RESEARCH AT THE INSTITUTE OF FOREST GENETICS RHINELANDER, WISCONSIN

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The Institute of Forest Genetics at Rhinelander, Wisconsin, was formally opened June 6, 1957, by the North Central (then Lake States) Forest Experiment Station, USDA Forest Service.

Originally, only the Forest Genetics Project was located at the Institute. Today, there are in addition: Pioneering Research and Radiobiological Studies of Northern Forest Communities. Information presented here will pertain only to recent findings of the Forest Genetics Project. The objectives of this project are fourfold:

1. Increase knowledge of the genetic constitution and the variation in populations of several forest tree species through basic research.
2. Develop guidelines that will enable tree breeders to plan realistic and efficient tree breeding programs.
3. Breed trees for local use in pilot size operations.
4. Develop efficient means for vegetative propagation of forest trees.

The genetics project has concentrated most of its research efforts on white spruce *(Picea glauca),* jack pine *(Pinus banksiana),* red pine *(Pinus resinosa),* and yellow birch *(Betula alleghaniensis).* In addition, a large number of other native and exotic species such as tamarack, balsam fir, northern white-cedar, Norway spruce, Serbian spruce, Engelmann spruce, and eastern white pine are being studied less intensively.

Variation of White Spruce Seed Sources

To date, the Institute has established provenance tests for white spruce, jack pine, red One, eastern white pine, tamarack, balsam fir, northern white-cedar, Engelmann spruce, Norway spruce, and yellow birch.

Results of a white spruce seed source test have been published recently by Nienstaedt (1969). White spruce *(Picea glauca* (Moench) Voss.) seed from 28 sources was collected over the entire range of the species from Alaska to Labrador and south to the limits of the species. They were field tested for 5 years in 14 field plantings in a region from 42° to 48° N. latitude from North Dakota to New Brunswick.

Survival exceeded 80 percent in all but three test locations. There were significant differences in seedling survival among seed sources. This was due largely to poor survival of seedlings from three Alaskan sources and one Yukon source. Seed from other sources showed only minor differences in seedling survival.

Seed-source differences in seedling height growth after 5 years were highly significant. The interaction between seed sources and plantation environment was also significant. A rank correlation analysis suggested that this significant genotype-environment interaction resulted mainly from the relative magnitude of response of seed from various sources to the changing environments and not to systematic changes in the ranking of seed sources.

An analysis suggested that the seed from the southeastern portion of the range of the species, including the Lake States, southern Ontario, and parts of Quebec and New England, were well adapted to all the test sites, and that some were growing better than the average for the plantations. Seedlings from sources on the Chippewa National Forest; McNally Lake, Quebec; and Ashley Mines and particularly Beachburg, Ontario, are among the 10 best in all 14 outplantings. Seedlings from some sources, particularly the northern ones, showed less than average adaptive stability and grew particularly poorly on the best sites. It is of interest to note that seedlings from a Douglas, Ontario, seed source still maintain a 22 percent superiority in height growth over those from seven other sources after 29 years in a plantation in northern Wisconsin. They are 17 percent taller than the local white spruce (King and Rudolf 1969).

The best individuals of the Beachburg source in four of the field plantings are being clonally propagated. Seed and seedlings from these grafts will be compared to seed and seedling progenies produced from white spruce seed orchards now being established in the Lake States area.

The data from this study suggest that individual tree selection, testing, and breeding of individuals from the southeastern portion of the species range may lead to improved new strains adapted to the test region used in this study. Selection in southeastern Ontario and adjacent areas in Quebec may yield particularly good genetic types.

Heritability Studies of White Spruce

Breeding for Delayed Budbreak

In the spring of 1958, 9 early-flushing and 16 late-flushing trees were selected in a white spruce plantation near Rhinelander, Wisconsin. These selections were cloned in 1962 and ultimately field planted in a replicated test in 1965.

Spring frost injury was recorded in the nursery in 1963 and again in the field in 1965. In 1963 an average of 80 percent of all buds on the early clones and 13 percent of the buds on the late clones were killed by frost. In 1965 the frost injury on these two types was 61 and 13 percent, respectively.

Flushing was recorded in the years without frost injury. On the average, the late clones were delayed 15 days in flushing compared to the early clones; the overall difference between the earliest and latest clones was 21 days.

Beginning in June 1968, terminal elongation of the clones was measured twice weekly until elongation ceased. Late clones completed 95 percent of their elongation 10 days later than the early clones. On the average, late-flushing parental trees were 42 percent taller than early-flushing parents at the end of the 1968 growing season. Total elongation of the late clones in 1968 exceeded that of the early clones by 25 percent. Since the average growth period was essentially the same for the early and late types (35.3 and 31.7 days, respectively), the superiority in total height elongation of the late clones resulted from a greater growth rate. The daily growth rate of the late clones was more than 50 percent greater than that of the early clones.

In 1967, early-flushing, late-flushing, and average individuals were crossed with 10 of the original and three additional selections (nine late-flushing and four early-flushing). The flushing and growth of the 27 progenies from the 9 late-flushing parents were studied in the greenhouse with day-night temperatures of 75°-65° F., and in growth rooms with temperatures of 65°-55° F., and 60°-50°F. The flushing differential was greatest in the greenhouse and flushing was delayed by lower temperatures. Heritability estimates (h2) varied with growth conditions and reached 0.705 for flushing in the greenhouse. The heritability of height growth, based upon a combined analysis of all 3 growth conditions, was h2 = 0.445.

In northern Wisconsin, selection and breeding of the two latest-flushing clones could increase frost avoidance by as much as 43 percent (Nienstaedt and King 1969) . The data suggest that simultaneous selection for late-flushing and rapid growth is possible in white spruce.

Half-Sib Studies

Since 1957 over 100 individual white spruce trees have been selected throughout the Lake States of Michigan, Minnesota, and Wisconsin. Open-pollinated seed from 32 of the selections was sown in the nursery in the fall of 1963; resulting seedlings were transplanted in the fall of 1965 and field planted in 1968. In the nursery, the 2-2 seedlings were measured for total height and current height growth. Two of the parents from Menominee County, Wisconsin, produced seedlings that made 63 percent more growth in 1967 than all of the 28 progenies included in the 1967 measurements.

The average annual height growth of the parents was strongly correlated with the current annual growth and total height of their respective progenies (r = .80 and .81, respectively) . When the progenies from the 11 parents of similar age (36 to 42-year-old) were compared, those from the 5 fastest growing parents were growing at a yearly rate (in 1967) nearly 21 percent better than the average for their age group. The data indicate the general feasibility of phenotypic selection in white spruce (Jeffers 1969) .

To date, 103 white spruce half-sib families have been field planted near Rhinelander, Wisconsin. Included in these plantings are 31 selections from the Ottawa Valley in Ontario, Canada. Some of the same families have also been outplanted in three additional areas including one southeast of Rhinelander (39 families), one in the eastern Upper Peninsula of Michigan (55 families), and one in Ontario, Canada (25 families).

Disease and Insect Resistance Breeding in Jack Pine

In a number of studies at the Institute, observations have been made on the differential susceptibility of jack pine to a variety of insects and diseases. One study includes trees from 30 sources in Michigan, Minnesota, and Wisconsin that have been in the field for 15 years in 17 locations throughout the Lake States. During the first 10 years the trees in these plantings showed significant seed-source-related differences In susceptibility to white pine weevil, red-headed pine sawfly, needle rust, jack pine needle-cast, bark beetles, eastern pine shoot-borer, and eastern gall rust]. (King and Nienstaedt 1965) .

The general approach in the study of pest resistance at the Institute is as follows:

Parents are selected in the seed source studies from sources that have demonstrated variation in pest incidence. This should insure genetic variation in the progenies. Occasionally, parents are seleted within natural stands, provided that pest incidence has been severe enough to suggest that undamaged trees did not escape infection by accident.

Selection of parents is followed by grafting to establish breeding arboreta.

The selected clones are crossed with several pollen testor parents to produce full-sib families.

Resulting full-lib progenies will be tested for pest resistance.

5. On the basis of the testing in step 4, a new cycle of selection will begin.

Six seed sources were selected in a Lake States jack pine seed source test on the Argonne Experimental Forest, Hiles, Wisconsin, on the basis of white pine weevil incidence — three low incidence and three high incidence sources. Four individual trees within each of the six sources were selected on the basis of good form and growth in the resistant sources and poor form and growth in the susceptible sources. All 24 individuals were clonally propagated in 1965 and outplanted near Rhinelander in 1968. Six additional parents, one from each of the six original sources, were selected for use as pollen parents. Many of the grafts flowered in the same year they were field planted, and controlled pollinations were started. The goal is to cross the six pollen parents with all of the 24 white pine weevil selections. These 144 full-sib families will be used to study the inheritance of variation in white pine weevil resistance.

Trees selected in the Institute's seed source studies, on the basis of eastern pine-shoot borer were grafted in 1966 and were field planted in 1968. Individual jack pines have also been selected in natural stands for resistance to jack pine budworm and pine tortoise scale. They have been grafted, and all the clones will be used in controlled pollinations as soon as they begin to bear female strobili in abundance.

Birch Genetics

A rangewide study of natural variation in yellow birch including 55 seed sources has been underway at the Institute since 1963. Ten test plantings have been established in the Lake States, New York, and New England, and three plantings in Canada. Second- and third-year height growth in the Rhinelander nursery varied greatly and was essentially random. Total height was not correlated with latitude, longitude, length of growing season, annual precipitation, average January temperature, or average July temperature. Diameter was only weakly correlated with latitude and length of growing season.

In contrast to its random variation in height and diameter, yellow birch exhibits a gradual north-south trend or clinal variation in growth initiation and cessation. In general, more northern sources begin growing earlier and cease growth earlier than more southern sources.

To determine whether the height growth variability noted in the seed source study might be due to individual tree variability within the sources, a study of 199 individual tree progenies representing 20 of the original 55 seed sources plus one additional source is now in progress. At the end of the first growing season there were highly significant differences in seedling height among the sources and among the individuals within each source (Clausen and Garrett 1969) .

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[1] *King, James P. Pest susceptibility variation in Lake States jack pine. (Manuscript in preparation.)*

Variation in DNA Content of Several Gymnosperms

A series of experiments has been conducted to determine the nuclear volumes and the amounts of DNA per cell in 13 coniferous species. The correlation between these two factors was determined, and the relationship between these factors and the distribution of the species was studies.

Slides of root meristems were prepared. The amount of DNA per cell was determined by Feulgen microspectrophotometry and biochemical analysis. The slides were also used to determine the nuclear volumes. Volumes were found to vary by a factor of 11.3 while DNA per cell varied among the 13 species by a mean value of 3.2. Red pine *(Pinus resinosa)* had the greatest nuclear volume and northern white-cedar the smallest. These two species also had the greatest and least amounts of DNA per cell.

The data suggest that nuclear size and DNA/cell may have an adaptive value. In the species studied, those with small nuclear volumes and less DNA/cell tend to have a wider distribution (Miksche 1967).

Intraspecific Variation of DNA per Cell in White Spruce and Jack Pine

The amount of DNA per cell was established chemically and cytophotometrically for 17 seed sources of *Picea glauca* and cytophotometrically for 11 sources of *Pinus banksiana.* DNA Feulgen absorption per cell varied from the lowest to the highest amount by factor of 1.6 and 1.5 for *P. glauca* and *P. banksiana,* respectively. Intraspecific variation of histone was similar to the observed DNA variation.

Intraspecific DNA also varied directly with intraspecific nuclear volumes; i.e., seedlings from sources with smaller nuclear volumes have less DNA per cell while seedlings from sources having larger nuclear volumes possess more DNA per cell.

A regression analysis between DNA per cell and latitude provided evidence that eastern and western population series of *P. glauca* exist in the seed sources studied. In the western series, DNA content per cell increased with increasing latitude. This relationship was not found for the eastern series. Two-year seedling height growth results also demonstrated that eastern sources are different from western sources. Seedling heights in the western provenances varied inversely with DNA content; i.e., seed from sources with small amounts of DNA per cell displayed greater growth. Seedlings from eastern sources, on the other hand, did not display the inverse relationship between DNA amount and 2-year growth (Miksche 1968).

Tree Improvement Opportunities in the North Central States Related to Economic Trends — A Problem Analysis

To determine the orientation and emphasis that tree improvement programs in the north-central States should take, a problem analysis exploring the economic needs for forest products has been developed by David H. Dawson of the Institute of Forest Genetics, and John A. Pitcher, Region 9, USDA Forest Service. The analysis indicates that most emphasis on tree improvement programs should be placed on *Populus* spp., white spruce, black spruce, *Betula* spp., *Larix* spp., shortleaf pine, jack pine, white pine, and black walnut. The analysis will be published soon by the North Central Forest Experiment Station, St. Paul, Minnesota (Dawson and Pitcher 1970).

Radiation Research

Until recently the radiation research at the Institute was conducted within the Forest Genetics Project. A significant portion of the research was devoted to the study of the relative radiosensitivity of various species of forest tree seed and seedlings. This type of research is being expanded to include a comprehensive study of the response of natural forest communities to gamma radiation. All radiation research is now under a new project entitled "Radiobiological Studies of Northern Forest Communities." Studies ranging from cell biology and genetics through general forest ecology will be conducted within the project. The program will include several seasonal exposures as well as a single long-term study of chronic irradiation. Support for this project will be provided by the Atomic Energy Commission as well as the USDA Forest Service. A wide variety of research in the program will be undertaken by University cooperators.

Leader of the new project is Dr. Thomas D. Rudolph, Principal Plant Geneticist, who has been on the Institute staff for more than 10 years.

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