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Genetic Variation Among Clones of *Picea abies* in Resistance to Growth of *Heterobasidion annosum*

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Summary

An inoculation experiment with *Heterobasidion annosum* on 98 four-year-old *Picea abies* clones was conducted on rooted cuttings under greenhouse conditions. One isolate of *H. annosum* and 10 ramets of each clone were used. After 34 days of incubation, fungal growth in sapwood and lesion length in the inner bark were measured. There were significant differences among clones in lesion length in the inner bark and in fungal growth in sapwood. Broad sense heritability was 0.35 for fungal growth and 0.27 for lesion length in the inner bark. Fungal growth and lesion length showed strong genotypic correlation. Bud-flushing index of the clones was correlated with mean fungal growth, whereas the growth termination index was not. Fungal growth in sapwood and lesion length in the inner bark of cuttings were not correlated with the mean height and provenance of 15-year-old ramets of the same clones in previously conducted field tests.

Key words: *Heterobasidion annosum*, *Picea abies* clones, Root rot, Norway spruce, resistance, gentic variation.

FDC: 165.53; 443; 416.3; 172.8 *Heterobasidion annosum*; 174.7 *Picea abies*.

Introduction

Investigations of genetic variation among Norway spruce (*Picea abies* (L.) KARST.) clones have revealed that several characters vary significantly. Results of an investigation by ERIKSSON *et al*. (1978) suggest that the photoperiod and temperature responses of Norway spruce are determined and influenced by a number of genes and/or alleles with small additive effects. SKRÖPPA and DIETRICHSON (1986) found that between-clone variation in height growth during a 7 year period accounted for 35% of the total variation in that particular character. Tree size, the wood specific gravity of *Picea sitchensis* (BONG) CARR. and height growth of *P. abies* were found to vary significantly between clones (CANNELL *et al*., 1983; ROULUND *et al*., 1985; SHAW *et al*., 1988). DIMITRI (1974 and 1976), VON WEISSENBERG (1975) and SWEDJEMARK and STENLID (1994 and 1996) showed significant between-clone variation in the growth of *Heterobasidion annosum* (FR.) BREF. in clones of Norway spruce.

Norway spruce has proved to be a good species for large-scale clonal tree improvement programs (BENTZER, 1993). Cuttings showed, on average, a 25% higher growth rate compared with seedlings in a Danish investigation (ROULUND and Bergstedt, 1982). Clonal selection is a good means of improving genetic gain (KLEINSCHMIDT, 1983), and the mass propagation of clones is an efficient way of exploiting genetically improved material. If resistance factors could be included in existing selection programmes for clonal production, the advantage of using cuttings for reforestation would be even greater since less resistant clones could be excluded.

H. annosum is the most serious of the pathogens attacking Norway spruce in Scandinavia. It causes root and butt-rot to conifers and broadleaf trees throughout the boreal and temperate zones of the Northern Hemisphere. Primary spread of the fungus is via spores that settle and germinate on freshly cut stumps or wounds on stems and roots to form a mycelium. The mycelium colonizes the stump, extends throughout the roots and infects healthy trees via root contacts between stumps and trees. Decay may spread up to 12 m in infected stems (STENLID and WÄSTERLUND, 1986).

The results of inoculation experiments under greenhouse conditions, used in several studies to test large amounts of plant material in a short period, correlate well with observations and inoculation studies in the field (KUHLMAN, 1970; BUTCHER *et al*., 1984; STENLID and SWEDJEMARK, 1988; CHASE *et al*., 1989; CAPRETTI *et al*., 1994; SWEDJEMARK and STENLID, 1995). DIMITRI and SCHUMANN (1989), showed that the rankings of *P. abies* clones in terms of *H. annosum* growth in sapwood was the same on cuttings as well as on 15-year old trees. However, negative results have also been reported by KUHLMAN (1972). He tested 185 families including some 10 000 seedlings of *Pinus taeda* and found no difference among the 6 provenances studied. Likewise, no difference was detected between two series of *Pinus elliottii* progenies.

The purpose of our study was to estimate the genetic variation in *H. annosum* growth in sapwood and lesion length in the

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inner bark between 100 clones of Norway spruce and look for correlations with other heritable characters.

Material and Methods

Originally the clones were produced in connection with a Swedish clonal forestry program. This original set of clones contained 632 clones of varying provenances and was primarily selected in 1980. Bud-flush was registered for the clones in Kolleberga Nursery in southern Sweden in the spring of 1982. On 10 occasions, each clone was observed to see if it had reached stage 3 according to KRUTZSCH (1975). The point in time (occasion 0 to 10) at which stage 3 was reached was taken as the bud-flushing index for the clone (SWEDJEMARK and STENLID, 1996). In mid-September of 1982, growth termination was scored as follows: 1 = early budset, 2 = proleptic growth and 3 = free growth. Another bud-flush assessment on remaining ramets of the 632 clones in the nursery was carried out in spring 1993 when KRUTZSCH's index was used. In the calculations, mean scores of the two bud-flush assessments are used. Within the clonal forestry program, field tests were established in 1983 when seven ramets of each clone were planted on each of two sites. The clones were planted in different Norway spruce seed zones (Anonymous, 1982) according to their pattern of growth rhythm. Total height, height increment, stem crooks and frost damage were measured after six growing seasons in the field. Best Linear Unbiased Predictor (BLUP) values were calculated for the measured traits (KARLSSON, unpublished).

The cuttings intended for resistance testing were randomely choosen among the 632 clones available. The scions were collected from 4-year-old nursery plants in the third vegetative cycle and rooted in 1989. They were transplanted as bare-roots in 1990 and potted in 20-cm-diameter (3-litre) pots in spring 1991. Two clones were lost during cultivation, thus, 98 clones ended up in the resistance testing programme in 1992. The provenances of the chosen clones varied: 63% were from Romania, 30% from Byelo Russia, 4% from Denmark and 3% from Sweden (*Table 1*).

The fungal isolate (Rb 175) used in the inoculation experiment was isolated in 1985 from a living Norway spruce in southern Sweden (STENLID, 1987). The isolate was of the S intersterility group of *H. annosum* (KORHONEN, 1978) and has been used in several inoculation experiments (SWEDJEMARK and STENLID, 1995, 1996). Results from similair investigations indicate that one fungal isolate may suffice for studying the variation in inoculation experiments (KUHLMANN, 1969; SWEDJEMARK and STENLID, 1988, 1995; ENTRY *et al.*, 1994. The inoculum was prepared by growing the fungus for 4 weeks on 5 mm x 5-mm spruce dowels at room temperature (STENLID and SWEDJEMARK, 1988).

The cuttings were randomised within five blocks, with two rametes/clone in each block. The cuttings were dehardened (HEIDE, 1974) so that each block had recieved identical light and temperature treatments prior to inoculation. The five blocks occupied separate growth chambers in the greenhouse and were inoculated at 1-week intervals.

The xylem was exposed on a 5-mm circular area by using a disinfected cork-borer. A *H. annosum* infected dowel was tightly attached to the wound by wrapping parafilm around the stem, about 8 cm above the soil surface (STENLID and SWEDJEMARK, 1988). The cuttings were thereafter randomly distributed in their growth chambers and incubated for 34 days in 18 h daylight and at 18 °C.

At the time of assessment, the cuttings were removed from the pots and vigour was scored based on the number of white unsuberized roots and the intensity of needle-fall, as follows: A score of 0 was assigned to a dead cutting. Below-ground, scores of 1 and 2 were assigned to cuttings with less than and more than three white unsuberized roots, respectively. Mycorrhiza was frequently present on the rootsystems. Above-ground, scores of 1 and 2, were assigned to cuttings with needle loss rates of more than and less than approximately 5% needle-fall, respectively. Scores used in the statistical analysis were the mean value of the sum of above-and below-ground values for each clone (SWEDJEMARK and STENLID, 1996).

The diameter at 5 cm above the soil surface and the height, excluding the new leading shoot, were measured for each cutting. The top, roots and branches were removed, and the total length of the inner bark lesion, extending from the wound was determined (SWEDJEMARK and STENLID, 1996).

Using sterilized tools, the stem was consequtively cut into 5-mm-thick discs, 20 pieces above and 20 below the point of inoculation. All discs from each tree were put separately into Petri dishes, and incubated under humid conditions for 5 to 7 days. The discs were then checked for the conidial stage of *H. annosum* under a dissecting microscope, and the extension of fungal growth was expressed in mm (STENLID and SWEDJEMARK, 1988).

When calculating fungal growth in sapwood and lesion length in the inner bark, all dead cuttings and all cuttings in which infection had failed were excluded (SWEDJEMARK and STENLID, 1996).

Table 1. – Distribution of provenances among clones.

Clone numbers	Number of clones	Provenance
0201-0822	30	Moldovita, Romania
0823-1375	24	Minsk, Logojskij, Byelo Russia
1376-1529	6	Minsk, Volozinskij, Byelo Russia
1530-2199	29	Cimpeni, Romania
2200-2363	5	Gustavsberg, 2nd generation Germany
2364-2387	1	Slogstorp, Denmark
2388-2446	3	Maglehem, Denmark

Table 2. – Distribution of bud flush and growth termination (bud set) classes in 1982 for the tested clones. Number of clones assigned to each budflush/budset index.

Budflush \ Budset	1	2	3	4	5	6	7	8	9	10	Sum
1	2	1	10	6	4	9	2	2	0	1	**37**
2	1	3	3	7	4	6	1	4	0	3	**32**
3	0	0	6	4	4	4	8	4	0	0	**30**
Sum	**3**	**4**	**19**	**17**	**12**	**19**	**11**	**10**	**0**	**4**	**99**

Analysis of variance using different GLM procedures, PEARSON's correlation coefficient test, and DUNCAN's multiple range test were performed using the SAS computer program. Genotypic parameters were estimated using mixed model software developed by HARVEY (HARVEY, 1990). BLUP values were calculated with the same software package. Genotypic correlations were estimated for the traits in the resistance test. For correlation estimates with field traits BLUP-values were used, and for growth rhythm traits phenotypic mean values were used.

Results

The size of the cuttings did not vary within, but was different between clones ($P < 0.00001$). Height among clones ranged between 25 cm and 70 cm (mean height 47 cm), and the diameter ranged between 4 mm and 14 mm (mean diameter 9 mm). The vigour condition mean score differed between clones ($p < 0.00001$) (Data not shown). About 18% of the clones were designated to bud-flushing index 3, 4 and 6, 10% of the clones to index 5, 7 and 8 and 3% of the clones to index 1, 2 and 10. The clones were evenly distributed among the growth termination classes (*Table 2*).

The *H. annosum* infection incidence was 99% and the mortality rate was 1.5% evenly distributed among the clones.

Mean fungal growth in sapwood for each clone ranged between 36 mm and 171 mm. Corresponding values for lesion length in the inner bark was 13 mm and 102 mm (*Fig. 1a, b*).

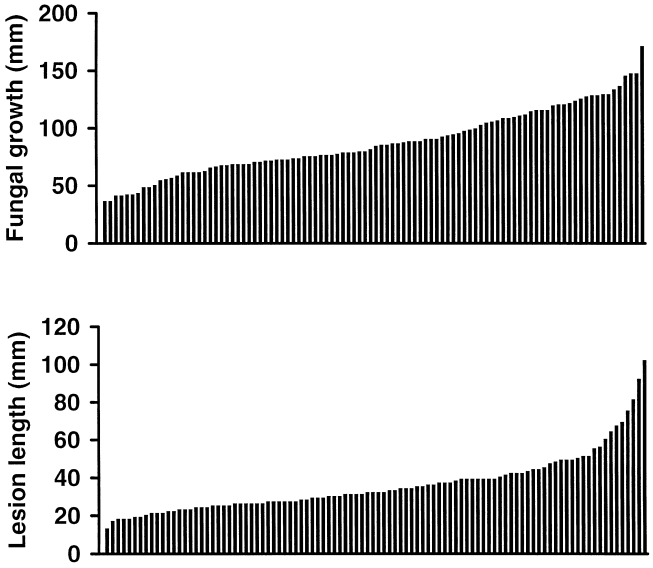

Fig. 1a and *b.* – Mean value (n = 10) for fungal growth (a) and lesion length (b) for each of 98 clones of Norway spruce.

There were significant genotypic variations in lesion length in the inner bark and fungal growth in sapwood among clones ($p < 0.00001$). Phenotypic and genotypic variances for mean lesion length were 595.6 mm^2 and 159.6 mm^2, and for mean fungal growth 1947.7 mm^2 and 684.5 mm^2. Broad sense heritability was 0.27 for lesion length, and for fungal growth 0.35. The genotypic coefficient of variance was 35.9% for lesion length and for fungal growth 30.2%. In the total material, mean fungal growth was 87 mm and for mean lesion length in the inner bark mean value was 35 mm. There was no significant difference in fungal growth up and down from the point of inoculation (*Table 3*).

No significant differences in fungal growth or bark lesion length were found among different provenances (Data not shown).

A significant genotypic correlation coefficient was found between fungal growth and lesion length ($r = 0.75$). Fungal growth and lesion length were negatively correlated with cutting diameter and vigour index ($r = -0.47$ and -0.59, respectively). Cutting height and diameter were positively correlated with vigour index ($r = 0.31$ and 0.44, respectively) (*Table 4*).

There was a correlation for both lesion length and fungal growth with bud-flushing index (BLUP-values), $r = 0.24$ and $r = 0.21$, respectively (*Table 5*).

In the field test performed within the clonal forestry program, mean values for height of the 6-year-old clones varied between 139 cm and 183 cm in the two seed zones. Phenotypic variances for height growth in seed zones 7 and 9 were 2044 mm^2 and 354.9 mm^2, respectively, and genotypic variances were 4065 mm^2 and 388.2 mm^2, respectively. The broad sense heritability (H^2) for height growth was 0.17 in seed zone 7 and 0.10 in seed zone 9. Corrersponding values for the genotypic coefficient of variation were 10% and 10.7% (*Table 3*).

Discussion

Our main results showed that there were differences in fungal growth in sapwood and lesion length in the inner bark among clones. Furthermore, the broad sense heritability was high for fungal growth in sapwood and lesion length in the inner bark. There were no correlations between fungal growth in sapwood with provenance groups or growth capacity in field tests.

A reliable inoculation method is a prerequisite when testing the relative susceptibility of a large set of host trees. The method in the present investigation has showed itself to be reliable, since the incidence of infection following inoculation is high, and the risk for experimental error due to technical problems is low. Fungal extension in the stem is also an economically important factor. The shorter the fungal

Table 3. – Mean values and genotypic parameters for some of the traits in field tests (mean values of 2 tests/zone) and resistance test in the greenhouse. σ^2P and σ^2G represents phenotypic variance, respectively. H^2 represents the broad sense heritability and CVg the genotypic coefficient of variation.

	Mean (mm)	σ^2P (mm^2)	σ^2G (mm^2)	H^2	Cvg (%)
Height age 6, zone 7	1391	2044	354.9	0.17	13.5
Height age 6, zone 9	1834	4065	388.2	0.10	10.7
Lesion of inner bark	35	595.6	159.6	0.27	35.9
Fungal growth up	43	534.4	167.4	0.31	30.0
Fungal growth down	43	551.2	181.2	0.32	31.0
Total fungal growth	87	1947.7	684.5	0.35	30.2

Table 4. – Estimates of genotypic correlations between traits in the resistance test. *) represents significance levels of 5%. NS = not significance, – indicates that the correlation coefficient is negative. D.F. = 96.

	Fungal growth up	Fungal growth down	Total Fungal growth	Cutting height	Cutting diam.	Cond. mean score
Lesion	0.75*	0.69*	0.72*	0.10 NS	(-)0.01 NS	(-)0.59*
Fungal growth up		0.97*	0.99*	(-)0.02 NS	(-)0.03 NS	(-)0.44*
Fungal growth down			0.99*	(-)0.10 NS	(-)0.15 NS	(-)0.50*
Total Fungal growth				(-)0.3*	(-)0.08 NS	(-)0.47*
Cutting height					0.77*	0.31*
Cutting diam.						0.44*

extension and the slower the spread of the fungus, the smaller is the volume of decayed wood.

Since this study was conducted on 4-year-old cuttings, which do not contain heartwood, our findings may not be applicable to older trees, in which heartwood is the main substrate of the fungus. However, in a previous study on *P. abies* clones, DIMITRI and SCHUMANN (1989) found a strong correlation between *H. annosum* extension in cuttings and that in trees. ZAK (1955) found that the relative resistance of *Pinus echinata* against littleleaf disease caused by *Phytophtora cinnamomi* in seedlings reflected that of the parent trees. Similarly, in unpublished studies of ours with Norway spruce cuttings there was good agreement between the results of inoculation experiments on young cuttings in the greenhouse and those obtained with 17-year-old ramets of the same clones in field tests. A large number of inoculated trees of the same clones used in this experiment will be sampled in the near future.

Any resistance barrier in the bark is bypassed by the inoculation method used in this study. However, when moving from one root to another, the fungus kills the bark as it grows through it before entering the sapwood (LINDBERG and JOHANSSON, 1991). In the present experiment as well as in

Table 5. – Correlation coefficients for BLUP values of mean lesion length, mean fungal growth, mean field height, and phenotypic values for bud-set index and bud-flush index. *) indicates that the correlation coefficient is significant at the 5% level, and NS indicates no significant correlation. A negative correlation coefficient is indicated by (–).

	Field height	Bud-set index	Bud- flush index
Lesion	0.17 NS	–0.01 NS	0.24*
Total fungal growth	0.11 NS	0.00 NS	0.21*
Field height		–0.07 NS	0.13 NS
Bud-set index			0.13 NS

earlier studies with *H. annosum* inoculations on Norway spruce seedlings, fungal extension in sapwood has been strongly correlated with the lesion length in the inner bark (STENLID and SWEDJEMARK, 1988; LINDBERG, 1992; SWEDJEMARK and STENLID, 1996). This correlation indicates that both fungal growth in sapwood and lesion length in the inner bark may be appropriate factors to consider when estimating the ability of the fungus to enter a living root.

In earlier studies (VON WEISSENBERG, 1975; STENLID and SWEDJEMARK, 1988; SWEDJEMARK and STENLID, 1995) no reduction in vigour has been observed in control seedlings (seedlings prepared with sterile wooden plugs in the same way as inoculated seedlings). This suggests that the incision in connection with the inoculation procedure does not influence the vigour of the plants. In the present study, the correlation data between vigour index score, lesion length and fungal sapwood growth are hard to interpret since they are all clone dependant. However, the negative correlation between vigour score and lesion length in the inner bark and fungal growth in sapwood indicates that the condition of the cuttings may be of importance for determining infection success (LINDBERG and JOHANSSON, 1992) and should be considered in future experiments in order to reduce the experimental error.

The lack of significant genetic correlations (*Table 3*) between lesion length and fungal growth with provenance and height in the field test is interesting. This is partly in accordance with a study by TRESCHOW (1958) who did not find any variation in growth of *H. annosum* among trees of different provenances of Norway spruce. Similarily, negative correlation between *H. annosum* infection rates and provenances of *Pinus taeda* was also reported by KUHLMAN (1972). If selection for resistance could be carried out without having to consider other characters, such as growth capacity or provenance, much could be gained. In contrast, results from field surveys and trials indicate that the rates of infection and extension of decay fungi are higher in larger trees than in smaller ones (DIMITRI and SCHUMANN, 1989; BLOOMBERG, 1990; SWEDJEMARK and STENLID, 1993). Whether this reaction is due to physiological, environmental or genetic factors has yet to be determined. Further studies on this theme should be made.

Mean fungal growth and mean lesion length were correlated with bud-flushing index. In a previous study (SWEDJEMARK and STENLID, 1996) it was found that fungal growth and lesion length were correlated with bud-flushing index only when the inoculation was carried out during bud- flush, which is in accordance with the present results.

There is little hope of finding totally resistant clones. However, the genotypic variation in fungal extension in the sapwood was quite large in this study. The genotypic coefficient of variation was more than twice that for height growth. This indicates that the proportion of the variation which is due to the genetic constitution of the cuttings is large. Good selection gains could be achieved, provided the correlation with fungal growth in mature trees is strong. The fastest gain will be attained by using cloned, mass-propagated material for outplanting of less susceptible clones. Planting a mix of such clones may reduce the frequency and spread of *H. annosum* in future populations of Norway spruce. Resistance testing could easily be applied in the Swedish breeding program for Norway spruce (KARLSSON and ROSVALL, 1992). This program includes vegetative propagation as a step in testing of new generation material. Since the present resistance testing procedure is fairly simple and inexpensive there is no reason not to use it, provided further research can verify the results in this study.

The relatively high H^2 indicates that there is also the potential for genetic gain. If more information about how the resistance mechanisms in Norway spruce are inherited, less susceptible clones could be used in future breeding populations. The offspring from such breeding populations would provide larger amounts of resistant material than mass-propagation of existing clones would, thus achieving a greater genetic variation in future clonal plantations.

Clonal effects in the field tests and the resistance test were predicted by the following statistical model for each observation: (1)

$$yijk = \mu + B_i + u_j + e_{ijk}$$

where:

y_{ijk} = character value for the ijkth observation
μ = mean value of the population
B_i = fixed effect of block i
u_j = random effect of clone j
e_{ijk} = random error term

Genetic parameters were interpreted as: (2)

$$\sigma^2_G = \sigma^2_u$$
$$\sigma^2_E = \sigma^2_e$$

where:

σ^2_G = genotypic variance
σ^2_E = environmental variance

BLUP values were calculated by: (3)

$$u_j = (\sigma^2_G/(\sigma^2_G + \sigma^2_E/n)\,(P_j - P)$$

where:

u_j = predicted clone effect for clone j
n = number of replications per clone
P_j = mean of clone j
P = total mean

Broad sense heritability was calculated as: (4)

$$H^2 = \sigma^2_G/\sigma^2_P$$

where:

σ^2_G = genotypic variance
σ^2_E = environmental variance
σ^2_P = phenotypic variance = $\sigma^2_G + \sigma^2_E$

The genotypic variation coefficient (CVg) was calculated as: (5)

$$CVg = (\sigma_G / \mu)\ 100$$

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Buchbesprechungen

Somatic Cell Genetics and Molecular Genetics of Trees. Edited by M. R. AHUJA, W. BOERJAN and D. B. NEALE. 1996. Kluwer Academic Publishers, Dordrecht. 292 pages. Hardcover NLG 200,– / US$ 130,–.

This volume is based on a joint meeting of the 2 International Union of Forestry Research Organizations (IUFRO) Working Parties, Somatic Cell Genetics (S2.04–07) and Molecular Genetics (S2.04–06) held in Gent, Belgium, 26 to 30 September, 1995. During the past decade rapid progress has been made in the biotechnology of forest trees, and this meeting provided a forum for the presentation and discussion of new developments in this area. This book documents some of these developments in somatic cell genetics and molecular genetics of trees. The book is divided into 4 sections. Section I deals with somatic embryogenesis and regeneration, and includes 10 chapters. Somatic embryogenesis has been investigated in a number of conifer and angiosperm tree species. However, *in vitro* regeneration of plants by somatic embryogenesis, or for that matter organogenesis, has been mainly achieved by employing juvenile tissues. Regeneration from tissues of mature trees is still very difficult by tissue culture. Several chapters discuss induction, early events, and markers of somatic embryogenesis. Questions regarding the stability or instability of somatic embryos-derived plants

(somatic seedlings) were also addressed in 2 chapters. Section II covers transformation and gene expression, and consists of 13 chapters. Most of the chapters in this section described the protocols for genetic transformation in trees using different gene constructs. Stability and expression of transgene expression in transgenic plants (Populus) was also discussed. A couple of papers outlined ideas for genetic engineering of wood (lignin) and floral genes for reproductive sterility. Section III deals with molecular markers and genome mapping, and contains 11 chapters. Several papers employed molecular markers for studies in bud dormancy and tissue differentiation, population genetics and disease resistance studies. In addition molecular markers have also been used for genome mapping. Identification and sequencing of genes and their function was discussed in loblolly pine. Section IV covers stress-related gene expression and is comprised of 4 chapters. Biotic/abiotic stress-related molecular characterizations in woody plants are presented in several papers in this section. Altogether there are 38 contributions in this book covering a wide range of topics in biotechnology of trees.

On the whole, this is an interesting and informative book on the recent advances in somatic cell genetics and molecular genetics of trees. This book would be useful for students, researchers, and managers in forestry interested in the biotechnology of trees.

H.-J. MUHS (Grosshansdorf)

Bäume und Wälder in Bayern. Herausgegeben vom Bayerischen Forstverein. 1997. ECOMED Verlagsgesellschaft, Landsberg. ISBN 3-609-65590-9. 285 Seiten mit zahlreichen 4farbigen Abbildungen. Gebunden DM 58,–/ öS 423,–/sFr 55,–.

Rund ein Viertel des deutschen Waldes liegt in Bayern. Die vorliegende geschichtliche, naturkundliche und kulturelle Darstellung der Baumarten und Waldgesellschaften in Bayern wurde vom Bayerischen Forstverein in 2., überarbeiteter Auflage herausgegeben. 27 Autoren geben in die historische, wirtschaftliche und kulturelle Bedeutung des Waldes und der Holzwirtschaft einen Einblick und beschreiben Verbreitung, Biologie, Standortansprüche, Waldbauliches, Vermehrung sowie Verwendung für 23 in bayerischen Wäldern vorkommende Baumarten bzw. Gattungen. Überwiegend allgemeine Literaturhinweise schließen die einzelnen Beschreibungen. Im folgenden werden 15 charakteristische Waldlandschaften Bayerns vorgestellt. Auf die Bedeutung der Wirtschafts-, Schutz- und Erholungsfunktionen des Waldes sowie auf die Gefahren für den Wald wird im letzten Abschnitt eingegangen. Das Buch ist durchgehend 4farbig illustriert und führt am Beispiel der bayerischen Wälder in verständlicher Weise in die komplexen Zusammenhänge der Lebensgemeinschaft Wald ein. Deren Verständnis ist eine Voraussetzung für einen wirksamen Schutz des Waldes. Auch außerhalb Bayerns kann dieses Buch allen an Wald und Landschaft Interessierten empfohlen werden.

M. LIESEBACH (Grosshansdorf)

Systemtheorie in der Ökologie. Schriftenreihe Angewandte Naturwissenschaften. Von K. MATHES, B. BRECKLING und K. EKSCHMIDT. 1996. Ecomed Verlagsgesellschaft AG & Co. KG, Landsberg. ISBN 3-609-69340-1. 128 Seiten mit Abbildungen, Tabellen und Übersichten. Broschiert DM 48,–/öS 350,–/sFr 44,80.

Die Ökologie hat sich als Teilgebiet der Biologie zu einer eigenständigen Naturwissenschaft entwickelt. Sie zeichnet sich vor allem durch das Wechselspiel von Theorie und Empirie aus. Daher nehmen systemtheoretische Ansätze gerade in diesem Forschungsbereich eine bedeutende Rolle ein. Aus der Forderung einer nachhaltigen Bewirtschaftung unserer natürlichen Ressourcen ergeben sich die aktuellen Fragestellungen zur Ökologie.

In diesem Buch wird eine Zusammenstellung von Beiträgen präsentiert, welche auf einer Tagung des Arbeitskreises »Theorie« in der Gesellschaft für Ökologie im März 1996, auf dem Schloß Rauischholzhausen vorgestellt wurden. Es ist den Buchautoren gelungen einen sehr guten thematischen Überblick über Geschichte, Gegenwart und Aussichten der Systemtheorie in der Ökologie zu geben.

Im 1. Teil des Buches werden die allgemeinen Konzepte der Systemtheorie, ihre geschichtliche Entwicklung sowie deren wissenschaftstheoretische Hintergründe erläutert. So wird nach einer kurzen Einleitung der Leser mit dem wohl zur Zeit bedeutendsten Konzept der Ökologie, der Hierarchie-Theorie, vertraut gemacht. In weiteren Beiträgen des 1. Teiles werden sowohl die geschichtliche Entwicklung behandelt als auch die modernen Theorien der Selbstorganisation in der Ökologie betrachtet. Schließlich wird in einem Beitrag noch auf die thermodynamischen Auffassungen der Ökologie eingegangen.

Vor dem Hintergrund des 1. Teils wird im 2. Teil die Relevanz systemtheoretischer Konzepte für die angewandte ökologische Forschung dargestellt. Mit der Auswahl der Beiträge wird ein repräsentativer Querschnitt der Ökosystemforschung der Bundesrepublik abgedeckt, welche eine gute Übersicht über mögliche Richtungen zuläßt. In diesen Beiträgen werden zunächst allgemeine Informationen zu den jeweiligen Forschungszentren gegeben und deren wesentliche theoretische Ansätze vorgestellt. Das Buch beinhaltet Vorträge der älteren Zentren in Kiel (PZÖ), Bayreuth (BITÖK) und Göttingen sowie der neuen Einrichtungen des UFZ Leipzig und des ZALF Müncheberg. Diese Beiträge zeichnen sich vor allem durch einen engen Bezug zum Umweltschutz aus. Es wird hierbei versucht, Konzepte für eine dauerhaft umweltgerechte Bewirtschaftung zu entwickeln.

Abgerundet wird dieser Band durch einen Beitrag zur Umweltschutzpraxis am Beispiel der ökotoxikologischen Risikobewertung. Gerade hier zeigt sich eine defizitäre Situation in Politik und Verwaltung.

Dieses Buch zeichnet sich durch eine vorbildliche Auswahl und thematische Zusammenstellung der Beiträge aus. Es gibt einen sehr guten Überblick über relevante Arbeiten in der Systemtheorie auf dem Gebiet der heutigen Bundesrepublik. Es ist sowohl für den Einsteiger in dieses Gebiet als Übersichtswerk geeignet als auch für jene, die sich bereits mit der Ökosystemforschung beschäftigen und sich über weitere Konzepte und Hintergründe informieren wollen. Außerdem eignet sich dieses Buch als Grundlage für weiterführende Diskussionen auf dem Gebiet der Systemtheorie in der Ökologie.

R. BIALOZYT (Grosshansdorf)

Genetic Data Analysis II. Methods for Discrete Population Genetic Data. By B. S. WEIR. 1996. Sinauer Associates, Inc. Publishers, Sunderland, Massachusetts, USA. 445 pages. £ 24.95.

This is a second edition of an earlier book "Genetic Data Analysis" by BRUCE S. WEIR. The author states in the preface that since the publication of the first volume, there has been a flood of information on the molecular markers developed by the PCR technology. Therefore, a revised, expanded, and an update version of the first edition of the book became necessary. In particular, the impact of microsatellite markers on population genetics has been substantial. These along with analysis of

restriction fragment length polymorphisms (RFLPs) and other co-dominant markers in plants, including trees, and animals and humans are also providing raw data for quantitative genetic analysis, construction of genome maps, and phylogeny profiles. In addition, forensic use of DNA markers in determining individuals identity and paternity disputes has attracted a lot of public attention and this requires quantification of data and use of paternity exclusion probabilities. All these developments and the availability of powerful new hi-tech computers are making the drab field of quantitative genetic analysis much more challenging and interesting. In this direction this book by BRUCE WEIR makes a real contribution. The book is divided into 10 chapters covering the essence of population genetics. The first chapter deals with the nature of discrete genetic data, starting with examples of genetic data, and then go on to molecular markers, including RFLPs, RAPDs, VNTRs, and STRs. Then there is brief discussion on genetic and statistical sampling, followed by notation and terminology. True to genetic tradition, the book does start with MENDEL. However, lingering questions regarding the exact nature of MENDEL's data by FISHER and others are also included. MENDEL's segregation ratios are too close to the expected as determined by chi-square statistics. Perhaps so. Nevertheless, MENDEL's work is the basis of genetics, and shows the importance of discrete data points. Now we also have molecular markers and DNA sequences as discrete genetic data, thus making a transition from the hypothetical genes to the DNA sequences. The next 2 chapters discuss estimation of frequencies within populations and testing hypothesis and HARDY-WEINBERG disequilibrium. Gene diversity, heterozygosity, population structure in fixed and random populations, and genetic distance are dealt with in the next 2 chapters. The identification of an individual in paternity disputes and forensic testing by DNA fingerprinting along with likelihood ratio is of interest in determining the frequency of matching profiles in the population. The last 3 chapters cover linkage, distance between genes, and estimation of recombination as basis of genetic maps, estimation of outcrossing, and selection, phylogeny reconstruction by distance matrix methods and parsimony methods, DNA sequence data analysis. Each chapter ends with set of interesting exercises. The book also contains 3 appendixes, including statistical tables, random numbers, and answers to the exercises. The book ends with a bibliography and author and subject index. The Genetic Data Analysis II is a valuable book not only for conventional plant and animal geneticist and breeders, but also for molecular biostatisticians.

M. R. AHUJA (Grosshansdorf)

Seeds of Forest Broadleaves – from Harvest to Sowing Techniques and Practices. By B. SUSZKA, C. MULLER and M. BONNET-MASIMBERT. Translated by A. GORDON. 1996. INRA Editions, Institut National de la Recherché Agronomique, Paris. ISBN 2-7380-0659-0. 295 pages. 310,– FF.

The irregular production of tree seeds, on one hand, and the difficulties of their storage over a number of years, on the other, pose a dilemma for a continuous supply of seeds. This problem comes to focus with increasing knowledge about adapted reproductive material and the requirements of planting specific seed sources. Above that there is a trend in Central Europe to plant more deciduous trees whose seeds are generally more difficult to handle than those of conifers. Thus, this book fills a gap by presenting techniques to handle seed in order to reach higher germination rates while extending the possible storing periods. The volume is divided into 2 parts. The first part, consisting of 94 pages covers general aspects of tree seed handling and gives background information about the biological processes occurring in seeds. The following topics are covered in short concise chapters: maturation, harvest, transport, provisional storage, cleaning, drying, conditioning before storage, storage, preservation strategies, breaking of dormancy, stratification, viability estimation, germination testing, and sowing. In the second part of the book (190 pages) seed handling of 15 Central European deciduous tree species of the genera *Acer, Alnus, Betula, Carpinus, Fagus, Fraxinus, Prunus, Quercus, and Tilia* is dealt with. The individual properties in seed handling according to the above mentioned topics are given. The many tables, figures, and excellent photographic illustrations help to understand the sometimes difficult seed treatment procedures of different species whose seed may exhibit 'recalcitrant' or 'orthodox' response when the water content is decreased in order to increase storing period. The 3 authors have gained adequate experience during many years of research in the field. The book is a summary of all the knowledge gathered and very useful not only as a seed handling manual but goes beyond that. For anybody handling seeds of deciduous forest trees (not only in Central Europe) the book is highly recommended.

G. VON WUEHLISCH (Grosshansdorf)

Illustrierte Flora von Mitteleuropa. Band I, Teil 3: Gramineae. Lieferung 8/9. 3., völlig neubearbeitete Auflage. Von G. HEGI. Bearbeitet von H. J. CONERT. 1996. Verlag Paul Parey, Berlin. ISBN 3-8263-3078-1. Seite 561 bis 736 mit 59 Abbildungen und 3 Tafeln. DM 90,–.

Der seit 1979 in einzelnen Lieferungen herausgegebene Teilband des „HEGI" über die Gräserarten Mitteleuropas wird mit der Doppellieferung 8/9 fortgesetzt. Nach neuesten Angaben sind insgesamt 10 Lieferungen vorgesehen. Aus der Unterfamilie *Pooideae* werden Arten der 5 Gattungen *Festuca* (Schwingel), *Lolium* (Weidelgras), *Vulpia* (Federschwingel), *Poa* (Rispengras) und *Bromus* (Trespe) ausführlich beschrieben und in vielen detailgenauen Zeichnungen im Text und auf 3 Farb- bzw. Schwarzweiß-Tafeln abgebildet. Die Beschreibungen enthalten umfassende und eingehende Angaben über die Artmerkmale und ihre Variabilität, über die allgemeine Verbreitung (teilweise ergänzt durch Verbreitungskarten) und das Vorkommen der jeweiligen Art im Gebiet, über Cytologie und Inhaltsstoffe, über Nutzen und Verwendung, über Krankheiten und Schädlinge sowie über wichtige Literatur. Ergänzend zu den in Mitteleuropa beheimateten Gräserarten werden auch die adventiv auftretenden Arten behandelt. Auch diese Lieferung des Standardwerkes ist von gewohnt hoher fachlicher Qualität und ist für alle an der mitteleuropäischen Flora Interessierten unentbehrlich.

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Identification of Heterobasidion annosum (S-type) genes expressed during initial stages of conidiospore germination and under varying culture conditions. FEMS Microbiol. Lett.Â Growth response of Norway spruce saplings in two forest gaps in the Swiss Alps to artificial browsing, infection with black snow mold, and competition by ground vegetation. Can. J. For.Â Infection of Picea abies clones with a homokaryotic isolate of Heterobasidion parviporum under field conditions. Can. J. For. Genetic variation in Heterobasidion annosum detected with M13 fingerprint-ing and ribosomal DNA probes. Esp. Mycol.Â Occurrence of Heterobasidion annosum in pure and mixed spruce stands in Southern Finland. Scand. J. For.Â Spread of S and P group isolates of Heterobasidion annosum within and among Picea abies trees in central Lithuania. Can. J. For.