Evidence of an Unbalanced Mating Pattern in a Seed Orchard Composed of Two Larch Species

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Summary

Mating patterns of a larch seed orchard composed of one clone of *Larix sibirica* and 6 clones of *L. decidua*, were investigated using allozymes as genetic markers. The studied orchard was designed to produce interspecific hybrid seeds. It was found that the orchard constitutes a population with a mating system that is far from panmixis. Studying outcrossing rates of individual clones by the *mixed-mating model*, some of the symptoms of non-random mating could be detected. They ranged between 0.096 for the Siberian larch clone, and 0.952 to l.019 for the European larch clones. However, the most profound insight into the mating patterns was possible through the use of the *mating model* methods. Detailed *mating model* analyses revealed that the Siberian larch pollinated almost 93% of all sampled ovules, while the remaining European larches only 7%, with some clones contributing less than 0.2% of all pollen gametes. The effectiveness of Siberian larch as a pollinator could be explained by its high flowering abundance and earlier flowering phenology, as well as by the specific design of the orchard, where a half of the grafts were of Siberian larch. The *neighborhood model* (variant of the *mating model*) applied in this study indicated that fecundity of males and their distance to maternal trees significantly influenced male mating success. The *mating model* studies allowed also for an in depth analysis of the hybridization pattern between the 2 species. Its level for European larches functioning as females averaged on 93.9%, while only 10.5% Siberian larch seeds were hybrids, which has significant implications for forest tree improvement programs. The advantages of applying the *mating model* approach in the studies of mating systems of forest trees, mainly seed orchards, are briefly discussed.

Key words: Larix decidua, Larix sibirica, isozymes, mating system, hybridization, mixed-mating model, neighborhood, paternity analyses, mating success, seed orchard.

FDC: 165.41; 181.521; 232.311.3; 174.7 *Larix decidua*; 174.7 *Larix sibirica*; (480).

Introduction

The last decades significantly benefited from progress in developing mating system estimation procedures in conifers (Neale and Adams, 1985; Ritland and El-Kassaby, 1985; Adams and Birkes, 1989) and many studies of mating systems have been done in natural and seed orchard populations (see for references: Muona, 1990; Adams and Birkes, 1991; Mitton, 1992; Wheeler and Jech, 1992). The analyses of mating patterns in seed orchards have theoretical as well as great practical importance. Knowledge of these patterns makes it possible to evaluate the genetic compositions of seed orchard crops and factors influencing their quality, including levels of inbreeding, variation in male fertility, patterns of pollen dispersal and amounts of background pollination. Thus, good estimates of mating system parameters are necessary for the proper management of existing orchards, as well as for planning breeding programs and designing seed orchards in the future (Muona, 1990).

The most widely used procedure for estimating plant mating systems is application of the *mixed-mating model* to genotypic arrays of mother plant offspring (Fyfe and Bailey, 1951; Brown and Allard, 1970; Neale and Adams, 1985; Ritland and El-Kassaby, 1985). This model makes several assumptions, one or several of which are usually violated (Brown et al., 1985; Mitton, 1992). The postulates are almost never met in small populations composed of few genotypes, mainly because of large differences in male fecundity or self-fertility.

Isozymes as genetic markers are ideally suited for *paternity* and *mating model* methods recently developed for mating system analyses of plant populations (Schoen and Stewart, 1986; Devlin et al., 1988; Roeder et al., 1989; Adams et al., 1992; Burczyk et al., 1996; Burczyk and Prat, 1997) and interest in such studies greatly increased (Broyles and Wyatt, 1990; Meagher, 1991; Devlin et al., 1992; Smouse and Meagher, 1994). This type of analyses appear to be very useful in predominantly outcrossing species, including most coniferous trees (Hamrick and Schnabel, 1985). The traditional *mixed-mating model* partitions mating events into 2 types – selfing or random outcrossing. Its application in coniferous populations explained very little, since their selfing accounted usually for less than 10% of successful fertilizations (Muona, 1990; Adams and Birkes, 1991), however patterns of outcrossing remained generally unknown. Outcross mating patterns can be investigated using *paternity methods* (Devlin et al., 1988). Once pollen parents of a large sample of offspring have been inferred, mating patterns can be directly determined (Wheeler et al., 1993). However, in order to obtain precise estimates exclusion probabilities (probabilities of being able to exclude potential males on the basis of genetic incompatibility alone) need to be high and the population must be isolated from external pollen sources (Devlin et al., 1988; Adams and Birkes, 1989).

In the *modeling approach* a theoretical mating model, designed to account for the distribution of genotypes in offspring (or pollen gametes in conifers), is applied to genotypic arrays of actual offspring and the mating parameters are estimated using various statistical procedures (e.g. maximum-likelihood). Reports to date indicate that these methods, including the *neighborhood model* (Adams and Birkes, 1989, 1991), may be powerful tools when investigating different aspects of mating systems in forest trees (Schoen and Stewart, 1986; Adams, 1992; Burczyk et al., 1996; Burczyk and Prat, 1997).

Our knowledge on mating behavior in seed orchards is still insufficient. Establishment of advanced generation seed orchards may involve the use of very few highly selected clones (Zobel and Talbert, 1984) and the knowledge of mating

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patterns in such orchards seems to be very important for their proper management. Although there are many papers describing outcrossing levels in multiclonal orchards, the investigations in seed orchards established with a few clones only are lacking (Müller-Starck and Gregorius, 1988). Hybrid orchards may also play an important role in advanced breeding programs. They are especially promising for larch (Paques, 1989) and results of some studies of mating patterns in hybrid larch seed orchards have recently been reported (Bergmann and Ruetz, 1987; Hacker and Bergmann, 1991; Ennos and Qian, 1994; Lewandowski et al., 1994). Presence of individuals from 2 species increases the potential for complexity in mating patterns due to the presence of restricted and perhaps directional hybridization. The assumption of random mating in such cases is probably totally unwarranted. A question then arises as to the best approach for evaluating mating patterns in orchards of this type.

The aim of this study was to investigate mating patterns in a larch orchard composed of one clone of *Larix sibirica* and a few clones of *Larix decidua*. It was hoped that *Larix sibirica* would act as the seed parent, since only hybrid seed (or selfs) would be found in this case. The interesting aspects of this orchard are the small numbers of clones and the absence of background pollination (no larch trees growing in surrounding stands) which can confound results of mating system analyses. In this paper using isozymes as genetic markers we studied the mating patterns based on various statistical procedures.

Materials and Methods

The Nahkamäki seed orchard is located in Central Finland (62°13'N, 25°24'E). The orchard is surrounded by a Norway spruce (*Picea abies* (L.) Karst.) forest and no larch trees are found within a distance of several kilometers from the orchard. The orchard consists of 7 clones: 1 clone of Siberian larch (*Larix sibirica* Ledeb.) (E1037 Raivola; initially originating from Arkhangelsk Province, Russia), and 6 clones of European larch (*Larix decidua* Mill.) (E1127 – from Switzerland; E1136 – from Scotland; E1138 – from Germany; E1139 – from France; E1149 and E1150 – from Austria). All the scions of the clones were collected from stands growing in the Punkaharju Research Station in Finland. In 1962, about 400 grafts were planted in an area of 1 ha at a 5 m x 5 meters spacing. One half of the grafts consisted of the Siberian larch and the other half of the European larch clones. The grafts of Siberian larch were distributed in the orchard in a systematic chequerboard pattern, while European larch clones were distributed randomly among the Siberian larch grafts. In Autumn 1991, at the time of seed collection, there were 118 grafts of Siberian larch and 98 of European larch (ranging from 7 to 22 ramets per clone) still alive in the orchard.

Cones were collected from 5 ramets of clones E1037, E1127, E1138 and E1139; 4 ramets from clone E1150, and only 1 ramet from clone E1149. About 20 seeds per graft were analyzed electrophoretically, with the total sample size being 507 seeds. The percentage of full seeds was determined by x-ray analysis. Genotypes of all clones in the orchard were determined based on megagametophytes of sampled seed, except clone E1136 due to the lack of seed. Based on flowering data, we assumed that clone E1136 did not produce pollen, or if any, its contribution was not significant compared to the others. Consequently, this clone was excluded as a potential father in the mating system analyses. Because of small number of seeds (20) sampled from clone E1149, it was not possible to obtain individual mating system parameters for this clone. However, the seeds of clone E1149 were included for calculating pooled estimates.

The seeds were subjected to standard horizontal starch gel electrophoresis, with methods similar to those described by Conkle et al. (1982), and Cheliak and Pitel (1984). We tried to analyze several enzyme systems, however only 4 systems revealed polymorphism, enabling precise genetic interpretation at 4 loci. Genotypes of megagametophyte and embryo seed tissues were determined based on 4 loci: fluorescent esterase (E.C. 3.1.1.1; locus *Fest-2*), malate dehydrogenase (E.C. 1.1.1.37; locus *Mdh-3*), shikimic acid dehydrogenase (E.C. 1.1.1.25; locus *Shdh*), and phosphoglucomutase (E.C. 2.7.5.1; locus *Pgm-1*). Pollen (paternal) contribution to each embryo was determined by assaying the haploid megagametophyte and the diploid embryo.

Statistical procedures

Mating patterns were investigated using the 3 general methods: *mixed-mating model, mating model* and *neighborhood model* approach. First, we used a standard *mixed-mating model* for estimating outcrossing rates (versus selfing). The model accounts for haploid genotypes in pollen gametes, assuming all matings due either to self-fertilizations (with probability s) or random outcrossing ($t = 1\text{-}s$). To estimate t, the model was applied to the observed pollen gamete data using maximum-likelihood procedures developed for conifers (Ritland and El-Kassabay, 1985). Outcrossing rates were calculated for the population as a whole (population-wide estimate), as well as for individual clones. Progeny arrays from ramets of the same clone were pooled together to analyze inter-clonal variation in outcrossing rate.

Mating model

The *mating model* was developed following Roeder et al. (1989) and modified for conifer data. The model assumes that a pollen gamete successful in fertilizing a viable offspring come from one of the individuals acting as male parents. In the model applied, the probability of observing a multilocus genotype g_i in pollen gametes of the sampled offspring is:

$$P(g_i) = \sum \phi_j P\left(g_i \middle| F_j \right) \qquad (1)$$

where $P(g_i|F_j)$ is the transition probability for the j-th (out of r) male to contribute to genotype g_i. It defines the proportion of a multilocus haploid genotype g_i among all possible gamete types produced by a male tree, and it depends on segregation likelihoods. It ranges from 0, when a gamete g_i may not be produced by a parent, to 1, when all gametes produced by a parent have multilocus genotype g_i (parental tree homozygous for all loci). The ϕ_j parameter indicates mating success of the j-th male (male fertility). The number of potential outcross males is restricted to the number of different clones. If the model is applied to the offspring sampled from an individual mother tree, its paternal contribution to the offspring indicates the proportion of self fertilization.

Individual fertilities (ϕ_j) were estimated by fitting the model to multilocus pollen gametic arrays in the offspring of individual clones (offspring pooled across ramets of the same clone) and the entire offspring sample using maximum likelihood (ML) methods (RAO, 1973) following the EM-algorithm (Roeder et al., 1989). Consecutive approximations of estimated parameters were calculated using the formula:

$$\phi'_j = \frac{1}{N}\left(\sum_{i=1}^{N} \frac{P(g_i|F_j)}{P(g_i)} \right) \bullet \phi_j \qquad (2)$$

Successive values of ϕ_j' were incorporated into equation 1 in order to calculate new $P(g_i)$ probabilities for every iteration. Iterations continued until all parameters converged to specified criteria (here, differences between consecutive estimates less than 0.001).

Individual fertilities calculated from the *mating model* were compared to those inferred basing on *fractional paternity* assignment (DEVLIN et al., 1988). Paternity of each offspring is assigned fractionally to non-excluded males (based on genetic compatibility) in proportion to their transition probabilities. In contrast to other paternity methods, paternity is assigned to all progeny, but some progeny will not be assigned a single male parent (ADAMS, 1992). Once pollen parents of a sample of offspring have been inferred, mating patterns can be directly determined.

Standard errors of individual fertility estimates, calculated basing on *mating model* and *fractional paternity* assignment, were approximated using the bootstrap method with resampling of progeny arrays (EFRON, 1979). This was done following 500 simulations ("bootstraps").

Neighborhood model

In order to determine potential factors influencing the individual male mating success (male fertilities) we applied the *neighborhood model* (ADAMS and BIRKES, 1989). In this model, an arbitrarily specified area around a mother tree (from which seeds are sampled) is designated its neighborhood. The neighborhood size in this study was established as 30 meters in radius, which included, on average, about 45 flowering trees (potential outcrossing pollen parents) around each mother-tree graft. This model partitions effective matings into tree groups: selfing, outcrossing within the neighborhood, and outcrossing with males outside the neighborhood (gene flow) (ADAMS and BIRKES, 1989, 1991; ADAMS, 1992). However, because in this study there was no larch trees growing around the orchard, and because no detectable pollen contamination from non-orchard sources was found, we assumed that all matings occurred within the orchard. On the other hand, the neighborhood size of 30 m in radius included generally all clones growing in the orchard. This made it impossible to separate outcrossing events with males located within a designated neighborhood, from outcrossings with trees located outside the neighborhood though still in the orchard. Taking into account the above considerations, we did not estimate the proportion of pollen migrant from outside the neighborhood.

Specific objectives of the *neighborhood model* analyses were to determine proportion of selfing (s), the effect of fecundity (γ) of male trees and of the distance (β) of males to the mother trees, on their mating success. For this purpose, progeny arrays were structured by sampled ramets and all flowering ramets, included within a neighborhood, were considered as potential fathers. In the model applied, the probability of observing multilocus genotype g_i in the pollen gametes of offspring from the mother tree was

$$P(g_i) = sP(g_i|M) + (1-s)\sum_{j=1}^{r} \phi_j P\left(g_i \middle| F_j\right) \qquad (3)$$

where s is the probability of selfing, $P(g_i|M)$ is the transition probability that the mother tree (or other ramets of this clone) produces gametes with genotype g_i, and $P(g_i|F_j)$ is the transiton probability for the j-th (out of r) outcross male in the neighborhood (excluding grafts of maternal clone) to contribute to genotype g_i.

In this model, the mating success of each outcross male in the neighborhood (ϕ_j) is assumed to be influenced by one or more factors in the order of an exponential function. In this study, we chose the pollen fecundity of the male and the distance of the male from the maternal tree as factors expected to influence mating success of individual males. Thus, the model (containing the two selected factors) was defined as:

$$\phi_j = \frac{e^{\beta d_j + \gamma f_j}}{\sum_{k=1}^{r} e^{\beta d_k + \gamma f_k}}, \qquad (4)$$

where d_j and f_j indicate respectively the distance and the pollen fecundity of the j-th male in the neighborhood. β and γ are the respective parameters describing the effect of particular factors. Pollen fecundity scores were expressed as number of male strobili per tree and were averaged among ramets of a clone, thus for every ramet of a particular clone the same fecundity score was assigned. Unfortunately, pollen fecundity data from 1990 (flowering season resulting in 1991 seed crop) was not available, but we did have data available for 1984. Field observations carried out in spring 1991 generally confirmed the clonal pollen fecundity rank as observed in 1984.

The three parameters (s, β, γ) were estimated by fitting the neighborhood model to the multilocus pollen gametic arrays in the offspring of individual mother trees using ML methods based on numerical procedures, that involved FISHER's method of scoring (NEWTON's method) (RAO, 1973). Parameters were estimated for individual clones (offspring polled across ramets of the same clone) as well as jointly for a combined sample over all mothers. This was done using the NEIGHBOR computer program (BURCZYK et al., 1993). Details on statistical procedures employed in the NEIGHBOR program were reported elsewhere (BURCZYK et al., 1996). The significance of the mating system parameters were tested by the log. likelihood ratio test (RAO, 1973) or by analyzing limits of their confidence intervals.

Results

Mixed-mating model outcrossing rate

The population multilocus outcrossing rate (t_m) was estimated to be 0.956, and was not significantly different from $t = 1.0$. Individual clonal outcrossing rates (t_{mi}) were calculated when pollen gene frequencies (p) were allowed to vary among clones (joint t_{mi} and p estimation) (RITLAND and EL-KASSABY, 1985). The outcrossing estimate calculated for Siberian larch was extremely low, accounting for only 9.6% of outcrossing. The highest value was observed for clone E1150, and it was 1.019 (*Table 1*). The estimate for clone E1138 did not converge.

Table 1. – Individual outcrossing rates (t_{mi}) calculated for clones based on *mixed-mating model.*

Clone	t_{mi} (SE)
E1037	0.096 (0.007)
E1127	0.952 (0.040)
E1139	0.982 (0.033)
E1150	1.019 (0.125)
mean t_{mi}	0.762

Estimates for clone E1138 did not converge

Mating model

Mating model provided estimates of male fertilities of clones realized among the offspring (seeds) of individual clones functioning as mothers (*Table 2*). The largest contribution was achieved by Siberian larch clone, and the estimate for the pooled sample accounted for more than 92.5% of all successful fertilizations. Among European larches only E1138 fertilized more than 5% (6.28%), with others generally much below 1%. A similar pattern was observed, when the progeny of individual maternal clones was considered. When the paternal contributions of individual clones into the offspring of every clone were estimated we could simply determine individual selfing rates. They ranged from 0 for the clone E1150 to 0.895 for E1037 (Siberian larch) (*Table 2*).

Table 2. – The estimates of paternal contribution (male fertilities) of individual clones into the progeny of individual clones functioning as mothers, based on *mating model* (a) and *fractional paternity* assignment (b) approaches.

(a) *mating model* approach:

Sampled Females	Clonal paternal contribution						log. likelihood
	1037	1127	1138	1139	1149	1150	
E1037	0.8950	0.0000	0.0835	0.0029	0.0000	0.0186	-159.5079
	(0.0457)	(0.0000)	(0.0492)	(0.0078)	(0.0000)	(0.0177)	
E1127	0.9538	0.0053	0.0332	0.0024	0.0053	0.0000	-160.7509
	(0.0295)	(0.0058)	(0.0290)	(0.0062)	(0.0058)	(0.0000)	
E1138	0.9638	0.0000	0.0323	0.0039	0.0000	0.0000	-147.0990
	(0.0262)	(0.0000)	(0.0277)	(0.0081)	(0.0000)	(0.0000)	
E1139	0.8521	0.0000	0.1177	0.0099	0.0000	0.0203	-167.1326
	(0.0480)	(0.0000)	(0.0549)	(0.0151)	(0.0000)	(0.0200)	
E1150	0.9854	0.0000	0.0038	0.0108	0.0000	0.0000	-114.9691
	(0.0131)	(0.0000)	(0.0072)	(0.0118)	(0.0000)	(0.0000)	
Pooled	0.9258	0.0012	0.0628	0.0015	0.0012	0.0075	-786.3069
	(0.0155)	(0.0012)	(0.0168)	(0.0037)	(0.0012)	(0.0052)	

(b) *fractional paternity* approach:

Sampled females	Clonal paternal contribution					
	1037	1127	1138	1139	1149	1150
E1037	0.6764	0.0026	0.2813	0.0102	0.0026	0.0270
	(0.0284)	(0.0018)	(0.0243)	(0.0072)	(0.0018)	(0.0122)
E1127	0.7042	0.0059	0.2738	0.0047	0.0059	0.0055
	(0.0276)	(0.0053)	(0.0250)	(0.0045)	(0.0053)	(0.0047)
E1138	0.7350	0.0012	0.2512	0.0050	0.0012	0.0063
	(0.0273)	(0.0012)	(0.0245)	(0.0050)	(0.0012)	(0.0053)
E1139	0.6680	0.0050	0.2670	0.0200	0.0050	0.0350
	(0.0313)	(0.0025)	(0.0248)	(0.0099)	(0.0025)	(0.0143)
E1150	0.7390	0.0015	0.2507	0.0059	0.0015	0.0015
	(0.0278)	(0.0015)	(0.0262)	(0.0062)	(0.0015)	(0.0015)
Pooled	0.7090	0.0032	0.2605	0.0088	0.0032	0.0153
	(0.0127)	(0.0013)	(0.0110)	(0.0030)	(0.0013)	(0.0039)

The mating pattern generated in the *table 2*, was analyzed in a f x m contingency table (where f and m were the numbers of functional females and males, respectively) by means of a G-test, to test for any incorporated heterogeneity (Sokal and Rohlf, 1981). Contribution of fathers was significantly different ($P < 0.001$) from the expectation of even contribution (null hypothesis $\varnothing_j = 1/r$, where r is the number of potential fathers). However, the proportions of male contributions was not heterogeneous across sampled females. One of the clones (E1138) sired females in significantly ($P = 0.004$) different proportions, than the rest of the clones (heterogeneous mating success). While most clones contributed more or less similar proportions of male gametes to every female, the clone E1138 differed in that contribution. Relative contributions of E1138 to the progeny of females E1037 and E1139 were higher than to the other clones.

The estimates of individual fertilities inferred based on fractional paternity assignment were lower for the Siberian larch clone and greater for the clones of European larch compared to the *mating model* estimates (*Table 2*). Devlin et al. (1988) found, that if substantial differences in fertilities exist in the mating population then the fractional paternity method gives the fertility estimates biased toward the null hypothesis (equal fertilities). The bias may exist additionally due to relatively low exclusion probabilities observed in this study (mean 0.55), which were determined empirically (Roeder et al., 1989; Adams, 1992). For each individual sampled mother tree the haploid genotype of a pollen gamete was generated randomly basing on diploid genotype of a randomly chosen potential father. The exclusion probability was calculated as the proportion of males which are excluded for each generated pollen gamete and it was averaged over all generated gametes following 10000 simulations per sampled mother tree (Roeder et al., 1989).

Neighborhood model

The *neighborhood model*, applied to all maternal trees analyzed jointly, demonstrated that all mating system parameters (s, β, γ) were significant in explaining mating patterns occurring within neighborhoods (*Table 3*). Selfing (s) accounted for 0.150 (outcrossing, assuming $t = 1\text{-}s$, was 0.850). An estimate of selfing of individual clones was obtained only for the Siberian clone (E1037), and was similar to selfing inferred from the outcrossing rate ($s = 1\text{-}t$) calculated basing on the *mixed-mating model* (0.940 vs. 0.904). Selfing estimates were not possible to obtain for the other clones, as the model including this parameter did not converge, but probably s is actually close to 0. Thus we excluded selfing from the model, estimating only the remaining parameters. However, for clone E1150 only the γ parameter was estimable. Distance effect appeared to be significant only for the pooled sample ($\beta = -0.2132$; $P = 0.039$), but not for individual clones (*Table 3*). The negative value indicates that mating success decreased with distance increase. In contrast, fecundity effect was significant ($P < 0.0001$) for the pooled sample and for all except the Siberian larch clone. The positive γ estimates show that the more fecund trees contributed more pollen to the progeny.

Table 3. – The estimates of selfing rate (s), distance (β) and fecundity (γ) effect calculated using the *neighborhood model* (standard errors in parentheses).

Clone	s	β	γ	log. Likelihood
E1037	0.9399[a]	0.0591	-0.0063	-162.5258
	(0.0238)	(0.2299)	(0.0066)	
E1127	–	-0.0096	0.0007[a]	-160.8849
		(0.1962)	(0.0002)	
E1138	–	-0.0129	0.0008[a]	-149.7738
		(0.6146)	(0.0003)	
E1139	–	-0.2901	0.0003[a]	-170.1384
		(0.1541)	(0.0001)	
E1150	–	–	0.0009[a]	-115.4923
			(0.0002)	
All	0.1496[a]	-0.2132[a]	0.0009[a]	-930.7235
clones	(0.0188)	(0.0558)	(0.0001)	
L. decidua	–	-0.0334	0.0007[a]	-630.2991
clones		(0.1282)	(0.00002)	

a) parameter significant at P < 0.05 level

Discussion

The mating system of larch species has already been studied in recent years. In tamarack (*Larix laricina*) the mean outcrossing rate in 5 populations was equal to 0.730 (Knowles et al.. 1987), which is one of the lowest values reported for conifers (Muona, 1990; Adams and Birkes, 1991). The outcrossing rates observed for European larch appeared to be higher, both in natural stands ($t = 0.943$; Lewandowski et al., 1991), and in seed orchards ($t = 0.929$; Burczyk et al., 1991), ($t = 0.852$; Paule and Gomory, 1992).

Outcrossing rates of individual clones, calculated on the basis of a *mixed-mating model* (*Table 1*), were similar to those inferred from the *mating model* analysis ($t = 1\text{-}s$; *Table 2*). While the values estimated for clones of European larch were close to unity (no significant difference from $t_{mi} = 1$) (*Table 1*), the estimate obtained for the Siberian larch clone was extremely low (0.096). This means that over 90% of successful fertilizations were due to selfing. Such a high level of self-fertilization was never reported for conifers, unless it resulted from controlled self-pollination. In our case no Siberian larch pollen was available to the grafts other than from the studied clone. It should be noted that the percentage of full seed of the Siberian clone was only about 6.34%, and was much lower than the respective values for the clones of European larch (from 13.3% to 31%, with a mean of 24%). It was found that in European larch, after controlled self-fertilization, embryo degeneration took place in 85% to 100% of pollinated ovules (Kosiński, 1987). Although self-fertilization is not the sole factor influencing empty seed production, it is probably the main reason for the low percentage of full seed in the Siberian larch clone.

Mating system analyses of outcrossing patterns in conifers, involving *mating model* or paternity methods, indicated great variation of individual male reproductive success (Hamrick and Schnabel 1985; Schoen and Stewart, 1986; Xie and Knowles, 1992; Wheeler et al., 1993). Additionally, the application of the *neighborhood model* to natural and seed orchard populations already indicated that a variety of factors, including relative location and distance from mother trees, pollen fecundity and flowering synchronization, may influence mating success of individual males (Adams and Birkes, 1991; Burczyk et al., 1996; Burczyk and Prat, 1997; Adams, Burczyk, Birkes, Hipkins and Wheeler, unpublished observations). It seems, that in this study the *mating model* approach gave the most profound insight into the mating patterns occurring in the orchard. Besides the estimation of selfing (versus outcrossing), it was also useful in describing the patterns of cross-fertilization within the seed orchard. Analyzing *table 2,* it is obvious that the mating system of the studied orchard is far from panmixis and that the Siberian clone may be considered as the exclusively dominant pollen parent in the orchard. It fertilized almost 93% of all viable embryos, while all clones of European larch fertilized only about 7%. Considering this, the high selfing detected for the Siberian clone is not surprising. Unfortunately, the method could not distinguish the male contribution between clone E1127 and E1149, thus for both clones the model assigned identical values. However, they contributed together only about 0.25% of total pollen in the orchard. Differential male contribution (pairwise fertility effect) of clone E1138 into different females could result from variation in genetic compatibility between mating clones or from differences in flowering phenology (Schoen and Stewart, 1987; Erickson and Adams, 1989; Skrøppa and Lindgren, 1994; Burczyk and Prat, 1997). The obtained results could be partially explained by flowering characteristics of particular clones (Nikkanen, 1993; Lewandowski et al., 1994). High male fecundity of the Siberian larch (about 8 times greater then the best clone of European larch) and its earlier pollen shedding, as compared to the European larches, could favor Siberian larch as the dominant pollen parent in the orchard. In fact the fecundity effect parameter (γ) calculated from the neighborhood model appeared to be very significant ($P < 0.0001$) (*Table 3*).

The distance effect was difficult to be noticed for any individual clone, although it was generally negative (*Table 3*). Since the distance parameter was estimable for all clones analyzed jointly, it seems that the relationship was similar for the majority of the studied ramets and thus was detectable for a large sample size. The negative β parameter indicated that mating success of male parents increased with decreasing distance to the females. The relationship between male mating success and distance to the mother tree may be strong in larch since pollen grains of this species have no air sacs and are probably dispersed over shorter distances than pollen of other coniferous trees. Burczyk et al. (1991) have found, that in the lower crown levels the percentage of seeds resulting from selfing was about 3 times greater than in the upper ones, probably due to the relatively ‘heavy’ pollen.

Information on interspecific hybridization in the orchard comes directly as part of the detailed study of the mating patterns. The fraction of mating events which occur between the Siberian larch and clones of European larch, detected by the *mating model*, denotes the degree of hybridization (*Table 2*). Its level ranged between 85.2% and 98.5% among the seed of clones of European larch, with a mean of 93.9%. In contrast, European larches pollinated together only 10.5% of Siberian larch ovules, the individual contributions ranging between zero (E1127 and E1149) and 8.35% (E1138). Thus, the hybridization pattern seems to be unidirectional. The percentage of hybrids among seeds of European larch, detected for the same investigated material using the rare marker alleles approach (Lewandowski et al., 1994) was similar to the values reported in this study. However, that method did not allow for a detailed analysis of the contribution of European larches into the progeny of the Siberian larch clone. Hybridization of *Larix* species was often observed (Bergmann and Ruetz, 1987; Hacker and Bergmann, 1991; Ennos and Qian, 1994), and generally high percentages of hybrid seed were found, ranging between 19% and 85%, depending mainly on the seed orchard design (number of clones of hybridizing species) and the species acting as the seed parent. However, all those studies used single-locus, or rare marker alleles methods.

The directional hybridization pattern should be taken into account when the progeny of the studied orchard will be genetically tested and used for reforestation, as well in the future planning of breeding programs based on hybrid seed orchards.

Acknowledgments

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Buchbesprechungen

Root Vitality and Decline of Red Spruce. Contributiones biologiae arborum 4. By P. M. Wargo, D. R. Bergdahl, D. R. Tobi and C. W. Olson. 1993. Verlag ecomed, Landsberg am Lech. ISBN 3-609-69930-2. 134 pages with many figures and 41 tables. DM 68,–.

Red spruce (*Picea rubens* Sarg.) stands show symptoms of decline throughout their natural range in the Appalachian Mountains of the eastern United States since the 1960's. While the above ground symptoms of declining trees were very well documented, little information exists on the status of the root system, especially of the non-woody fine roots. The very exact and detailed investigations give useful comparisons between crown deterioration and root vitality on basis of morphological and physiological indices on apparently healthy and declining red spruce trees at 2 sites in Vermont (1221 m elevation) and New York (1483 m elevation). The changes in the crown (various growth, stem, twig and needle characteristics) and in the root system are reported very precisely, and are discussed at the whole tree level. An appendix contains statistical models for the variables as well as figures for the annual radial and basal area increments of red spruce trees in three healthy classes. The studies are a significant contribution to the forest decline syndrom.

B. R. Stephan (Grosshansdorf)

Krankheiten der Wald- und Parkbäume. Diagnose, Biologie, Bekämpfung. 3., neubearbeitete und erweiterte Auflage. Von H. BUTIN. 1996. Verlag Georg Thieme, Stuttgart und New York. ISBN 3-13-639003-2. 261 Seiten mit 130 Abbildungen in 520 Einzeldarstellungen und 2 Sporentafeln. Kartoniert DM 79,–.

Das 1983 erstmals erschienene Buch über Diagnose, Biologie und Bekämpfung der Krankheiten der Wald- und Parkbäume liegt jetzt in 3., neubearbeiteter und erweiterter Auflage vor. Diese Tatsache unterstreicht das große Interesse an diesem hilfreichen und sehr empfehlenswerten Buch. Die bewährte Gliederung, die Krankheiten nach dem Ort ihres Auftretens zu beschreiben, wurde beibehalten, wobei nur die Reihenfolge der Baumarten teilweise geändert wurde. Die 10 Hauptkapitel behandeln Schäden an Blüten und Samen, Schäden an Keimlingen und Jungpflanzen, Schäden an Nadeln und Blättern, Schäden an Knospen, Trieben und Ästen, Rindenschäden, Gefäßkrankheiten, Wurzel- und Stammholzschäden, Lagerschäden, Epiphyten, Symbionten und parasitische Blütenpflanzen, sowie Formveränderungen und Wuchsanomalien. Neben nichtparasitären bzw. abiotisch bedingten Schäden sowie einigen Viruskrankheiten gilt das Hauptaugenmerk den durch Pilzarten verursachten Krankheiten und Schäden. Wichtige Krankheiten werden mit ihren Symptomen, ihren Erregern und deren Biologie ausführlich beschrieben und anhand sehr guter und genauer Zeichnungen abgebildet. Gelegentlich schädigend auftretende Pilzarten werden nur kurz vorgestellt. Auf Gegenmaßnahmen wird dem Kenntnisstand entsprechend hingewiesen. Gegenüber der vorigen Auflage wurden manche Texte präzisiert, einige Pilzarten ausführlicher beschrieben, andere neu aufgenommen und die Zahl der Zeichnungen um 14 erweitert. Leider mußten etliche lateinische Pilznamen, den neueren taxonomischen Erkenntnissen folgend, geändert werden, doch findet man auch die alten Synonyme. Etwas stärkere Berücksichtigung fanden Erkrankungen an Robinie, Zierapfel, Kirsche, Pflaume und Weißdorn. Beibehalten wurden die 2 Sporentafeln am Ende des Buches, sowie Übersichten zur Klassifikation der erwähnten Pilzgattungen, zu den lateinisch-deutschen Namen der genannten Baumarten und -gattungen, zur Erklärung der Fachausdrücke. Überarbeitet wurde das Literaturverzeichnis mit 240 Zitaten. Abschließend folgt ein Verzeichnis der erwähnten Krankheiten, Schäden und Symptome. Mit dieser Neuauflage steht dem Fachmann und interessierten Laien ein Leitfaden zur Verfügung, der die Identifizierung von Baumkrankheiten erleichtert. Dem Buch ist wiederum eine weite Verbreitung zu wünschen.

B. R. STEPHAN (Grosshansdorf)

Birken in den Alpen. Taxonomisch-ökologische Untersuchungen an *Betula pubescens* EHRH. und *Betula pendula* ROTH. Contributiones biologiae arborum, **6**. Von C. HIBSCH-JETTER. 1994. ecomed, Landsberg am Lech. ISBN 3-609-69940-X. 170 Seiten mit 21 Abbildungen und 50 Tabellen. DM 68,—.

Obwohl Birken in den Alpen weit verbreitet und von großer ökologischer Bedeutung sind, fehlen bisher eingehende Untersuchungen zum Vorkommen und zur Standortsökologie der beiden baumförmigen Birkenarten *Betula pendula* und *B. pubescens*. Solche Fragenkomplexe sind jedoch nur zu klären, wenn bekannt ist, welche Birkensippen in den Alpen autochthon vorkommen, und hierzu muß man sie taxonomisch unterscheiden können. Wegen der großen Variation innerhalb und zwischen Birkenarten stellen sie eine taxonomisch schwierige Gruppe dar. In der vorliegenden Arbeit wurde anhand morphologischer und karyologischer Untersuchungen der Frage nachgegangen, welche Birkensippen in den Alpen vorkommen, inwieweit *B. pendula* und *B. pubescens* zu unterscheiden sind und ob von *B. pubescens* Sippen (Unterarten) nachzuweisen sind, die bereits für andere europäische Gebiete beschrieben wurden. Etwa 400 Einsammlungen aus dem Alpengebiet wurden um etwa 200 Individuen aus dem nördlichen Alpenvorland, aus Südpolen und aus Lappland ergänzt. Die alpinen Birken konnten anhand mehrerer Blatt- oder Fruchtschuppen-Formparameter in der Regel eindeutig den beiden Arten *B. pendula* (2n = 28) und *B. pubescens* (2n = 56) zugeordnet werden. Morphologisch intermediäre Formen waren Chromosomenzählungen zufolge nicht hybridogenen Ursprungs. Die außeralpinen Referenzsippen der Unterarten *B. pubescens* ssp. *pubescens*, ssp. *tortuosa* und ssp. *carpatica* waren nur durch die gleichzeitige Berücksichtigung mehrerer Behaarungs-, Blatt- und Fruchtschuppen-Merkmale zu trennen. Diese intraspezifischen Taxa ließen sich bei den alpinen Moorbirken nicht nachweisen, doch waren sie den Unterarten *carpatica* und *tortuosa* ähnlicher als der Unterart *pubescens*. – Die an der Universität München gefertigte Dissertation ist ein wertvoller Beitrag zur Klärung der systematisch-taxonomischen Gliederung innerhalb der Gattung *Betula*.

B. R. STEPHAN (Grosshansdorf)

Neophyten. Biologie, Verbreitung und Kontrolle ausgewählter Arten. Umweltforschung in Baden-Württemberg. Von E. HARTMANN, H. SCHULDES, R. KÜBLER und W. KONOLD. 1995. ecomed, Landsberg am Lech. ISBN 3-609-65450-3. VIII und 302 Seiten mit 121 Abbildungen, 43 Tabellen im Text und 14 Tabellen im Anhang. Paperback DM 78,—.

Pflanzenarten, die nach dem Jahre 1500 infolge der weltweit zunehmenden Handelsbeziehungen in die heimische Flora einwanderten, werden im allgemeinen als Neophyten bezeichnet. Manche Arten haben sich zu „Problemarten” entwickelt, da sie durch ihr starkes Ausbreitungs- und Konkurrenzverhalten die heimische Vegetation bedrängen, vielfach auch unterdrücken. Die in dem vorliegenden Buch behandelten 7 Neophyten-Arten haben ihren Verbreitungsschwerpunkt in den Hochstaudensäumen von Wasserläufen. Veränderungen in der Ufervegetation von Fließgewässern durch Eutrophierung oder Dezimierung bzw. Vernichtung von Weichholzauen, z. B. Auenwälder mit Weiden- oder Erlen-Arten, haben die Massenausbreitung sehr begünstigt und zur Bildung von hohen, kaum durchdringbaren Dickichten geführt. In Baden-Württemberg befaßte sich eine Studie mit der Verbreitung, Ökologie, Vergesellschaftung und den Bekämpfungsmöglichkeiten der Kanadischen und Riesen-Goldrute (*Solidago canadensis, S. gigantea*), des Indischen Springkrautes (*Impatiens glandulifera*), des Topinambur (*Helianthus tuberosus*), des Riesen-Bärenklaus (*Heracleum mantegazzianum*) sowie des Japanischen und Sachalin-Knöterichs (*Reynoutria japonica, R. sachalinensis*). In einem allgemeinen Teil wird sehr ausführlich auf die Biologie, Ökologie und Verbreitung der einzelnen Arten eingegangen, wobei einzelne Abschnitte vor allem auch dem Wachstum, der Reproduktion und dem Einfluß ökologischer Faktoren (Licht, Temperatur, Wasser, Nährstoffe) gewidmet sind. Von besonderem Interesse ist ein Kapitel über die unterschiedlichen Auswirkungen dieser Neophyten auf die Fauna. – In einem speziellen Teil werden Notwendigkeit und Möglichkeiten einer Bekämpfung diskutiert. In umfangreichen Versuchen wurden Verfahren geprüft, die sich als unterschiedlich wirksam herausstellten. Insgesamt bietet das Buch sehr wertvolle Informationen, die in solchem Umfang und solcher Ausführlichkeit über die genannten Neophyten-Arten bisher nicht zur Verfügung standen.

B. R. STEPHAN (Grosshansdorf)

Ökologie und Interdisziplinarität – eine Beziehung mit Zukunft? Herausgegeben von PH. W. BALSIGER, R. DEFILA und A. DI GIULIO. 1996. Birkhäuser Verlag, Basel. ISBN 3-7643-5317-1. 202 Seiten mit Abbildungen und Tabellen. Paperback DM 46,–.

Zum Verständnis der komplexen Beziehung von Mensch und Natur reicht angesichts des Fehlens einer einheitlich ausgerichteten Umweltforschung eine einfache additive Anhäufung wissenschaftssoziologischer, -philosophischer und -historischer Kenntnisse nicht aus. Auch wenn der Ökologie die Schutzwürdigkeit der Natur und die Harmonievorstellung („ökologisches Gleichgewicht") zugrunde liegen, fehlen z. B. normierte Handlungen und allgemein anerkannte wissenschaftskonstituierende Sätze. Eine wissenschaftliche Fundierung der Merkmale einer interdisziplinären Ökologie läßt sich mit integrativen Ansätzen der Wissenschaftsforschung erzielen.

Im vorliegenden Buch geben Autoren aus unterschiedlichen Disziplinen und Richtungen in 12 Beiträgen einen Einblick in empirische und analytische Ansätze einer integrativen Wissenschaftsforschung. Nach einer allgemeinen Einführung folgen 3 Beiträge, die sich mit der wissenschaftlichen Fundierung der Ökologie auseinandersetzen. Grundlegende wissenschaftstheoretische und -historische Fragen werden im Zusammenhang mit Interdisziplinariät behandelt. Der Schwerpunkt der folgenden 4 Beiträge liegt auf der Forschung. Empirisch und analytisch beschäftigen sich die Autoren mit Fragen der Wissensproduktion, der Methoden, der Forschungsorganisation sowie der Forschungsevaluation in der inter- bzw. transdisziplinären Umweltforschung. Darunter ist auch ein Beitrag aus dem forstlichen Bereich von Prof. KROTT, Leiter des Instituts für Forstpolitik und Naturschutz der Georg-August-Universität Göttingen. 3 weitere Beiträge beschäftigen sich empirisch und theoretisch mit der Lehre. Hier werden u. a. Probleme dargestellt, mit denen Forschende in der interdisziplinären Zusammenarbeit konfrontiert werden. Auf Fragen im Zusammenhang mit der Schnittstelle Gesellschaft und Wissenschaft gehen 2 Beiträge ein. Ersichtlich wird, daß in der Umweltforschung Interdisziplinarität auch ein Informationsproblem ist.

Das vorliegende Buch stellt eine Synopse sonst nur getrennt vorliegender Ansätze der Wissenschaftsforschung dar und zeigt deren Stellenwert sowie Nutzen am Beispiel der Umweltforschung auf. Für Verantwortliche im Bereich Umwelt, die sich damit beschäftigen, wie die Wissenschaft gesellschaftliche Probleme angemessen angehen kann, enthält das Buch wertvolle Informationen.

M. LIESEBACH (Grosshansdorf)

Molekulare Entwicklungsbiologie. Vom Gen zur Pflanze. Herausgegeben von P. WESTHOFF. 1996. Georg Thieme Verlag, Stuttgart, New York. ISBN 3-13-102021-0. 192 Seiten mit 97 Abbildungen und 19 Tabellen, Glossar. DM/SFr 58,–/öS 429,–.

Das vorliegende Lehrbuch 'Molekulare Entwicklungsbiologie' richtet sich an Studenten der Botanik im Hauptstudium sowie an Pflanzen- und Entwicklungsphysiologen. Es stellt einen ersten Versuch dar, das Gesamtgebiet der pflanzlichen Entwicklungsbiologie in mehreren Hauptthemen zu behandeln. Für dieses Vorhaben haben sich 5 Hochschullehrer aus 5 Universitäten in Deutschland zusammengefunden, die in unterschiedlichen Forschungsgebieten dieses Faches tätig sind. In insgesamt 7 Kapiteln versuchen sie, Grundlagen der Entwicklung sowie angewandte Aspekte wie den Einfluß von Phytohormonen und Interaktion von Pflanzen mit anderen Lebewesen zu behandeln. Die einzelnen Kapitel sind jeweils übersichtlich in Vorspann, Basiswissen, Definition und Zusatzwissen gegliedert und erleichtern somit dem Studenten das Erlernen des behandelten Stoffes der einzelnen Kapitel. In den ersten 5 Kapiteln werden neueste Ergebnisse zu altbekannten Themen dargestellt, die in vielen pflanzenphysiologischen Lehrbüchern bereits einen festen Platz haben. Ein besonders interessantes Thema der molekularen Entwicklungsbiologie, auf dem besonders in den letzten Jahren intensiv gearbeitet wurde, ist die Erforschung der molekularen Grundlagen der Blütenentwicklung. In dem Buch sind diese leider sehr kompakt und dadurch für einen Laien schwer nachvollziehbar in nur einem Unterkapitel berücksichtigt worden. Unverständlich bleibt der Umstand, warum scheinbar keiner der Wissenschaftler am MAX-PLANCK-Institut für Züchtungsforschung in Köln, die maßgeblich mit an der Entschlüsselung von Entwicklungsgenen geforscht haben, an der didaktischen Gestaltung dieses Unterkapitels mitgewirkt hat. Insgesamt gesehen jedoch stellt dieses Lehrbuch eine wertvolle Hilfe für jeden Studenten dar, das faszinierende Thema der pflanzlichen Entwicklungsbiologie selbständig zu erarbeiten. Neben den zahlreichen Abbildungen und Tabellen finden sich zahlreiche sogenannte Boxen, die über neueste Forschungsergebnisse und Methoden informieren. Somit ist das Buch, das den vielsagenden Untertitel 'Vom Gen zur Pflanze' trägt, jedem Interessierten sehr zu empfehlen.

M. FLADUNG (Grosshansdorf)

Gebietsfremde Tierarten. Auswirkungen auf einheimische Arten, Lebensgemeinschaften und Biotope – Situationsanalyse. Herausgegeben von H. GEBHARDT, R. KINZELBACH und S. SCHMIDT-FISCHER. 1996. ECOMED Verlagsgesellschaft, Landsberg. ISBN 3-609-69420-3. 314 Seiten mit Abbildungen und Tabellen. Paperback DM 68,–/öS 531,–/sFr 66,–.

Teil natürlicher Evolutionsprozesse ist die Besiedlung neuer Lebensräume durch gebietsfremde Tierarten (Neozoen). Die zunehmende Mobilität des Menschen sowie die Intensivierung internationaler Handelsbeziehungen haben diesen Prozeß nachhaltig unterstützt. Eingeschleppt oder bewußt ausgebracht, haben sich zahlreiche Tierarten im Laufe der Zeit mehr oder weniger stark ausgebreitet. Zu den bekanntesten Beispielen zählen die Kaninchen in Australien und das Rotwild in Neuseeland. Aber auch in Deutschland sind Tierarten (z. B. Waschbär, Bisam, Nutria, Dreiecksmuschel, Amerikanischer Flußkrebs), die man als Neubürger unserer Fauna bezeichnen kann, anzutreffen. Für den Naturschutz, aber auch die Land- und Forstwirtschaft können einige Arten ein ernst zu nehmendes Problem darstellen. Das Auftreten gebietsfremder Tierarten und deren Auswirkungen auf einheimische Arten, Lebensgemeinschaften und Lebensräume sowie mögliche ökonomische Folgen wurden im Mai 1995 während eines Kolloquiums in Fellbach bei Stuttgart diskutiert. Die vorgetragenen 21 Beiträge sind im vorliegenden Band in der Reihe Umweltforschung in Baden-Württemberg erschienen. Das Buch ist nicht nur für Zoologen wertvoll, sondern bietet Biologen, Ökologen, Landschaftspflegern, Forstwissenschaftlern, Umweltverbänden und Umweltbehörden neue Erkenntnisse für eine differenzierte Betrachtungsweise der Neozoen-Problematik. Mit zahlreichen Tabellen, Abbildungen, Verbreitungs- bzw. Ausbreitungskarten und umfangreichen Literaturverzeichnissen ist das Buch als Informationsquelle uneingeschränkt zu empfehlen.

M. LIESEBACH (Grosshansdorf)

Induced Mutations and Molecular Techniques for Crop Improvement. By International Atomic Energy Agency, Vienna. 1995. 748 pages with 94 figures. Paperback öS 2160,–

This proceedings is based on an International Symposium on the "Use of Induced Mutations and Molecular Techniques for Crop Improvement", which was jointly organized by the Plant Breeding and Genetics Section of the International Atomic Energy Agency (IAEA), and the Food and Agriculture Organization (FAO) of the United Nations, in Vienna, 19 to 23 June, 1995. A somewhat related symposium on "Plant Mutation Breeding for Crop Improvement" was organized by the same organizations in 1990, indicating the commitment of IAEA/FAO to application of mutation breeding to crop improvement. Induced or spontaneous mutations have played a very important role in crop improvement. However, all types of mutations are not always useful; many are deleterious and some may even lead to genetic instability. The objective of this symposium was to review the current status of induced mutations in plants and the use of molecular biology techniques in practical crop breeding and improvement. The application of molecular biology techniques has been valuable in elucidating the nature and mechanisms of mutations. Therefore, use of induced mutations, combined with molecular techniques, would be crucial for future genetic improvement of agricultural crops. The symposium was divided into 12 sessions, including one evening session, and there were 2 additional 2 poster sessions. The following topics are included in this volume: 1) Plant breeding: problems and current techniques; 2) Seed quality; 3) Apomixes and F_1 hybrids; 4) Plant pathology and disease resistance; 5) Genome architecture, genome manipulation and comparative gene mapping; 6) Methylation and gene expression; 7) Molecular markers, Part 1: Application of DNA based marker mutations for improvement of cereals and other sexually reproduced crop species; Part 2: Use of novel DNA fingerprinting techniques for the detection and characterization of genetic variation in vegetatively propagated crops; 8) Stress tolerance; 9) Genetic transformation; 10) Looking into the future: Looking into model plants; 11) Biotechnology in developing countries; and 12) Current application of mutation techniques. In addition, there were 2 poster sessions devoted to: 1) Molecular markers and genetic transformation for crop improvement; and 2) Mutation techniques and biotechnology for crop improvement. There were altogether 46 invited papers and some 66 posters presentations in this symposium. Papers on molecular markers, molecular techniques, genetic engineering and biotechnology were well represented in this symposium. As it turns out, mutations are not only induced by physical and chemical agents, but also by tissue culture (somaclonal variation), and by transgenes (somatoclonal variation). Most of the somaclonal variation may be undesirable for crop improvement. Instability of transgenes in plants following genetic engineering may also pose a certain genetic risk. However, some genotypes produced by tissue culture or genetic engineering may be useful. The utility of a mutation would, invariably, depend on the environment in which it is tested. Therefore, it is important to specify the environmental conditions under which a new crop mutant is grown. This book deals with the prospects of induced mutations and bears on some of the related problems. Altogether, this is a useful volume on the induction of mutations and molecular techniques for crop improvement, and would be of interest to those working in this area.

M. R. AHUJA (Grosshansdorf)

Ausgewählte Schriften von Dr. h. c. WALTER KREMSER. Schriftenreihe „Aus dem Walde“, Mitteilungen aus der Niedersächsischen Landesforstverwaltung, Heft 49. Herausgegeben vom Niedersächsischen Ministerium für Ernährung, Landwirtschaft und Forsten. 1996. Bezug: Bezirksregierung Hannover, Postfach 203, D-30002 Hannover. 344 Seiten. DM 20, –.

Mit dem vorliegenden Band würdigt die Niedersächsische Landesforstverwaltung ihren ehemaligen Waldbaureferenten Dr. h. c. WALTER KREMSER und dessen herausragenden Leistungen. Der Band vereinigt 20 Aufsätze des langjährigen Waldbaureferenten, die in den Jahren 1967 bis 1984 erschienen sind. Viele der KREMSER'schen Ausarbeitungen haben zeitlosen Charakter und gehen weit über das rein Forstfachliche hinaus. Sie sind in einer forstlich und gesellschaftlich rasch sich ändernden Zeit aktuell geblieben und regen auch unter den heutigen Gegebenheiten zum Nachdenken an. Da der Schriftleitung eine thematische Zusammenführung der Aufsätze nicht sinnvoll erschien, wurden sie in der Reihenfolge ihres zeitlichen Erscheinens abgedruckt. Der Dokumentation bleibt zu wünschen, daß sie über Niedersachsen hinaus Beachtung findet, zumal einige der abgedruckten Arbeiten in Publikationsorganen erschienen sind, die heute nicht mehr existieren und daher nur schwer zugänglich sind.

M. LIESEBACH (Grosshansdorf)

Danksagung

Mein Dank

zunächst meinem Fachkollegen Professor H. HATTEMER für die sachkundige Darstellung meiner Bemühungen um unser gemeinsames Forschungsgebiet als Einleitung der letzten beiden Hefte des Jahrganges 1996 dieser Zeitschrift. Zusammen mit seiner Laudatio anläßlich meines 90. Geburtstages an meiner alten Wirkungsstätte sind seine Ausführungen für mich ein nachdenklicher Rückblick über 6 Jahrzehnte, in denen mich genetische Fragen meines Berufszweiges beschäftigten.

Ebenso erfreute mich die Zueignung einiger Originalarbeiten, Aufmerksamkeiten und besonders zu schätzende Geburtstagsgeschenke der Autoren.

Ritzerau, am 20. Juni 1997 W. LANGNER

My Thanks

First of all I want to thank my colleague Professor H. HATTEMER for the knowledgeable presentation of my endeavors with respect to our common field of research as introduction to the dedicated issues of the 1996 volume of this journal. Together with his laudation on the occasion of my 90th birthday at my old working domain are his remarks a thoughtful reflection over the past 6 decades in which genetical questions of my working field occupied me.

Also, I was pleased by the dedication of original papers to me, tokens of friendship, and especially appreciated birthday presents of the authors.

Ritzerau, 20. 6. 1997 W. LANGNER

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