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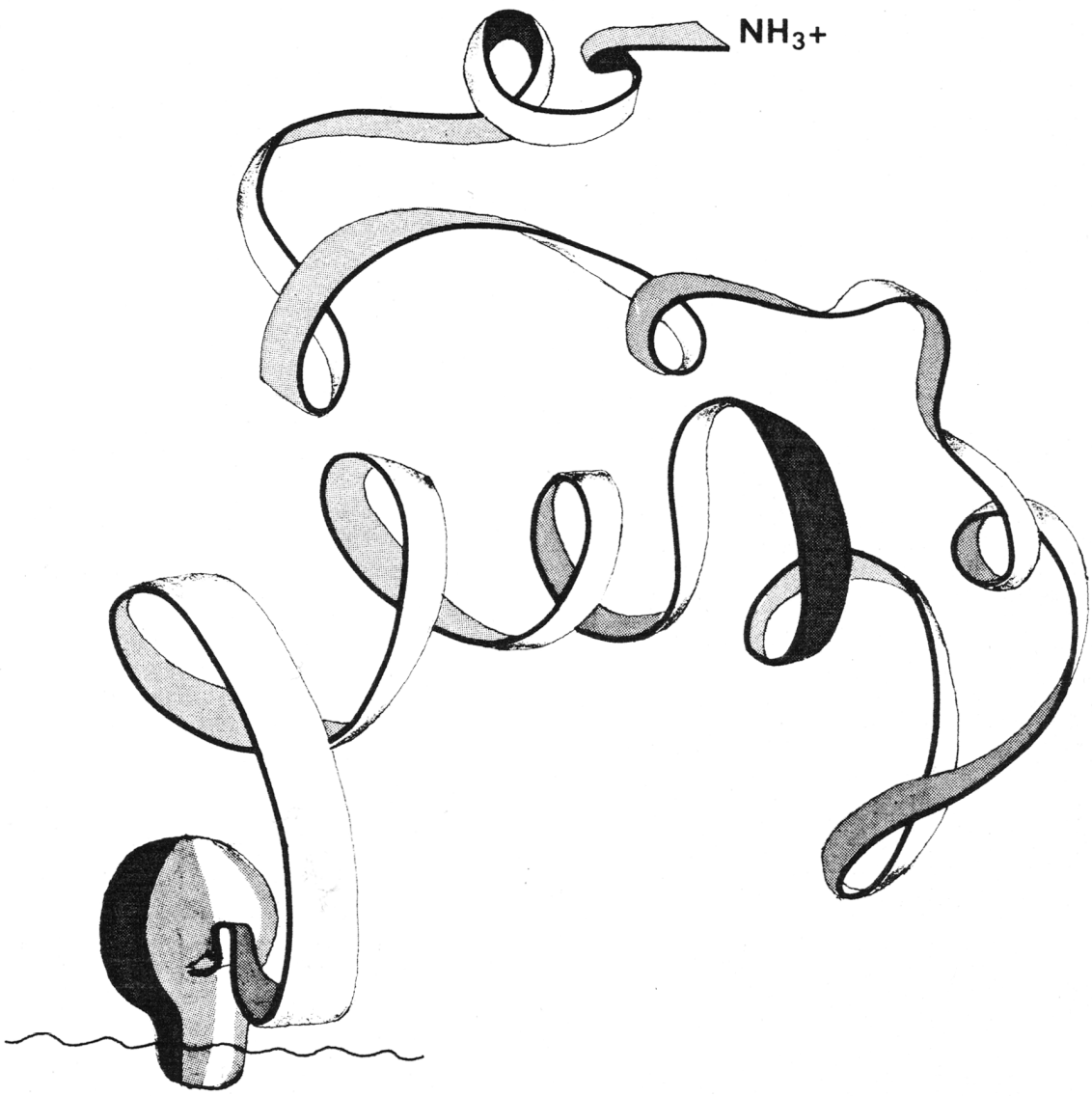
Proceedings of the Symposium on

Isozymes of North American Forest Trees and Forest Insects

July 27, 1979, Berkeley, California



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Cover: The polypeptide strand forming will become an enzyme. A ribosome translates genetic information as it moves along a messenger-RNA molecule.

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PREFACE

Isozyme techniques are currently the best means for evaluating the genetic structure of forest populations. Data from isozyme studies can help researchers evaluate, sample, and conserve the genetic variation of forest tree species. Our perception of genetic variation in forest populations has been significantly enlarged by new findings from studies detecting enzyme alleles of numerous genes of forest trees and insects.

The 1979 meeting of the Western Forest Genetics Association in Berkeley, California, provided an opportunity for a symposium, on July 27, to present some of these findings. It was appropriate to hold the symposium in conjunction with the Western Forest Genetics Association meeting, since most researchers of isozymes of North American forest organisms work in Western North America. The symposium was sponsored by the Pacific Southwest Forest and Range Experiment Station's Institute of Forest Genetics, which maintains a center for isozyme research in population genetics of forest trees.

The gathering of researchers and their presentations attested to the high value and multiple uses of isozyme technology for resolving genetic variation in forest organisms. Participants reported the distribution of genetic variation between and within several species, and proposed strategies for maintaining the variation through future generations. The population structure of species was evaluated at several levels—from broad regional comparisons to groups of trees on mountain slopes.

For many years, growth tests coupled with quantitative analyses of forest trees have estimated the proportion of total phenotypic variation that is attributable to genetic causes. But almost all the observed variation in isozymes stems from genetic differences: species and populations can be compared on the basis of the amount of genetic variation each possesses. The amount of genetic variation, whether considering an entire species or a small group of trees, is measured by the average heterozygosity of numerous loci. Presentations in the proceedings give information that relates average heterozygosities to growth rates and to life history characteristics of trees.

The relationship between a host tree and its pests adds another dimension to the study of forest genetics. Both the trees and the pests can differ in the genetic structure of their respective populations and in the amount of genetic variation each possesses. One presentation in this symposium points to the importance of the genetic variation of insects in designing effective pest management strategies.

Forest trees generally are difficult to work with in genetic studies because of their large sizes and slow developmental rates. One feature of conifers, however, elevates their value in isozyme studies. The female gametophyte tissue—the endosperm of conifer seeds—and its egg cells develop from a single haploid nucleus; mature seeds contain a haploid gametophyte and a diploid embryo. The genes segregating among the gametophytes of a tree permit direct genetic tests of allelism. One presentation in the proceedings uses segregation from multiple loci to determine linkage relationships. Others analyze the gametophytes and accompanying embryos from individual seeds to determine the seed tree and pollen parent genotypes. The proportion of outcrossing and selfing are evaluated for open-pollinated seed. Knowledge of the seed tree genotype and of pollen parentage are shown to be valuable for a variety of uses in tree breeding programs.

In all, an impressive diversity of information is represented in the papers of this symposium. It is obvious that a technology that yields precise genetic information for numerous genes, with great efficiency of time and space and at relatively low cost, will be a great aid in tree improvement and gene conservation.

We, at the Pacific Southwest Forest and Range Experiment Station in Berkeley, were delighted with the enthusiasm of our friends and colleagues who attended the symposium and prepared papers for these proceedings. To each participant, we extend our warmest appreciation for current, advanced information of the highest quality. Their successful efforts in resolving genetic variation in forest organisms will undoubtedly stimulate new work in forest genetics and greatly assist in the wise management of genetic resources.

We extend appreciation to the Western Forest Genetics Association for publicizing the symposium and providing local arrangements. Special thanks are due Ray Steinhoff, 1979 Chairman of the Western Forest Genetics Association, and William B. Critchfield and William J. Libby, co-chairmen of the 1979 meeting of the Association.

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