

as to bring particular genes (e. g. frost or drought resistance).

The provenances are to be sown and planted as ordinary provenances experiments provided numerous and small plots per provenances are assumed.

Measures are to be made when the considered characteristics exhibit a sufficiently high early test value (NANSON, 1967 or 1968).

On the basis of these results, early selections are made successively and for example, only the best individuals of the best provenances are kept for reproduction. So, all individuals of any provenance that are not adapted to the environment of the seed orchard are discarded. Therefore, bad provenances will disappear almost entirely and will not participate to reproduction.

Since the provenance seedling seed orchard is not intended to be pruned, selections may continue after flowering, particularly for those characteristics whose early test value reaches a sufficient level only at older stages. Provenances seedling seed orchard has thus an evolutionary character, genetic gain ever improving, on the contrary of clonal seed orchards.

Provenances seed orchard constitutes also a valuable basic genetic material for further breeding.

III. Discussion

III.1. — Advantages

1) Rapidity, security, low costs

As seen in the introduction, provenances seedling seed orchard assures rather low delays before commercial harvests can begin. Very often, not more than 5 to 20 years from the start, according to species and conditions, are necessary before first seeds are produced. By the classical way of provenance tests followed by seed orchard establishment, many tens of years are necessary.

Moreover, provenances seedling seed orchards permit to escape to different risks involved in genetic material recovery. These risks are generally very important, and often, the results from the provenances experiments are difficult or impossible to use because the original provenance stands are not more available.

Finally, provenances seedling seed orchards involve not much more costs and labour than an ordinary provenances experiment.

2) Broad genetic basis

A very broad genetic basis is assured by the diversity of provenances and seedlings constituting the seed orchard. The synthetic variety produced by the provenances seedling seed orchard is in fact a sort of genetic synthesis of the individuals of the species or of individuals of a part of its range which are the best adapted to the planting site.

Of course, this synthesis will be somewhat different according to the environment of the seed orchard. In fact, the selective pressure to which the components of the seed orchard will be submitted, will vary more or less with the situation of the seed orchard.

This type of seed orchard will increase considerably the gene richness of the created synthetic variety, principally by way of multiple allelism. This synthetic variety will therefore exhibit more "flexibility" (see REHFELDT and LESTER, 1969) i. e. ability for adaptation to many different sites, changing environments and diverse utilizations.

The broad genetic diversity makes also this synthetic variety a good if not the best basic material for future breeding in many directions.

3) Gene pool conservation

The provenances seedling seed orchard can also play an important role in the conservation of the gene pool of a species. This role can become in some cases the most important purpose or consequence for species which are threatened by excessive exploitation, as many precious broadleaved species in West Africa, *Pinus caribaea* var. *bahamensis*, soon perhaps also *Pseudotsuga menziesii*, etc. With the limitation said above, the provenances seedling seed orchard is to a certain extent a genetic synthesis of the species or of a part of its range.

4) Heterosis effects

Crossing between unrelated individuals has often a heterosis effect as a consequence. This effect bears generally on vigour ("luxuriance"), but also on flexibility and "developmental homeostasis" of every heterotic genotype to different sites, and on its resistance against adverse ecological conditions (frost, drought, etc.) as against biotic agents (fungi, insects).

The actual genetic gain realized by the offspring of the seed orchard will be therefore probably superior to the genetic gain which could be estimated from performance of parents in the seed orchard.

5) Advantages peculiar to seedling seed orchards

Among these advantages are rapidity of establishment of the seed orchards (seedling plantations) and no problem proper to grafting, i. e. no technical ability, no greenhouse investments, no graft incompatibility, no delays, etc. (see TODA, 1964).

This type of seed orchard is thus particularly convenient for many developing countries, especially with tropical pines.

Moreover, the provenance seedling seed orchard escape to the danger of inbreeding, peculiar to half-sibs or full-sibs seed orchards as pointed out by ZOBEL and McELWEE (1964) and BARBER and DORMAN (1964). Indeed, if two individuals from the same provenance mate together, because for example they share the same plot, their offspring will not suffer from inbreeding depression.

III.2. — Drawbacks

1) Collection of provenances

A rather large sample of provenances is needed so as to contain a sufficient number of the best one.

Therefore, a seed collection must be organized on a large scale. Since this collection represents high costs and many serious operational problems, it should be organized at the international level. Provenances seed collections made in the frame of IUFRO under the direction of BARNER for diverse species of Western North America (e. g. douglas) are a model to be followed.

2) Testing location

Since the provenances seed orchard is first a provenance test, it must be realized in the region of utilization of its offspring, so as to avoid interactions which would diminish genetic gain.

This region of plantation is not necessarily the best region for flowering and fructification of the seed orchard.

Therefore, the optimum compromise between absence of interaction and massive seed-setting must be sought.

3) *Late flowering of the species*

Though early flowering is not absolutely necessary, it is an important advantage. When late flowering takes place, the unpruned trees are already tall and difficult to climb.

However even with such species, some measures can be taken to promote earlier flowering: large distance at plantation (e. g. 2×2 m or 3×3 m) followed by heavy selective thinnings; possibly fertilizer treatments, if no interaction is demonstrated.

4) *Spacing at plantation and selection intensity*

On one hand, large distances at plantation reduce the intensity of selection and genetic gain.

On another hand, too narrow distances present the risk that competition takes place before planting shock and related disturbances are overcome; then individuals with poor genotype but favoured by accident have more chances to suppress individuals with better genotypes but less favoured; this results in a lessening of heritability and genetic gain.

For species used in Western Europe, it seems at first sight that the best compromise lies in spacings ranging between 1.5×1.5 m and 2×2 m.

In the first case, the basic population will be of about 4.440 plants/ha being thinned successively to 10% (4.7×4.7 m) or 5% (6.7×6.7 m); the resulting selection intensities are $i_{10} = 1.75$ and $i_5 = 2.06$ (NANSON, 1967).

In the second case, we shall have 2500 plants/ha being thinned successively to about 20 or 10%, with $i_{20} = 1.40$ and $i_{10} = 1.75$. In this case however, selection could be made later, before competition takes place, what will increase the heritability.

5) *Isolation barriers between provenances*

Some fecundation barriers can occur between provenances: mainly phenological differences, but perhaps also physiological or genetic incompatibilities. However, concerning this last point since sterility at fecundation of ovule by pollen tube is induced by multiple allele genes "s" of the same kind in the two gametes, and since the probability to have different "s" genes in individuals from different provenances is high, the rate of success of inter-provenances crosses might be higher, other factors being considered as equal.

These problems should be nevertheless better studied in the future.

To sum up, it seems that complete incompatibility between two provenances, even remote, is scarce. In fact in general, these problems do not prevent fecundation but can reduce the rate of crossings between certain provenances.

6) *Loss of information and demonstration*

The structure of the provenances seedling seed orchard is so that it contains many replicated small plots (often one-tree plots) and that many provenances will completely disappear in earlier stages.

It results that a certain amount of information will be lost very early, mainly on the worst provenances.

On another hand, this structure is not favourable for demonstration purposes. This last point can be important when the problem is to convince responsible persons or foresters not yet aware of the importance of between-provenances variation.

7) *Problems of lay-out, mapping, measures and analysis*

A provenance seed orchard can make important problems of lay-out, labelling, mapping, control, measure, analysis, selection, etc.

These operational and conceptual problems will be discussed more in details in the next chapters.

IV. Lay-out

The basic principle is to have small and numerous replicated plots so as to promote random mating between individuals of different provenances. However it must be noted that matings between individuals of the same provenance are allowed since they are not related, on the contrary of the case of full-sibs and half-sibs seed orchards, where the risk of inbreeding can be important.

There are many different possible designs able to meet this principle and it is not possible to discuss them in detail here. However practical constraints and operational difficulties play an important role and limit their number.

Therefore and so as to give a concrete model, we give here procedures similar to those we actually use or plan to use for establishment of our provenances seedling seed orchards of Douglas fir composed of the best provenances collected by BARNER.

Sowing

The provenances are sown in generally four (but possibly more) completely randomized blocks. Incomplete blocks designs and other sophisticated designs are avoided because too difficult and costly to realize practically; they are also uneasy to analyse even with computers, especially when missing values occur, what is not uncommon.

The amount of seed sown is carefully calculated so as to provide about the same number of trees per provenance and to cover the scheduled area.

Extraction and lining-out

After one or two years (and measures in the meantime) seedlings are lined out in the nursery with the same design but as far as possible with another randomization. At extraction, a certain massal selection (culling or roguing) of seedlings may take place; this selection removes a certain amount (preferably constant) of the worst seedlings per plot.

Some of the worst provenances could also be eliminated completely on the basis of certain characteristics (height, etc.) in so far the value of early test of the characteristics be sufficiently high and well established.

After one or two years more (e. g. 2/2 plants) measures are made and analyzed; for every characteristic, genotypic heritability (h^2_G) on the means per provenance are calculated (NANSON, 1970) as the corresponding genotypic correlation (r_G).

At this stage, some of the worst provenances might be eliminated on the basis of economic characteristics for which: early test value and h^2_G are high enough; selection of provenances might also be envisaged from Selection Index combining different characteristics (NANSON, in press).

Within the plots, a more or less severe massal selection may take place. Because of lack of time and costs, this selection may be carried out visually eliminating with shears plants which are ill, badly shaped, too small, etc., up to about a certain proportion fixed in advance.

Choice of Field design

This choice must be made at the latest at this stage. Each nursery block should be considered and handled as a separate unit. Within each block, plots may be grouped in the field in complete (sub)-block design or in complete randomization. Plots may take the form of a rectangle, a square, a line, or a point (one-tree plot).

Taking account of facility, and of promotion of random mating between individuals of different provenances, linear plots or better one-tree plots, seem to be the most adequate.

Labelling

In the nursery, the remaining plants of the remaining provenances are labelled according to the field design. Since numerous labels are needed, cheap plastic labels presented in rolls can be used.

If linear plots of for example 20 trees are retained, the first and last 20th trees in the nursery plot are labelled with provenance numbers; and so on for the other plants of the plot; the last set in the plots will thus contain 20 plants or less.

If one-tree plots are retained, every plant must be labelled.

Lifting — Randomization

Each nursery block is handled apart.

At extraction, singles plants or bundles corresponding to a plot are immediately randomized, for example by scattering them at random along a trench. This randomization will still be improved at loading on vehicle and unloading in the field.

Planting

Each nursery block being handled apart, bundles, or single plants in case of one-tree plots, are planted in the (randomized) order they come; in linear plots, the first and last plants are those labelled.

This procedure permits planters to plant quickly and well during good weather conditions without being disturbed by proper allocation of numbers to planned places.

Spacing

As said before, the best compromise between competition and low intensity of selection seems in our conditions, to lie in a spacing ranging from 1.5×1.5 m to 2.0×2.0 m.

Mapping

As plantation is finished, mapping of plots may begin. It is in fact a "post-mapping" as opposed to "pre-mapping" which is generally practiced. This post-mapping has advantages: no problem of allocation of plants to planned places and therefore no error, rapidity of plantation during good weather conditions, important increase in plant survival and decrease in planting shock. — WRIGHT (1970) uses also such a procedure in some provenance experiments.

Many-tree plots, especially linear plots, are generally easy to map, since the number of plots is relatively limited.

On the contrary, mapping of one-tree plots represents an important work.

It can be done independently by two operators. The two maps are then compared, non concordant numbers noted, and afterwards corrected in the field. Then, the definitive map is written and multiplied.

This map must lay sufficient intervals between numbers so as to serve for inscription of measures (one to three

measures) under the number of each tree. The map becomes thus a measure form.

Other more complicated and elaborated procedures based on integrated use of computers have been also described with details by BARADAT *et al.* (1970) for half-sibs and full-sibs seedling seed orchards of *Pinus pinaster*. The authors use pre-mapping by computers for one-tree plots in complete (sub)-blocks designs. This has the drawbacks of pre-mapping and of the difficulties represented by missing values since families are often of very unequal size. This require also high capacity computers, as highly elaborated sets of computational programs what can increase considerably computations costs.

This procedure has however many advantages, mainly with large amounts of trees, for automatic calculation of selection index, automatic mapping of the selected trees, etc. It could be used also to a certain extent for provenances seedling seed orchard when high capacity computers facilities are easily available and when index selection on an individual basis is possible.

V. Measures

Characteristics to be measured must not be too numerous, because of operational and computational difficulties especially with construction of selection index.

These characteristics must be restricted to those for which early test value is high enough for prediction of economic characteristics at rotation end.

These last are generally: volume growth (m^3/ha), form (bole straightness and branch fineness), possibly wood quality, and resistance to physical and biotic agents.

This pose one of the most important and difficult problem in tree breeding: the value of early tests.

We have studied this problem theoretically and experimentally mainly for growth (NANSON, 1967, 1968). It was done on the basis of 13 field tests, chiefly provenances experiments, 7 of which have already reached an age superior to 40 or 60 years. It appears that early selection of provenances or of offsprings for future growth may be very efficient when made on the basis of height at an age of 5 to 10 years from the seed, i. e. when planting shock and grass competition are overcome, and when height reaches about 1 to 3 m in conditions of Western Europe.

For what concerns form, results are lacking almost entirely. Adult form is possibly not yet well marked at juvenile stage, but it seems that marked defects at this stage (repetitive forking, etc.) cannot bring good adult form. Therefore individuals exhibiting such defects might be eliminated. This removal is to repeated at each successive selective thinning.

Wood qualities (basic density, fibre length, etc.) could also be assessed with validity at a rather early stage as some studies tend to show it (cfr. ZOBEL *et al.*; POLGE et ILLY, 1968). These determinations are however expensive to realize on a large scale and they often oblige to destroy the plants. Therefore, it seems sometimes advisable to postpone these measures to later stages.

Resistance against physical and biological factors (early, winter and late frosts, fungi, insects, etc.) may be sometimes validly assessed at early stages; this is naturally the case when resistance is only of concern at these early stages (many frost resistances, some fungi diseases).

For what concerns record of measures, one possible way to proceed is to write them down on the map under the number of the tree; measures intended to form selection index should be grouped on the same map.

VI. Analysis and Selection

Analysis should be conducted in function of the types of selection which are chosen.

VI.1. — Types of selection methods

For one characteristic, the following methods of selection are to be recalled.

1) *Individual selection* (Mass selection), where individuals are selected solely according to their own phenotypic values, irrespective of their provenance.

2) *(Among) Provenance selection*, where all individuals of a provenance are selected or rejected according to the mean phenotypic value of this provenance.

3) *Within provenance selection*, where the best individuals of every provenance are selected according to their phenotypic value compared within the provenance.

4) *Combined selection*, where individuals are selected according to an indice taking into account their individual phenotypic value appropriately weighted by their provenance mean.

When more than one characteristic is taken into account for selection, the following types of selection must be also considered and combined with the preceding ones to give all possible combinations.

a) Independent culling levels

Selection is made for one characteristic at a time, independently of the others. Thus, selection is made for the first characteristic, then for the second on the selected individuals of the first, etc.

b) Index selection

Selection is made on the basis of an index in the form:

$$I = a_1 X_1 + a_2 X_2 + \dots + a_n X_n,$$
 where X_i are the phenotypic values of the different characteristics and a_i are their weights, themselves dependent on heritabilities, genotypic (or genetic) correlations, and economic weights.

c) Tandem selection

Selection is made for one characteristic at a time in every generation. This type of selection seems to be inappropriate to forest tree breeding with long generation intervals; it will not be envisaged here.

VI.2. Discussion

1) Present possible methods

In theory, "combined selection" joint to "Index selection" will give the optimal results provided genetic parameters can be estimated, and then estimated without important errors, what is not often the case.

The first question is to know if combined selection is possible.

Since individuals from the same provenance are according to the existing theory of population genetics in principle unrelated, no combined selection seems at first sight possible nor desirable. It seems however that individuals from the same population are more related than individuals from different populations. Then, the genetic correlation (r) between individuals from the same provenance as compared to all individuals of all provenances would be different from zero and combined selection could be envisaged if methods to estimate r existed.

This is a type of question that could be more thoroughly studied in the frame of quantitative genetics.

At any rate, it must be observed that combined selection has seldom a great superiority on other good methods whatever r may be; this superiority is generally less than 10% (FALCONER, 1961) and it can be easily compensated by a slight increase in the intensity of selection.

For instance, for $n = 50$ trees per provenance and if r were equal to 0.05 or 0.10, we should have for an intraclass correlation (t) ranging from 0.1 to 0.3 the following figures for Individual (I), Provenance (P) and Within-provenance (W) selection in percentage of Combined selection:

		I	P	W
$r = 0.05$	$t = 0.1$	99	20	98
	$t = 0.2$	94	14	99
	$t = 0.3$	88	11	99
$r = 0.10$	$t = 0.1$	100	34	94
	$t = 0.2$	97	25	97
	$t = 0.3$	92	19	98

For $n = 20$ or $n = 100$, the figures are very similar.

In this case, provenance selection must not be made, whereas Within provenance or Individual selection may be performed with little loss of efficiency.

On another hand, for the most defavorable case above with individual selection, the same response will be obtained for Individual-as for Combined selection if the following relation takes place between the selection differential:

$$i_I = i_C / 0.88$$

If we select $a_C = 50\%$ of individuals by combined selection, we will have $i_C = 0.80$ (NANSON, 1967); then $i_I = 0.80/0.88 = 0.91$, that corresponds to $a_I = 43\%$ (remaining after selection).

Therefore, a little more severity at selection, or a larger number of individuals with the same severity, can make individual or within provenance selection as effective as combined selection could be if r were known with accuracy.

From the practical point of view, individual selection is also generally the easiest to perform, especially in case of one-tree plots. Furthermore, in case of emergency, or when men and money are lacking, or when measures and computation facilities are not available as this can occur in developing countries, this individual selection could be performed visually as an ordinary selective thinning, probably without an important loss in response. In this case, individual selection is thus an easy, flexible and rather efficient method.

Within provenance selection can be advisable mainly between plants of the same plot for they share a common environment which reduces environmental deviations between trees and thus increases the efficiency of selection. With plots containing only a few trees, selection might keep finally only the best tree per plot; then individual selection can proceed as seen above.

The second question concerns the possible use of an index.

Since the value of early tests becomes sufficient only at different ages for the diverse economic characteristics and since there is a periodic necessity of thinning, independent culling levels will be often the necessary mode of selection. This procedure is also the easiest to realize in practice.

2) Gains evaluation

In the provenances seedling seed orchard, matings will be made on one hand between individuals of the same provenance, and on the other hand between individuals of different provenances; the proportion between these two

kinds depends on the spatial structure of the seed orchard, on the ratio of the number of provenances to that of individuals per provenance and on crossability between provenances.

Crosses between individuals of the same provenance will result in a first genetic gain Δ_{Gp} coming from the selection of the best provenances and in a second gain (Δ_{Gi}) coming from the selection of the best individuals within provenances. Of course it is perhaps difficult to set a border between the two since individual selection is performed irrespective of the provenances.

If selection would be performed by provenance selection followed by within-provenance selection, the respective gains would be:

$$\Delta_{Gp} = i_p h^2_{Gp} \sigma_p$$

and

$$\Delta_{Gi} = i_i h^2_{Ai} \sigma_i$$

where i_p and i_i are the respective standardized selection differential, h^2_{Gp} is the genotypic heritability (broad sense) of the means per provenance, h^2_{Ai} the genetic heritability (narrow sense) of individuals within provenance, σ_p and σ_i the respective phenotypic standard deviation of the means of tested provenances and of individuals within provenances.

Δ_{Gp} is the genotypic gain that could be obtained by use in practice of the selected provenances, and Δ_{Gi} is the supplementary gain obtained by use of the offspring of the selected individuals.

Example:

Let us have 40 provenances of douglas with 100 trees per provenance in a fully randomized one-tree plot design; for tree height, let $\sigma_p = 20\%$ of the general average and $\sigma_i = 25\%$ of their provenance mean; $h^2_{Gp} = 0.7$ and $h^2_{Ai} = 0.2$. We select 20 provenances, so $i_p = 0.78$, and one fourth of the trees within provenance, so $i_i = 1.27$. We have then:

$$\Delta_{Gp} = (0.78) (0.7) (20) = 10.92\%$$

$$\Delta_{Gi} = (1.27) (0.2) (25) = 6.35\%$$

or a total of 17.27%. Since individual selection is probably more efficient than the succession of the two above selections, real figures must be higher.

Crosses between individuals from different provenances will add to the preceding gains an heterosis effect which can be a priori negative, null or positive.

From what we know from previous crossing experiments between species, provenances or unrelated forest trees, it is unlikely that this heterosis effect could be negative. At worst it can be null but very often positive especially for what concerns growth ability (luxuriance) which is generally the main purpose of breeding.

To certain extend, provenances seedling seed orchard can therefore cumulate in one cycle of selection gains arising from provenance selection, individual selection and probable heterosis effect between provenances.

3) Further research

Of course, further research would be useful to improve the present methods and increase the gains.

The question of the genetic correlation between individuals of the same provenance should be reconsidered.

The building of index of selection should also be studied mainly for selection at the individual level. Index can be useful when different economic variables exhibit a sufficient early test value at about the same period.

This type of seed orchard provide also a good and easy basic material for the study of crossing between prove-

nances. It permits progeny testing and possible determination of general and specific combining ability. It allows after a certain period the study of the value of early tests and therefore permits a further selection of the parents on the basis of their progeny tests. At this stage, gains can still be considerably increased.

VII. Conclusions

The provenances seedling seed orchard presents many advantages, particularly for new species which are still genetically unknown or for species already under breeding where it appears now that the programme has started with bad or medium provenances. The most important of these advantages seems to be: low costs, no peculiar technical ability, short delays, gains already important, probable heterosis effects and no inbreeding risks, great flexibility of population, broad genetic basis and gene richness, gene pool conservation and good basis for further breeding.

This type of seed orchard raises however problems as: proper collection of provenances, genotype \times environment interaction, knowledge of early test value, appropriate choice of spacing and selection intensity, possible isolation barriers between provenances, system of mapping, measure and analysis, loss of information and demonstration. Furthermore, the rather simple selection method proposed, i. e. individual selection following an independant culling level system, might be improved so as to increase gains.

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Summary

The "provenances seedling seed orchard" is proposed as a new method of forest tree breeding.

Its description and practical execution are developed with some details.

Its advantages and drawbacks are discussed. It appears that the provenances seedling seed orchard is generally easy to establish rapidly and to handle. It can provide in a rather short delay an offspring characterized by a great flexibility and a broad genetic basis and representing a gain already important even without taking probable additional heterosis effects into account. However, more research could be useful to improve the methods of selection of the components of the orchard.

Key words: Seed orchard, provenance, breeding methods, gene pool, gene conservation, heterosis, flexibility, early selection.

Résumé

Le «verger à graines de semis de provenances» est proposé en tant que nouvelle méthode de l'amélioration des arbres forestiers.

Sa description et son exécution pratique sont exposées avec quelques détails.

Ses avantages et inconvénients sont discutés. Il apparaît que le verger de semis de provenances est en général facile à établir rapidement et à traiter. Il peut procurer endéans un délai assez court une descendance, caractérisée par une grande adaptabilité et une large base génétique, et représentant un gain déjà important sans compter un effet d'hétérosis probable supplémentaire. Cependant, des recherches nouvelles pourraient être utiles en vue d'améliorer les méthodes de sélection des composants du verger.

Zusammenfassung

Die „Herkunfts-Sämlings-Samenplantage“ wird als eine neue Methode der Forstpflanzenzüchtung vorgeschlagen. — Beschreibung und praktische Durchführung werden im einzelnen dargestellt. — Vorteile und Nachteile werden diskutiert. Es zeigt sich, daß Herkunfts-Sämlings-Samenplantagen ganz allgemein leicht und schnell zu erstellen und zu handhaben sind. Man kann innerhalb kurzer Zeit eine Nachkommenschaft erhalten, die durch große Anpassungsfähigkeit und eine breite genetische Basis ausgezeichnet ist und die auch schon ohne den zusätzlich zu erwartenden Heterosis-Effekt einen wertvollen Gewinn darstellt. Jedoch dürften noch weitere Untersuchungen nötig sein, um die Selektionsmethoden für die Auslese der Baum-Komponenten für solche Samenplantagen zu verbessern.

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Statistical Efficiency in Wood Quality Study Based on a Black Pine Plantation

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A randomized complete block design containing four-tree plots has been a popular experimental design for the assessment of geographic variation patterns in tree species. Frequently plot means are used as items in the analysis of variance and other statistical computations.

Since tree breeding is time consuming and costly, tree breeders are in constant search of techniques that will help evaluate genetic constituents of the species under investigation at its early stage of life. Numerous publications established strong nursery-plantation, juvenile-mature age, trunkwood-branchwood and increment core-entire tree relationships.

In the assessment of European black pine (*Pinus nigra* ARNOLD) wood properties, plot means were used as items in the analysis of variance. They were satisfactory to show the geographic variation pattern in specific gravity and tracheid length (LEE and WRIGHT, in press). However, a number of questions remained unanswered. What would be statistical efficiency if study material were collected from less than four trees per plot and from less than 10 replications? If reduced plot size and smaller number of replications could yield equally acceptable information, they would imply that time and land can be saved. The present paper was intended to analyze the impact of different plot sizes and replicate numbers on the evaluation of branch-

wood specific gravity and tracheid length in 27 different European black pine seed sources.

Material and Methods

I measured tracheid length and alcohol-benzene extractives free specific gravity on one lateral branch collected from the south aspect of the top-most whorl of each of 4 trees per plot on each of 10 blocks of a 27-origin black pine plantation (MSFG 5-61) in Kellogg Experiment Forest, Kalamazoo County, southwestern Michigan.

Each of 4 trees per plot and all 10 replications were numbered and with the aid of random number table I selected four different plot sizes (1-, 2-, 3-, 4-tree plots) and eight different numbers of replications (1-, 2-, 3-, 4-, 5-, 6-, 8-, and 10-replications) in the laboratory following a sampling scheme technically called sampling with replacement. Regardless of what the first number may be, every number has an equal chance of being drawn in the second drawing. Analysis of variance and correlation analysis were conducted by an electronic computer, IBM 1130.

Results and Discussion

Study of Plot Sizes: Since the study plantation had 16 (= 5.93 percent) missing plots, substituted values were calculated by computing the average for surviving plots of the same provenance and treatment. After substituting the missing plot values and reducing the degrees of freedom accordingly each set of measurements was subjected to analysis of variance for which the degrees of freedom

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