STRATEGIES FOR THE GENETIC IMPROVEMENT OF IMPORTANT TREE SPECIES IN THE MARITIMES

by

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Fredericton, New Brunswick

Information Report M-X-156

Government of Canada

1986

Catalogue no. Fo46-19/156E
ISBN 0-662-14573-9
ISSN 0704-769X

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ABSTRACT

Multigeneration breeding strategies for the genetic improvement of tree species that are important for reforestation in the Maritimes Region of Canada are presented. The species include: black spruce (*Picea mariana*), white spruce (*P. glauca*), red spruce (*P. rubens*), Norway spruce (*P. abies*), jack pine (*Pinus banksiana*) and tamarack (*Larix laricina*). The strategies presented here are based on available biological and genetic information and can be modified or changed as more information or improved techniques become available.

RESUME

Les stratégies de la reproduction de génération multiple en vue de l'amélioration génétique des essences d'arbres sont d'importance potentielle pour le reboisement dans les Maritimes du Canada. Ces essences comprennent: l'épinette noire (*Picea mariana*), l'épinette blanche (*Picea glauca*), l'épinette rouge (*Picea rubens*), l'épinette de Norvège (*Picea abies*), le pin gris (*Pinus banksiana*) et le mélèze (*Larix laricina*). Les stratégies sont basées sur les renseignements biologiques et génétiques disponibles et peuvent être modifiées, ou changées à mesure que surviennent nouveaux renseignements ou techniques.

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INTRODUCTION

"There are two aspects to any successful tree improvement program. The first relates to obtaining an immediate gain of desired products as rapidly and as efficiently as possible. ... The second aspect ... is concerned with the long-term need to provide the broad genetic base that is essential for continued progress over many generations" (Zobel and Talbert 1984).

Reforestation by planting has increased dramatically in the Maritimes Region over the last two decades. In 1967 less than 12 million trees were planted annually, by 1977 this number had risen to almost 30 million (Fowler 1979) and currently over 90 million trees are planted. The numbers of trees planted by species in 1985 are summarized in Table 1.

Concurrent with the increase in reforestation efforts, there has been a dramatic increase in tree improvement activities in the Region. With the exception of red pine (Pinus resinosa, Ait.) and balsam fir (Abies balsamea (L.) Mill.), all the species important in the reforestation programs are now the subject of tree improvement efforts (Coles 1979; Mullin 1985). To date, attention in the breeding programs has centered on first generation improvement with considerably less effort on long-term planning. Conventional selection, testing, and mass production techniques have been adopted for the different species based on currently available information on the genetic and biological characteristics of each species.

Effective development of a strategy for genetic improvement of a species requires detailed information on the amount and pattern of genetic variation, inheritance, correlations among traits, and mating system. Unfortunately, tree breeders are faced with the problem of initiating selection and breeding programs before much of this information is available. Initially, breeding strategies are often based on intuition and experience with other species as much as on scientific fact. As new information becomes available from the program and

Table 1. Seedling production in the Maritimes Region, 1985. Compiled by R.D. Hallett and L. Lanteigne, Canadian Forestry Service - Maritimes

	Seedlings production ('000)			
	Province			
Species	P.E.I.	N.S.	N.B.	Region
Black spruce	348	17 327	33 842	51 521
White spruce	442	5 640	3 255	9 337
Red spruce	---	4 157	237	4 394
Norway spruce	---	1 797	575	2 372
Jack pine	---	620	17 105	17 725
Red pine	279	2 968	1 665	4 912
White pine	62	200	2	264
Larch species	179	243	309	731
Balsam fir	210	930	850	1 990
Other	84	129	160	373
Total	1 604	34 011	58 004	93 619

related research it may be desirable to modify or change the breeding strategy. Therefore, breeding strategies must be flexible to accommodate anticipated changes.

For any long-term tree improvement program, i.e., a program that is designed to span several generations, one can identify different groups of trees. These include the trees in the natural forest, trees in plantations, trees in seed orchards, trees in family and progeny tests, and trees in the selection plantations and breeding gardens. These groups of trees can be, and often are, genetically different, and they generally serve distinctly different functions in a tree improvement program.

Natural forests are the source of all the genetic variability upon which tree improvement relies. Plantations represent a sample of the natural forest and can also be an important source of genetic variability, especially for non-native species. The trees in the seed orchards represent a select sample of the genetic variation. The family tests and progeny tests are composed of open-pollinated and control-pollinated offspring, respectively, of selected trees and can be used to evaluate these trees. The trees used for second and subsequent generation breeding are genetically diverse populations (or groups) used to provide material for future generations of selection and breeding. Trees in the selection plantations are full-sib progenies derived from control-pollinations within the breeding population. Selections made in these plantations are used to form the next breeding population. Controlled pollination and pedigree control are an essential aspect of the breeding procedures.

Most forest tree species are outbreeders. Inbreeding in many species has been shown to result in reduced numbers of viable seed and reduced growth. It is widely accepted that inbreeding is to be avoided, or at least stringently controlled in the mass production phase of a breeding program, i.e., seed orchards. Inbreeding would also confound progeny tests used to evaluate parent trees. Inbreeding in the production and progeny test populations can be avoided. On the other hand, inbreeding in the breeding population is unavoidable after only a few generations. Fortunately, a high level of inbreeding can be tolerated, and even may be used to advantage in the breeding population (van Buijtenen and Lowe 1979).

It is the intent of this paper to set out in a formal way the long-term breeding strategies thought to be most appropriate for the different species used for reforestation in the Maritimes Region. These strategies are based on current biological and genetic information on the species, and while more reliable than earlier information, it is still incomplete. As more information becomes available and as techniques improve, it will undoubtedly be desirable to modify or even dramatically change the strategies.

GENERAL STRATEGY

The Maritimes Region has been divided into **breeding zones.** Within each breeding zone, the breeding population will be divided into **breeding groups.** For those species in which first generation improvement is through seedling seed orchards, information from open-pollinated family tests, will be used to rogue the orchards and to identify "best" families in which clonal selections will be made for second generation breeding. Subsequent improvement with these species, as with the other species, will be through selection, testing, and mass production in clonal orchards. A complementary mating design consisting of **polycrosses** and **single pair matings** or **partial diallel matings** will be used for all species.

Representative unimproved populations, **standards,** will be used to assess the actual genetic gains attained throughout the life of the program. Provisions are also made for the

introduction of new selections into the program as well as **gene conservation** and changes in selection criteria, e.g., **wood quality**.

It is recognized that the breeding strategies, as presented, are rather rigid and somewhat optimistic in terms of generation times and consolidation of entries. In reality, the strategies represent a goal to strive for, recognizing that one will have to contend with serious economic and biological constraints in their implementation.

Breeding zones

The Maritimes Region has been divided into eco-geographic seed zones based on forest classification, climate, and phenology (Fowler and MacGillivray 1967). These seed zones are used to control the movement of tree seeds and seedlings within the region. Current information from provenance, stand, and family tests suggests that in most instances breeding zones can be considerably larger than seed zones. New Brunswick and Nova Scotia have separate but integrated breeding programs. New Brunswick is treated as a single breeding zone for all species except Norway spruce (*Picea abies* (L.) Karst). Nova Scotia, except for the Cape Breton Highlands, is also a single breeding zone. Prince Edward Island, with its smaller reforestation program, is cooperating with the other programs to develop improved materials specifically for Prince Edward Island. The breeding zones and seed zones are illustrated in Figure 1. Supporting information on the rationale for the eco-geographic seed zones is provided by Fowler and MacGillivray (1967).

If, in the future, it becomes evident that a further subdivision of the breeding zones is desirable the strategies can be modified. For example, it is not necessary to represent all breeding groups or to use the same clonal selections in orchards designed to service different parts of a breeding zone. Although most of the proposed strategies indicate clonal orchards composed of 20 or more clones, the actual minimum number is 9, if ramets of the same clone are to be separated by two unrelated clones (Langner and Stern 1955).

Breeding groups

The breeding population for each breeding zone will be divided into breeding groups as suggested by van Buijtenen and Lowe (1979). For all species, except Norway spruce and the alternate strategy for tamarack (*Larix laricina* (Du Roi) K. Koch), the strategies call for the establishment of 20, 20-tree breeding groups. For each breeding zone, selected trees will be assigned to breeding groups with the constraints 1) that all related trees are assigned to the same breeding group, and 2) that all trees within a group come from the same general area (seed zone). In this way, inbreeding will be confined to within breeding groups and can be eliminated from the production phase of the program. If it is necessary in the future to subdivide the breeding zones it will be possible to segregate or reassemble the breeding groups to service the new zones.

Polycross

A polycross test is one in which the performance of progenies derived from different seed parents (selected trees) but pollinated with a common mix of pollens is compared. The polycross test is used to assess general combining ability (GCA) of selected trees and, in turn, to identify full-sib families having high GCA parents. A 20-tree pollen mix consisting of equal volumes of pollen from each of 20 or more trees will be used for all polycrosses. This pollen mix should 1) be from trees unrelated to the trees being tested, 2) be repeatable through subsequent generations, 3) be similar, at least in respect to geographic origin, to pollen expected to be produced in the orchard, and 4) be in adequate supply to service all selected trees. Wherever possible, 20 clones that do not quite meet the criteria for second generation selection

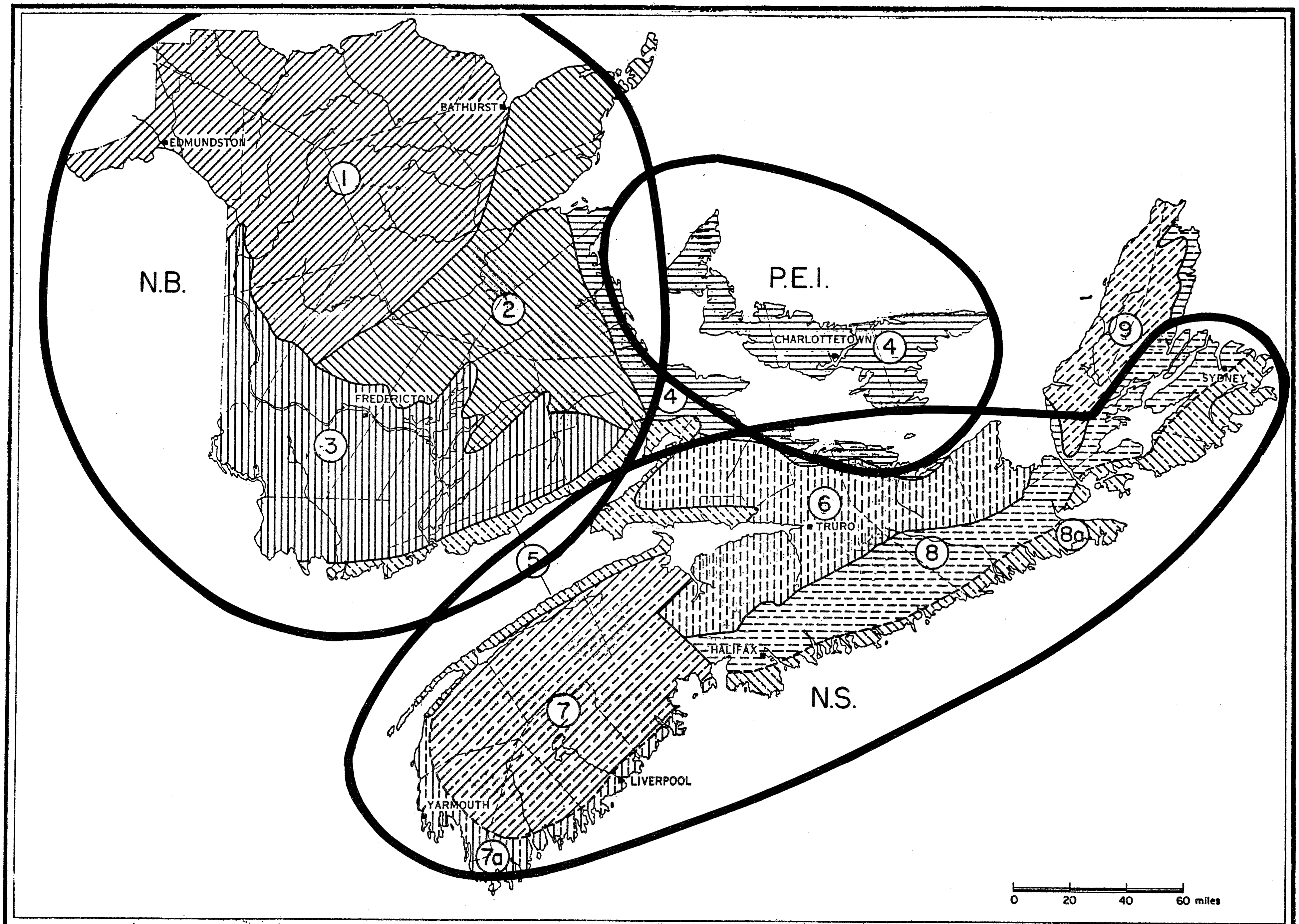

Fig. 1. Breeding zones ▬ and seed zones ◯ of the Maritimes Provinces.

will be identified and propagated as a pollen source for the polycrosses. Constraints 3 and 4 create problems in the first breeding cycle of some species, e.g. black spruce (Picea mariana (Mill.) B.S.P.), where pollen production will not be adequate (constraint 4) it will be necessary to use some less representative pollen.

The polycross progeny tests will be planted in small (4-tree) plots in replicated tests at five or six locations distributed throughout the area where the species is considered important for reforestation.

Single pair mating

In a single pair mating design, each clone is artifically crossed with one other clone to produce full-sib progenies. Single pair mating will be made between clones originating from the same seed zone to produce materials 1) from which selections will be made for the next breeding population, and 2) for direct use in seed orchards, i.e., the best individuals in progenies from parents with the best average GCA. This design maximizes the number of unrelated progenies created and minimizes the cost. It has the disadvantage that genes from some high GCA parents may not be included in the resulting breeding population. This disadvantage can, in part, be overcome if the strategy allows for the inclusion of exceptional GCA parents in the next breeding population.

Unlike the progeny tests from the polycross, the full-sib families will be planted out in 49 or 100 tree plots in two locations to increase the efficiency of within-family selection. These selection plantations will be established on good uniform sites to increase the efficiency of within-family selection. The reason for planting in two locations is to insure against unknown contingencies such as damage by fire or insects.

Partial diallel mating

In a partial diallel mating design, each clone is crossed with two or more other clones to produce full-sib progenies. The breeding strategies for black, white (Picea glauca (Moench) Voss), and red spruces (P. rubens Sarg.), jack pine (Pinus banksiana Lamb.), and tamarack call for the use of partial diallel matings once the breeding population has been divided into breeding groups. The partial diallel matings will be used to produce materials 1) from which selections will be made for the next breeding population, and 2) for direct use in seed orchards. In this mating scheme (Fig. 2) each clone will be crossed with two unrelated clones, each from a different family, for a total of 20 crosses per breeding group. Where it is not possible to make a cross in the specified direction because male or female flower production is inadequate, the reciprocal cross will be substituted. As with the single pair matings the full-sib families will be planted out in 49 or 100 tree plots in one or two locations.

A disconnected half diallel (factorial) mating design will be used for the improvement of Norway spruce and its use is proposed in an alternative strategy for the improvement of tamarack. In this design the breeding population is divided into five-clone sets and each clone crossed once with six other clones in two other sets (Fig. 3). The full-sib families will be planted out in progeny tests in four or five representative locations. Information from the progeny tests will be used to identify pairs of clones with high specific combining ability whose progenies can provide material for mass vegetative propagation, and to identify clones with high GCA parents for the next breeding population.

Standards

Standard populations of trees, representative of those currently used for reforestation, are required to assess the actual gains attained in subsequent generations. For some species such as black spruce and jack pine, stands have already been reserved for long-term seed production and conservation of genetic

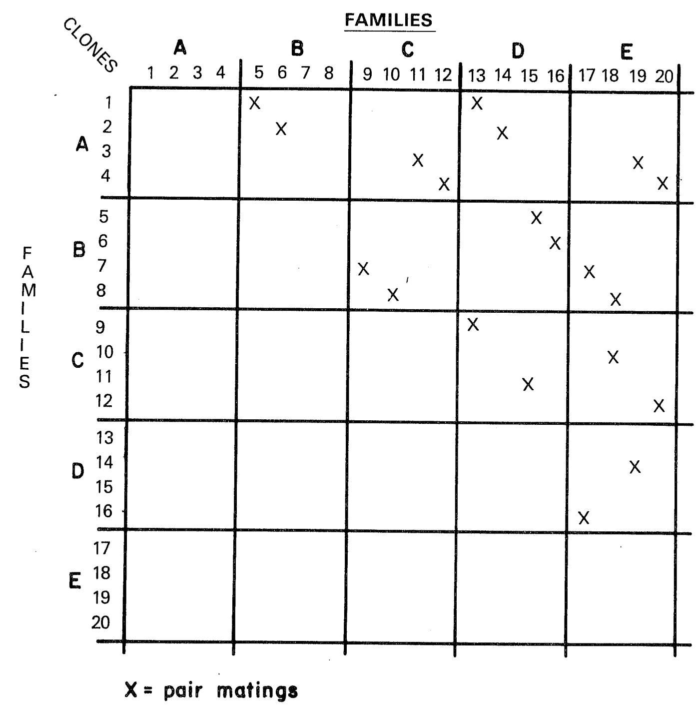

Fig. 2. Design for partial diallel matings in each breeding group.

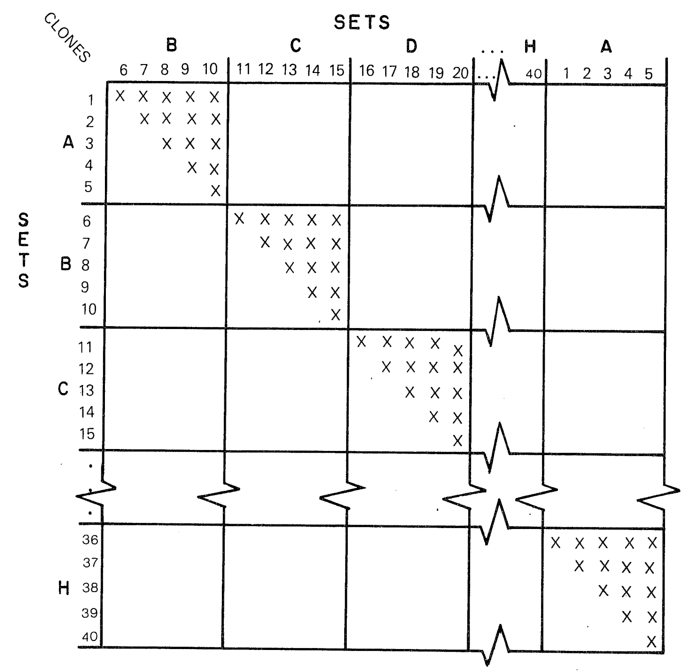

Fig. 3. Design for first 5-tree disconnected half-diallel.

resources. General collections from two or three of these stands will provide adequate standards. For other species, it will be necessary to make special provisions. Several options exist 1) long-term storage of seed from representative general collections, 2) use of seeds from stands in National Parks or other genetic reserves, and 3) identification and reservation of additional stands.

Wood quality

In the current programs, emphasis has been placed on improving growth and stem quality. It is recognized that a substantial improvement could also be attained in wood quality, especially wood density. Unfortunately, more information is required on juvenile-mature correlations to determine if selection for wood characteristics can be made at the time family and progeny tests are evaluated. Information on wood specific gravity is available for most trees involved in the clonal orchard programs, e.g., white spruce, red spruce, and tamarack.

Gene conservation

Over the course of any selection and breeding program there will be an increase in frequency of "desirable" genes and a decrease in frequency of **currently** "undesirable" genes. Neutral genes, although not selected against, may be either lost or fixed in small breeding populations. In fact, the use of breeding groups such as in the proposed strategies should maintain or enhance the frequency of neutral genes (van Buijtenen and Lowe 1979).

There is a high probability that some currently unimportant genes will be important in the future, e.g., genes for disease or insect resistance. It follows that steps should be taken now to insure that these genes (or gene complexes) will be available if, and when, required. In situ conservation is undoubtedly the most effective method for preserving gene complexes. The current reserve-stand policy for black spruce and jack pine in New Brunswick, provides a reasonable level of in situ conservation for these species. The extensive natural forests, existing plantations, and reserves should provide adequate protection for the gene resource for all species in the present improvement programs.

Introduction of new selections

It is difficult to introduce new materials into a breeding program after the first or second breeding cycle without reducing the level of improvement in traits already selected, e.g., growth. It is possible, using the polycross test described earlier, to establish the relative value of new selections. Selections that have a GCA that exceeds the minimum currently used in the breeding population(s) can be added to the program or substituted for earlier selections. This will be important for species in which the initial selection intensity was low, e.g., Norway spruce, or where selection criteria have changed, e.g., there is a need to incorporate disease or insect resistance into the program. It will also be of considerable importance if the established breeding zones have to be divided.

BLACK SPRUCE TREE IMPROVEMENT STRATEGY

Black spruce is the most important reforestation species in the Maritimes, especially in New Brunswick, where current seedling production approaches 34 million annually. Reasonably good information is available on genetic variation at the provenance (Morgenstern 1975; Fowler and Park 1982) and stand levels (Park and Fowler 1984; Boyle 1985). Family tests have been established to provide information on genetic variation among individual trees. Information from provenance tests suggests that there is little advantage in going outside the Region to obtain breeding materials. By far the greatest component of variation resides among individuals within stands (Boyle 1985).

Black spruce is a precocious species, producing flowers at age 8-10 years from seed. Seed production from seedlings is expected to exceed that from grafts of comparable age after about 10 years. Black spruce is generally of good quality and parent-progeny correlations for growth attributes based on wild selections are low (Morgenstern et al. 1975). Primarily for these reasons, a seedling seed orchard approach was considered appropriate for first generation improvement.

Separate, but coordinated, tree improvement programs are carried out in New Brunswick, Nova Scotia, and Prince Edward Island. Nova Scotia has a separate improvement program with black spruce for the Cape Breton Highlands. To date, over 1300 plus trees have been selected in the Region and their wind-pollinated progenies have been used to establish 80 ha of seedling seed orchards and 50 family tests. The largest program is that of the New Brunswick Tree Improvement Council (NBTIC). The NBTIC program started in 1976.

A flow chart outlining the strategy for the improvement of black spruce is presented in Figure 4. Over the first 10 years of the program, 1200 unrelated plus trees will be selected (1). Seeds have been collected from each plus tree and used to establish seedling seed orchards (2) and family tests (3). To date, over 1000 trees have been selected, open-pollinated progenies from 730 of these have been planted in family tests. All selections will be made and family tests established by 1987.

At age 10 years, the family tests will be evaluated and the information used for roguing the seedling seed orchards (4). This process will be continued from years 10 to 20, and the orchards will be further rogued on the

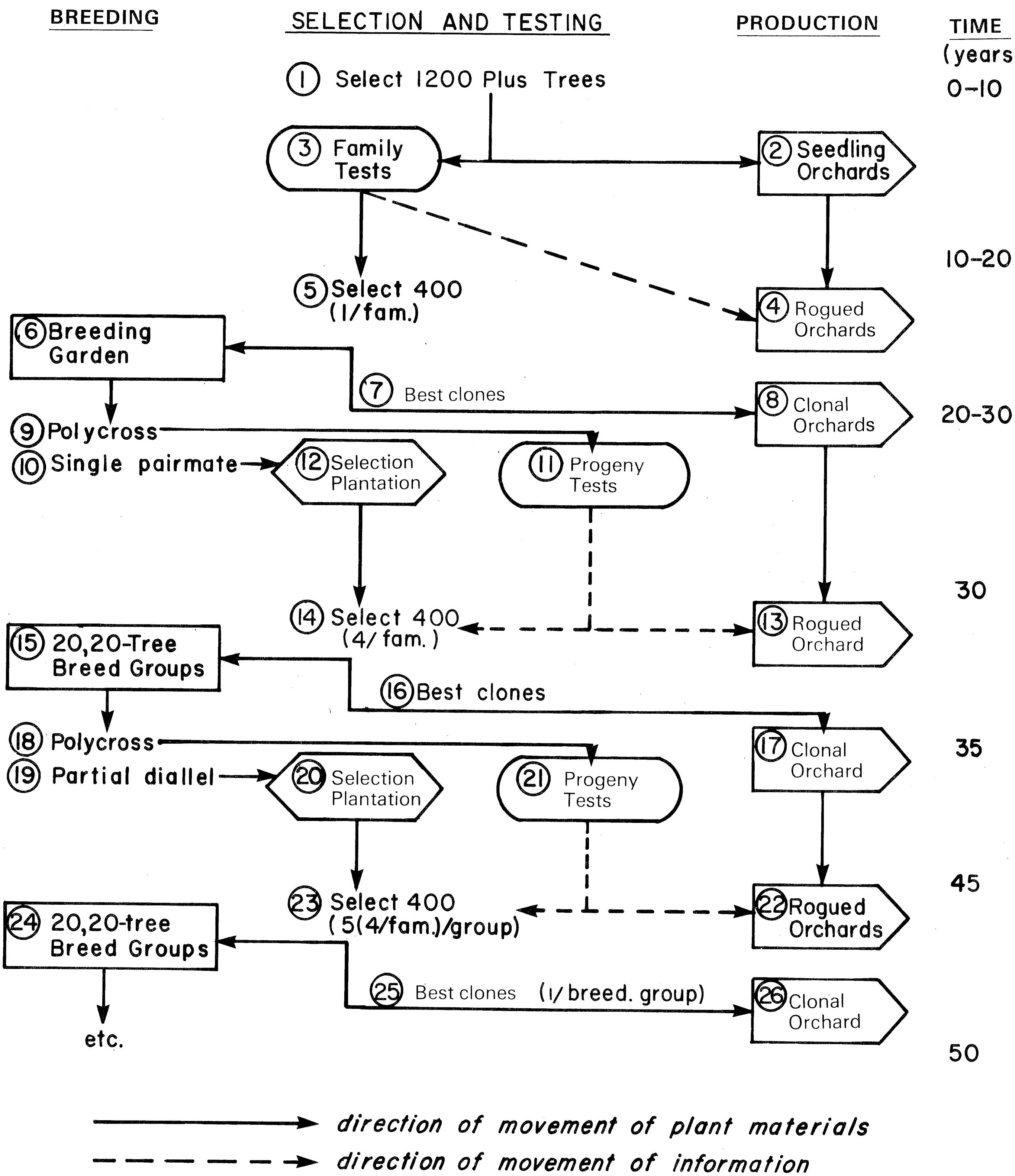

Fig. 4. Flowchart for black spruce tree improvement strategy NBTIC Program, (initiated 1976)

basis of 15- and 20-year evaluations. The 400 phenotypically best trees, one from each of the best 400 families will be identified (5), vegetatively propagated (rooted cuttings), and planted in a breeding garden (6). These 400 clones will form the base breeding population. The best 30-40 clones (7) will be used to establish clonal seed orchards (8) (year 14-24).

At year 24, when the 400 clones have reached flowering age in the breeding garden or in the family tests, each tree will be crossed with a standard pollen mix (polycross) to determine its general combining ability (9). The earlier selections will be crossed using ramets in the breeding garden. To avoid waiting for selections, which were made late in the program, e.g., years 5-10, to flower in the breeding garden, crosses will be made on ortets in the family tests. In this way, it should be possible to complete all first cycle breeding work and bring the program into phase at year 24. The polycross families will be raised in progeny tests (11). Each of the trees will also be used as a male or female parent for single pair matings (10). The only constraint in determining which trees will be crossed is that they originate in the same seed zone. The 200 full-sib families from the single pair matings will be planted into selection plantations (12) designed to facilitate selection of the best individual tree in each family, i.e., one 49-tree block of each family in each of two locations. Results from the progeny tests will be used to identify the parents with the best GCA for roguing the clonal orchard (13) and to identify the full sib families whose parents have the best average GCA. The four phenotypically best trees in the best 100 GCA families i.e., best average GCA of seed and pollen parents, will be selected (14) to form the next generation breeding population. These 400 trees will be assigned to 20, 20-tree breeding groups (15) with all related trees being assigned to the same group (year 34). Each breeding group will consist of 4 full-sibs from each of 5 unrelated families located in the selection plantations. The best tree from each of the best 30-40 unrelated families (16) will be propagated and used for a new clonal seed orchard (17). The clones used in the orchard should be in phase, phenologically, to maximize panmixia in the orchard.

When the 400 selected trees in the selection plantations flower (about year 35), each tree will be polycrossed (18) and mated with two unrelated trees in the same breeding group (19), i.e., 20 matings per breeding group using a partial diallel mating design (Fig. 2). As in the last cycle of breeding, selection, and testing, progeny test (21) results will be used to identify best parents for roguing the earlier clonal orchards (22) and to identify the full-sib families, in the selection plantations (20), whose parents have the highest average GCA. The best four individuals in the five best GCA families within each breeding group will be selected (23) to perpetuate the breeding group and form the next breeding generation (24). The results will also be used to identify clones (25) for the establishment of new orchards (26). However, unlike the last cycle, only the best clone from each breeding group will be included in the new orchards.

Anticipated problems and opportunities

Polycross The pollen mix used for the polycross should be consistent and repeatable over time. Pollen production in black spruce at age 10 years will be adequate to carry out the planned single pair matings, but will probably not be adequate to provide a 20-tree mix for the polycrosses. If this is the case, a 20-tree mix composed of equal volumes of pollen from trees growing on the Acadia Forest Experiment Station (AFES) will be used for first generation breeding. Twenty unrelated clones, growing in the family tests, that do not quite meet the criteria for next generation selection will be propagated as a pollen source for future polycrosses.

Vegetative propagation The black spruce breeding strategy outlined above relies on seed orchards for mass production of improved seeds and is designed to capture only a part of the available genetic variation. Advances in propagation methodology indicate that vegetative propagation of this species by juvenile stem cuttings is becoming a viable alternative to sexual reproduction. In fact, operational-scale programs exist in Ontario (Armson et al. 1980) and Nova Scotia (Hallett 1985). An opportunity exists to utilize a larger portion of the available variation with vegetative propagation. To utilize this variation effectively, more sophisticated and more expensive mating and testing designs are required to determine specific combining ability (SCA). A logical approach would be to select a manageable-sized population of high GCA trees on the basis of family or progeny tests. These trees would then be crossed using a disconnected, partial diallel design with resulting progenies planted out in replicated tests to determine the best SCA combinations. This material could also be used immediately for mass vegetative propagation. After progeny testing, the best crosses could be repeated and mass propagated. In essence, vegetative propagation could replace clonal orchards in the proposed strategy.

WHITE SPRUCE TREE IMPROVEMENT STRATEGY

White spruce is of considerable importance as a reforestation species throughout the Region. Annual planting of the species is usually between 5-10 million seedlings. Nienstaedt and Teich (1971) provide a detailed review of the genetics of white spruce. The species is highly variable at the provenance and within provenance levels. Provenance information indicates that trees of southeastern Ontario provenance will grow as fast or faster than trees of local provenance over a wide range of environments from the Maritimes to the northern Lake States. At the individual tree level, the species is highly variable in respect to many growth and quality characteristics. Growth of white spruce can be increased if the level of inbreeding that occurs in natural stands can be eliminated (Park et al. 1984).

Cones have been observed on white spruce as early as 4-6 years of age, however, it generally does not produce abundant cone crops until at least age 15 years (Nienstaedt and Teich 1971). The species is fairly easy to graft and grafts will produce reasonable quantities of flowers within 5-6 years. Cone production from grafts is expected to exceed that of seedlings of comparable age for at least 20 years. These facts suggest a clonal seed orchard approach for the improvement of white spruce. Two distinctly different programs have been implemented for the genetic improvement of white spruce in the Region: 1) seedling seed orchards will be utilized to capture genetic variation at the provenance level, and 2) clonal seed orchards will be used to capture within provenance variation. The strategies for the two programs will be presented separately.

Southeastern Ontario white spruce

Trees of southeastern Ontario provenances of white spruce have performed consistently well in tests in New Brunswick (Fowler and Coles 1977). Although it is questionable if the same is true in Nova Scotia (T.J. Mullin, pers. comm.).[1] Unfortunately, commercial quantities of seed from these provenances have not been available for direct use in the Region. The objective of this program is to develop a reliable seed source of southeastern Ontario provenance that has been selected and improved in respect to growth and quality under Maritimes conditions. All three Maritime provinces are cooperating in this program.

A flow chart outlining the improvement strategy adopted by NBTIC is presented in Figure 5. Open-pollinated

[1]T.J. Mullin, 1985. N.S. Dep Lands Forests. Debert, N.S.

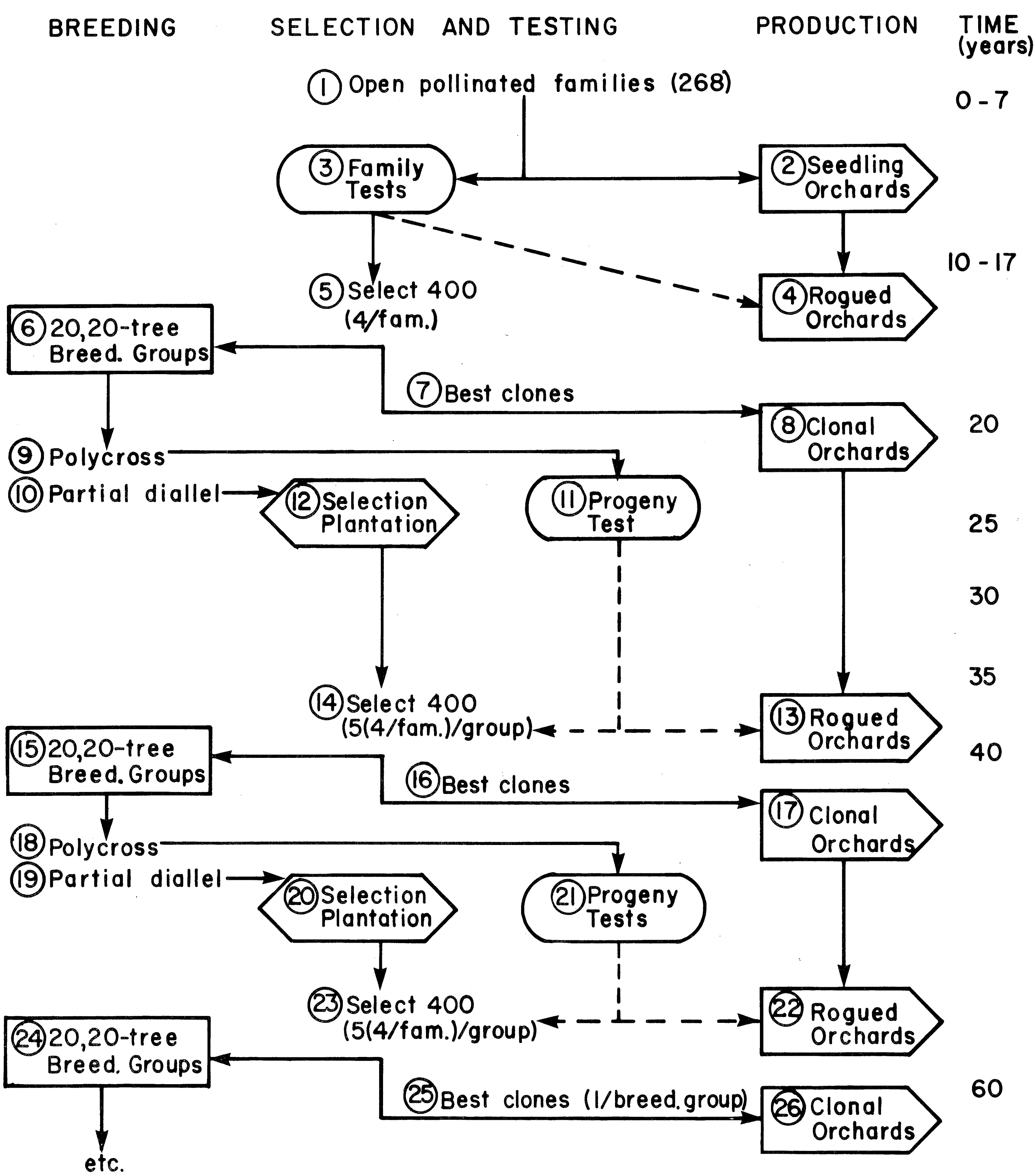

Fig. 5. Flowchart for white spruce tree improvement strategy - southeastern Ontario Provenances, NBTIC, initiated 1978.

seeds from phenotypically good white spruce from southeastern Ontario have been provided by the Petawawa National Forestry Institute and the Ontario Ministry of Natural Resources. The first seed collections were obtained in 1972, however, the first operational seedling orchard was not planted until 1978. To date, seeds representing 268 open-pollinated families have been obtained (1) and used to establish 12 ha of seedling seed orchard (2) and family tests (3).

When the family tests are 10 years old they will be evaluated and the best families will be identified. The seedling orchards will be rogued (4) with subsequent roguings based on 15- and 20-year measurements. At age 15 years, the 400 best individuals in the 100 best families (4 per family) will be selected (5) to form the next breeding population. The 400 clones will be divided into 20, 20-tree breeding groups with ramets of related clones going to the same group (6). Each breeding group will consist of four full-sibs from each of five unrelated families. The phenotypically best clone (7) in each of the best 30-40 families will be used for a clonal orchard to be planted about year 22 (8).

Each of the 400 selected clones will be polycrossed (9) and mated (10) to two unrelated clones in the same breeding group (Fig. 2). Crossing of the earlier selections will be done on grafts in a breeding garden, whereas more recent selections will be crossed using ortets in the family tests (see p. 14, age to flowering). This will bring the program into phase about year 22. The resulting progenies will be planted in progeny tests (11) and selection plantations (12), respectively. When the progeny tests are 15 years of age they will be evaluated and the best families identified. The clonal orchard will be rogued (13) and the 20 best trees in the families with best GCA parents in each breeding group (4 per family) will be selected (14). These 400 clones will be assigned to their originating group (15). The phenotypically best clone from the best 30-40 unrelated families (16), regardless of their group of origin, will be used to establish the second clonal orchard (17) at about year 42.

In the next breeding cycle, scheduled for about year 44, each tree will be polycrossed (18) with the common pollen mix and each tree will be mated (19) to two other trees in the breeding group. Some inbreeding within breeding groups will be unavoidable at this stage. The selection (20) and testing (21) procedures will be the same as in the preceding cycle. Progeny test results will be used to identify the families with the best GCA parents and to rogue the clonal orchard (22). The best 20 individuals in the families with best GCA parents in each breeding group (4 per family) will be selected (23) and returned to their original breeding group (24). The best clone in each breeding group (25) will be used for the clonal orchards (26) about year 65.

Maritimes Region white spruce

All three Maritime Provinces have active programs for the genetic improvement of white spruce based on conventional clonal seed orchards. Each province is treated essentially as a separate breeding zone with only a limited exchange of materials between zones. The Nova Scotia and New Brunswick programs are similar in strategy, scope, and rate of progress to date. A strategy for the Nova Scotia program is presented (Fig. 6). The Nova Scotia Tree Improvement Working Group (NSTIWG) program was initiated in 1976. The plus tree selection aspects of this program were completed in 1985. To date, 468 plus trees have been selected (1). These trees are grafted and used to establish clonal orchards (2) and a breeding garden (3). To date 6 ha of clonal orchards have been established and an additional 25-30 ha are planned.

When the grafts flower (year 10-15) each clone will be polycrossed (4) and crossed with two other clones from the same seed zone in a partial diallel design (Fig. 2) (5), and planted into progeny tests (6) and selection plantations (7), respectively. The pollen mix

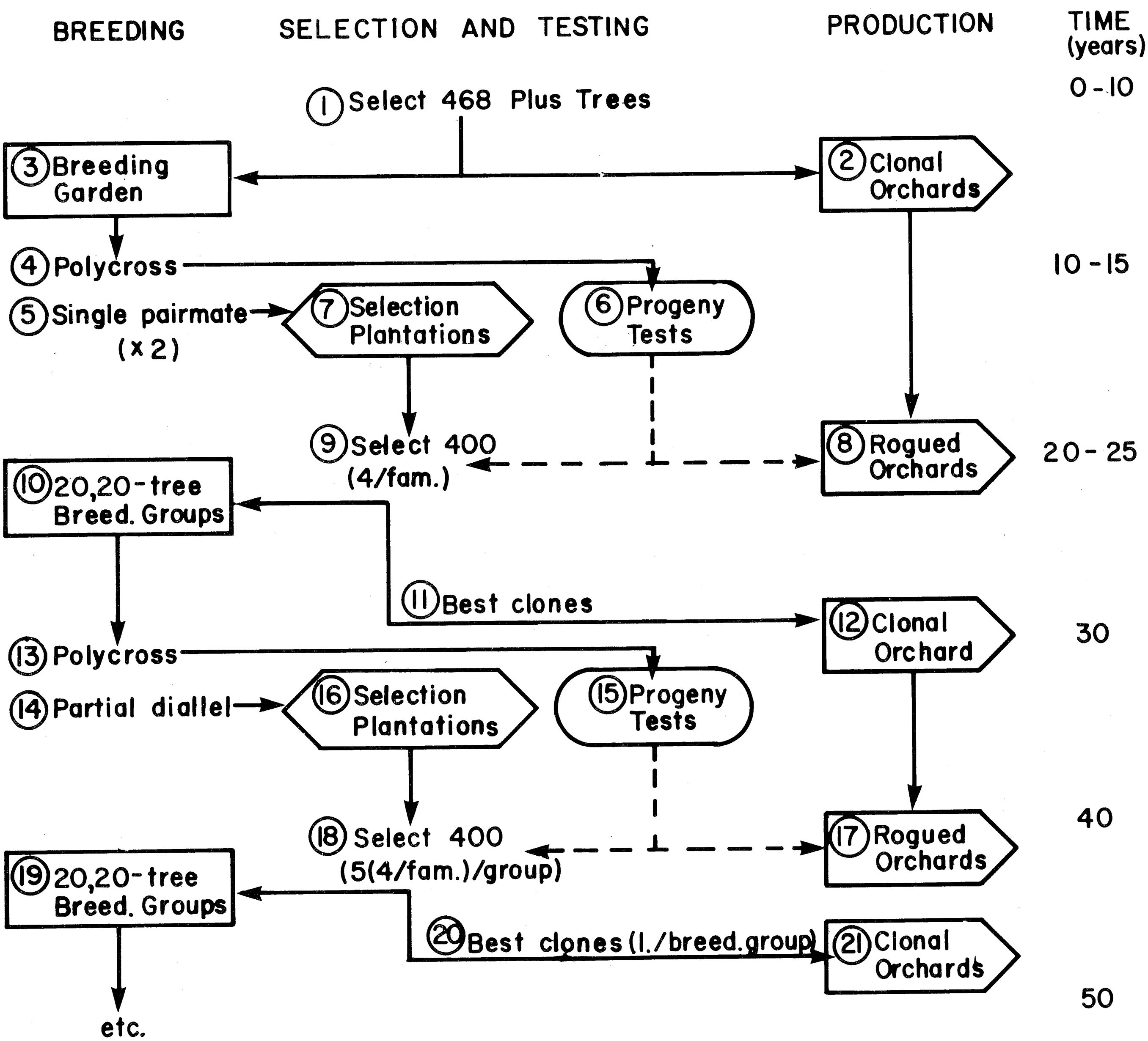

Fig. 6. Flowchart for white spruce tree improvement strategy Maritimes Provenances, NSTIWG Program, initiated 1986.

for the polycross will consist of equal volumes of pollen from each of 20 phenotypically good clones growing in a demonstration seed orchard at Lawrencetown, N.S. None of these clones are included in the current breeding program.

At age 10 years (year 20-25), information from the progeny test will be used to rogue the clonal orchards (8). These orchards will be further rogued on the basis of 15- and 20-year data. At age 15 years, families in the selection plantation having the best GCA parents will be identified. The four phenotypically best trees in each of the 100 best families, i.e., best average GCA of seed and pollen parents, will be selected (9) and assigned to 20, 20-tree breeding groups (10) with all related trees going to the same group. All trees within a group will also be from the same seed zone. The phenotypically best tree in the best 30-40 unrelated families (11) will be used to establish second generation clonal orchards (12) at about year 30.

The selected trees are expected to flower at about age 15 (year 25-30) (see p. 14, age to flowering). Each tree will be polycrossed with the common pollen mix (13) and crossed with two other unrelated trees in the same breeding group (14). To synchronize the program better, crosses involving the earliest selections will be made on ramets in a breeding garden and crosses on the most recent selections will be made on ortets in the selection plantations. All crosses should be completed about year 30. The resulting seedlings will be planted into progeny tests (15) and selection plantations (16), respectively.

As in the preceding breeding cycle the information from the progeny tests will be used for a first roguing of the clonal orchards (17) and to identify families in the selection plantations having the best GCA parents. The four phenotypically best individuals in the five best GCA families in each breeding group will be selected (total 400) (18) and assigned to their originating breeding group (19). The best clone in the best family in each breeding group (20) will be propagated for clonal seed orchards (21) at about year 50.

Anticipated problems and opportunities

Age to flowering The white spruce breeding strategy assumes that trees selected for the next generation of breeding in the family tests and selection plantations will produce the required numbers of male and female flowers at age 15. It is highly probable that at least some of the trees will not. If the proposed schedule is to be maintained it will be necessary to induce flowering on these trees. Application of gibberellin A 4/7 has been demonstrated to be effective for inducing flowering in 12-year-old white spruce (Cecich 1985). It is highly probable that application of GA 4/7 in conjunction with spacing and fertilization can be used effectively to produce the required numbers of male and female flowers. Studies to develop effective methods of flower induction in white spruce are currently underway in the Maritimes (M.S. Greenwood pers. comm.).[2]

RED SPRUCE TREE IMPROVEMENT STRATEGY

Red spruce is an important forest species in the Region, however, it is currently not widely planted. Annual seedling production for the Region is less than 5 million seedlings of which almost all are produced in Nova Scotia (Table 1). It is predicted that over 14 million red spruce seedlings will be required annually for planting in Nova Scotia in the future (Mullin 1983).

Red and black spruce hybridize in nature and although there is some question as to the full significance of this hybridization, there is little doubt that it is of importance in parts of the Region (Gordon 1976). Provenance information for red spruce is confounded by the fact that tests have often included

[2]M.S. Greenwood. 1985. Univ. of Maine; Orono, ME 04469.

hybrids that contribute substantially to the observed variation (Morgenstern and Farrar 1964; Manley 1972; Morgenstern et al. 1981). Information on genetic variation at the stand or individual tree levels is not yet available. There is no evidence to suggest that there is any advantage in using trees from outside the Region in a tree improvement program.

In the absence of special treatment, red spruce cannot be relied upon to produce female and male flowers in abundance until age 20 years or more. The species can be grafted with reasonable ease and grafts from mature trees will flower within five years. The species is moderately variable in respect to quality traits and it is assumed that branch and stem characteristics can be improved genetically. A clonal seed orchard approach has been accepted for improvement of the species. The Nova Scotia Tree Improvement Working Group (NSTIWG) is actively engaged in improvement work with red spruce. A strategy for this program is presented in Figure 7.

The NSTIWG red spruce program started in 1976. The selection of plus trees was completed in 1984-85. At this time, year 10, 546 trees have been selected (1) and grafted. Over 8 ha of clonal orchard have been planted (2) and plans call for an additional 35 ha by 1988. The selected clones are also being planted in breeding gardens (3). As soon as the clones flower in the breeding garden or orchards (year 7-17), each clone will be polycrossed (4) and single pair mated to one other clone from the same seed zone (5). The progenies from the 546 polycrosses and 273 single pair matings will be planted in progeny tests (6) and selection plantations (7), respectively. Information from the progeny test will be used to rogue the seed orchard (8) and to identify families in the selection plantations that have high GCA parents. The first roguing of the orchard will be done when the progeny tests are 10 years of age (year 18-28). A second 1.5 generation clonal orchard (optional) could be established using the 30 clones with the highest GCA (9) based on 10- or 15-year data from the progeny test. A second roguing of the original orchard will be based on 15- to 20-year measurements.

The 400 best individuals in families from the best GCA parents will be selected (10) in the selection plantations at age 15 years. Selections should be completed and the program brought into phase about year 33. Two selections will be made in each of the best 200 families. These 400 clones will be randomly assigned to 20, 20-tree breeding groups (11) with the constraints that related clones be assigned to the same breeding group and that all clones in the group come from the same seed zone. Each breeding group will consist of two full-sibs from each of 10 unrelated families. The selected clones will be vegetatively propagated and planted in a breeding garden to encourage earlier flowering. The 30-40 best unrelated clones (12), i.e., those having the best GCA parents, will be used to establish a second generation clonal orchard (13) at year 35.

As in the previous breeding cycle each clone will be polycrossed (14) and progeny tested (15). Each clone will also be crossed with two other unrelated trees in the same breeding group (16) (Fig. 2) and the resulting progenies planted in selection plantations (17). Information from the progeny tests will again be used to rogue the new clonal orchard (18) and to identify families in the selection plantations with high GCA parents. The four best individuals in the five best families in each breeding group will be selected (19) and assigned to the breeding group from which they originated (20). The best clone from each breeding group (21) will be used to establish a third generation clonal orchard (22) at about year 57.

Anticipated problems and opportunities

Polycross The pollen mix used for the polycross will consist of equal volumes of pollen from 20 phenotypically good clones growing in an experimental seed orchard at Lawrencetown, N.S. These clones are not included in the current

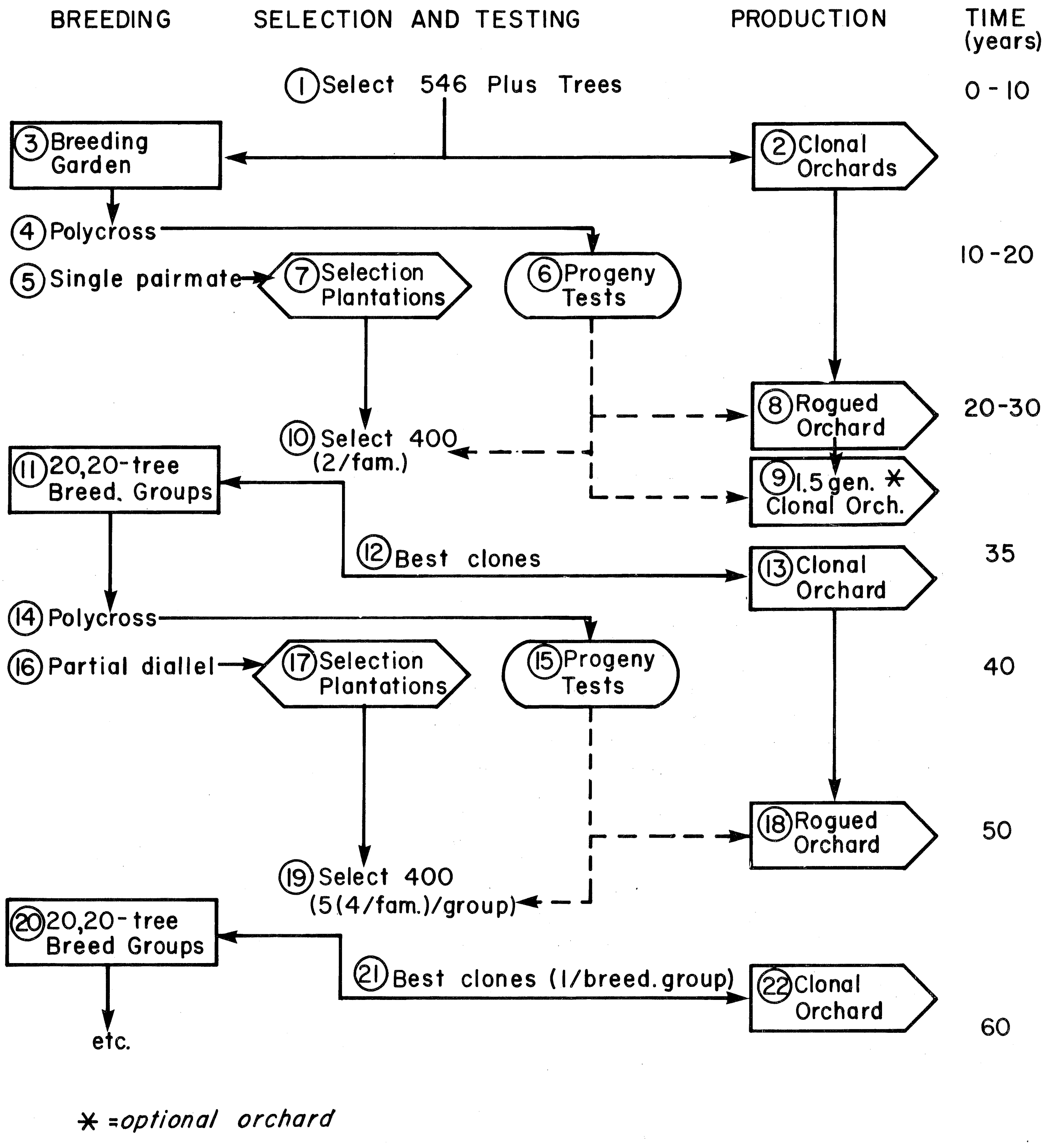

Fig. 7. Flowchart for red spruce tree improvement strategy NSTIWG Program, initiated 1976

improvement program and are representative of good red spruce in Nova Scotia. Only clones, the ortets of which are not growing in close proximity to plus trees, will be used. These clones are currently producing pollen in reasonable quantities. This pollen source has the additional advantage that the orchard is located in one of the phenologically advanced parts of the province so that fresh pollen should be available for all polycrosses.

Time-to-flower Even under good plantation conditions red spruce does not usually flower until age 20 years or more. In the strategy presented above, selections for next breeding generation are made at age 15. These clones are grafted and it is assumed controlled crosses can be made when the grafts are 5 years old. This assumption may not be realistic unless other steps are taken to reduce the time-to-flower. There is a need to develop accelerated breeding techniques for this species, e.g., breeding greenhouses and appropriate fertilizer and (or) growth regulator applications. The optional clonal seed orchard, suggested for year 30, would speed-up production of improved seeds, if accelerated breeding techniques are not developed.

JACK PINE TREE IMPROVEMENT STRATEGY

Jack pine is the second most important tree species planted in New Brunswick. It is of minor importance in Nova Scotia and Prince Edward Island. Current annual seedling production of jack pine is about 18 million. Rudolph and Yeatman (1982) provide a detailed review of the genetics of the species and present a general strategy for improvement. There is reasonably good information available on genetic variation at the provenance and within provenance (stand) levels, and family tests have been established to provide information on genetic variation among individual trees. Provenance information suggests that tree improvement efforts should concentrate on local materials.

Jack pine is a precocious species, capable of producing male and female flowers in abundance at less than 8 years of age with cone production on seedlings greatly exceeding that on grafts of comparable age (Rudolph and Yeatman 1982). Parent-progeny correlations for growth attributes based on wild selections are low (Canavera 1975) although the potential for stem form and wood quality improvement appears high. A seedling seed orchard approach utilizing a large number of families appears reasonable for first generation improvement of the species. The New Brunswick Tree Improvement Council has undertaken a major program for the improvement of jack pine. A strategy for the NBTIC program is presented in Figure 8.

Jack pine plus tree selection started in 1977 with the first family tests and seedling orchards being planted in 1979. Over the first 10 years of the program, 1000 unrelated plus trees will be selected (1). Seeds will be collected from each plus tree and used to establish seedling seed orchards (2) and family tests (3). To date, 850 trees have been selected, 590 of which have been included in seedling seed orchards (43 ha) and 21 family tests. Plus tree selection will be completed and all family tests established by 1987 (year 10).

At age 7 years, the family tests will be evaluated and the information used for the first roguing of the seedling seed orchards (4). This will take place from year 9 to 17. The orchards will be rogued again when they are 12 and 17 years of age. At age 7 years the best clones, one from each of the best 400 families will be selected (5), vegetatively propagated, and planted in a breeding garden (6) to form the base breeding population. The best 30-40 clones (7) will be vegetatively propagated to establish clonal seed orchards (8) (year 11-21). Flowering will be reasonably heavy after the ramets have been in the breeding garden for 5 years. Controlled breeding will begin at this time. To avoid waiting for selections that were made late, e.g., years 5-10 in the program, to flower in the breeding

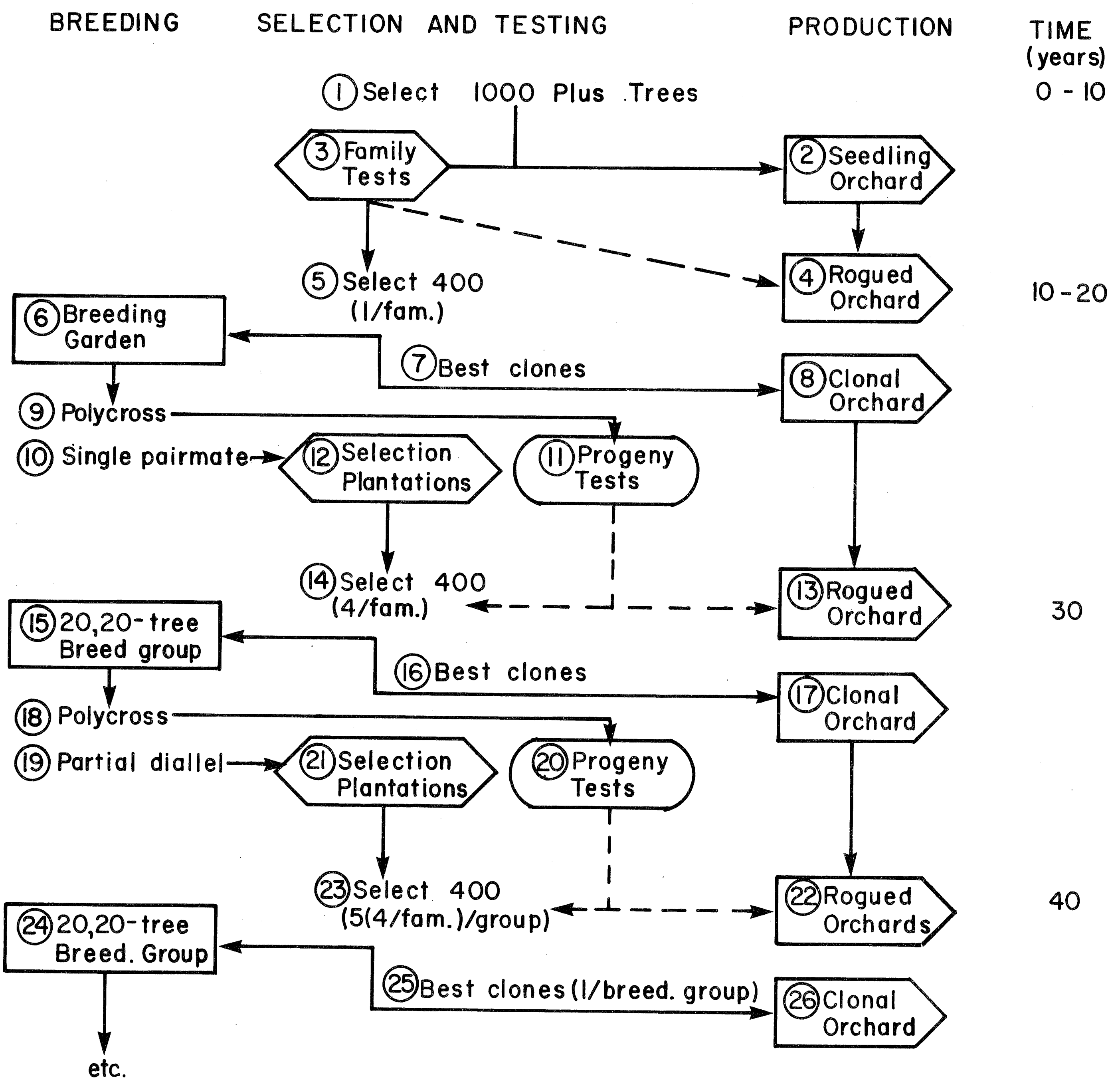

Fig. 8. Flowchart for jack pine improvement strategy NBTIC Program, initiated 1977

garden, crosses will be made on ortets in the family tests rather than on ramets in the breeding garden. In this way, it should be possible to complete all first cycle breeding work over a 2-year period and bring the program into phase by year 22.

Each of the 400 selected trees will be polycrossed (9) and single pair mated (10) to another tree from the same seed zone. The 400 polycross progenies will be planted into progeny tests (11) and the 200 full-sib families from the single pair matings will go to selection plantations (12). The progeny tests will be evaluated at age 7 years. Information on general combining ability from the progeny tests will be used to rogue the clonal orchards (13) and to identify full-sib families having parents with high average GCA. The 4 phenotypically best trees in each of 100 full-sib families identified as having highest parental average GCA will be selected (14). These 400 clones will be assigned to one of 20, 20-tree breeding groups (15) at about year 30. Assignment will be random with the constraint that related trees must go to the same breeding group and all trees in the group come from the same seed zone. The 30-40 best unrelated clones (16) will be used for new clonal seed orchards (17).

The second cycle of breeding will begin in the selection plantations as soon as the individual trees have been identified. Each of these 400 selected trees will be polycrossed (18) and progeny tested (20). Each tree will also be crossed with two other unrelated trees in the same breeding group (19) (Fig. 2). The resulting full-sib families will be planted in selection plantations (21) to provide materials for the third cycle of breeding. Based on results from the progeny tests the third generation clonal orchards will be rogued (22) and the best GCA families will be identified (year 40). The best four trees in each of the best five families will be selected (22) in each breeding group, based on average GCA of the parents. These 20 trees from each breeding group will be assigned to their originating groups (24). The best clone from each breeding group (25) will be used to establish new clonal orchards (26).

Anticipated problems and opportunities

Polycross Pollen production in plantation-grown jack pine is adequate at age 7 years to provide pollen for the polycrosses. Twenty-five good trees from families that do not quite meet the requirements for second generation selection have been selected in a southern New Brunswick family test. Pollen from 20 of these trees will be used for all polycrosses. These selections have been grafted and will be maintained for pollen production.

Family tests Evaluation of the family tests and selection of superior individuals at age 7 years may be optimistic. The oldest family tests will be 15 years of age when the newest ones reach age 7. If the correlation for growth for individuals at 7 and 15 years is not high enough, it may be necessary to postpone selection of the best individual trees, e.g., age 12 years.

TAMARACK TREE IMPROVEMENT STRATEGY

Tamarack is one of the most rapid growing of the northeastern American conifers and is reported to outgrow other native conifers over much of its native range (Park and Fowler 1982). Despite its rapid growth, at least over short rotations, tamarack is not an important reforestation species. On average, less than a million seedlings are planted annually in the Maritimes Region. However, largely because of its potential, it is one of the four species chosen by the NBTIC for their tree improvement program (Coles 1979).

Tamarack is a precocious species, producing male and female flowers at 7-10 years from seed. Seed yields, at least in the wild, are low and cone and seed yields are frequently further reduced by insect feeding. Information on genetic variation of the species is limited. Jeffers (1975) and Cech et al. (1977) reported significant differences among provenances in respect to height and survival. Rehfeldt (1970) found differences among stands within a single geographic area (Wisconsin) to be substantial. Both Rehfeldt (1970) and Jeffers (1975) considered the species to be highly variable at the intrapopulation level. There is no information to suggest that tree improvement efforts should concentrate on anything other than local materials.

Park and Fowler (1982) studied the effects of inbreeding in a tamarack population in central New Brunswick. They found the species to be highly variable at the intrapopulation level and demonstrated that trees growing in close proximity to one another were often related. In comparison with other conifer species, tamarack is below average in self-fertility and above average in number of lethal equivalents. Tamarack exhibits relatively large specific combining ability variances for early seedling height, a fact which must be considered if growth rate of the species is to be improved effectively.

The species is easy to graft and because of its indeterminate growth pattern it is possible to produce plantable grafts in 1 or, at most, 2 years. Tamarack exhibits considerable phenotypic variation in stem form and branching habit. Primarily because of the ease of grafting and the assumption that large gains can be made in quality characteristics, a clonal seed orchard approach has been followed. The strategy for the NBTIC program is presented in detail in Figure 9.

The first selections of tamarack under the NBTIC program were made in 1977. To date, 150 plus trees have been selected in New Brunswick. An additional 32 plus trees are available from Maine and Prince Edward Island. It is anticipated that 300 plus trees will be selected by 1986 (1). Grafting will be completed and the 300 plus trees planted into clonal seed orchards (2) and breeding gardens (3) by 1987. This will be the base breeding population for tamarack in New Brunswick. Flowering should begin within 5 years of grafting. At that time, each clone will be crossed with a standard pollen mix (polycross) (4) and each clone will be single pair mated (5) to one other selected clone originating in the same seed zone. These crosses should be completed about year 15 (1992). The seedlings obtained from the polycross will be planted in progeny tests (6) to provide GCA information for roguing the seed orchard (7) and identification of superior full-sib families. The seedlings from single pair matings will be planted into selection plantations (8) to provide materials for second generation selection and breeding.

At age 10 years, the 400 best phenotypes, four from each of the 100 best families, will be selected (9). These 400 trees will be divided into 20, 20-tree breeding groups (10) with related trees from the same seed zone being assigned to the same group. Based on family test rankings, the phenotypically best 30-40 unrelated clones (11) will be used for a clonal seed orchard (12) to be planted about 2002 (year 25). The second cycle of breeding will start on trees in the selection plantations about this same time. Each clone will be polycrossed (13) and crossed to two other unrelated clones in the same breeding group (14) in a partial diallel design (Fig. 2). As in the preceding breeding cycle the full-sib families will go to selection plantations (15) and the seedlings from the polycrosses to progeny tests (16). Based on the results of the progeny tests, the clonal orchards will be rogued (17) and the best full-sib families identified. The four best trees in each of the five best families in each breeding group will be selected (18) for the next cycle of breeding. These clones will be assigned to the same breeding group from which they originated (19). The best clone (20) from each breeding group will be propagated to establish the third clonal orchard (21) (year 36).

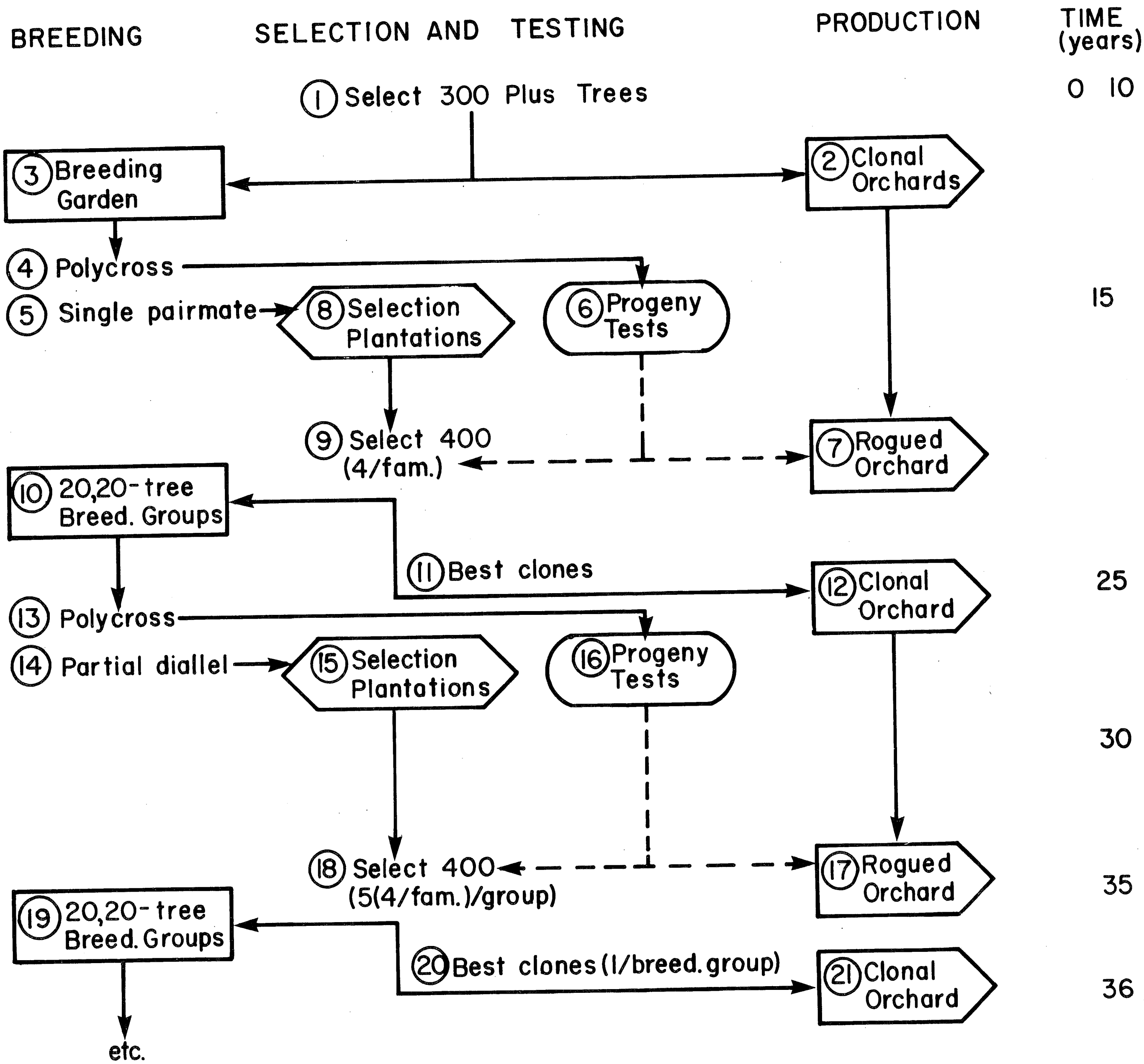

Fig. 9. Flowchart for tamarack improvement strategy NBTIC Program, initiated 1977

Anticipated problems and opportunities

Polycross The pollen used for the polycross should be consistent and repeatable over time. Tamarack is not a heavy pollen-producer. It is doubtful if enough pollen from any 20 clones will be available at age 10 years, to provide for all the polycrosses. Because of this, a pollen mix obtained from equal volumes of male flowers from 100 randomly distributed trees growing in a plantation at MacDonalds Corner, N.B. will be used. The trees in this plantation result from controlled crosses involving 20 female and more than 40 male trees of AFES origin (Park and Fowler 1982). The plantation is replicated at AFES. This pollen source has the advantage of being located in one of the phenologically most advanced areas in New Brunswick.

Vegetative propagation The preceding breeding strategy has been presented on the assumption that methods of propagating tamarack will not change over the next several decades. In fact, there is a strong probability that tamarack will be propagated vegetatively, first from rooted cuttings and eventually via tissue culture. This will result in substantial changes especially in the production aspects of the strategy. Changes in propagation techniques could logically take place as early as data are available from the first progeny tests.

ALTERNATIVE STRATEGY FOR IMPROVEMENT OF TAMARACK

Experiments with tamarack in central New Brunswick (Park and Fowler 1982) revealed a high level of SCA. The improvement strategy outlined above is designed to capture only GCA. An opportunity exists, through vegetative propagation, to capture and mass produce a higher proportion of the available genetic variation. To do this, a more appropriate mating design will be required.

The alternative improvement strategy (Fig. 10) will begin the same as the preceding strategy (Fig. 9) in that 300 plus trees will be selected (1) and will be established in a breeding garden (2). No clonal orchards need be established. Most clones in the breeding garden will flower about age 5 years.

The breeding population will be divided into two groups. Each clone will be polycrossed with a 20-tree pollen mix from the other group (3). The resulting progenies will be planted in progeny tests (4) and extra seed used to produce cuttings for mass vegetative propagation (5). The resulting propagules will be equivalent to what could be produced in a first-generation clonal orchard. The crosses can be repeated annually, or as required, to provide a continuous supply of juvenile cuttings.

Information from the polycross progeny test at age 10 years will be used to identify clones in the breeding garden with high GCA. The 40 best clones will form the new breeding population (6). Each of the 10 best GCA clones will be crossed with a pollen mix from the other nine best clones (7) to provide materials for mass vegetative propagation (8). The genetic quality of the propagules will be as good as, or better than, seedlings from a 100-clone clonal orchard after 90% roguing and the elimination of self pollination and pollen contamination. This is a much higher level of roguing than is possible under any currently accepted seed orchard scheme. The 40 best GCA clones in the breeding garden (6) will be divided into 8, 5-clone sets. Each clone will be crossed with six clones from two other sets in a disconnected half diallel design (9) (Fig. 3) and the resulting progenies planted in progeny tests (10):

Information from the progeny tests at age 10 years, will be used to identify pairs of trees in the breeding garden with high SCA (11). These high SCA crosses will be repeated (12) to provide juvenile materials for mass vegetative propagation (13). Information from the progeny test will 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

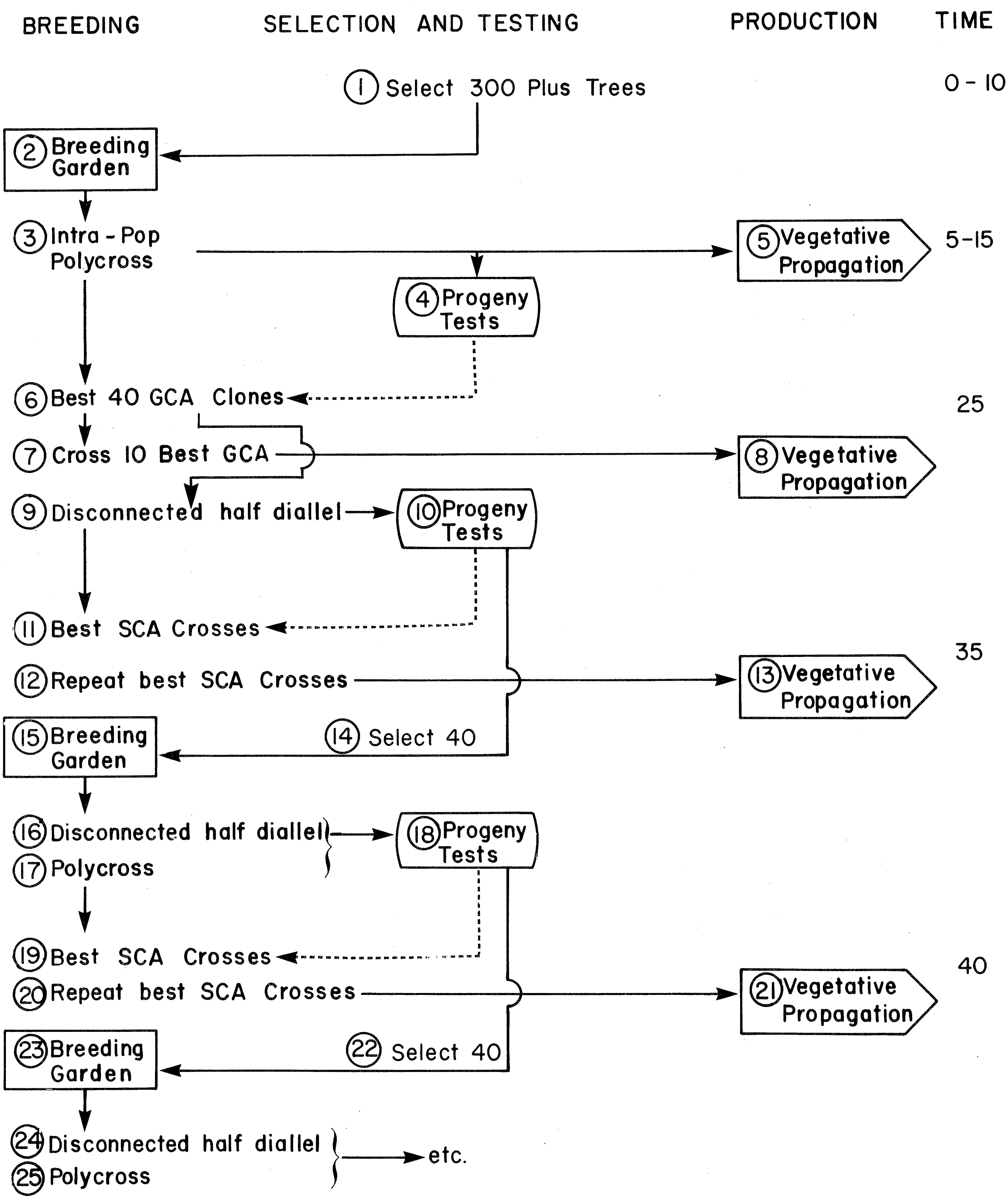

Fig. 10. Flowchart for alternative strategy for improvement of tamarack

the 8 sets of crosses, will be selected (14) to form the next breeding population (15). No more than 1 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. 11). As some trees within each set will be related, each tree will also be polycrossed (17) to provide reliable GCA information. The resulting progenies will be tested (18).

As in the preceding breeding cycle, the progeny tests will be evaluated at age 10 years 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 phenotypically 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 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 6 clones from completely unrelated sets of crosses, e.g., set (AxB) x (CxD) crossed with (ExF) x (GxH) (24) (Fig. 12). Each of the 40 clones will also be polycrossed to provide reliable data on GCA (25). Testing, evaluation, and selection procedures will be as in the preceeding 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 utilize inbreeding in subsequent breeding efforts effectively.

NORWAY SPRUCE TREE IMPROVEMENT STRATEGY

Norway spruce currently is not an important reforestion species in the Maritimes Region. However, tests have demonstrated that trees of this species from good provenances are capable of outproducing native spruces when planted on appropriate sites (Fowler and Coles 1979). Interest in Norway spruce has increased considerably in recent years and current plans call for the planting of 2-3 million seedlings annually. The best provenances for most parts of the Maritimes are from mid-elevations (700 m) in the Sudeten and Carpathian Mountains of Poland. For the climatically more rigorous parts of the Region, provenances from east of the Baltic Sea in Lithuania, Latvia, or western Russia are superior. Unfortunately, it is difficult to obtain commercial quantities of seed from any of these provenances.

Norway spruce 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, cone crops within 5 years of grafting. Flowering on grafts of immature trees is even less reliable. The most widely accepted method of mass production of improved seeds is via clonal seed orchards. This approach is being followed on a small scale in Nova Scotia. Norway spruce is also propagated vegetatively on a commercial scale in northern Europe.

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 one breeding zone, the southern zone. The second, northern breeding zone, corresponds to seed zone 1 of Fowler and MacGillivray (1967). Planting of Norway spruce in the Cape Breton Hills and Highlands cannot be recommended until more information is available on appropriate provenances. Phenotypically good trees of known good provenance have been selected; 100 for the southern zone and 40 for the northern zone. Additional plus trees of known good provenance have been made available by the Petawawa National Forestry Institute and will be included in this program. Because of the limited amount of material available, selection intensity has ranged from only 1 to 5%. Additional

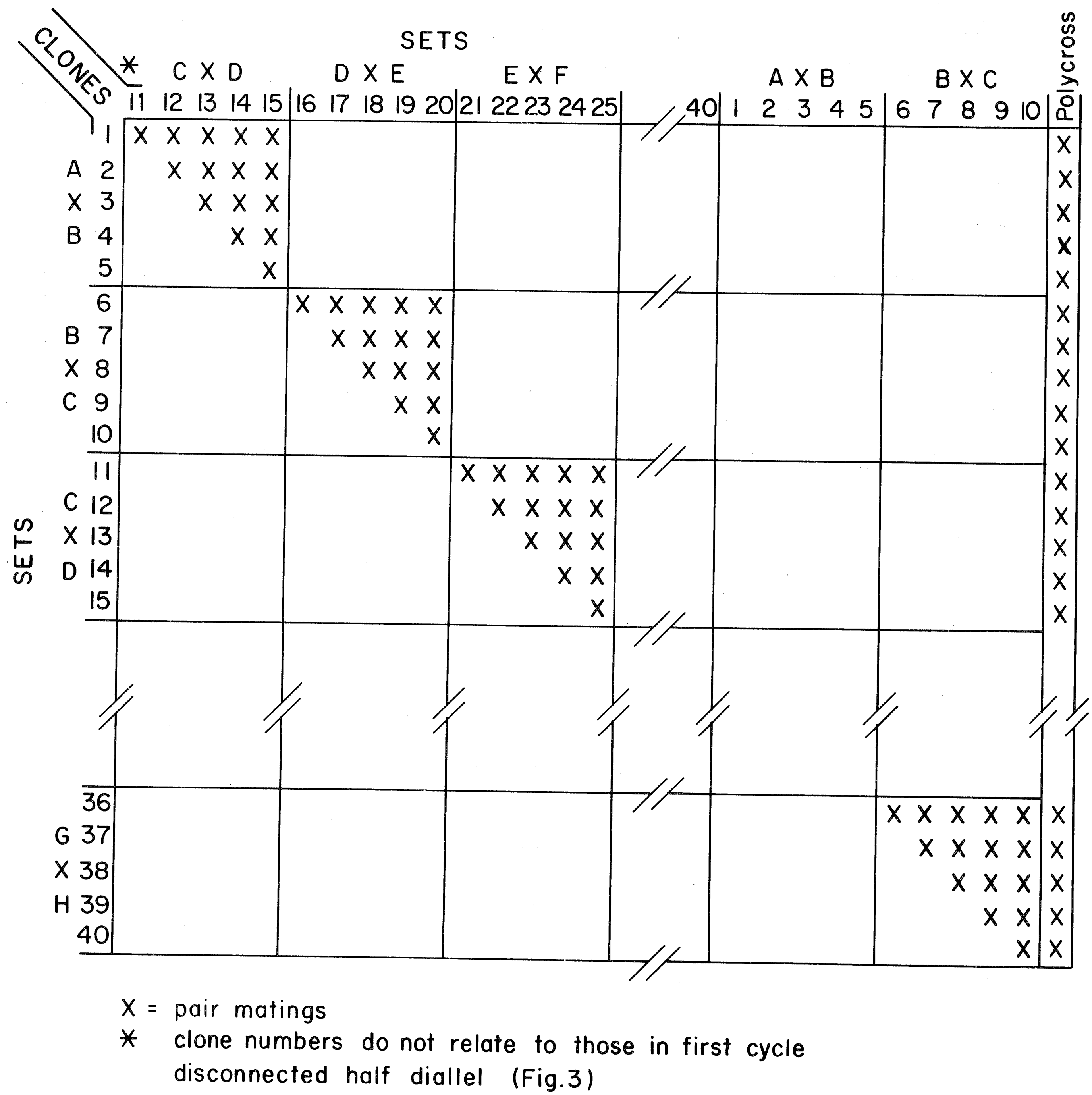

Fig. 11. Design for second 5-tree disconnected half diallel

SETS

SETS	CLONES *	(EXF) X (GXH) 21	22	23	24	25	(FXG) X (HXA) 26	27	28	29	30	(GXH)X (AXB 31	32	33	34	35	(DXE)X(FXG) 16	17	18	19	20	Polycross
	1	X	X	X	X	X																X
(AXB)	2		X	X	X	X																X
X	3			X	X	X																X
(CXD)	4				X	X																X
	5					X																X
	6						X	X	X	X	X											X
(BXC)	7							X	X	X	X											X
X	8								X	X	X											X
(DXE)	9									X	X											X
	10										X											X
	11											X	X	X	X	X						X
(CXD)	12												X	X	X	X						X
X	13													X	X	X						X
(EXF)	14														X	X						X
	15															X						X
	36																X	X	X	X	X	X
(HXA)	37																	X	X	X	X	X
X	38																		X	X	X	X
(BXC)	39																			X	X	X
	40																				X	X

X = pair matings

* clone numbers do not relate to those in first or second cycle disconnected half diallel (Fig. 3, Fig. 10).

Fig. 12. Design for third 5-tree disconnected half diallel

selections will be difficult to obtain until recently established "good provenance" plantations are old enough to provide meaningful selections. The selected trees have been grafted and planted in a breeding garden - clone bank. To date, only 2.4 ha of clonal orchard has been planted.

The current breeding strategy is essentially the same as for red spruce (Fig. 7) except that the number of original selections is much less. Even if orchard establishment proceeds at an accelerated rate, it is doubtful if significant quantities of improved Norway spruce seed will be available until well into the next century. An accelerated breeding program, coupled with a production program based on vegetative propagation is proposed for this species. A flow chart for such a program is presented in Figure 13.

For the southern breeding zone, 100 plus trees have been selected (1), grafted, and are, or will be, planted in a breeding garden. Additional clones will be available from PNFI and other cooperators. Several ramets of each clone will be potted and moved to an accelerated breeding facility (2). When the grafts are large enough to support a cone crop they will be induced to flower using appropriate accelerated breeding techniques such as those that have proven satisfactory for other spruce species. The clones will be divided into two groups and group 1 clones will be pollinated 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 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 at age 5 and 10 years can be used to rogue poor GCA clones from the program and will result in some genetic improvement in the materials used for mass vegetative propagation.

Information from the progeny test at age 15 years will be used to identify the 40 best GCA clones in the breeding garden, which will form the new breeding population (6). The 10 best GCA clones will be intercrossed (7) to provide cuttings for mass vegetative propagation (8). These crosses will be repeated as required. The resulting propagules should be equivalent to seedlings from a 100-clone clonal orchard after 90% roguing. The 40 best GCA clones in the breeding garden will be divided into 8, 5-clone sets and crossed in a disconnected half diallel design (9) (Fig. 3). The resulting progenies will be tested (10).

Information from the progeny test at ages 10, 15, and 20 years will be used to identify pairs of trees in the breeding garden with high 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 net breeding population (15). Only 1 tree will be selected in any family. Subsequent breeding, testing and production procedures will follow the strategy presented as an alternative breeding strategy for tamarack (Fig. 8).

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 efforts to obtain Norway spruce seed of known good provenance are successful, e.g., the Canada - USSR scientific exchange, a reliable source of new selection 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.

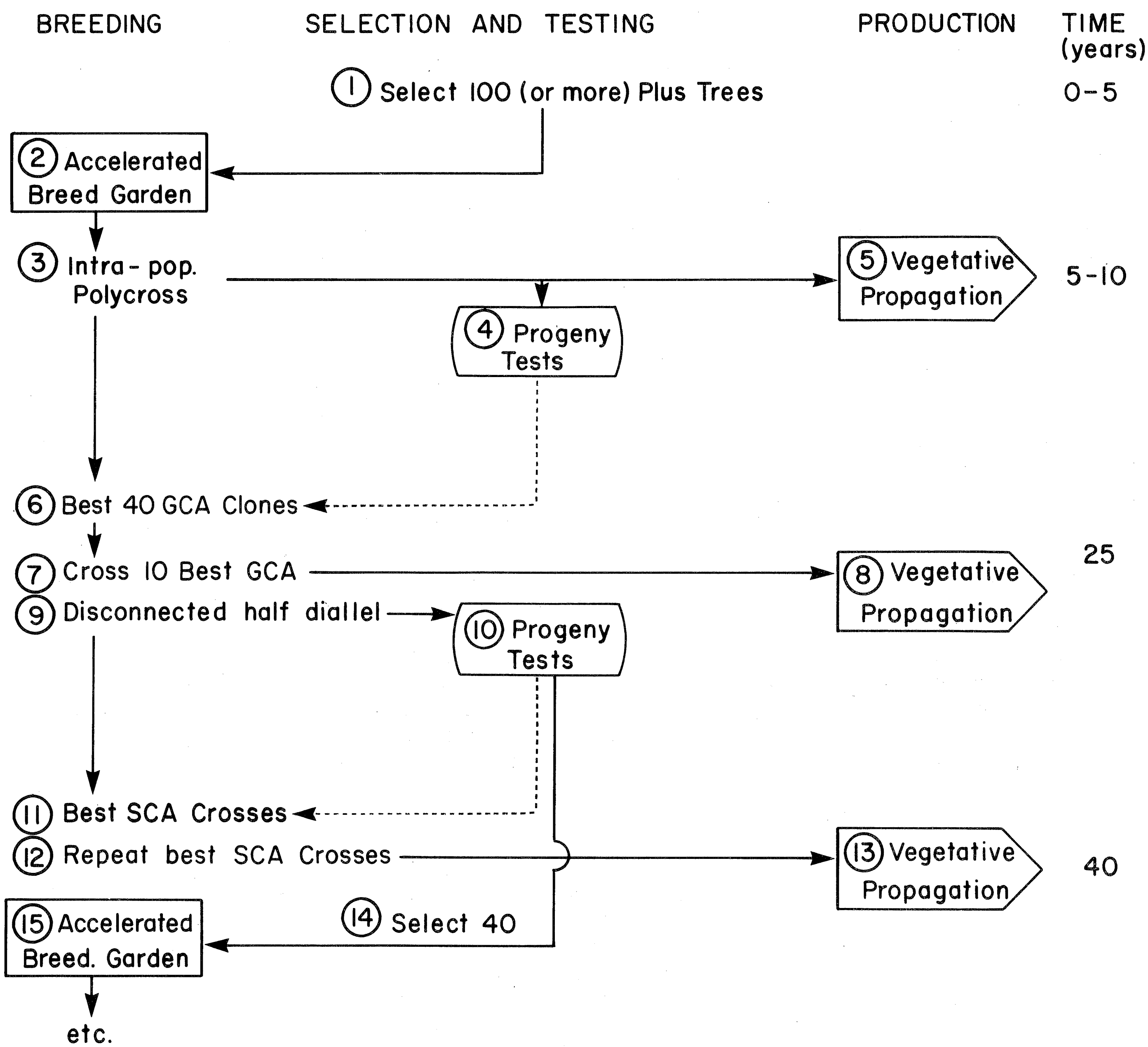

Fig. 13. Flowchart for Norway spruce improvement strategy Southern breeding zone, initiated 1982

ACKNOWLEDGEMENTS

The author wishes to acknowledge the in-depth discussions and assistance provided by Y.S. Park, E.K. Morgenstern, J.D. Simpson, R.F. Smith, and T.J. Mullin. Their assistance with the proposed strategies is appreciated. I also wish to thank C.W. Yeatman for his critical review and helpful suggestions which resulted in some significant changes in the strategies.

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