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Strategy for long-term breeding of *Picea abies* in Lithuania: short overview

Abstract: This paper presents the newly suggested long-term breeding strategy for Norway spruce in Lithuania to share with the optimisation approach, which may be useful in synchronising the long-term breeding and gene conservation plans in neighbouring regions. The breeding programme in Lithuania is at a stage where the long-term plans need to be developed. Our strategy is to proceed with a closed-nucleus breeding population which is structured into subpopulations according to adaptation zones (4–5 subpopulations). The size of each subpopulation is 50 unrelated and progeny-tested individuals. The breeding cycle consists of double-pair mating and a balanced within-family selection forward. The candidates will be clone-tested. Advanced genotypes will be selected into an advanced nucleus; an isolated foreign breeding population is planned. Positive assortative mating is used for deployment. An experimental "shuttle-breeding" strategy may be tested: selection with a very high intensity, controlled crosses, nursery tests for vigour and growth rhythm, cloning by hedges into short-rotation clonal plantations.

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Future strategy of Norway spruce breeding in Lithuania

The problem with the present-day breeding programmes for Norway spruce and Scots pine in Lithuania is that these programmes were developed to increase the genetic gain, without long-term plans or optimisation of cost and time efficiency. The following questions remained unanswered: (a) How long will we be able to cope with the inbreeding depression caused by mating among the relatives? (b) Are the selected methods fast enough to achieve the genetic gain? (c) Are the methods cost-efficient? The gene diversity in the breeding population may soon become too narrow to allow new selections. Selection backwards usually takes a long time, and its accuracy in assessing the breeding values may be outweighed by a faster and more precise testing when selecting forward. The efficient breeding strategy should allow

one to achieve maximum genetic gain per unit loss of gene diversity by using cost- and time-efficient methods. This means that optimisation of the breeding plans is needed to simultaneously consider the genetic gain, gene diversity in the breeding population, and the cost and time of certain breeding methods.

After a number of optimisation studies (e.g. Danusevičius and Lindgren 2002a, b), the suggested outline of the breeding strategy for Norway spruce is the following (Fig. 1): 5–6 closed-nucleus breeding populations with 50 members each (one population for foreign individuals); controlled crossings by the double-pair mating design, which will produce 50 full-sib families; cloning of each full-sib family member and establishment of clonal tests; selection of one best full-sib family member by the performance of its clonal copies; crossing of these 50 best individuals as the new breeding population members for the next breeding cycle. Such strategy will allow one to main-
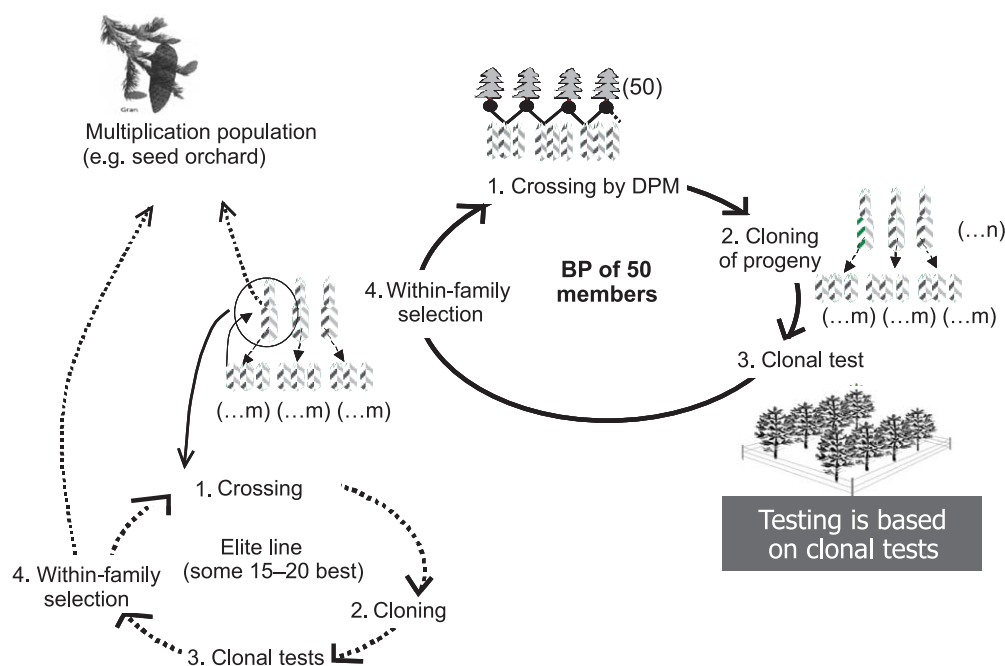
Fig. 1. Suggested long-term breeding strategy for Norway spruce in Lithuania

tain gene diversity in the breeding population at a sufficient level, and generate genetic gain for many breeding cycles by using cost- and time-efficient methods. The breeding population founders will be selected as progeny-tested parents. If necessary, forward selections based on a combined index will be used.

Orchard deployment strategy will be based on a restricted linear deployment method (Lindgren and Matheson 1986). After testing, one individual within
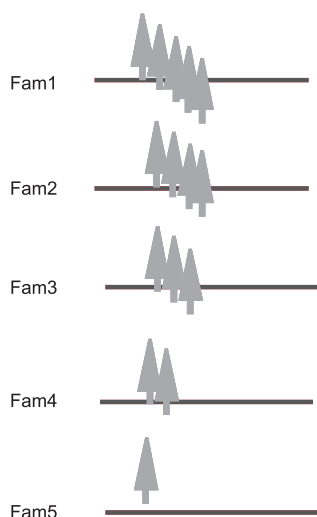

Fig. 2. Principle of the seed orchard deployment strategy by linear deployment of unrelated individuals. Only the top-ranking individual in each family is considered for deployment. The selections are deployed in the proportions linearly related to their breeding value. The number of families is chosen based on the diversity needed in the seed orchard

certain number of superior families (to be chosen to result in the status number of approximately 12 in the seed orchard) will be deployed proportionally to its breeding values, i.e. the number of ramets will be linearly related to the individual's breeding value. This strategy was found to be near to the optimum if large diversity is available for deployment, which usually is the case in progeny tests (Fig. 2) (Danusevièius and Lindgren 2008).

We used computer simulation as an efficient tool to develop and optimise breeding strategies. Our optimisation of long-term breeding strategies showed that clonal testing is by far the best cycling method (Danusevičius and Lindgren 2002a, b). If it is not available for species like Scots pine, a two-stage breeding strategy is suggested where phenotypic pre-selection is used at the first stage, followed by progeny testing of the pre-selected genotypes, and selection backwards of a balanced number of individuals within each family (Danusevičius and Lindgren 2002a, b).

Where development is needed?

Commercial forests in northern Europe are given increasingly more conservation and protective functions. The proposals to ban clear cuts and prolong the rotation age of natural forests are pending. On the other hand, the demand for such natural products as wood is increasing. A good solution is to invest more in short-rotation plantations of many species among which Norway spruce is a good candidate, especially on abandoned agricultural land. Specific breeding plans then may be needed for natural "green" forest

stands (forestry with long rotations: soft breeding with diversity reserves, orchards with many clones) and for short-rotation plantations. These plans may combine short-rotation forestry with aggressive breeding. The aggressive breeding strategies need to be developed, like for instance the following: cloning of 5 best genotypes from 3 tests (15 clones); establishing a cutting plantation which also serves as a test; recombining 5 best and testing the clonal copies of the full-sibs; selecting 10 superior individuals for commercial multiplication.

A suggestion by El-Kassaby and Lindgren (personal communication) for more efficient use of molecular markers in "half-full-sib breeding" is currently under examination: the male parent of the progeny can be identified with the aid of molecular markers. To test this suggestion, we need to develop genotype-specific markers for some N best genotypes in a test or orchard, find several forest or experimental plantations established with this orchard's seed, identify N good growing phenotypes in these plantations, and identify the parents of good performing phenotypes with the aid of genotype-specific DNA markers. To screen the efficiency of the above-mentioned breeding strategy, several pilot studies are planned to assess the success of fertilisation in seed orchards: is it a random process or are there certain clones dominating as fathers? In the same seed orchard, we will (a) collect seeds from another N best genotypes and identify their fathers by cpDNA markers; (b) collect pollen of 20 clones and use this pollen mixture for polycross to identify the winning fathers in the seed.

Another issue is the use of epigenetic technologies to manipulate trees (without genetic transformation), e.g. silencing by RNRi. This technique was successfully applied for poplar by Bohlenius et al. (2006). A better understanding of genomic imprinting and paramutation in trees may be acquired by reciprocal crossings among individuals with contrasting flowering traits with known specific-allele markers to identify the presence or absence of a particular allele and phenotypic expression of the trait. The following hypothesis could be tested: even though the allele failed to get into the progeny, but its remains – the siRNR – did and affect the expression of the allele from the other parent.

There is good news for old provenance tests: we may use them in breeding to exploit hybrid vigour. The strategy is to make a polycross with local pollen in the provenance tests. Cloning of the superior hybrid progeny may efficiently exploit the hybrid vigour from inter-provenance crosses. In one of our experiments, we compared the performance of the intraspecific hybrid progeny with the progeny of the autochthonous populations of Scots pine at age 23 in a field trial (Danusevičius 2008). The polycross prog-
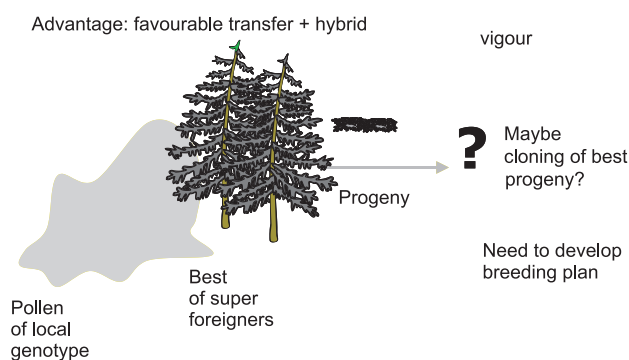

Fig. 3. Suggested strategy to use old provenance trials to capture hybrid vigour from the polycross with the local pollen

eny were markedly taller and of better stem quality than their autochthonous counterparts (Fig. 3 and 4). The local population was by far the best in both wood yield and stem quality. The study showed that (a) the local male parent introduced by a pollen mixture in a polycross markedly improved the wood yield and quality of Scots pine progeny, (b) the short- or long-distance transfer did not markedly improve the adaptation traits given the climatic conditions of Lithuania. An idea was suggested for practical breeding to use a pollen mixture of known foreign origin to pollinate superior local females in seed orchards, or vice
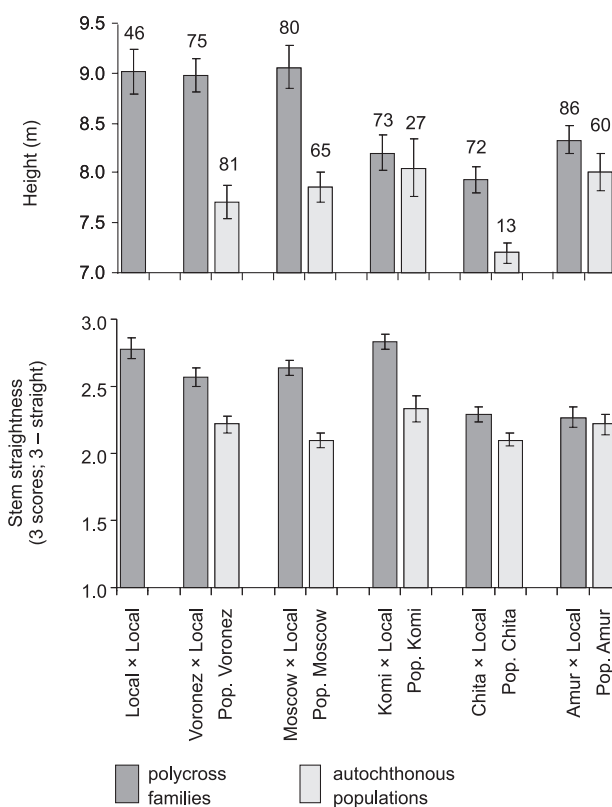

Fig. 4. Results for a provenance hybrid (local × foreign) test: hybrid polycross progeny were superior over autochthonous at age 23 years

versa, to give new life to old provenance trials by pollinating the desired foreign clones with the pollen of the best locals. Old provenance tests may also be used to assess the effects of climatic change; especially interesting is how it affects the reproduction traits.

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