given as the correlation between the true and predicted breeding value. The results refer to single trait evaluations of parents in the two sets.

sets of parents	diameter		pilotdyn		spiral grain
	east region	west region	raw	adjusted	
set 1 (parents in groups I and II)	0,81	0,70	0,70	0,73	0,79
set 2 (parents in group III)	0,68	0,83	0,77	0,83	0,81

In a previous study, raw and adjusted PL measures showed similar favourable genetic correlations with SG, and the estimates tended to be low (COSTA E SILVA *et al.*, 2000). Reports on the relationship between WD and SG are scarce in the literature: in young pine wood, an additive genetic correlation of -0.07 was found by ALLEN (1977) and a phenotypic correlation of -0.05 was reported by BURDON and LOW (1992). In the current work, a correlation of -0.15 was found between the basic density of 90 mature parents and their breeding value predictions for SG based on the performance of the offspring (data not shown). All of these estimates are low in magnitude and negative in sign and, from this information, a value of -0.1 was assumed for the genetic correlation between WD and SG.

Prediction of breeding values

The methodology followed here to predict breeding values for DM assumed no serious genotype by environment interactions within the defined planting regions, which amounts to assume unit genetic correlations across the respective sites. From the data analysis, there was no indication of important violations of this assumption for trials in the eastern region only although, for the western zone, the results from group III pointed out that the examined sites were equally correlated with a common estimate of 0.55 (COSTA E SILVA *et al.*, 2000). To verify possible bias in the BLUP analysis applied in this study, that assumed unit genetic correlations, a second evaluation was also carried out for parents in group III, following a multivariate approach that used a common additive genetic correlation of 0.55 across the trials within the western region. Apart from this, both of the analyses used the same estimates for the other parameters (i.e. the genetic variance within each region and the genetic covariance across the two regions).

The predictors of parent effects from the second evaluation were averaged for the western sites, and then the predictions obtained from the two BLUP analysis were compared within each region. Spearman rank correlations between predictions from the two analysis were close to 0.99 in both regions and, when comparing breeding value ranks, both of the approaches identified the same top 7 parents (i.e. nearly the top 20% of 37 parents). However, as expected, the predicted breeding values in the western region were more regressed toward their mean of zero after the second evaluation: when comparing mean values of r_{aa} , the estimate for the western region was 0.83 under the analysis applied here (Table 4) but only 0.72 following the second evaluation. For the eastern region, the r_{aa} values were similar under both approaches. Moreover, when averaging the predicted breeding values of the top 7 parents, the difference between the two analysis was 1.0 mm in the western region, but only 0.1 mm in the eastern region. These results indicate that the BLUP analysis applied here may over-evaluate the parents in group III for selections targeting the western region, thus overestimating expected genetic gains. Yet, when all parents (from all groups) were ranked on the basis of predicted breeding values in the western region, the two analysis led to marginal differences in expected genetic responses (around 0.4 mm, by selecting either the 10 or 20 best parents).

In summary, compared with the applied analysis assuming unit correlations, the parental evaluations were not substantially affected by using across-site genetic correlations of 0.55, albeit the lack of sufficient precision in trial F242 (COSTA E SILVA *et al.*, 2000) limits possible inferences concerning the homogeneity of correlations for the sites in the western region.

Expected genetic gains from parental selection

The poor correlations between wood properties result in some genetic progress in both spiral grain and basic density

(Table 3, option 1). On the other hand, the adverse relationship between diameter and the wood properties (COSTA E SILVA *et al.*, 2000) restricts simultaneous genetic gains in growth rate and wood quality. Thus, an aggregate breeding objective combining spiral grain, wood density and diameter growth may either emphasize selection on a trait (or a combination of traits) or compromise the gains in all characters (Table 3, options 2).

Diameter growth was generally the most weighted character under multiple trait selection (Table 3, options 2). This result reflects the structure of the relationships between traits, but does not necessarily bear a useful interpretation in economic terms. In fact, diameter may be the trait with less relative economic importance, as the FP241 orchard is intended to supply improved seed for the production of structural timber from Norway spruce plantations in fast growing conditions and under shorter rotations. Studying stability, visual grading outcome and strength properties of structural boards from spruce, DANBORG (1996) concluded that diameter growth rate has a direct negative impact on twist, longitudinal shrinkage, knot-tiness (i.e. size and frequency of knots), stiffness and bending strength. Faster diameter growth will also increase the size of the juvenile wood. This contributes further to lower structural performance, particularly because inner boards tend to twist more than outer boards (DANBORG, 1996).

These results suggest that some control of growth rate is required to produce acceptable timber for structural use. Selections based on either 2b or 2c (Table 3) are reasonable options for the specified end use and growth environment, because they are expected to increase the quality of the juvenile wood and reduce its amount in the harvested log. Lower left-handed grain angles in spruce juvenile wood contribute to reduce twist in sawn wood, and thus may improve the grading outcome (BRAZIER, 1985; DANBORG, 1996; HANSEN, 1999). Particularly for small and medium inner boards from fast-grown Norway spruce plantations, the grading outcome can be poor even for a low incidence of spiral grain (DANBORG, 1996). Recently, HANSEN (1999) reported that reducing the grain angle (measured in ring numbers 6 and 8 from the pith) by 1° may increase the proportion of the best quality grade by 8% for inner boards from Sitka spruce. As also noted by BRAZIER *et al.* (1985), for sawn timber from fast-grown spruce plantations, the reduction of the proportion of the best quality grades is likely to be not compensated for by an increase in yield associated with a larger stem diameter. In Norway spruce, the basic density level of the juvenile wood may be higher than that of the mature wood (DANBORG, 1994). However, the low value of 325 kg/m³ (Table 2), estimated for a mean ring width of 4.7 mm, may be below the limit of acceptance for structural use (i.e. the strength properties of the sawn timber may be poor), and thus a further improvement of 7 kg/m³ or 8 kg/m³ in basic density is judged to be worthy. Therefore, optimizing selection for diameter growth over wood quality (option 2d) is not currently considered to be appropriate for structural timber, and selection options 2b or 2c are more desirable than a lower risk solution (option 2e) that compromises the gains in all traits (Table 3). Finally, although it may be reasonable to emphasize selection on wood properties in relation to diameter growth in spruce, the same strategy may not apply to other conifers with other patterns of variation (within the annual ring, as well as within the tree) for anatomical and physical properties.

Conclusion

The results obtained in this work give strength to the actual breeding strategy of Norway spruce in Denmark, which uses a structure based on a large central population and a number of

smaller specialized units or elite populations (WELLENDORF *et al.*, 1994). The presence of a reasonably strong genotype by environment interaction for diameter (WELLENDORF *et al.*, 1999; COSTA E SILVA *et al.*, 2000) gave some support for an environmental zonation, and thus for a definition of distinct breeding populations for improving growth rate. In this context, growth rate may be combined with health (i.e. resistance to needle cast) to achieve simultaneous gains targeting the wind-exposed sites of the western part of the country. On the moderate to low site indices of this region, wood quality is considered to be satisfactory. For the more productive sites of the eastern region, the simultaneous gains in growth rate and wood quality are limited because the genetic relationships are adverse. Thus, improvements in growth and wood quality traits may be faster accomplished through separate elite populations.

Although current short-term objectives for the deployment population placed more emphasis on wood properties relatively to growth rate for improving the quality of sawn timber, the structure of the breeding population is flexible in the sense that it can accommodate other end-use goals or future changes in market conditions. Furthermore, the structure of small elite breeding populations combined with a good environmental zonation will be an advantage for a strategy applying marker-aided selection (MAS). The breeding value predictions enabled the identification of superior parents for individual traits, and then the aim is to map a restricted number of quantitative trait loci (QTL) for the target trait in the outstanding parents and their progeny. This entails the screening of molecular markers for co-segregation with the individual characters in the progeny from the best parents (as described by O'MALLEY and McKEAND, 1994; WELLENDORF and SKOV, 1997; SKOV and WELLENDORF, 1999). The objective is then to employ MAS in the offspring of crosses between mapped parents from different elite populations, for selecting and mass-propagating individuals that have favourable trait combinations. If feasible, this strategy will be particularly useful for achieving simultaneous genetic gains in adversely correlated characters, as the growth and wood quality traits studied here. Finally, MAS can also be applied for accelerating recurrent selection within each of the elite breeding populations.

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Buchbesprechungen

Niedersächsische Forstliche Biographie. Ein Quellenband. Schriftenreihe „Aus dem Walde“, Mitteilungen aus der Niedersächsischen Landesforstverwaltung, Heft 51. Von F. KROPP und Z. ROZSNYAY. Herausgegeben vom Niedersächsischen Ministerium für Ernährung, Landwirtschaft und Forsten. 1998. Bezug: Niedersächsisches Forstplanungsamt, Forstweg 1A, D-38302 Wolfenbüttel. 628 Seiten. DM 28,-.

Nach Baden-Württemberg, Hessen und Bayern hat die niedersächsische Landesforstverwaltung eine forstliche Biographie herausgegeben. Das Buch ist in zwei Teile gegliedert. Der erste Teil (497 Seiten) enthält 218 Lebensbilder namhafter Forstleute mit „niedersächsischem Bezug“. Dabei fanden neben forstlichen Praktikern auch Forstwissenschaftler der Forstakademie, forstlichen Hochschulen und forstlichen Fakultäten in Hann. Münden/Göttingen – ihr Anteil beträgt im vorliegenden Band 33% – auch Beachtung. Eine zeitliche Einschränkung der breitgefassten Personenauswahl wurde nicht getroffen. Die Lebensbilder reichen bis ins 16. Jahrhundert zurück und enden im Sommer 1998. Jedes der alphabetisch geordneten Lebensbilder wurde nach Nennung der persönlichen Lebensdaten und einer Darstellung der Verbindung zum Land Niedersachsen in drei Abschnitte aufgeteilt: (1) eine knapp gehaltene oder stichwortartig abgefasste Kurzbiographie, die Informationen über Werdegang und Verdienste des Forstmannes bietet und Hinweise auf allgemeinpolitische Entwicklungen und Umbrüche der Zeit gibt, (2) Quellen, welche für die Biographie benutzt wurden und die dem Leser weitergehende Nachforschungen ermöglichen, und (3) soweit vorhanden, eine Auswahl an Veröffentlichungen des Dargestellten. Durch die umfassende Präsentation der Forstliteratur ist die niedersächsische forstliche Biographie zugleich ein wesentlicher Beitrag zur forstlichen Bibliographie dieses Bundeslandes. Im zweiten Teil (128 Seiten) des Buches werden vier besonders profilierte

Forstleute – J.G. v. LANGEN, H.D. WILCKENS, H.C. BURCKHARDT und F.A.C. ERDMANN – näher beschrieben. Beiträge zur Entwicklung der forstlichen Ausbildung in Niedersachsen runden diesen Teil ab.

Dem im Geleit geäußerten Wunsch des Schriftleiters Prof. Dr. OTTO, dass auch Forstleute anderer Bundesländer, Naturschützer, Heimatkundler und alle Freunde des Waldes diese verdienstvolle Arbeit mit Interesse zur Kenntnis nehmen, kann man sich uneingeschränkt anschließen.

M. LIESEBACH (Grosshansdorf)

Waldzustandsanalyse mit multivariaten Verfahren: theoretische Grundlagen und Anwendungen. Von G. BECHER. 1999. Springer-Verlag, Berlin, Heidelberg, New York, London, Paris, Tokyo, Hong Kong. ISBN 3-540-65239-6. XII und 312 Seiten mit 67 Abbildungen und 63 Tabellen. Gebunden DM 149,- / öS 1088,- / sFr 136,- / GBP 57,50 / US\$ 85,15.

Das vorliegende Buch geht auf die Auswertung der in den 80er Jahren durchgeführten immissionsökologischen Waldzustandserfassung (IWE) zurück. Angesichts der Tatsache, dass sich die neuartigen Waldschäden nicht auf einzelne Einflussfaktoren zurückführen lassen, wurden die Messprogramme erweitert. Damit stieg die Anzahl der gemessenen Variablen an, und die Datensätze erhielten einen multivariaten Charakter. In der Arbeit wird mit einer mehrdimensionalen Datenanalyse den Fragen, die für das Erkennen der anthropogenen Waldgefährdung und für die Erfassung der bereits eingetretenen Schäden (Nadelverluste) relevant sind, nachgegangen.

Nach einer Einführung in die Problematik der Ökosystemanalyse bei flächenhaften Waldschäden stellt der Autor die mathematischen Grundlagen der mehrdimensionalen Datenanalyse umfassend vor. Anhand von multivariaten Modellen (Diskriminanz-, kanonische Korrelations-, Regressions-, Hauptkomponenten- und Faktorenanalyse) werden Versauerungshypothesen zur Klärung der neuartigen Waldschäden am Beispiel eines flächendeckend erhobenen Datensatzes aus Schleswig-Holstein überprüft. Die kausale Kette von den anthropogen induzierten Versauerungsprozessen über Störungen des Fließgleichgewichtes im Boden als Reaktionsmedium bis hin zu den äußerlich sichtbaren Schäden kann nachvollzogen werden.

Der Autor zeigt, (1.) dass im Bereich der Zuwachskunde eine Neuorientierung notwendig wird; (2.) dass zusätzliche Parameter erhoben werden müssen, um den anthropogen bedingten Teil am ursachenunspezifischen erhobenen Nadelverlust spezifizieren zu können; (3.) welche von den gemessenen bzw. abgeleiteten Parametern die größte Aussagekraft hinsichtlich des Potentials, anthropogen bedingte Waldschäden zu klären, besitzen; und nennt (4.) geeignete Methoden zur Verknüpfung dieser Parameter mit den okular geschätzten Nadelverlusten.

Das Buch zeichnet sich durch seinen systematischen Aufbau aus und vermittelt anhand zahlreicher Abbildungen und Tabellen dem ökologisch denkenden und mathematisch interessierten Leser aus den Bereichen Forstwissenschaft, Bodenkunde, Biologie, Geographie und Umweltwissenschaften in nachvollziehbaren Schritten die Theorie der multivariaten Datenanalyse am Beispiel der neuartigen Waldschäden. Durch die fachübergreifende Konzeption des Buches werden auch Biometriker, Physiker und Statistiker angesprochen, die Anregungen für ihre Arbeit mit den Anwendern multivariater Verfahren im Bereich der Ökologie suchen.

M. LIESEBACH (Grosshansdorf)

Handbuch zum deutschen und europäischen Sortenschutz. Systematische Darstellung mit Gesetzestexten. Von F. WUESTHOFF, H. LESSMANN und G. WÜRTEMBERGER. 1999. Wiley-VCH Verlag, Weinheim, New York, Chichester. ISBN 3-527-28810-4. 2 Bände mit XVI und 840 Seiten. Gebunden DM 498,- / Euro 254,62 / sFr 443,-.

Als Ergebnis einer grundlegenden Neubearbeitung des anerkannten Standardwerks „Sortenschutzgesetz“ von WUESTHOFF, liegt ein Handbuch vor, das sowohl den deutschen als auch den europäischen Sortenschutz in zwei Bänden mit drei Teilen ausführlich darstellt. Der erste Band enthält zwei Teile. Im ersten Teil sind im Originalwortlaut das Sortenschutzgesetz (SortG), die EG-Verordnung über den gemeinschaftlichen Sortenschutz (EGSVO) und das Internationale Übereinkommen zum Schutz von Pflanzenzüchtungen (UPOV-Übereinkommen) abgedruckt. Sie sind die Grundlage für den sich anschließenden Erläuterungsteil (432 Seiten). In ihm werden in 7 Abschnitten die einzelnen rechtlichen Vorschriften in systematischem Zusammenhang erläutert. Im ersten Abschnitt werden Ausführungen zum Schutzzanliegen gemacht. Es folgen Erläuterungen und Kommentare zu den Voraussetzungen zur Sortenschutzerteilung, zum Inhalt des Sortenschutzes sowie zu den Berechtigten aus dem Sortenschutz, zum Schutzerteilungsverfahren und zur Dauer des Sortenschutzes. Mit Ausführungen zu Sortenschutzverletzungen und ihren Folgen schließt der 7. Abschnitt. Im zweiten Band folgt der dritte Teil, in dem weitere rechtliche Grundlagen (Gesetze, Verordnungen, Bekanntmachungen, Empfehlungen, Mitteilungen, Formulare usw.) zusammenge-

stellt sind. Die Auswahl der im Zusammenhang mit dem Sortenschutz bedeutenden Quellen besticht durch ihre Vollständigkeit. Der zweite Band schließt mit einem zehnteiligen Stichwortverzeichnis, das sich auf rund 1500 Randnummern im Erläuterungsteil bezieht. Das Handbuch ist für alle am Saatgutmarkt Beteiligten als systematisches Nachschlagewerk eine unentbehrliche Informationsquelle bei der Gestaltung ihrer Arbeit.

M. LIESEBACH (Grosshansdorf)

Holzfacetten – Begegnungen mit dem Schönen. Von G. WITT. 1999. DRW-Verlag Weinbrenner GmbH & Co., Leinfelden-Echterdingen. ISBN 3-87181-350-8. 144 Seiten mit 192 zum Teil doppelseitigen Farbfotos. Fester Einband DM 128,-/6S 934,-/sFr 114,-.

Dieser außergewöhnliche Bildband stellt eine wertvolle Ergänzung der bisher erschienenen, in erster Linie auf die Vermittlung von Sachwissen orientierten DRW-Fachbücher für die Holzwirtschaft dar. Er bringt dem Betrachter das „Element“ Holz aus ganz anderem Blickwinkel als gewohnt nahe. Durch eine Dreiteilung des Buches wird der Entwicklungsweg des Rohstoffs Holz deutlich gemacht, von seiner Entstehung über die Verarbeitung bis zur Verwendung in den verschiedensten Bereichen des Lebens. Im ersten Abschnitt zeigt der Autor den Baum in seinem Lebensraum Wald in wunderbaren Fotografien zu den verschiedensten Jahreszeiten und Altersstufen. Besonders ansprechend sind die Nahaufnahmen von Holz- und Rindenstrukturen, aber auch die Darstellung des Zusammenspiels von Wald und Wasser. Zum zweiten Teil leiten Bilder über, die Bäume nach dem Fällen zeigen, also auf dem Wege ihrer Nutzbarmachung durch den Menschen. Es folgen Motive vom Transport, von der Lagerung und Trocknung des Holzes bis zu seiner Verarbeitung im Sägewerk. Mit Ausschnitten aus dem Verbund von Stämmen bei der Errichtung von Blockhäusern wird der Übergang zum letzten Abschnitt des Bildbands gefunden. Hier werden die vielfältigen Verwendungsmöglichkeiten des Holzes für nützliche und zugleich schöne Dinge gezeigt, vom Haus- und Schiffsbau über Brücken und Treppen bis hin zu Spielzeug und Intarsienarbeiten. In allen Fotografien beeindruckt ihre brillante Farbkomposition und der sichere Blick des Fotografen für die Ästhetik des Details. Ein kurzer Anhang mit Informationen zu einigen Bildern insbesondere aus dem letzten Teil des Buches hätte die Gesamtdarstellung abgerundet. Vermutlich ist bewusst darauf verzichtet worden, um den Blick für das in diesem Band Wesentliche zu schärfen: die Schönheit des Holzes in all seinen Erscheinungsformen in Harmonie mit seiner Umgebung. Man wird angeregt zum Nachdenken über die Langlebigkeit des Individuums Baum, das schon zu Lebzeiten und erst recht in seiner endgültigen Gestalt als genutzter Werkstoff Holz den Menschen durch die Jahrhunderte seiner Geschichte begleitet hat. Diese komplexe Betrachtungsweise wird dem Leser schon durch das einführende Vorwort von DIETER GÖRLACH nahe gebracht. Die im Bildteil ergänzend eingefügten Zitate und Gedichte verschiedener Autoren verstärken die von den Bildern auf den Betrachter übertragene Stimmung. Die zitierten Worte von THEODOR HEUSS: „Holz ist ein einsilbiges Wort – aber dahinter steht eine Welt voller Märchen und Wunder“ spiegeln die Wirkung dieses Buches wider, dessen Faszination man sich kaum entziehen kann.

Der Bildband „Holtzfetzen“ ist ein schönes Geschenk für alle, die dem Holz in irgendeiner Weise zugetan sind, sei es aus beruflichen Gründen oder einfach aus Interesse für die Natur.

G. NAUJOKS (Waldsiefersdorf)

Bibliographie – Umweltaspekte der Gentechnik. Reihe UMPLIS – Informations- und Dokumentationssystem Umwelt. Bearbeitet von E. DÖRNER und A. SCHUBERT. Herausgegeben vom Umweltbundesamt. 1999. Erich Schmidt Verlag, Berlin, Bielefeld, München. ISBN 3-503-05835-4. Format 17 cm x 24 cm. 622 Seiten. Kartoniert DM 98,-/Euro 50,11/6S 715,-/sFr 89,-.

Der erste Eindruck des Buches ist abschreckend. Der stechend-rot gehaltene Einband und der Umfang des Werkes vermitteln etwas Bizarres, gar etwas Unheimliches. Und tatsächlich, das Thema „Umweltaspekte der Gentechnik“ könnte etwas Bedrohliches darstellen, wenn nicht, wie im vorliegenden Werk gelungen, eine breite Palette umweltrelevanter Publikationen zum Thema Gentechnik zusammengestellt worden wäre. Gentechnik und ihre Anwendungsgebiete in der Medizin, Pharmazie, Umweltschutz und Lebensmittel beschäftigen seit Verabschiedung des Gentechnikgesetzes im Jahr 1990 immer mehr die breitere Öffentlichkeit in Forschungseinrichtungen, Politik, Verwaltung, Umweltverbände und Wirtschaft. Dabei wird die Diskussion über die Anwendung der Gentechnik und ihre Folgen nach wie vor sehr kontrovers geführt. Die in der vorliegenden Bibliographie zusammengestellte Sammlung von Publikationen befasst sich bevorzugt mit Fragen der Sicherheits- und Begleitforschung zum Thema Gentechnik. Verschiedene Literaturdatenbanken wurden durchsucht und schließlich 2100 Fachveröffentlichungen zusammengetragen. Nach Sachgebieten geordnet und mit anhängenden Autorenregister lässt sich eine gesuchte Publikation leicht finden. Somit stellt das vorliegende Buch insgesamt eine gelungene Zusammenstellung des aktuellen Stands der bis heute veröffentlichten umweltrelevanten Arbeiten zum Thema Gentechnik dar. Dennoch wird sich vielleicht dem unvoreingenommenen Leser der Eindruck aufdrängen, dass die Auswahl an Publikationen eine leichte Unausgewogenheit zwischen Pro und Contra Gentechnik darstellt.

M. FLADUNG (Grosshansdorf)

Illustrierte Flora von Mitteleuropa. Band IV. Teil 2C, Rosaceae. Lieferung A. Bogen 1 bis 7, Rosa. 2., vollständig neubearbeitete Auflage. Von G. HEGI. Bearbeitet von H. HENKER. 2000. Verlag Parey, Berlin. ISBN 3-8263-3296-2. 108 Seiten mit 77 Abbildungen und 2 farbigen Tafeln. Broschiert DM 78,-.

Die 1906 von GUSTAV HEGI zunächst in 6 Bänden begründete und seither in über 20 Teilbänden zumeist vollständig neubearbeiteten 2. bzw. 3. Auflagen sind für die Flora Mitteleuropas das unverzichtbare Standardwerk. Band IV, Teil 2C, erscheint in Lieferungen mit den Gattungen *Rosa*, *Potentilla* und *Sibbaldia*. Hiervon liegt als erste Lieferung die Neubearbeitung der Wildrosen-Arten vor. Von den weltweit bekannten 100 bis 250 Arten (je nach Artauffassung) kommen in Europa 30 bis 60 heimische oder eingebürgerte Arten vor, von denen wiederum für das Gebiet der Flora 33 Arten beschrieben werden. Obwohl es sich hierbei um eine relativ kleine, überschaubare Anzahl handelt, ist ihre eindeutige Bestimmung in vielen Fällen außerordentlich schwierig. Hierzu tragen die große genetische Vielfalt der als Arten betrachteten Sippen, die hybridogenen Formenschwärme und die komplizierten Fortpflanzungsverhältnisse bei. Das führt beispielsweise in der Sektion *Caninae* (Hundsrosen) dazu, dass „alle Arten dieser Sektion in vielfältigen Kombinationen ineinander überzugehen scheinen, die häufig als Zwischen- oder Übergangsformen bezeichnet werden und nicht selten regional gehäuft auftreten“ (S. 30). Hinzu kommt, dass die nomenklatorische Situation der

Wildrosen sehr verworren ist, viele Arten mit zahlreichen synonymen Namen versehen wurden und Prioritätsregeln vielfach nicht konsequent einzuhalten sind. In der vorliegenden Bearbeitung werden daher sehr eingehend die diagnostisch wichtigen Merkmale dargestellt und wichtige Hinweise zum Bestimmen von Wildrosen gegeben. Die einzelnen Rosen-Arten werden in der für den „HEGI“ gewohnten, genauen und ausführlichen Weise beschrieben. Detailliert wird auf das Vorkommen, die allgemeine Verbreitung, die Verbreitung im Gebiet der Flora, auf Variabilität und Taxonomie sowie auf Bastarde (allerdings ohne Beschreibung der einzelnen Hybrid-Formen) eingegangen. Bei der Gattungsbeschreibung finden sich Ausführungen zur systematischen Stellung, Morphologie und Anatomie, Cytotaxonomie und Bastardierung, Blüten- und Ausbreitungsökologie, Ökologie und Soziologie, Inhaltsstoffe, Nutzen und Verwendung, Krankheiten und Schädlinge, Kulturgeschichte, Florengeschichte (erste Fossilfunde stammen aus dem Tertiär), Artkonzept sowie zu einem historischen Überblick auf die Erforschung der Gattung. Verbreitungskarten, s/w-Zeichnungen und s/w-Fotos ergänzen den Text, wobei die fotografierten Herbar-Belege leider weniger gut die Einzelheiten zeigen als die Zeichnungen. Wertvoll sind die ausführlichen Literaturangaben zur Gattung sowie zu den einzelnen Arten. – Rosen sind typische Vertreter von Gebüschgesellschaften und spielen häufig in Sukzessionsstadien bei der Wiederbewaldung eine bedeutende Rolle. Manche Arten sind inzwischen gefährdet oder sogar vom Aussterben bedroht. Ihre Erhaltung wird im Rahmen der Erhaltungs-Konzepte von Baum- und Straucharten gefördert. Hierzu muss man die Arten jedoch identifizieren können, wozu diese Lieferung des „HEGI“ einen wesentlichen Beitrag liefert.

B. R. STEPHAN (Grosshansdorf)

Kurzumtriebsbewirtschaftung auf landwirtschaftlichen Grenzertragsböden. Biomasseproduktion und bodenökologische Auswirkungen verschiedener Baumarten. Berichte aus der Agrarwissenschaft. Von R. UNSELD. 1999. Shaker Verlag, Aachen. ISBN 3-8265-4829-9. 193 Seiten mit 39 Abbildungen und 63 Tabellen. DM 98,-.

Bei der vorliegenden Arbeit handelt es sich um eine Dissertation, die im Rahmen des Sonderforschungsprogramms „Nachwachsende Rohstoffe“ des Landes Baden-Württemberg erstellt wurde. Neben Pappeln und Weiden wurden 16 weitere Laubbaumarten auf ihre Eignung für den Kurzumtrieb geprüft. Auf 4 ehemaligen Ackerstandorten in Baden-Württemberg und einem Waldstandort in Rheinland-Pfalz wurden wachstumskundliche und bodenökologische Fragestellungen untersucht. Im wachstumskundlichen Teil wurden Anwuchserfolg, Biomasseproduktion und vegetative Regenerationsfähigkeit untersucht. Balsampappel- und Korbweidenstecklinge überzeugten, während Birken und Aspen mäßigen Anwuchs zeigten. Bei allen Baumarten gefährdete Wildverbiss und konkurrierende Begleitvegetation den Anwuchserfolg. Die Biomasseproduktion wurde nach einer Produktionszeit von 8 Jahren ermittelt, als der Bestandeszuwachs bei den meisten Baumarten kulminierte hatte. Abhängig von Baumart und Standort wurden bis 20 t Trockenmasse je Hektar und Jahr (Grauerle auf ehemaligem Niedermoorstandort) produziert. Die bodenökologischen Untersuchungen beinhalten Durchwurzelungsvermögen, Lagerungsdichte, chemische Bodenanalysen des Bodenwassers und der Festsubstanz, Nährelementanalysen der Biomasse, Nährstoffein- und -austräge sowie Untersuchungen zum Wasserhaushalt. Einige der bodenökologischen Untersuchungen erfolgten beispielhaft und bedürfen daher vor

einer Generalisierung einer differenzierten Betrachtung. Die Ergebnisse belegen, dass im Kurzumtriebswald viele Eigenschaften des Hochwaldes gefunden werden und eine Einstufung als ackerbauliche Monokultur dem Kurzumtriebswald nicht gerecht wird. Der Kurzumtriebswald ist durch seine typischen ökologischen Eigenheiten eine eigene Landnutzungsform. Abschließend werden die Untersuchungsergebnisse im Hinblick auf die Baumartenwahl für den Kurzumtrieb diskutiert und Anbauempfehlungen ausgesprochen. Ein 14seitiges Literaturverzeichnis berücksichtigt wesentliche Arbeiten bis 1997. Der hohe Verkaufspreis steht jedoch einer weiten Verbreitung des Buches entgegen.

M. LIESEBACH (Grosshansdorf)

Teil I: Dokumentation der Sturmschäden vom 29. 6. 1997 in Niedersachsens Wäldern verursacht durch „schwere lokale Stürme“. Von M. HUBRIG.

Teil II: Die betriebswirtschaftliche Entwicklung des Niedersächsischen Landesforstbetriebs. Von H. RIPKEN. Schriftenreihe „Aus dem Walde“, Mitteilungen aus der Niedersächsischen Landesforstverwaltung, Heft 52. Herausgegeben vom Niedersächsischen Ministerium für Ernährung, Landwirtschaft und Forsten. 1999. Bezug: Niedersächsisches Forstplanungsamt, Forstweg 1A, D-38302 Wolfenbüttel. 230 Seiten. DM 25,-.

Im ersten Teil des vorliegenden Heftes aus der Schriftenreihe „Aus dem Walde“ dokumentiert MARTIN HUBRIG (135 Seiten) die schweren Gewitterstürme vom Abend des 29. Juni

1997 mit über $\frac{1}{2}$ Mio. Efm Schadholz im südlichen Niedersachsen. Einem historischen Abriss ähnlicher Ereignisse in Deutschland folgen die Darstellung der meteorologischen Situation und für die einzelnen Schadensbereiche eine Beschreibung des Schadensereignisses und des Schadensverlaufs sowie eine Fotodokumentation. Der Fototeil verdeutlicht, welche potentiellen Gefahren von urplötzlich auftretenden und mit brachialer Gewalt hereinbrechenden Stürmen ausgehen. Anders als bei vielen Winterstürmen zeichnen sich die Schäden der Sommergewitterstürme durch hohe Anteile an Bruch- und Splitterholz sowie durch die Zerstörung junger Bestände aus. Auch wenn letztlich kein noch so stabiler Einzelbaum einem derartigen Sturm gewachsen ist, so müssen hinsichtlich der höheren Stabilität standortgerechte Mischbestände als notwendige waldbauliche Ziele weiterhin verfolgt werden.

Im zweiten Teil (95 Seiten) gibt der langjährige Leiter des Referats Betriebswirtschaft, Controlling, Organisation der Landesforstverwaltung, HEIKO RIPKEN, eine Bestandsaufnahme betriebswirtschaftlicher und organisatorischer Entwicklungen der niedersächsischen Forstverwaltung. Im Zuge der allgemeinen Verwaltungsreform des Landes Niedersachsen hatte auch die Niedersächsische Landesforstverwaltung eine Reorganisation beschlossen. Auf der Grundlage von Analysen und kritischen Beurteilungen der betriebswirtschaftlichen Entwicklung wurden Leitbilder und künftige Ziele sowie Strategien erarbeitet. Dargestellt wird am Beispiel der Niedersächsischen Landesforstverwaltung, wie der gesamte Prozess der planmäßigen betriebswirtschaftlichen Entwicklung (einschließlich der sog. Non-Profit-Leistungen) einer Forstverwaltung gestaltet werden kann. Dieser Bericht, der nachvollziehbar macht, wie es zu der großen Verwaltungsreform kam, ist auch als Dokumentation eines persönlichen Lebenswerkes zu lesen.

M. LIESEBACH (Grosshansdorf)