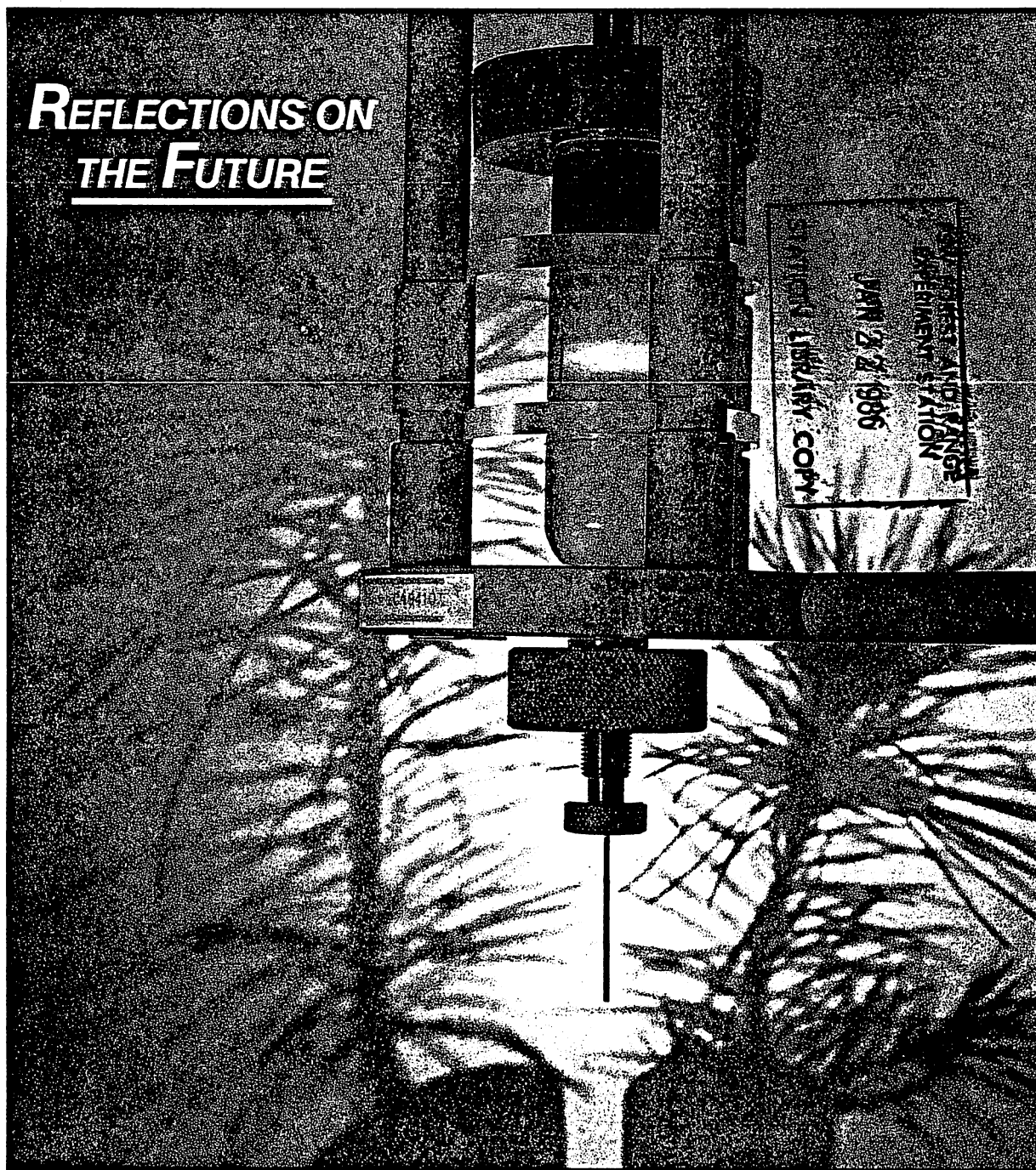


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**REFLECTIONS ON
THE FUTURE**



Plus: A New International Forestry Department

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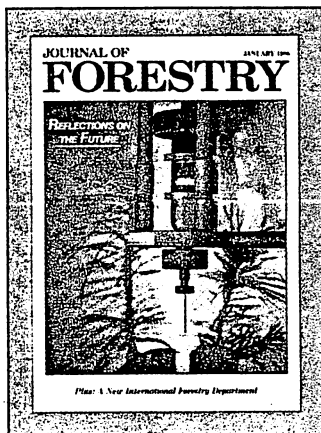
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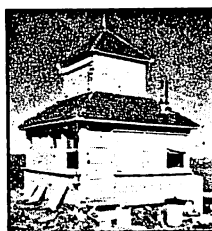
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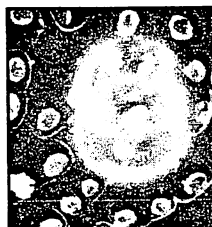
Cover: A band of purified DNA from sugar pine needles fluoresces under ultraviolet light. The DNA was stained with ethidium bromide and concentrated in a cesium chloride density gradient. Photographs by Carol A. Loopstra and Paul D. Hodgskiss, USDA Forest Service.



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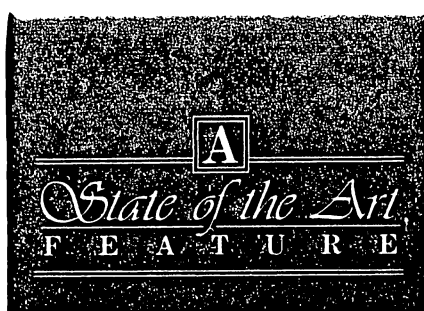
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Part I. The New Genetics

TREE GENETICS AND IMPROVEMENT

We've come a long way from the fifties, and we're just on the threshold of genetic engineering.

By Calvin F. Bey, Daniel B. Houston, and Ronald J. Dinus

In 1958, when the *JOURNAL* devoted an entire issue to "Progress in Tree Improvement," the topic was a novelty to the forestry profession. Since then we have come a long way. Although still not a household word, tree improvement is increasingly recognized as an essential part of forest management. Consideration of the genetic resource now begins with forest planning. Stanley Krugman discusses conservation of the natural genetic base in "The Ethical Question" on page 40. Genetic considerations are now part and parcel of silvicultural prescriptions, stock propagation, seed deployment, and maintenance treatments.

Tree improvement is a complex science and a multifaceted art. Not only the scope has broadened—regional conferences, short courses, international programs, new forest-genetics textbooks, and a multitude of articles in numerous journals attest to a flurry of activity in the field.

Tree improvement, as with any specialty, is most valuable when integrated within land-management programs. Major efforts are currently geared to

developing improved seed for reforestation programs, though W.J. Libby, in "Clonal Propagation" on page 37, tells us that mass cloning is on the horizon. Michael Greenwood, in "Shortening Generations" on page 38, reports that nursery managers and reforestation specialists are joining tree-improvement specialists as key participants in the process of realizing genetic gains. Coordinated efforts are essential in matching seed needs and supply.

With improved seeds come new questions: Is it better to establish plantations of single- or multi-family lines? Can we match genotypes with specific sites? As plantations develop from improved seeds, additional questions emerge: Are old thinning and harvest schedules still appropriate? Can we ignore insects and disease, or will they

(Continued on page 36)

Calvin F. Bey is program leader, USDA Forest Service, Pacific Northwest Forest and Range Experiment Station, Juneau, AK; Daniel B. Houston is associate professor, Department of Forestry, Ohio State University, Wooster; and Ronald J. Dinus is with International Paper Company, Tuxedo Park, NY.

Decoding Tree

Biochemical geneticists refine tools for the future.

By M. Thompson Conkle

Check the laboratory reports after your next physical. You'll find information on a number of biochemical processes. Procedures like those used in the medical sciences are yielding valuable information about genetic differences among trees and tree pests. New procedures that provide ways to isolate and move genes are advancing progress in tree improvement. These procedures can be applied to forestry because life processes are remarkably similar in all organisms.

Living organisms code and transmit genetic information by means of deoxyribonucleic acid—DNA. This nucleic acid has a four-letter molecular alphabet that codes the basic structure for genes, which are the blueprints for making different enzymes. And enzymes—like machines in factories—modify raw materials to make products. Cells—like factories—are sites for thousands of metabolic reactions. Clusters of cells differentiate to become tissues. Production, differentiation, and

DNA

assembly of component tissues give rise to the integrated structure of organisms.

Changing the spelling in the DNA code by one letter can alter gene products and modify metabolic reactions. One altered enzyme may work a little faster than the original; another may work slower or not at all. Different forms of the code and variation in gene products are the sources of genetic variation among organisms. Decoding DNA and identifying different forms of enzymes and cellular products help us measure variation.

Studies on variation help explain forest-tree evolution and can be applied to tree breeding. Analyses have provided information for setting seed-zone and breeding-population boundaries, determining the probable geographic origin of unmarked seed collections, selecting parents for improvement programs, and fingerprinting vegetative propagules to maintain close control of clones.

Data on variation in DNA, enzymes, and cell products complement information gained from progeny tests. Biochemical tests detect genetic variation unaffected by environmental variation. Such tests identify specific DNA codes, enzymes, and cellular products in a tree. They detect alternative genes (al-

les) and gene products in populations of trees.

In forest trees, as in other organisms, early work using biochemical procedures began when techniques were developed for analyzing special classes of compounds. Procedures for separating enzymes were developed later, and now laboratories are beginning to isolate and decode DNA.

Monoterpenes

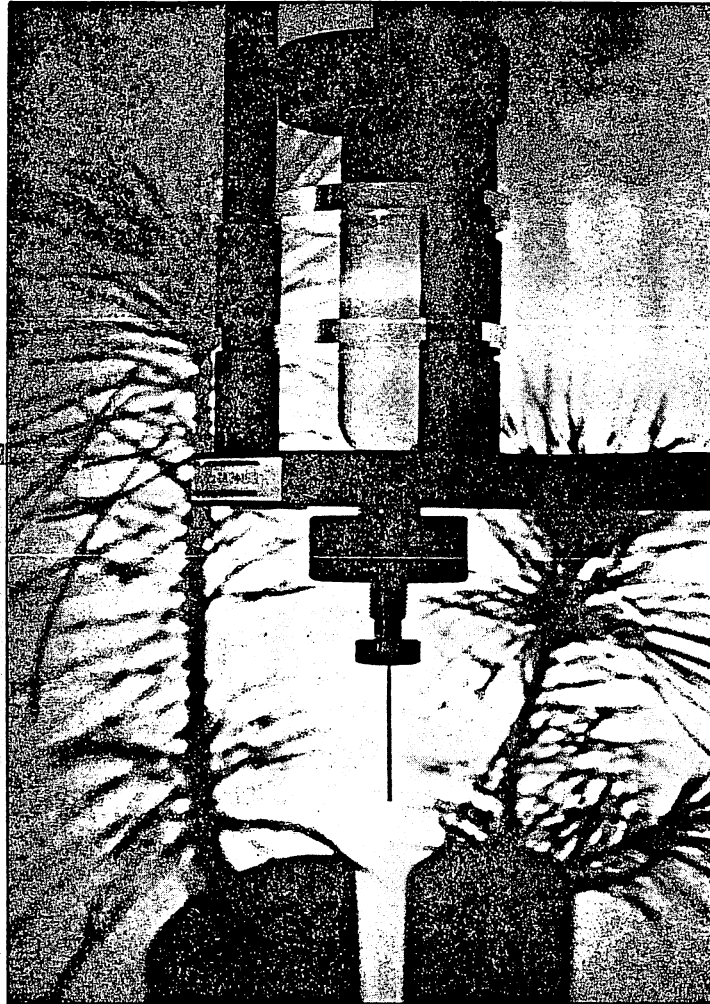
Many cellular products exist in trees, but the monoterpenes in conifer resin were among the first molecules thoroughly studied. Monoterpene surveys of resin from the wood, bark, and leaves of individual trees became common

when equipment for rapid and precise analyses (gas chromatographs) became available.

Monoterpenes are separated as nitrogen gas carries them through a chromatographic column. Signals from a detecting device record kinds and proportions of monoterpenes in each sample. Geneticists, having determined the inheritance of several monoterpenes, can now classify trees by genetic types and closely predict the components of resin in progeny of controlled crosses.

Forestry will benefit from new research on metabolic products, as progress is made in developing even more sensitive equipment. Detecting varia-

(Continued on page 36)



(Bey, continued from page 34)

become more troublesome? Tree-improvement workers are doing more than generating improved seeds. They are taking part in a network of specialists to answer land-management questions.

All tree-improvement programs are not alike. Dissimilarities are due to biological differences among species, such as flowering habits, traits for improvement, disease problems, graftability, and seed production. Differences also result from geography, landowner objectives, and demand for improved seeds. The result has been the develop-

ment of specialists for related species and even for individual species.

Different programs have also developed because of differing philosophical approaches to tree improvement. When programs were getting started in the 1950s, tree-improvement workers had no standard textbooks for guidance. While some programs followed European traditions, others developed their own. Philosophical differences have

been healthy. Workers in each program have been forced to look critically at their approach and to develop sound biological and economic justifications.

Research has helped identify and solve problems in tree improvement. Researchers began working on provenance trials, but full-fledged progeny testing is now a routine part of tree-improvement programs. Topics such as advanced-generation breeding, shortened generations, resistance breeding, and control of cone and seed insects are being given priority. While emphasis has been on solving practical problems, activity continues in basic research, involving genetic engineering, tissue cul-

(Conkle, continued from page 35)

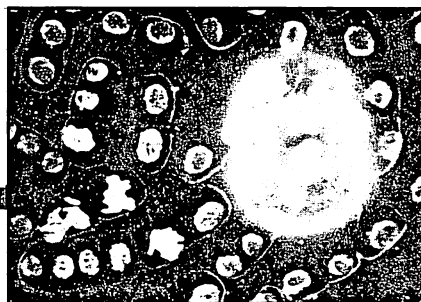
tion in compounds present in only minute quantities may lead to a better understanding of how trees grow, how they differentiate, and how they resist pests.

Enzymes

Workers in forestry laboratories can analyze enzymes from seeds, needles, buds, and cambium for genetic information on as many as 60 genes. That number is increasing. Dissimilar enzymes separate after being loaded on gels and subjected to high-voltage direct current. Histochemical stains then reveal the location of each enzyme.

Conifer seeds are particularly useful for these studies because the nutritive tissue surrounding the embryo has the same genetic makeup as the egg from which the embryo developed. This feature allows researchers to distinguish between genetic factors coming from the seed parent and those from the pollen parent.

By analyzing enzymes, breeders can learn much about variation among trees, progeny, and populations. As with monoterpenes, knowing geographic patterns of enzyme variation may help in deciding where to put boundaries for seed zones and breeding zones. Enzymes are excellent for iden-



Autoradiography of pine root tip.

T. Hillson

tifying clones and determining the parentage and purity of seed lots. Enzyme differences among pollen parents are used to determine pollination effectiveness, estimate the proportion of selfing, and monitor contamination from sources outside seed orchards.

In general, progress from artificial selection depends on the amount of genetic variation present in breeding populations, and enzyme analyses provide a good estimate of this value. Some lines of research suggest that trees with the most variation have the highest growth potential. Others lead to quite different conclusions. If a variation-growth potential relationship can be verified and if the relationship is strong, it could be an efficient way to select and breed trees.

Genes for known enzymes are also important for mapping chromosomes. Using the nutritive tissue in conifer seeds, researchers estimate the distance between genes and map their positions relative to one another. Such maps will be useful for locating and studying other genes that control growth and pest resistance.

Tree DNA

Studying DNA helps us to understand genes: how they are constructed, how they vary, and how they function. This understanding is leading to the means for isolating and moving genes into new host plants.

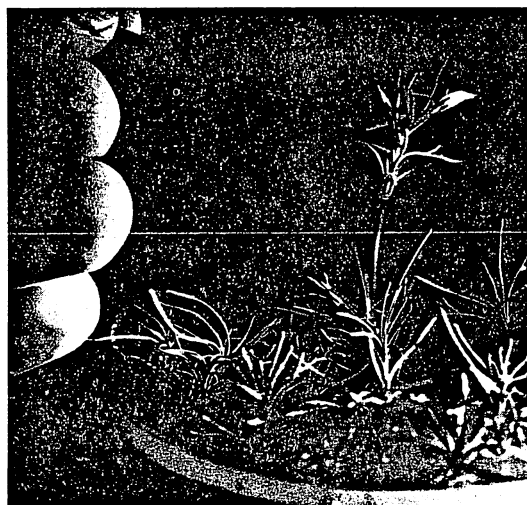
Special enzymes are used to cut long DNA molecules into short fragments. The fragments are separated using direct electric current in gels—a process similar to that used for separating enzymes. They can then be labeled with radioactive chemicals to reveal variation similar to the way in which enzymes are stained with histochemicals. Analyzing the DNA code of a fragment can yield fundamental information about genetic variation. Comparing codes from similar fragments of several species helps explain the evolution of genes. Mapping the location of DNA codes will add new markers to linkage maps of trees.

A DNA fragment with the code for a specific gene can be captured by putting it into specially "engineered" particles in bacteria. Then, when the bacterium infects a plant, some fragments with the gene fuse into the plant's DNA. If all processes are successful, the transferred gene will function in cells of the new host. A variant of this

Clonal Propagation

The clones are coming!

By W.J. Libby



ture, and population theory. Thompson Conkle, in "Decoding Tree DNA" on page 34, describes trends in biochemical genetic research. These supportive efforts will supply the information needed for tree-improvement programs of the future.

The SAF Working Group on Tree Genetics and Improvement prepared this series of articles to bring together information on current approaches and programs and to highlight special-interest topics relevant to land management. Our intent is to present a survey of the field that will inform other natural-resource professionals and place useful information in their hands. ■

procedure bypasses the infection step by injecting engineered particles into single cells growing in tissue culture.

Research is now under way in tissue-culture laboratories to discover how to grow whole trees from single cells. Growing trees from cells is necessary after injecting particles, but the procedures have another important use. Geneticists plan to select variant cells that either arise naturally during culture or are induced by chemical and environmental stimulants. For example, cells surviving high salt concentrations or cold shock might produce hardier trees for such conditions.

Several major problems must be solved before desirable genes are identified, replicated, and put into recipient trees. But research is advancing. Before too many years, forest scientists will bypass breeding blocks and long-term tests to move pest-resistant genes into trees lacking them; to develop trees resistant to herbicides; to engineer trees with small branches and strong apical dominance; and even to develop trees as sources of new, high-value, secondary products.

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A sexual or vegetative propagation—cloning—of trees has been a useful tool in traditional tree improvement. Cloning also promises to be the basis of a revolution in tree improvement with important effects on silviculture, forest policy, forest harvesting, and wood utilization. Reasons for cloning and the ability to clone effectively vary among species, and even among age classes within species.

Grafting and rooting have been the traditional methods. Grafting can be performed reliably with most species. In some species, graft incompatibilities develop anywhere from a year or so to over a decade after grafting, resulting in failure of the graft union. The cost per graft is generally high, and the effects of the rootstocks are an additional variable. These factors limit grafts to a set of specialty uses, mostly as a way of moving select genotypes to breeding orchards or expanding such genotypes in seed orchards.

By contrast, stecklings (plantable rooted cuttings) can in some cases be produced for costs similar to those of seedlings; in a few cases for even less. Low costs plus freedom from delayed mortality and from rootstock interactions mean that stecklings can be considered for many uses, from mass propagation for production plantations to research requiring high genetic control. Unlike grafting, the rooting of cuttings is highly sensitive to the effects of maturation of the donor tree. In general, cuttings from juvenile donors root easily and subsequently grow like seed-

(Continued on page 38)

*W.J. Libby
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The goal is to produce embryoids from cell culture and encapsulate them to produce artificial seeds with high clonal fidelity.