STRATEGY FOR THE GENETIC IMPROVEMENT OF NORWAY SPRUCE IN THE NORTHEAST

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Abstract. — A multigeneration strategy for the genetic improvement of Norway spruce for northeastern North America is presented. The strategy is based on available biological and genetic information and will be modified as new information or techniques become available.

A breeding program, coupled with a production program utilizing vegetative propagation of superior half- and full-sib families is proposed. Clonal propagation of proven genotypes is also considered. The benefits of incorporating accelerated breeding and testing methods into the program are discussed.

Additional keywords: Breeding strategy, Picea abies, genetic improvement, accelerated breeding, accelerated testing, vegetative propagation.

Norway spruce, Picea abies (L.) Karst. has been the most widely planted non-native tree species in eastern North America. Extensive planting of this species began in the mid 1800s and by 1936 over 48 000 ha (120,000 acres) of plantation existed in New England (Hosley 1936). Norway spruce was never extensively planted in eastern Canada. The oldest forest planting recorded for eastern Canada was carried out about 1918 (Hughes and Loucks 1962).

Norway spruce is currently not an important reforestation species in either the northeastern United States or eastern Canada. Although detailed information is lacking, annual planting of Norway spruce in the northeast probably does not exceed 6 million seedlings annually.

Growth of Norway spruce, planted on suitable fresh, rich sites in the northeast is generally recognized to be superior to that of native spruce species growing on comparable sites (Hosley 1936, Hawley and Lutz 1943, MacArthur 1964, Hughes and Loucks 1962). Average mean annual increment (MAI) of 57 plantations in New England, the oldest of which was 70 years, was reported to be 10.7 m^3/ha and the greatest MAI was about 17 m^3/ha (Hosley 1936). MacArthur (1964) reported that good, unmanaged plantations of Norway spruce growing on suitable sites in the Great Lakes - St. Lawrence Forest Region of Quebec had a MAI of 6-7 m^3/ha at 40 years. The most productive plantation in New Brunswick produced 15 m^3/ha per year at age 50 years (Hughes and Loucks 1962) while production of 8.8 m^3/ha per year was reported for good plantations in Nova Scotia (Bailey 1973).

Provenance trials of Norway spruce in the Maritimes Region of Canada have identified mid-elevation (700 m) provenances in the Sudeten and Carpathian

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Mountains of Poland as being best for all except the most rigorous parts of the Region (Fowler and Coles 1979). Provenances from east of the Baltic Sea in Lithuania, Latvia, and western Russia are recommended for the New Brunswick Highlands. Considerably less information is available on "best" provenances to use in New England. Holst (1963) in reviewing the results of the 1930 IUFRO provenance trials suggested that the choice of seed source for use on good spruce sites in New England was not critical. He suggested that any fast-growing, moderately hardy provenance from Romania, Czechoslovakia, Poland, or White Russia would produce more wood than native red spruce P. rubens Sarg. or white spruce P. glauca (Moench) Voss. This generally supports the recommendations of Ashman (1958) for Maine and Baldwin (1953) for the northeastern United States. Intuitively, I suggest that sources from east of the Baltic Sea and White Russia will do best in northern Maine, Polish sources best in coastal and southern Maine, New Hampshire, and Vermont, and Czechoslovakian and Romanian Sources from the Carpathian Mountains will probably do well in southern New England.

Renewed interest in Norway spruce as a reforestation species, coupled with the difficulty in obtaining commercial quantities of seed of known good provenance, emphasize the need to develop and implement appropriate improvement strategies and programs. In the following I will present a strategy for the genetic improvement of Norway spruce in eastern Canada. A similar strategy should be appropriate for this species in northern New England.

It is assumed that progress in an improvement program with a non-native species will be most effective if the base breeding population is from known, well-adapted provenances, (e.g., juvenile-mature correlations are expected to be higher than with unproven materials). Based largely on the results of provenance tests (Fowler and Coles 1979), two breeding zones are recommended for Norway spruce in the Maritimes. All of the Maritimes Region except northern New Brunswick and the Cape Breton Hills and Highlands is considered the southern zone, while the New Brunswick Highlands (Seed zone 1 of Fowler and MacGillivray 1967) is the northern zone. The improvement strategy for each of these zones is essentially the same, except that trees of eastern Baltic and White Russian provenances will be used for the northern zone and trees from the Carpathian and Sudeten Mountains of Poland will be used for the southern zone.

Norway spruce has proven to be a rather recalcitrant species in respect to flowering and seed production. In nature, the species does not produce substantial cone crops until age 20-30 years or later. The species is easy to graft and grafts of mature trees will produce reasonable, although highly periodic, crops within 5 to 10 years of grafting. Flowering on grafts of younger trees (<20 years) is less reliable. The most widely accepted method of mass producing improved seeds is via clonal seed orchards. However, young Norway spruce can be mass propagated with relative ease from stem cuttings. In fact, vegetative propagation of dormant cuttings is used on a large scale in several improvement programs in Europe (Kleinschmidt and Schmidt 1977, Lepisto 1977 and Benzer 1981). We have found that young Norway spruce seedlings, especially during the neoform (indeterminate) growth phase, are amenable to mass vegetative propagation using techniques similar to those described by Rauter (1971) and Armson et al. (1980). Five hundred, or more, plantable ramets per clone can be produced in one year from neoform seedlings compared

with <20 from 2-year-old seedlings that have entered their preformed growth phase.

BREEDING STRATEGY

A tree improvement program, coupled with a production program based on vegetative propagation of half- and full-sib families obtained from controlled pollinations is proposed for this species. A flowchart adapted from Fowler (1986) is presented in Fig. 1.

For the southern breeding zone, one hundred plus trees of known good provenance have been selected (1). These have been grafted and are currently growing in a breeding garden (2). Additional selections of good provenance will be available from the Petawawa National Forestry Institute and other cooperators. When flowering begins the 100 clones will be divided into two groups and group 1 clones will be crossed with a group 2 pollen mix and vice versa (3). The resulting progenies will be planted in progeny tests, (4) and extra seed used to produce juvenile cuttings for operational vegetative propagation (5). The genetic quality of the resulting propagules will be equivalent to seedlings produced in an unrogued clonal seed orchard. The crosses can be repeated annually, or as required, to provide a continuous supply of juvenile materials. Information from the progeny tests will be used to identify the 40 clones with the best general combining ability (GCA) and will form the new breeding population (6). The 10 best GCA clones will be intercrossed (7) with a pollen mix of the other 9 best clones to provide cuttings for mass vegetative propagation (8). These crosses will be repeated as required. The genetic quality of the resulting propagules should be equivalent to seedlings from a 100-clone clonal orchard after 90% roguing and the elimination of self pollination and pollen contamination.

The 40 best GCA clones in the breeding garden will be divided into 8, 5-clone sets. Each clone will be crossed with five clones from another set in a disconnected half-diallel design (9) (Fig. 2) and the resulting progenies tested (10). Information from the progeny tests will be used to identify pairs of trees in the breeding garden with high specific combining ability (SCA) (11). These crosses can be repeated (12) to provide cuttings for mass vegetative propagation (13). Progeny test data will also be used to identify families in which selections will be made for the next breeding cycle. The 40 phenotypically best trees, in families with high GCA parents, 5 from each of the 8 sets of crosses will be selected (14) to form the next breeding population (15). Only one tree will be selected in any family. In this breeding cycle the 5 trees from set A x B will be crossed with 5 trees from set C x D, and B x C will be crossed with D x E, etc. (16) (Fig. 3). As some trees within each set will be related, each tree will also be polycrossed (17) to provide reliable GCA information. Equal volumes of pollen from each of 20 clones that do not quality in the best 40 will be used for the polycrosses. The resulting progenies will be tested (18).

As in the preceding breeding cycle, the progeny tests will be evaluated and the pairs of trees with high SCA will be identified (19). These crosses will be repeated (20) to provide juvenile material for mass vegetative propagation (21). The 40 best trees in families with high GCA parents, 5 from each of the 8 sets of crosses, will be selected (22) to form the next breeding

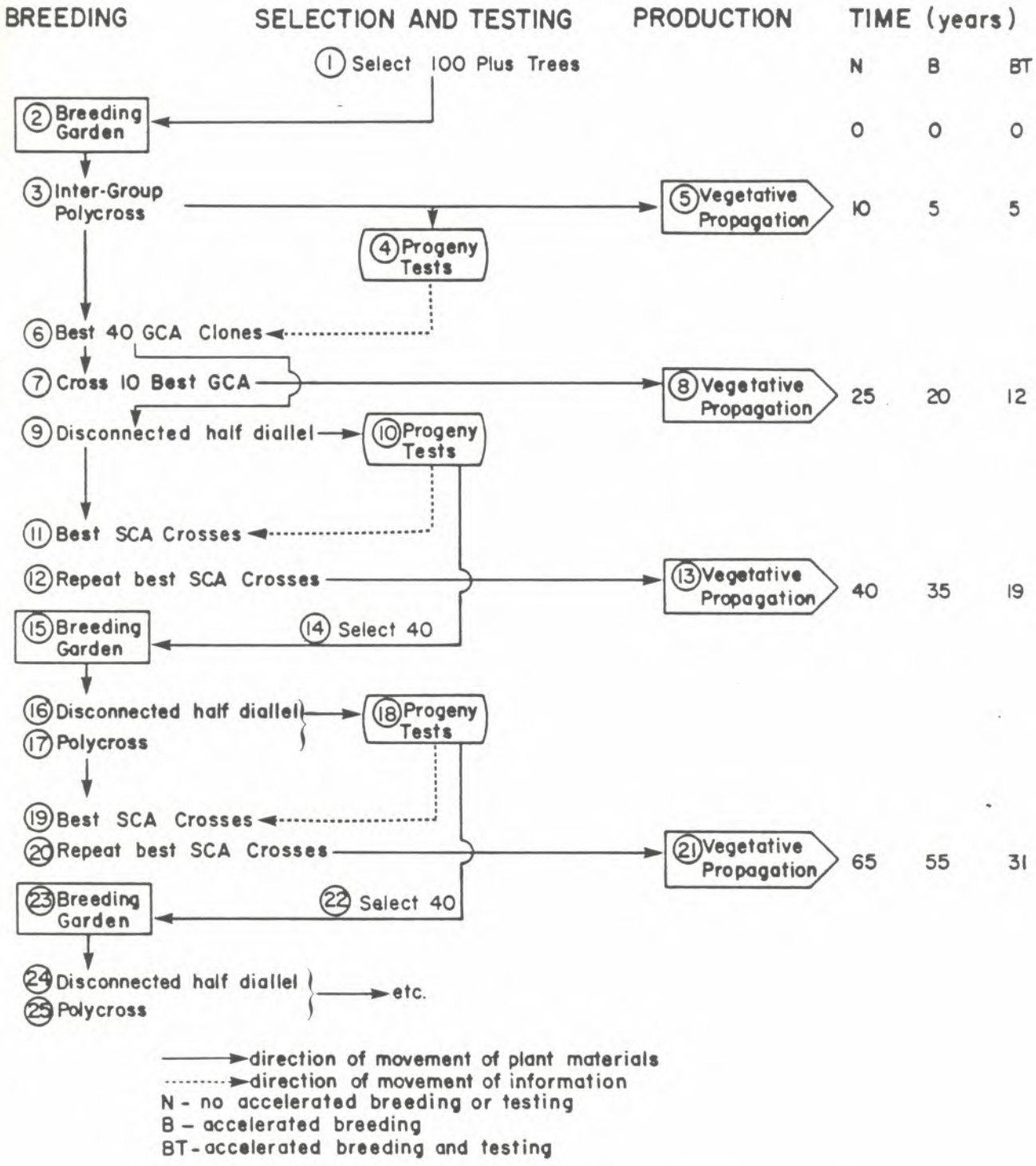

Fig. 1. Flow chart for the Norway spruce tree improvement program.

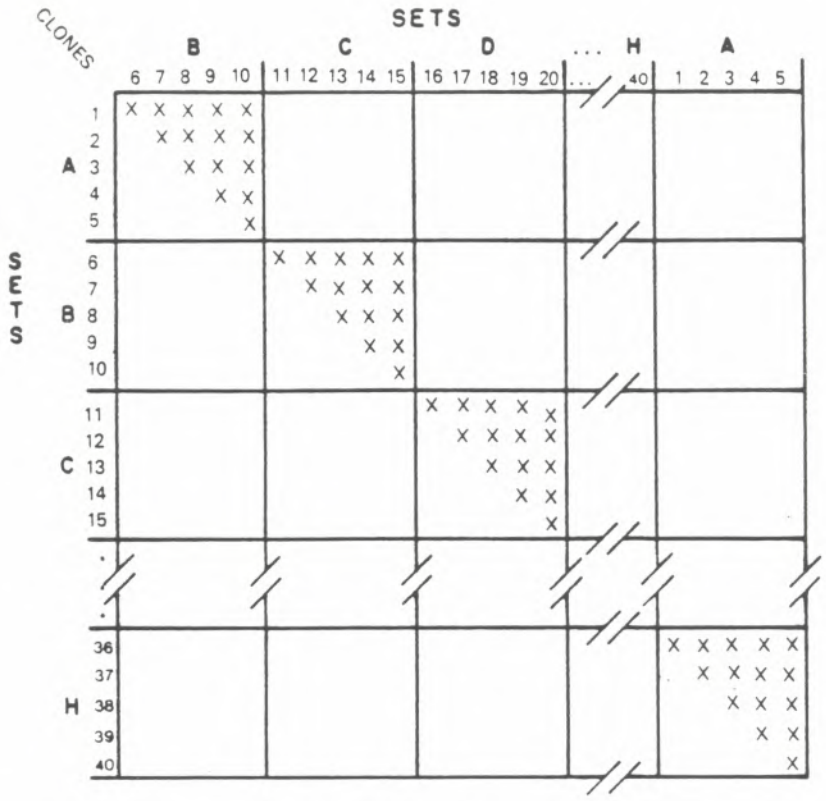

Fig. 2. Design for first 5-tree disconnected half-diallel.

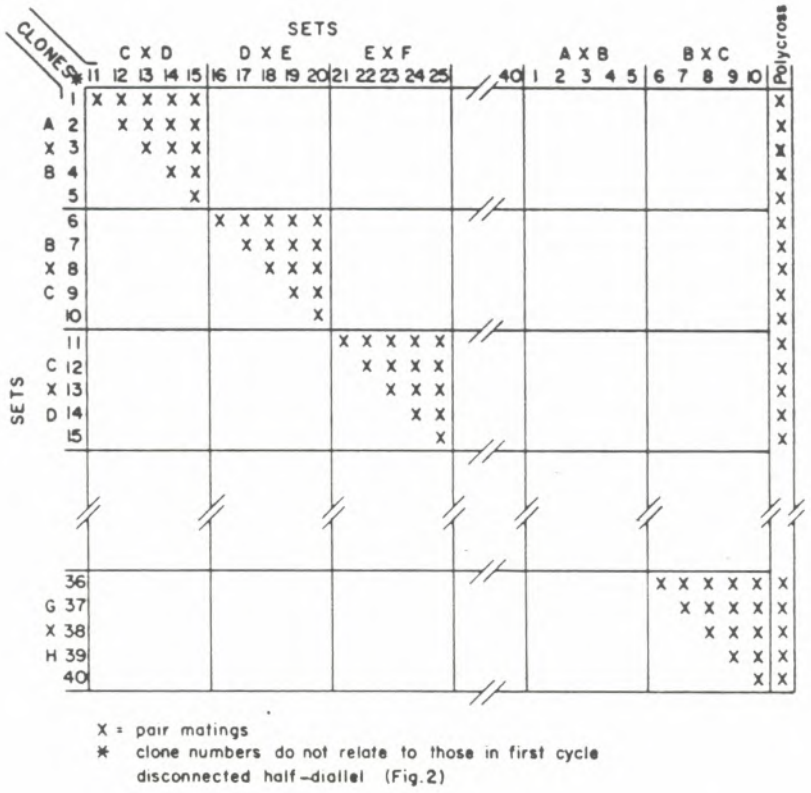

Fig. 3. Design for second 5-tree disconnected half-diallel.

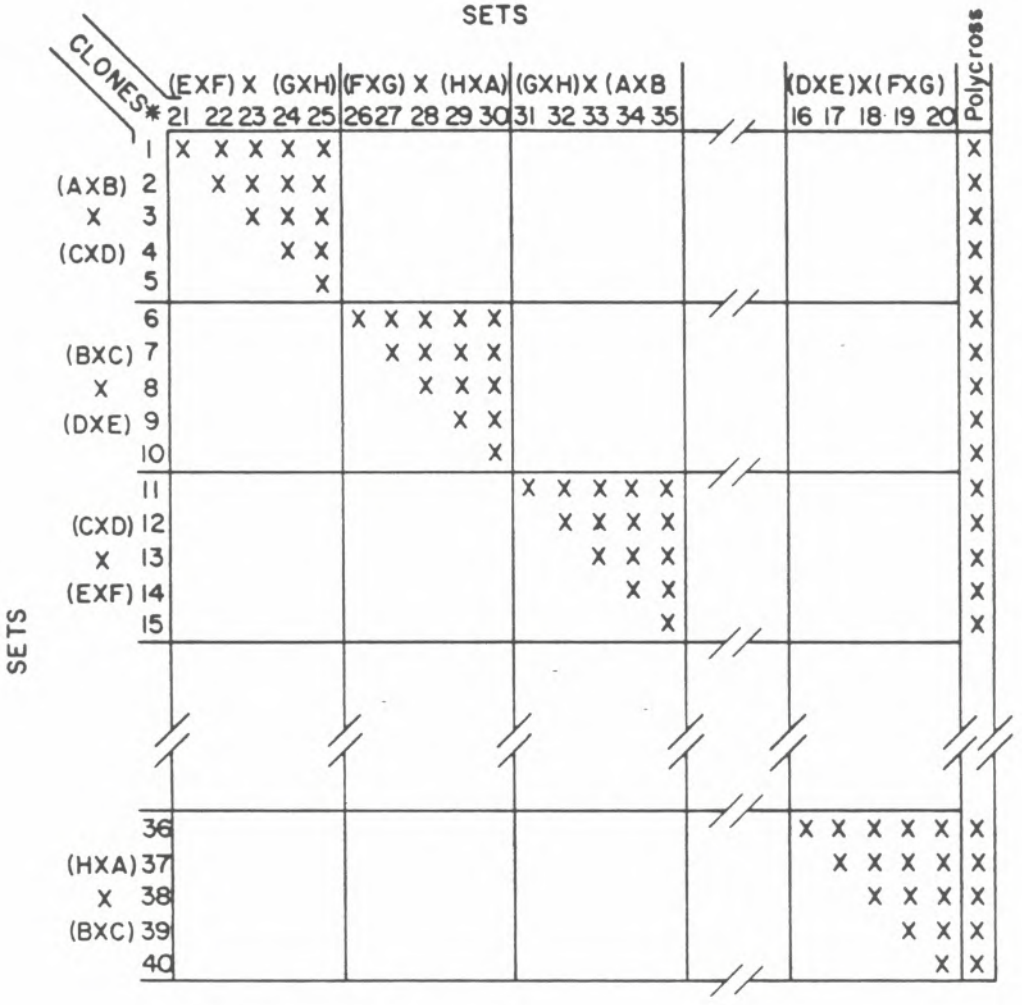

Fig. 4. Design for third 5-tree disconnected half-diallel.

population (23). No more than 1 tree will be selected in any family. As in the preceding breeding cycle the 5 clones from each set of crosses will be crossed with 5 clones from a completely unrelated set of crosses, e.g., set (AxB) x (CxD) crossed with (ExF) x (GxH) (24) (Fig. 4). Each of the 40 clones will also be polycrossed, using the same mix as above (17) to provide reliable data on GCA (25). Testing, evaluation, and selection procedures will be as in the preceding breeding cycle.

In the next breeding cycle, inbreeding is unavoidable as most of the selections will be related. It is essential that pedigree records be maintained throughout the program so that the level of inbreeding can be controlled. It may be possible to effectively utilize inbreeding in subsequent breeding efforts.

The limited number of selections and the low selection intensity upon which this program is based, limits the level of gain attainable. It will undoubtedly be desirable to bring new selections into the program as they become available. If current efforts to obtain Norway spruce seed of known good provenance are successful, a reliable source of new selections will be assured for the future. These new selections will be polycrossed using a common pollen mix and those with high GCA added to the program either as new breeding sets or replacements in poor breeding sets.

ACCELERATED BREEDING AND TESTING

Using current progeny testing and breeding techniques, it is assumed that 15 years will be required for progeny testing and an additional 10 years will be needed before selected clones flower in a breeding garden and crosses can be made for the next generation of testing and selection, i.e., the breeding/testing cycle 25 years. The genetic gains and approximate time when the gains are anticipated are presented in Fig. 5. This figure assumes that without accelerated breeding or testing, gains from the first cycle of selection and vegetative propagation will be 10%, i.e., equivalent to a clonal

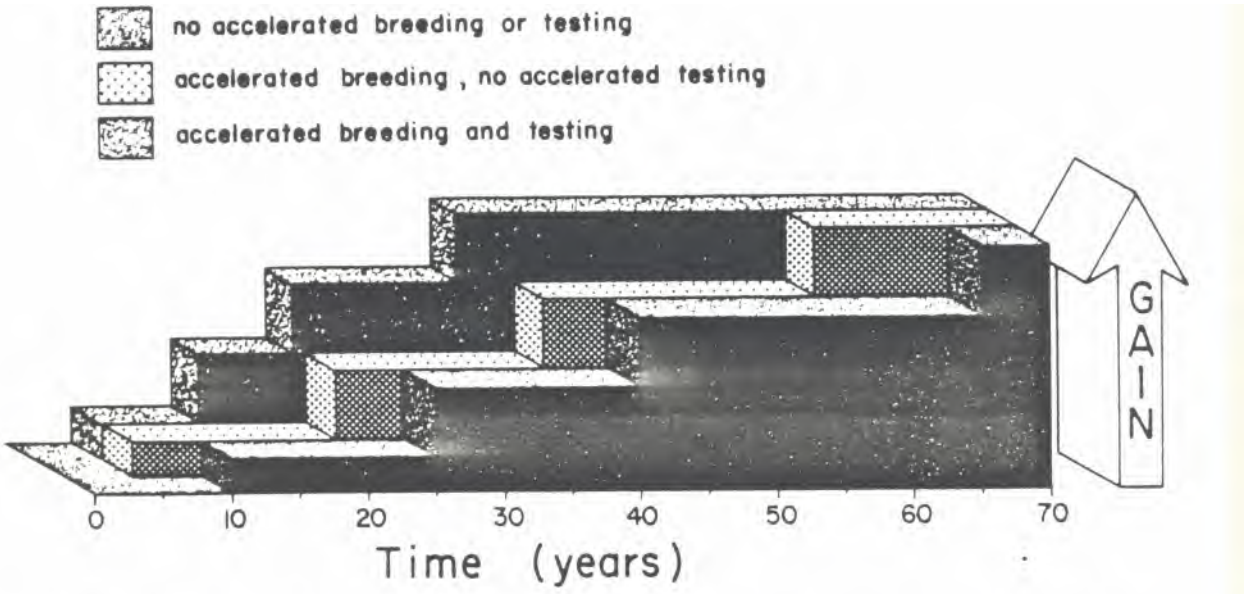

Fig. 5. Diagram showing the magnitude of genetic gains to be attained in a Norway spruce breeding program with and without accelerated breeding and accelerated testing.

seed orchard with no selfing or outside pollen contamination. The second set of vegetative propagules are expected to exhibit an additional gain of 20%, i.e., equivalent to a clonal orchard after 90% roguing, no selfing, and no contamination. It is also assumed that vegetative propagules from high specific combiners will have gains of an additional 20% per generation. The first gain of 10% is expected at year 10, a second gain of 20% at year 25, a third gain of 20% at year 40, and additional gains at 25-year intervals.

It should be possible to reduce the time it takes Norway spruce grafts to flower from 10 years to 5 years using accelerated breeding techniques such as those described by Luukkanen (1980), Luukkanen and Johnsson (1980) Cecich (1985) and Pharis et al. (1986). If successful the first gain of 10% would be anticipated at year 5, the second gain of 20% at year 20, a third gain of 20% at year 35, and additional gains at 20-year intervals (Fig. 5).

Accelerated testing offers even more opportunities to reduce the breeding cycle and speed up the rate at which genetic gains can be made. If the testing period could be reduced from 15 to 7 years, without adversely affecting juvenile-mature correlations, the first gain of 10% could be expected at year 10, a second gain of 20% at year 17, a third gain of 20% at year 24, and additional gains at 17-year intervals. If both accelerated breeding and accelerated testing techniques could be perfected and employed (Fig. 5), corresponding gains could be anticipated at year 5 (10%), year 12 (20%), year 19 (20%) and additional gains at 12-year intervals.

CLONAL TESTING AND PROPAGATION

The strategy described in the preceding sections deals with the capture and utilization of genetic variation at the family level. It is essentially the same approach that is used in a clonal orchard program except that vegetative propagation replaces the clonal orchard for mass production, and SCA as well as GCA can be utilized. Also, an opportunity exists to capture and utilize genetic variation at the within family, or clonal level.

If mature conifers could be rejuvenated, as some angiosperms can, clonal propagation and testing would be a relatively straight-forward procedure. Unfortunately they cannot, and it will likely be several years before reliable techniques for conifer rejuvenation are perfected. In the absence of techniques for rejuvenating conifers, it is essential that (1) some ramets of each clone be maintained in a juvenile condition, at least until the clones have been adequately tested, and (2) early test procedures be developed to identify superior clones.

Currently, hedging is used to retain selected clones in a juvenile or near-juvenile condition until the clones can be field tested. Unfortunately, the cuttings produced in hedges have already entered their preformed growth phase. An alternative to hedging would be to keep selected seedlings or their propagules in the neoform phase by nursing them in a long-day, good growth environment. Judicious pruning and serial propagation (St. Clair et al. 1985) could keep the seedlings to a manageable size. A Norway spruce seedling could probably be kept in a neoform growth phase for several years, hopefully long enough to complete the clonal tests.

Recent advances in the use of tissue culture for the long-term storage of clonal materials (Aitken-Christie and Singh, in press) may provide another alternative to hedging and retain clones in a neoform growth phase. In this method, tissues from first-year seedlings are cultured and placed in cold storage until clonal tests have been completed (5-7 years). They can then be used as a source of material for mass production of identified superior clones. We are currently exploring the use of this technique with Larix and if successful, plan to expand the work to include Picea.

Even with the best techniques, it will not be feasible to clonally test large numbers of clones. It is important that all clones selected for testing have a high probability of being superior. Conversely, it is important that seedlings that have a low probability of being superior be culled from the program before the cloning stage. Seedlings in families from known high GCA parents and eventually those from parents with known high SCA have the highest probability of being superior. Clonal selection should be restricted to within such high GCA - SCA families.

It is difficult to over emphasize the need to develop reliable early testing procedures. Such procedures would make it possible to reduce the breeding cycle substantially. In the suggested clonal improvement program, the existence of such testing is crucial.

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