OPTIMIZATION OF LONG-TERM BREEDING STRATEGIES FOR CYCLIC WITHIN-FAMILY SELECTION

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INTRODUCTION: Long-term forest tree breeding proceeds through repeated cycles of testing, selection and recombination. We searched to optimize the breeding strategy for such a cycle using within-family selection. We focus on the most important factors for tree improvement: the raise of genetic gain, the disadvantage of increased relatedness, the cost of the testing methods, and the duration. A complete cycle is studied; the factors could be expressed as the gain per cycle, the drop in gene diversity per cycle, the cost per cycle, and the duration of a full cycle. The situation we envisaged was usually that the breeding population was double-pair mated and one selection was done per full-sib family based on phenotype, clone testing or progeny testing. Thus, a fully balanced breeding strategy was assumed. The possibility to make selection in two stages was considered.

METHODS: The breeding cycle is composed of a number of moments (Fig. 1), each of which takes certain time. The duration of the whole breeding cycle is a sum of a number of time components. The gain is depending on the duration of the field-testing, the longer the test the higher the gain. Cost is often expressed per breeding population member. There is a cost per genotype tested and a cost per test plant. There are also genetic parameters (additive variation in the goal character and additive, dominance and environmental variation in the measurement character, the weight factor for gene diversity versus breeding value) and rotation time, which is of importance for the accuracy of genetic testing as a function of testing time.

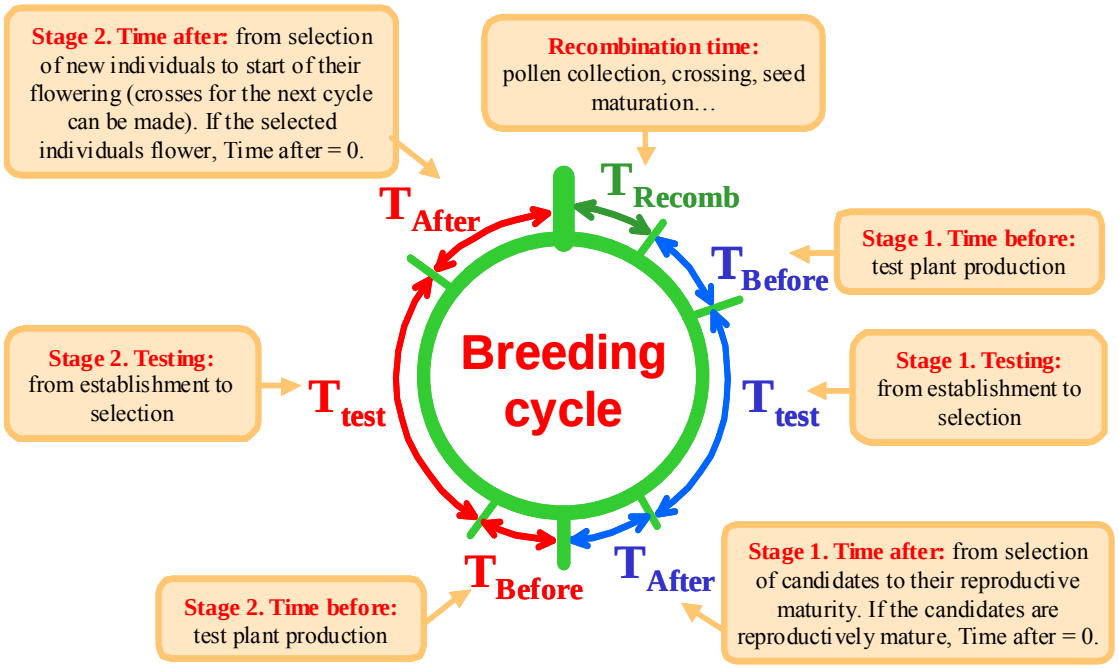

Figure 1. Illustration of the breeding cycle subdivided into time components used in the simulations. Cost components can be connected with the time components. Testing can be done in one or two stages.

The parameter maximized is annual Group Merit progress at a given annual cost, where Group Merit is a weighted average of genetic gain and gene diversity. In our studies we tested a set of scenarios for the northerly conifer breeding within reasonable bounds of the genetic, cost and time parameters. By using a deterministic approach, we have combined gain, diversity, cost and time in the "Breeding Cycler"- a simulator based on MS Excel. Breeding cycler is mainly aimed for optimizing closed-nucleus long-term breeding strategies based on repeated cycles of controlled mating, testing and selection. We choose the MS Excel platform to make the simulator more available and understandable.

MAIN FINDINGS: Clone testing, progeny testing and phenotypic testing were the major testing strategies compared. Clone testing of the candidates appears as the most efficient testing strategy (Fig. 2).

Clone testing was superior even if cost for cloning is high, time for cloning is long and there is some dominance

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variation. Norway spruce can be operationally cloned by rooted cuttings, although the propagation method is too expensive for operational forestry. Clone testing is used routinely in long-term breeding of Norway spruce in Sweden. Given what we consider relevant parameter values, the model suggested the following recipe for optimally efficient long-term breeding of Norway spruce: (1) mate each individual in the breeding population to two others; (2) produce 18 full-sibs from each cross; (3) propagate 15 cloned copies of each full-sib; (4) field test; (5) make selections based on performance of the cloned copies at age 15; (6) select the best tested clone within each full sib for the new breeding population; (7) make the next cycle of crosses for the next generation of the breeding population.

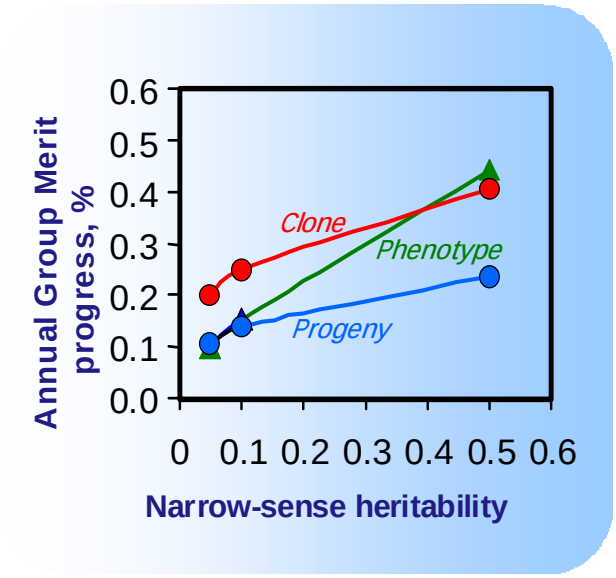

Figure 2. Comparison of annual progress in Group Merit using the main testing strategies at a variable heritability. Note, the efficiency of the Phenotype strategy, which becomes greater than for clonal testing at heritability above 0.4.

These numbers generated by the model are based on certain assumptions on a number of parameters considering a typical situation, for a real case under other assumed parameter values the most efficient numbers may be somewhat different.

Progeny testing appeared less efficient (Fig. 2), because of relatively longer cycle time dependent on the need for the candidate to reach their sexual maturity. Phenotypic testing was more efficient than progeny testing except for the lowest heritability, when it was about equally efficient as progeny testing (Fig. 2), when heritability is low, selection based on family performance becomes more reliable. At high heritability phenotypic selection is more efficient than clone testing, the phenotype approaches the clonal mean when heritability is high so cloning become an unneeded extra step at high heritability. Note, that the heritability here means individual narrow sense within-family heritability.

It is possible to have two stages in a breeding cycle: start with a phenotypic-based pre-selection and go on with a more careful test of the remaining candidates. It did not appear advantageous letting clone testing be preceded by phenotypic pre-selection. But it turned out more favorable to let progeny testing be proceeded by pre-selection based on phenotypic testing than either of the testing strategies alone for typical heritability. Phenotype pre-selection generates extra gain by taking advantage of the time before the candidates reach their sexual maturity. The advantage of phenotypic pre-selection increases the longer it takes till progeny testing can be performed (Fig. 3), even if there is not waiting time at all to sexual maturity (e.g., the perfect flowering stimulation recipe was invented) it still is more efficient to wait 10 years for the progeny testing to start.

The two-stage strategy seems a good strategy for the species, which are difficult to clone. Given what we consider relevant input parameter values, the model suggested (with same reservations as above) the following recipe for optimally efficient long-term breeding of Scots pine: (1) mate each individual in the breeding population to two others; (2) propagate 70 full-sibs from each cross; (3) field test; (4) make phenotypic pre-selection of 5 genotypes at age 10; (5) initiate progeny-test of these five candidates; (6) field test with 30 offspring from each candidate; (7) make evaluation of performance at age 10; (8) select the best progeny-tested candidate within each full sib for the new breeding population; (9) make the next cycle of crosses for the next generation of the breeding population.

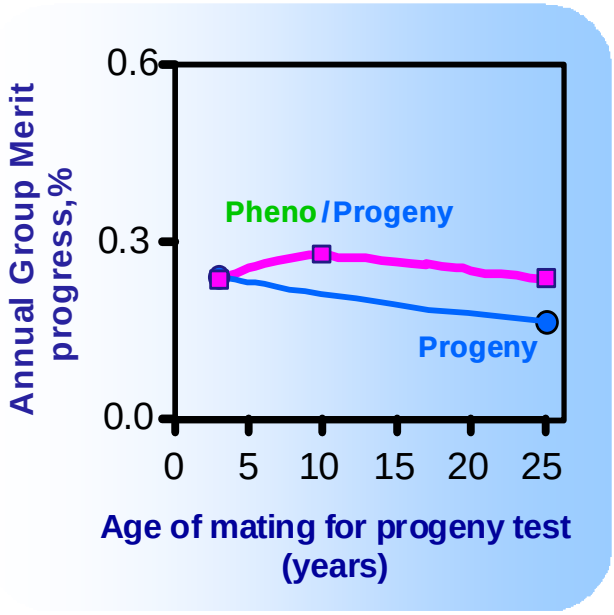

Figure 3. Comparison of annual progress in Group Merit from single stage progeny testing strategy and two-stage phenotype/progeny strategy at a variable age of mating for progeny test (basically age of sexual maturation). The optimum age of mating for the two-stage strategy varied between 10 to 15 years.

Ten years may be early to get seeds for progeny-test on Scots pine; it depends on the system used. But a delay to 15 years has little effect on the efficiency (Fig 3), thus efforts to promote early flowering may have limited practical value.

We have also developed a model for optimization of the long-term breeding population size by considering genetic gain, relatedness, time and cost components. It optimized the allocation of resources between the breeding and testing populations. The size of the breeding population was regarded optimal, when the annual increase in group merit was maximized at a budget constraint. The optimum breeding population size ranged between 30 and 70 (Fig. 4). High heritability, more efficient breeding strategy (clone or progeny versus phenotype), high additive variance at mature age, low annual budget, expensive testing method and a low value assigned to gene diversity favored a small breeding population size.

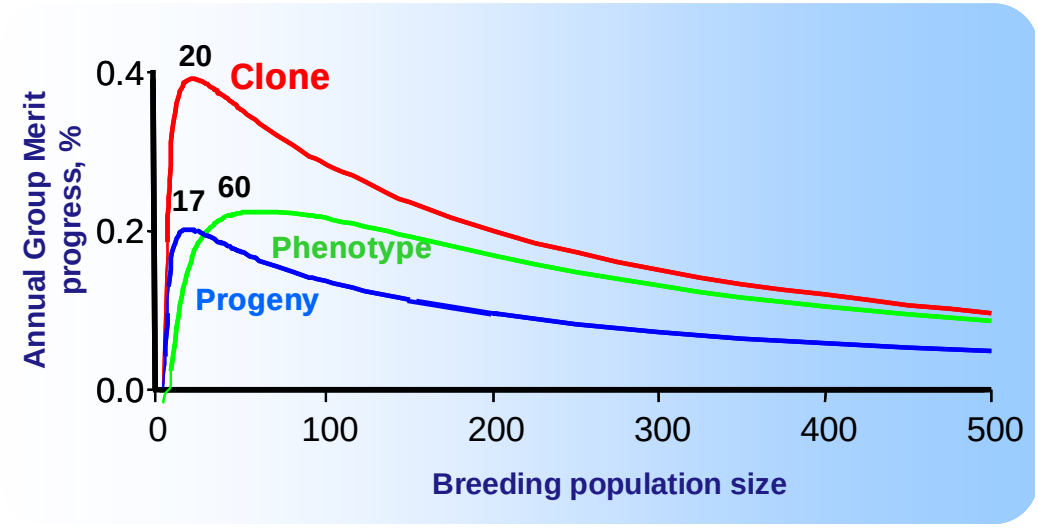

Figure 4. Breeding efficiency (annual group merit progress) as a function of the breeding population size for three testing strategies. The optima basically reflect the allocation of recourses between the breeding (meaning diversity) and testing (meaning testing precision) populations.

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The simulator can currently be downloaded at:
http://www.genfys.slu.se/staff/dagl/Breed_Home_Page/Breeding_Cycler/Breeding_Cycle_Menu.htm