Treebreedex

A working Model Network of Tree Improvement towards a Competitive, Multifunctional and Sustainable European Forestry

Activity 5 “Optimization of breeding strategies”;

task E “State-of-the-art synthesis on scientific and technical methodological aspects”

Efficiency of tree breeding strategies in Europe

Report from the Questionnaire “Testing strategies in tree breeding”

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This report presents results form the questionnaire “Testing strategies in tree breeding”, which was carried out for Activity 5 “Optimization of breeding strategies”; task E “State-of-the-art synthesis on scientific and technical methodological aspects”; sub-task “Optimizing testing strategies: balancing gain and diversity”

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Contents

Summary

Efficient breeding implies optimum allocation recourses between high and low input breeding and optimal combination of genetic gain, gene diversity, costs and time. This combination strongly depends on the long-term breeding plans and the input in breeding. The experience is gained, but not equally among the European countries, where breeding is driven by variable ownership types and interests. To maximise the efficiency of breeding at the pan-European perspective, it is beneficial to gain from experience of scientifically-sound strategies. The objective of this questionnaire is to prepare a review on how breeding programs of forest trees are designed and what testing strategies are used in European countries. The ultimate goal is to improve efficiency of breeding by taking advantage of the efficient practice. The questionnaire consists of 3 parts: (I) breeding strategies and testing/selection methods used for each species,(II) tools available to optimise the testing strategies and (III) literature list on optimization of breeding strategies of forest trees. In total, answers on 115 breeding programs from 28 forest tree species were obtained from 19 Treebreedex institutions (representing 19 countries). The main forest countries responded. No breeding programmes were reported for such wide-spread conifers as *Juniperus* and *Taxus bocata*. Most breeding efforts are focused 3 coniferous species (*Pinus sylvestris, Picea abies and Larix sp.*) and on 4 broadleaved species (*Populus sp., Betula sp., Fraximus sp. and Prunus avium*). The general statistics on breeding is as follows: 60% of all are long-term programmes; 52% high input; 30% do not subdivide the breeding stock into breeding populations and as much as 40% use the site type and natural species distribution as the main criterion for subdividing into breeding populations (meaning not eco-climatic zones or adaptive environments); only 10% maintain nucleolus breeding population for generating high gain; 47 % uses closed breeding populations with no infusion of genetic material from outside; only 33% use controlled mating among breeding populations members; 87% use the same testing strategy for different traits; 48% breeding and multiplication populations are not separated; 69 % use among and within family selection; 50% uses two-stage phenotype-progeny testing strategy; 8 % use molecular markers in breeding and 5% use simulations to optimise breeding (most were willing to use simulations). In the analyses of the answers, the breeding strategies were subdivided into 4 categories based on terms and input: "long-term high-input"; "long-term-low-input"; "short-term high-input” and “short-term low-input” and methods of breeding with each of these 4 strategies were analysed.

1. Introduction

Efficient breeding implies optimum allocation recourses between high and low input breeding and choice of efficient testing strategies. It may not be easy to optimally combine genetic, gene diversity costs and time depending on the economic and ecological importance of a series of species (Fig. 1.1.1). Allocation of the recourses may reach its optimum when the input is associated with the economical importance of the species. Efficiency of breeding mainly depends on appropriate testing strategy to control the relatedness and to provide maximum genetic gain per unit of time and the genetic diversity lost. The experience is gained, but not equally among the European countries, where breeding is driven by variable ownership types and interests. To maximise the efficiency of breeding at the pan European perspective, it is beneficial to gain from experience of scientifically-based strategies. A first step to achieve this goal is to prepare analysis of the present situation with breeding and testing strategies in Europe.

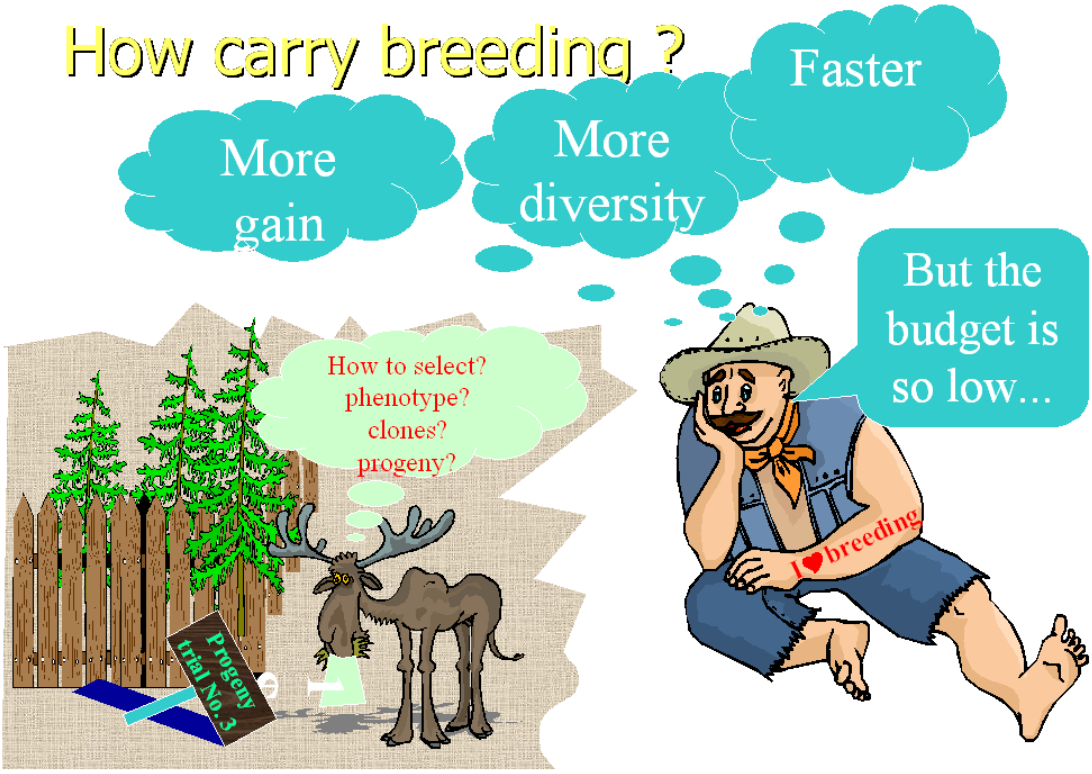

Fig. 1.1.1. When drafting breeding programmes, decisions need to be made on allocation of recourses (inputs) for a number of species, terms of breeding and all subsequent methods, such as mating, testing, selection. This makes a complex task, which if not properly solved could lead to inefficient breeding.

The objective of this questionnaire is to prepare a review on how breeding programs of forest trees are designed and what testing strategies are used in European countries. The ultimate goal is to improve efficiency of breeding by taking advantage of efficient experiences and excluding repetition of common mistakes, in this way raising efficiency and compatibility of European forest sector. It will also allow establishing “testing tools shelf” in the Virtual Breeding center containing the tools and demonstrations to be used as guidelines when searching for the optimum testing method for a given situation in tree breeding.

This questionnaire consists of 3 parts. Part 1: What breeding strategies and testing/selection methods are used for certain species? Part 2: What tools are available to optimise the testing strategies? Part 3: Literature list on optimization of breeding strategies of forest trees.

2. Material and methods

2.1. Terminology.

For the sake of common understanding of what is addressed in the questionnaire the following terms were suggested and distributed with the questionnaire.

Long-term breeding: breeding planned for long-term with specific plans to maintain sufficient level of gene diversity in breeding population for many breeding cycles.

Short-term breeding: breeding aimed for rapid generation of genetic gain with no specific plans to maintain required level of gene diversity inbreeding population for more than a few breeding cycles.

High-input breeding: high intensity genetic improvement system aimed at generation of high and reliable benefit at the cost of comparable large investment.

Low-input breeding: a low intensity genetic improvement activity, which does not require large investment (e.g. seed collection stands).

Multiple population breeding system: the breeding population is subdivided in several smaller populations that are bred for different objectives.

Breeding population: the group of individuals that will carry the advancement of breeding into future generations.

Candidate (testing) population: group of individuals that carry the recombined genes of the breeding population members and are tested to qualify as breeding population members for the next breeding cycle.

Multiplication (propagule) population: the group of individuals primarily aimed for sexual or vegetative multiplication of the genetically advanced material for commercial purposes (seed orchard, hedges for cloning).

Nucleus breeding: breeding scheme where populations in breeding cycle are divided into intensively managed nucleus with top-ranking genotypes and less intensively managed genetically less advanced main population.

Breeding cycle: the successive alternation of recruitment, candidate and breeding populations in one breeding generation.

Testing/selection strategy in recurrent breeding (cycling strategy): the testing/selection method used repeatedly over a series of identical breeding cycles (long term breeding)

Single-pair mating (SPM): each BP member mated to another BP member only once (need to select 2 best within each family to maintain constant BP size)

Double pair mating (DPM): each BP member mated to two other BP members (need to select 1 best within each family to maintain constant BP size)

Single-stage selection strategy: selection of the candidates carried out at one occasion within breeding cycle (nursery pre-screening may be ignored).

Two-stage selection strategy: selection made at 2 stages within one breeding cycle: a pre-selection of certain number of candidates at stage one followed by further testing of the pre-selected candidates and selection of the new BP members at the second stage (testing methods may differ between the stages).

Phenotype testing: testing and selection is based on the individual's phenotype and phenotypes of its relatives (if available).

Clone testing: individuals are tested and selected based on performance of their clonal copies. (alternative definition: individual's breeding value is predicted based on performance of its clonal copies)

Progeny testing: individuals are progeny tested and selected based on the performance of their progeny. (alternative definition: individual's breeding value is predicted based on performance of its progeny copies)

Open nucleus breeding is a method to maintain gene diversity in the breeding populations by recurrent infusion of genetic material from outside (e.g. from natural stands).

Closed nucleus breeding is a method to maintain gene diversity in the breeding populations by using certain selection strategies but no infusion of material from outside.

Deterministic simulator performs simulations based solely on algorithms and formulas.

Stochastic simulator performs simulations allowing random factors in addition to algorithms and formulas.

2.2. The questionnaire explained.

Table 2.1. Explanation of the questions, the possible answers and their aim.

Question	Possible answers	Comment to the question	Aim of the question
1. Are there specific plans to maintain sufficient level of gene diversity in breeding populations for many breeding cycles?	1. Yes (long term breeding)	Long-term breeding is breeding planned for long-term with specific plans to maintain sufficient level of gene diversity in breeding population for many breeding cycles. Short-term breeding is breeding aimed for rapid generation of genetic gain with NO specific plans to maintain required level of gene diversity in breeding population for more than a few breeding cycles.	This question is essential and shall be addressed before starting any breeding programme, because main design and strategy depends on the long-term aims of the programme and shall be chosen to provide optimum balance genetic gain and diversity.
	2. No (short term breeding)		
2. Are you aiming at high intensity breeding to obtain high benefit at the cost of large investments?	1. Yes (high input breeding)		It connects to the question above, because usually if a program is long term, it consumes large resources and is high input. However, there could be short term strategies with high input efforts, for instance plantation forests for fast timber or biomass production in a 50-100 year perspective and perspective. If answer is high input and long term then it can be ignored as it givens no sense.
	2. No (low input breeding)	High-input breeding is high intensity genetic improvement system aimed at generation of high and reliable benefit at the cost of comparable large investment. Low-input breeding is a low intensity genetic improvement activity, which does not require large investment (e.g. seed collection stands).	
3. How among-population gene diversity is captured by the breeding program?	1. Multiple breeding populations, one in each breeding zone	Multiple population breeding system: the breeding population is subdivided in several smaller populations that are breed for different objectives (e.g. different adaptive zones).	It is important not to make mistake with adaptedness and in each adaptive environment to start with the most adapted material Failure
	2. Multiple breeding populations, established by administrative districts		

	3. Multiple breeding pops. based on site type or natural species range 4. Other, state which 5. No attention is paid: all range is one breeding zone		to consider adaptedness may lead low breeding efficiency and low return from the investments.
4. Do you divide breeding population into intensively managed nucleus with top-ranking genotypes and less intensively managed main population	1. Yes 0. No	Nucleus breeding: separation of a smaller group of genetically advanced trees within the breeding population.	In case of long term breeding, where the need to carry gene diversity load slows dawn the genetic gain, such division allows to achieve higher gains for the near future and satisfy the stakeholders in faster returns.
5. How is gene diversity maintained in (or planned) in the breeding population (BP)?	1. Open population, recurrent infusion of genetic material. 2. Closed population, no infusion of new material. 3. Other method (state which) 4. No long-term plans,	Open breeding population (nucleus) breeding is a method to maintain gene diversity in the breeding populations by recurrent infusion of genetic material from outside (e.g. from natural stands) Closed breeding population (nucleus) is a method to maintain gene diversity in the breeding populations by using certain selection strategies (e.g. within-family selection) but no infusion of material from outside.	There alternatives to maintain gene diversity, having own advantages at specific cases. Is the most appropriate chosen? If one is planning for long term breeding and makes no thinking on how to maintain gene diversity in long run, he is seriously mistaken …
6. Which mating system among breeding population members is used (or planned) to create the candidate population?	1. Controlled pollination (SPM, DPM, diallel, factorials, polycross, other) 0. Open pollination	Single-pair mating (SPM): each BP member mated to another BP member only once (need to select 2 best within each family to maintain constant BP size) Double pair mating (DPM): each BP member mated to two other BP members (need to select 1 best within each family to maintain constant BP size) Breeding population (BP): the group of individuals that will carry the advancement of breeding into future generations. Candidate (testing) population: group of individuals that carry the recombined genes of the breeding population members and are tested to qualify as breeding population members for the next breeding cycle.	It is simple but important decision, where OP suppose to lead because it is cheap. However, loss of the genetic gain by using OP in certain cases may not be tolerated. How one will control relatedness and prevent inbreeding depression in an OP population?
7. Are different testing strategies used for different traits	1. Yes, different strategies (indicate which for which) 0. No, the same strategies	An example of different: progeny testing for wood yield (low heritability) and phenotype testing for growth rhythm (high heritability).	Is such complex approach really efficient?
8. Is breeding population and multiplication population separated from each other as regards location and genetic composition?	1. Yes, separated geographically 2. Yes, separated genetically 3. Yes, separated geographically and genetically	Breeding population (BP): the group of individuals that will carry the advancement of breeding into future generations. Multiplication (propagule) population: the group of individuals primarily aimed for	This question is important as regards optimum deployment of the genetic gain (keeping all BP as MP in one seed orchard is very

	4. No, not separated	sexual or vegetative multiplication of the genetically advanced material for commercial purposes (seed orchard, hedges for cloning). Example of geographic separation is when set of genotypes located in a crossing archive (breeding population) close to institute and the same set of their copies in a "milder" location to get more seeds. Example of genetic separation is family seed orchard thinned based on own performace or clonal orchard thinned on based on progeny test. Example of genetic and geographic separation is when certain number of the best genotypes located in a crossing archive (breeding population) is deployed in a seed orchard, established at another site. Example NO separation is a clonal seed orchard with progeny of the clones under test but no thinning is planned. Or 2nd generation seed orchard with backwards selected clones.	inefficient)
9. Level of selection	1. Within families 2. Among families 3. Among and within families 4. Other, free comment	Breeding cycle the successive alternation of recruitment, candidate and breeding populations in one breeding generation. Note, when establishing BP, selection may be made among families, but later for each new breeding cycle, it is made within fmailies. In such case the answer is "within families".	It concerns how efficient one may control the coancestry in BP
10. What testing strategy is used/planned to select the BP members (pre-screening in nursery for growth rhythm or vitality may be considered as single-stage):	1. Single-stage: phenotype testing 2. Single-stage: clone testing 3. Single-stage: progeny testing 4. Two-stage: phenotype/progeny testing 5. Two-stage: phenotype/clone testing	Single-stage selection strategy: selection of the candidates carried out at one occasion within breeding cycle (nursery pre-screening may be ignored). Two-stage selection strategy: selection made at 2 stages within one breeding cycle: a pre-selection of certain number of candidates at stage one	This addresses the testing efficiency and many are forgetting that it is not the only genetic gain but also time and cost are equally important factors. Are they considered?

	6. Other, free comment	followed by further testing of the pre-selected candidates and selection of the new BP members at the second stage (testing methods may differ between the stages). Phenotype testing: testing and selection is based on the individual's phenotype and phenotypes of its relatives (if available). Clone testing: individuals are tested and selected based on performance of their clonal copies. (alternative definition: individual's breeding value is predicted based on performance of its clonal copies) Progeny testing: individuals are progeny tested and selected based on the performance of their progeny. (alternative definition: individual's breeding value is predicted based on performance of its progeny copies).	
11. Is information on molecular markers used to aid the selection?	1. Yes (list the traits)		What is use of markers in practice? Main perspective SNPs in major genes.
	2. No		
12. Have you used simulations?	1. Yes		What are the tools available to help breeders
	2. No		

3. Results

3.1 General

In total, answers on 114 breeding programs of 28 forest tree species from 23 Treebreedex institutions (representing 19 countries) were obtained. The main forest countries responded.

No breeding programmes were reported for such wide-spread conifers as *Juniperus* and *Taxus bocata*.

Most of the breeding efforts are focused on 3 coniferous species (*Pinus sylvestris, Picea abies* and *Larix* sp.) and on 4 broadleaved species (*Populus sp., Betula sp., Fraxinus sp. and Prunus avium*) (Fig. 2.1.1). *Pseudotsuga menziesii* is among the leading in breeding effort among the exotic species and ranks as forth as regards numbed of breeding programmes.

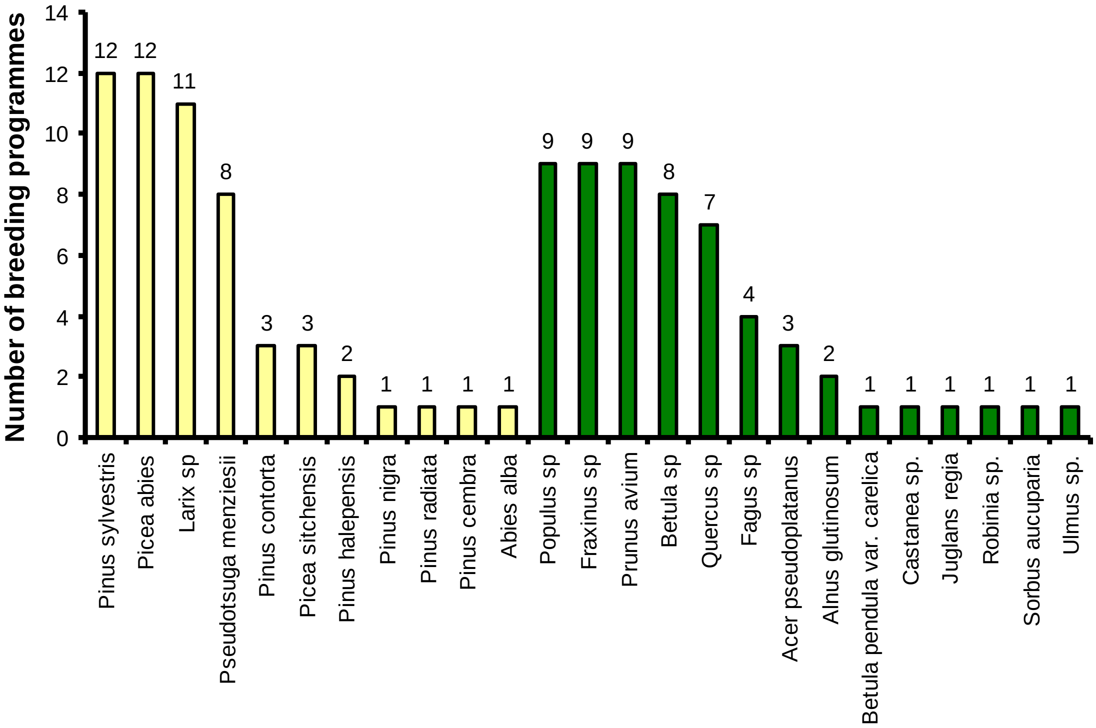

Fig. 3.1.1. Number of breeding programmes for each tree species sorted by coniferous (left) and broadleved (right).

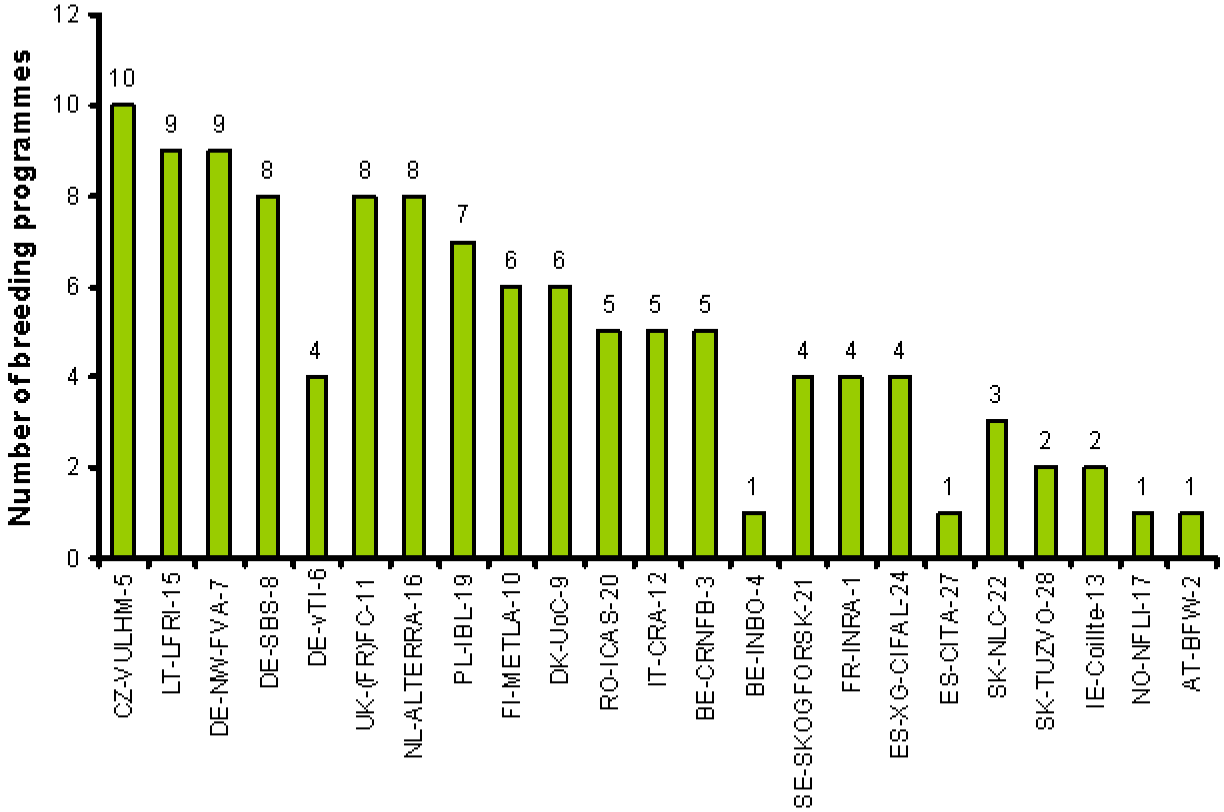

Fig. 3.1.2. Number of breeding programmes per Treebreedex institution. Abbreviation explained "LT-LFRI-15" means "country code - institution's abbreviation – Treebreedex number".

As regards number of breeding programmes per country, central European countries with landscapes suitable for forestry are leading, starting from the absolute leader Germany with 21 breeding programme (Fig. 3.1.2). There is no strong connection between the county's woodenness and number of species included in breeding (Fig. 3.1.2).

For the reference when interpreting the later results, all answers are summarised by species in Table 3.1. The general statistics on breeding is as follows: 60% of all are long-term programmes; 52% high input; 30% do not subdivide the breeding stock into breeding populations and as much as 40% use the site type and natural species distribution as the main criterion for subdividing into breeding populations (meaning not eco-climatic zones or adaptive environments); only 10% maintain nucleolus breeding population for generating high gain; 47 % uses closed breeding populations with no infusion of genetic material from outside; only 33% use controlled mating among breeding populations members; 87% use the same testing strategy for different traits; 48% breeding and multiplication populations are not separated; 69 % use among and within family selection; 50% uses two-stage phenotype-progeny testing strategy; 8 % use molecular markers in breeding and 5% use simulations to optimise breeding.

Table 3.1. Summary of the questionnaire by presenting the number of answers counted for each species. Hints of the questions and the answers are given in the heading (full questions see Table 2.1).

Species	Species code	Long term?		High input?		Multiple breeding populations?				
		Q1		Q2		Q3				
		0	1	0	1	1	2	3	4	5
		no	yes	no	yes	by zones	by district	site type or spec. distrib.	other	no attention
Pinus sylvestris	1	3	9	5	7	3	1	4	0	4
Picea abies	2	3	9	3	9	3	1	7	0	1
Pinus contorta	3	1	2	3	0	1	0	0	1	1
Larix sp	6	5	6	3	8	2	1	4	0	4
Quercus sp	7	2	5	5	2	2	1	3	0	1
Fraxinus sp	8	5	4	5	4	2	1	4	0	1
Betula sp	9	3	5	5	3	3	1	3	0	1
Betula pendula var. carelica	9.1	1	0	1	0	0	0	0	0	1
Fagus sp	10	1	3	2	2	1	1	2	0	0
Populus sp	11	5	6	3	8	0	1	3	1	6
Prunus avium	13	6	3	3	6	1	0	4	0	3
Robinia sp.	14	1	0	1	0	1	0	0	0	0
Pseudotsuga menz.	15	3	5	4	4	3	0	3	1	1
Picea sitchensis	16	0	3	1	2	0	0	1	0	2
Alnus glutinosum	18	0	2	2	0	2	0	0	0	0
Acer pseudoplatanus	19	3	0	2	1	0	0	1	0	2
Pinus cembra	20	0	1	0	1	0	0	1	0	0
Pinus nigra	21	1	0	1	0	0	0	0	0	1
Pinus radiata	22	1	0	1	0	0	0	0	0	1
Castanea sp.	23	0	1	1	0	1	0	0	0	0
Ulmus sp.	24	1	0	0	1	0	0	0	1	0
Sorbus aucuparia	25	0	1	1	0	0	0	1	0	0
Juglans regia	26	0	1	0	1	0	0	1	0	0
Abies alba	27	0	1	1	0	0	0	1	0	0
Pinus halepensis	28	1	1	2	0	0	0	2	0	0
	Total	46	68	55	59	25	8	45	4	30
	Percent	40	60	48	52	22	7	40	4	27

Table 3.1 continued. Number of certain answers given by species. Hints of questions and answers are given in the heading (full questions see Table 2.1).

Species	Species code	Nucleus breeding population?		How keep gene diversity in long-term?				Mating type?	
		Q4		Q5				Q6	
		0	1	1	2	3	4	1	2
		no	yes	open BP	closed	other	no long term plan	CP	OP
Pinus sylvestris	1	11	1	5	4	1	2	5	7
Picea abies	2	9	3	2	7	0	3	5	7
Pinus contorta	3	3	0	0	2	0	1	1	2
Larix sp	6	11	0	1	6	1	3	5	6
Quercus sp	7	7	0	2	4	0	1	0	7
Fraxinus sp	8	9	0	1	5	0	3	0	9
Betula sp	9	8	0	2	4	0	2	3	5
Betula pendula var. carelica	9.1	0	1	0	1	0	0	1	0
Fagus sp	10	4	0	2	2	0	0	0	4
Populus sp	11	9	2	6	2	3	0	9	2
Prunus avium	13	9	0	3	4	0	2	1	8
Robinia sp.	14	1	0	0	1	0	0	0	1
Pseudotsuga menz.	15	7	1	1	5	1	1	3	5
Picea sitchensis	16	2	1	1	2	0	0	2	1
Alnus glutinosum	18	2	0	0	2	0	0	1	1
Acer pseudoplatanus	19	3	0	0	1	0	2	0	3
Pinus cembra	20	0	1	0	1	0	0	1	0
Pinus nigra	21	1	0	0	1	0	0	0	1
Pinus radiata	22	0	1	1	0	0	0	0	1
Castanea sp.	23	1	0	0	0	0	1	0	1
Ulmus sp.	24	1	0	0	0	1	0	1	0
Sorbus aucuparia	25	1	0	1	0	0	0	0	1
Juglans regia	26	1	0	1	0	0	0	0	1
Abies alba	27	1	0	1	0	0	0	0	1
Pinus halepensis	28	2	0	1	0	1	0	0	2
	Total	103	11	31	54	8	21	38	76
	Percent	90	10	27	47	7	18	33	67

Table 3.1 continued. Number of certain answers given by species. Hints of questions and answers are given in the heading (full questions see Table 2.1).

Species	Species code	Different testing for different traits		Is MP and BP separated?				Level of selection			
		Q7		Q8				Q9			
		0	1	1	2	3	4	1	2	3	4
		no	yes	yes geography	yes genetically	yes 1+2	no	within	among	within+ among	other
Pinus sylvestris	1	11	1	2	0	4	6	2	3	6	1
Picea abies	2	11	1	2	0	4	6	2	1	7	2
Pinus contorta	3	2	1	0	0	1	2	1	1	1	0
Larix sp	6	10	1	4	0	4	3	1	4	5	1
Quercus sp	7	6	1	2	0	1	4	0	1	4	2
Fraxinus sp	8	8	1	3	0	1	5	1	1	4	3
Betula sp	9	7	1	1	0	2	5	2	1	4	1
Betula pendula var. carelica	9.1	1	0	0	0	1	0	0	0	1	0
Fagus sp	10	3	1	1	0	1	2	0	0	3	1
Populus sp	11	8	3	3	1	1	6	0	1	7	3
Prunus avium	13	8	1	3	1	1	4	0	1	5	3
Robinia sp.	14	1	0	0	0	0	1	0	0	0	1
Pseudotsuga menziesii	15	8	0	3	0	0	5	0	2	4	2
Piceaw sitchensis	16	3	0	0	0	1	2	1	0	1	1
Alnus glutinosum	18	2	0	1	0	1	0	1	0	1	0
Acer pseudoplatanus	19	3	0	1	0	0	2	0	1	1	1
Pinus cembra	20	1	0	1	0	0	0	0	0	1	0
Pinus nigra	21	1	0	0	0	1	0	0	1	0	0
Pinus radiata	22	0	1	0	0	1	0	0	0	1	0
Castanea sp.	23	0	1	0	1	0	0	0	0	1	0
Ulmus sp.	24	0	1	0	1	0	0	0	0	1	0
Sorbus aucuparia	25	1	0	0	1	0	0	1	0	0	0
Juglans regia	26	1	0	0	1	0	0	0	1	0	0
Abies alba	27	1	0	0	1	0	0	0	1	0	0
Pinus halepensis	28	2	0	0	0	0	2	0	1	1	0
	Total	99	15	27	7	25	55	12	21	59	22
	Percent	87	13	24	6	22	48	11	18	52	19

Table 3.1 continued. Number of certain answers given by species. Hints of questions and answers are given in the heading (full questions see Table 2.1).

Species	Species code	Testing strategy						MAS		Simulations		Total no of prog.s
		Q10						Q11		Q12		
		1	2	3	4	5	6	0	1	0	1	
		1stage PH	1stage CLO	1stage PRO	2stage PH/PR	2stage PH/CL	pther	no	yes	no	yes	
Pinus sylvestris	1	1	0	3	8	0	0	11	1	11	1	12
Picea abies	2	0	3	1	6	0	2	12	0	10	2	12
Pinus contorta	3	1	0	2	0	0	0	3	0	3	0	3
Larix sp	6	2	0	3	6	0	0	10	1	11	0	11
Quercus sp	7	1	0	1	4	0	1	7	0	7	0	7
Fraxinus sp	8	3	0	1	4	0	1	9	0	9	0	9
Betula sp	9	2	1	0	3	1	1	8	0	8	0	8
Betula pendula var. carelica	9.1	0	0	0	1	0	0	1	0	1	0	1
Fagus sp	10	1	0	0	3	0	0	4	0	4	0	4
Populus sp	11	0	3	0	5	3	0	9	2	11	0	11
Prunus avium	13	0	1	0	5	1	2	7	2	9	0	9
Robinia sp.	14	0	0	0	1	0	0	1	0	1	0	1
Pseudotsuga menziesii	15	0	0	2	5	0	1	8	0	6	2	8
Piceaw sitchensis	16	0	0	1	1	0	1	3	0	3	0	3
Alnus glutinosum	18	1	0	0	0	1	0	2	0	2	0	2
Acer pseudoplatanus	19	1	0	1	1	0	0	3	0	3	0	3
Pinus cembra	20	0	0	0	1	0	0	1	0	1	0	1
Pinus nigra	21	0	0	1	0	0	0	1	0	1	0	1
Pinus radiata	22	0	0	0	1	0	0	1	0	0	1	1
Castanea sp.	23	0	0	0	0	1	0	0	1	1	0	1
Ulmus sp.	24	0	0	0	0	0	1	1	0	1	0	1
Sorbus aucuparia	25	0	1	0	0	0	0	0	1	1	0	1
Juglans regia	26	1	0	0	0	0	0	0	1	1	0	1
Abies alba	27	1	0	0	0	0	0	1	0	1	0	1
Pinus halepensis	28	0	0	0	2	0	0	2	0	2	0	2
	Total	15	9	16	57	7	10	105	9	108	6	114
	Percent	13	8	14	50	6	9	92	8	95	5	

3.2. Choice of the breeding strategy: duration and input.

Aim of this question and the interpretation of the results.

When preparing breeding strategy, the first decision is on the durability (meaning long terms such a uncertain future) and the financial input into the breeding programme. Most of the subsequent components of the breeding programme depend on the long-term durability of the programme, i.e. finding optimum balance between the two opposite factors – the genetic gain and gene diversity. If the species possess a high capacity for long-term commercial interest, it deserves to receive a long term breeding effort. Usually in the respect “long-term” is meant “uncertain future”- that is gene diversity reserve should be sufficient for centuries of breeding. This means that such programme may also serve for gene conservation. Long-term breeding is breeding planned for long-term with specific plans to maintain sufficient level of gene diversity in breeding population for many breeding cycles. Long-term breeding means commitment for a long-term investment, which requires significant amount of resources. Such investment is profitable for commercially important species or from gene conservation point of view. Whereas, short-term breeding is breeding aimed for rapid generation of genetic gain with no specific plans to maintain required level of gene diversity inbreeding population for more than a few breeding cycles. The answers may allow analysing the efficiency of the methods used for certain cost and durability scenario as compared with the scientific evidence form simulations studies and practice.

This chapter summarises answers of the following two questions:

1. Are there specific plans to maintain sufficient level of gene diversity in breeding populations for many breeding cycles? (answers: yes, no).
2. Are you aiming at high intensity breeding to obtain high benefit at the cost of large investments? (answers: yes, no).

The review of the answers showed that long-term breeding plans are intended for 60% of the breeding programs and intentions to invest much in intensive breeding are foreseen in 58% of the breeding programs. Among the top leading with 6 to 9 long tem breeding programmes are Czech Republic, Poland and Lithuania. As regards the inputs, the top three leaders with 8 to 9 breeding programmes are the Netherlands, Göttingen (Germany) and the Czech Republic.

As regards the duration and the financial input (cost) and the following types of breeding strategies were emerging (Fig. 3.2.1):

1. **Long-term and high-input breeding strategy here defined to as "commercial forestry" breeding strategy,** where the motivation is obtain maximum benefit at a high cost (input) and the investments are intended to maintain the gene diversity reserve for uncertain future. This strategy is optimal for a widespread dominant species of high commercial value.
2. **Short-term and high input breeding strategy here defined as "plantation forestry breeding strategy"**, where the main aim is to produce high gain at a short time without long-term plans. It seems to suite immediate demands for fast gain, without caring much for the diversity reserve such as for short rotation plantations.
3. **Long-term- low input here defined as "conservation forestry breeding strategy".** Here the emphasis is on preserving the gene diversity and other ecological functions, where economical gains are less important than gene diversity for conservation but if possible efforts for improving forests are also foreseen. State-driven companies and countries with less importance of forest sector or some of the exotic species earlier thought as important and now conserved for uncertain needs. Also it may be considered as an upper grade of low-input strategy with thought to do more than minimum but no complex and costly strategies. This strategy emerged in the countries were breeding activities were initiated and later abandoned or left al a low priority but the intentions are to conserve what was earlier achieved (e.g. DK).
4. **Short-term and low-input, here defined as "classical low input breeding",** where the aim is to conserve or improve as minimum cost (good to do something when we can). This category mainly includes economically less important species.

The detailed results are presented by species groups below. The species were divided into groups: widespread native conifers (*Picea abies, Pinus sylvestris, Larix sp*.), exotic conifers (*Pinus contorta, Picea sitchensis, Pseudotsuga menziesi*), southern conifers (*Pinus halepensis, Pinus nigra, Pinus radiata, Pinus cembra, Abies alba)*, fast-growing broadleaves (*Populus sp., Alnus glutinosum, Betula sp*.), slow growing broadleaves (*Quercus sp., Fraxinus sp., Prunus avium, Fagus sp*.) and scattered broadleaves (*Acer pseudoplatanus, Robinia sp., Sorbus aucuparia, Ulmus sp., Juglans regia, Betula pendula var. carelica, Castanea sp.)*

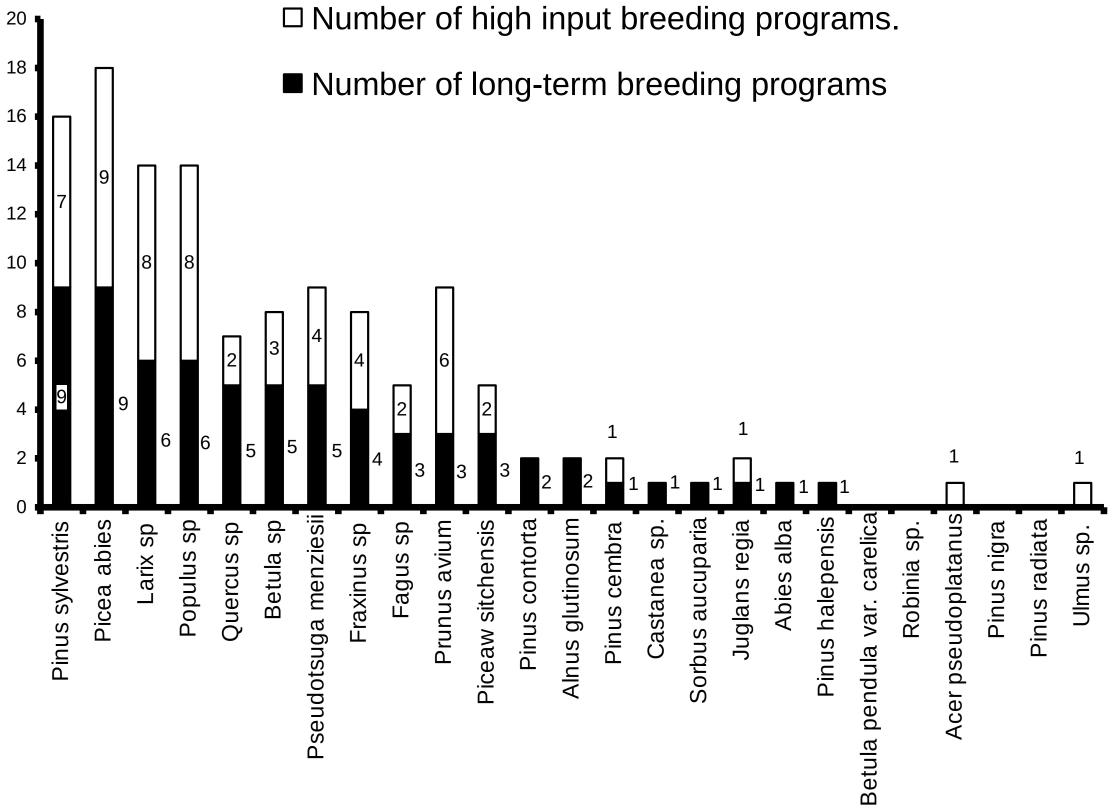

Fig. 3.2.1. Number of long-term and high-input breeding programmes for each. Numbers at the bars show the total number of breeding programmes for each species.

Widespread native conifers

Pinus sylvestris

As regards the most widespread and native European conifer *Pinus sylvestris*, most of the programmes use commercial or conservation forestry strategies (Fig. 3.2.1, 3.2.2). The conservation forestry strategy is used more than the commercial forestry strategy (Fig. 3.2.2). As a widespread conifer Pinus sylvestris is know for its ecological function. LT, PL, DE, SK, IE prefer to put more emphasis on the conservation than to commercial goals, whereas CZ, FI, UK, SE vice versa. The reasons of this conservational approach in breeding could be relatively lower forest cover and industrial importance (DE, IE) or environmental policy and availability of better candidates under constrained financial resources (LT, PL, SK). Commercial interest in such widespread commercial species as *Pinus sylvestris* is important in forest industry countries (FI, SE). By choosing long-term commitment for high input, UK and CZ may indicate their strategic interest to strengthen benefits from forestry. DE and NL chose breeding at high cost without long-term commitment. This hardly is an efficiently approach, because of long-rotations of Pinus sylvestris and availability of better candidates. Probably, owing to limited distribution and commercial importance, ES indents for low-input breeding.

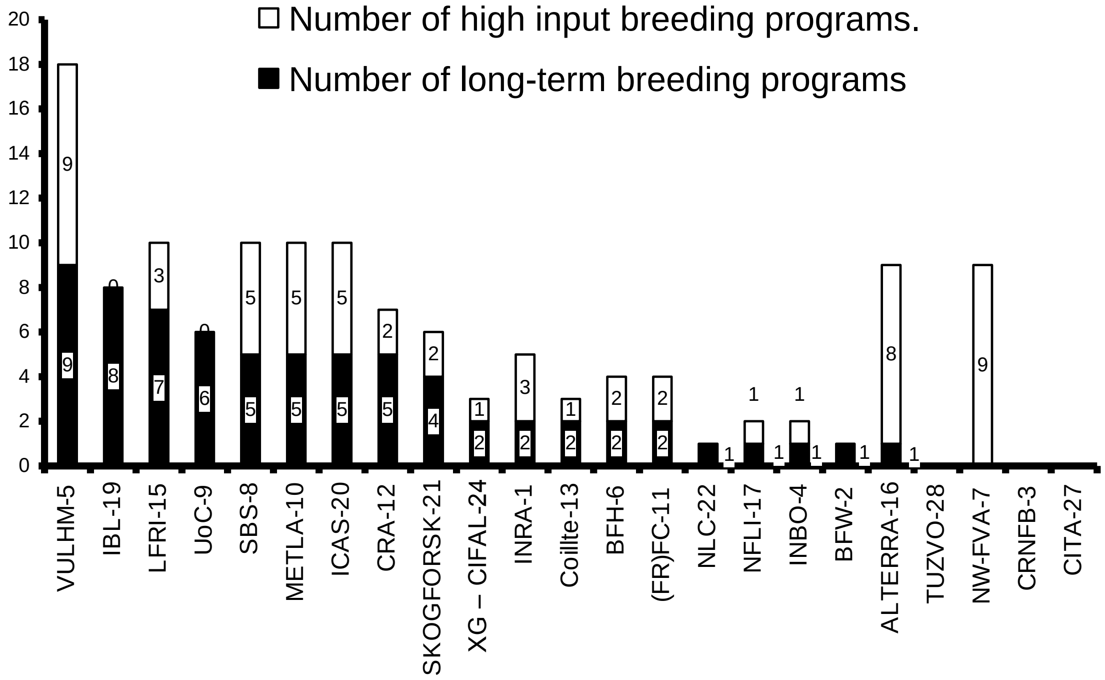

Fig. 2.2.2. Number of long-term and high-input breeding programmes for each participant of Treebreedex. The plot is summarising the answers to the questions 1 and 2. Numbers at the top of the bars show that total number of breeding programmes for each species.

Picea abies

In comparison to *Pinus sylvestris*, more breeding strategies of Picea abies are aimed at commercial forestry breeding- 7 out of 12 and these were the main EU forest countries: CZ, DE, FI, LT, NL, RO, SE (Fig. 2.2.3). As for *Pinus sylvestris*, plantation forestry breeding of *Picea abies* is planned by NL and DE (less afforested countries). *Picea abies* has a potential for short rotation plantations especially in the countries with surplus of agricultural land. It could be recommended for such countries to consider such short-term high-input breeding of *Picea abies* with full sib breeding and clonal deployment of the best performing clones directly to the commercial plantations. Conservation forestry breeding is intended by DK and PL and could be logical in the regions were *Picea abies* in threatened as it is at the marginal areas of its natural distribution (e.g. southern PL). In SK *Picea abies* breeding is downgraded to low-input by setting the priorities on gene conservation..

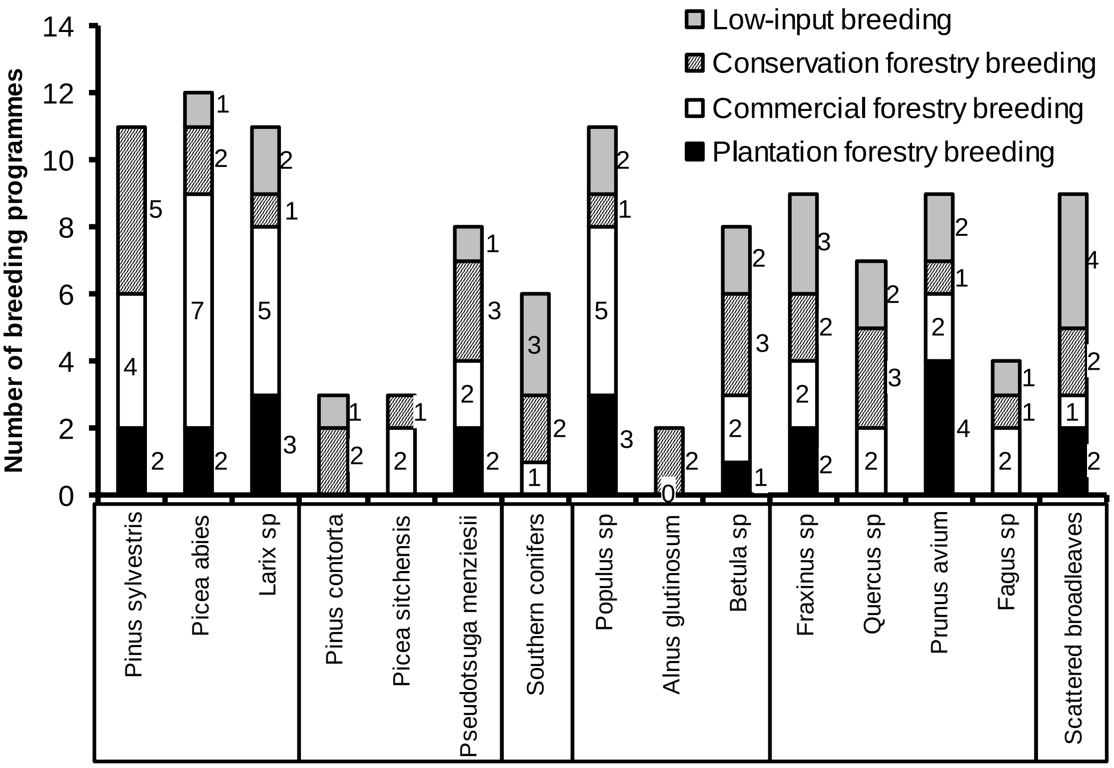

Fig. 2.2.3. Species comparison based on the 4 strategies regarding the balance of economic versus conservation goals. “Low input breeding” means low cost and short term programs; “Conservation forestry breeding” means long-term and low-input programs; “Commercial forestry breeding” means long-term and high-input programs and “Plantation forestry breeding” means short-term and high-input programs. The numbers at the bars show number of breeding programs. The outlined groups on the X axis are as follows (left to right): widespread native conifers, exotic conifers, southern conifers, fast-growing broadleaves, slow-growing broadleaves, exotic and scattered broadleaves. Southern conifers include: *Pinus halepensis, Pinus nigra, Pinus radiata, Pinus cembra, Abies alba*. Scattered broadleaves include: *Acer pseudoplatanus, Robinia sp., Sorbus aucuparia, Ulmus sp., Juglans regia, Betula pendula var. carelica, Castanea sp.*

Larix sp.

Larix sp. provide fast growing resinous timber. Its future needs are uncertain, may be therefore, it has relatively more high input short term breeding strategies (2 DE, NL). There are 5 serious long-term undertakings (FR, FI, DE, RO, CZ). Only PL intends for conservation forestry breeding. LT and UK uses low input breeding (LT to conserve what was achieved earlier). If there will be market, Larix sp. could be suitable for fast growing plantations and together with *Picea abies, sitchensis* form the coniferous part in plantation forestry programmes.

Exotic conifers

From the three exotic conifers only *Pseudotsuga menzisii* received more attention with 8 breeding programmes versus 3 for *Pinus contorta* and 3 for *Picea sitchensis*. With *Pseudotsuga menzisii* FR and DE intend for serious investment into high-input and long-term breeding (defined here as commercial forestry breeding); DK, IT, ES aim at conservation forestry breeding; NL and DE (NW_FVA) – at plantation forestry breeding and BE at low input breeding. For *Pinus contorta*, CZ, SE intends for long-term low-input breeding (perhaps, to retain what was achieved earlier) and LT aims for short-term low input breeding to preserved current achievements until a decision is made. As regards *Picea sitchensis*, UK and IE intends for commercial forestry breeding, whereas, DK – short rotation forestry breeding.

Southern conifers

Low-input breeding is intended for *Pinus halapenis* (ES*)*, *Pinus nigra* (UK), *Pinus radiata* (ES). Commercial forestry breeding is indented for *Pinus cembra* in RO. *Abies alba* is breed by PL and IT towards short-rotation forestry breeding.

Fast growing broadleaves

Populus sp. has achieved most of attention with 11 breeding programs, of which 5 are high-input long –term strategies (NL, LT, DE(2), CZ), 3 high-input short-term (FI, DE (2)), 2 low-input short-term (SK, ES), 1- long-term and low input conservation approach (AT). *Alnus glutinosum* is bred by LI and FI both with long-term low-input strategy here defined as conservation approach. For *Betula* sp., there are 2 long-term high – input programs (FI, CZ), 3 long-term low input strategies (SE, PL, LT), 1 short-term high input (DE) and 2 short –term low input strategies (DE, UK).

Slow growing broadleaves

For *Fraxinus* sp., there are 2 commercial forestry breeding strategies (CZ, RO), 2 conservation forestry breeding (LT, DK), 2 short rotation forestry breeding (DE, NL) and 3 low-input (FR, DE, UK) breeding strategies. For *Quercus* sp., there are 2 conservation forestry breeding (RO, CZ), 3 short rotation forestry breeding (DK, LT, PL) and 2 low-input (UK, BE) breeding strategies. For Prunus avium, there are 2 commercial forestry breeding (BE, IT), 1 conservation forestry breeding (DK), 4 short rotation forestry breeding (ES, NL, DE (2), FR) and 2 low-input (DE, BE) breeding strategies. For Fagus sp., there are 2 commercial forestry breeding (DE, CZ), 1 conservation forestry breeding (PL), and 1 low-input (BE) breeding strategies.

Exotic and scattered broadleaves

4 of 9 programmes are intended for short-term low-input breeding (*Robinia sp., Acer pseudoplatanus, Betula pendula var. carelica*), 2- short-term high-input (Ulmus *sp., Acer pseudoplatanus*), 1- long-term low-input (*Castanea* sp.), 2- long-term and high-input (*Juglans regia*).

3.3. Principles of delineating breeding zones and establishing breeding populations.

Aim of this question and the interpretation of the results.

It is important not to make mistake with adaptedness and in each adaptive environment to start with the most adapted material Failure to consider adaptedness may lead low breeding efficiency and low return from the investments.

This chapter summarises answers of the question number 3:

How among-population gene diversity is captured by the breeding program?

Possible answers:

1. Multiple breeding populations, one in each breeding zone
2. Multiple breeding populations, established by administrative districts
3. Multiple breeding pops. based on site type or natural species range
4. Other, state which
5. No attention is paid: all range is one breeding zone.

For detailed answers by species see Table 3.1.

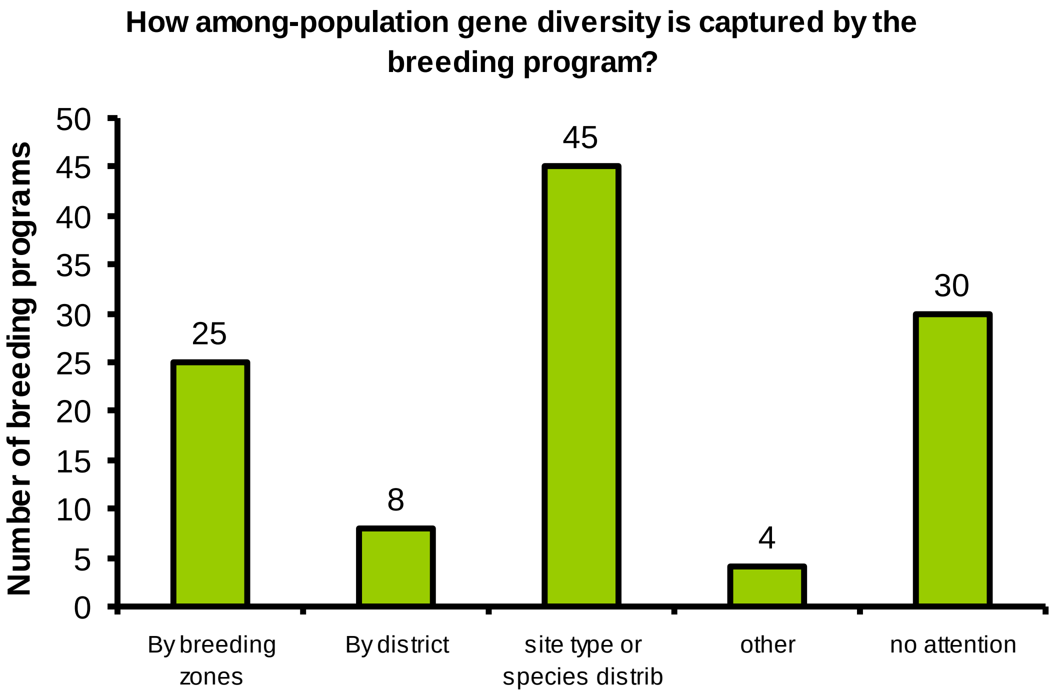

Fig. 3.3.1. Summary on how species gene diversity is captured by a breeding program overall all breeding programs in this survey.

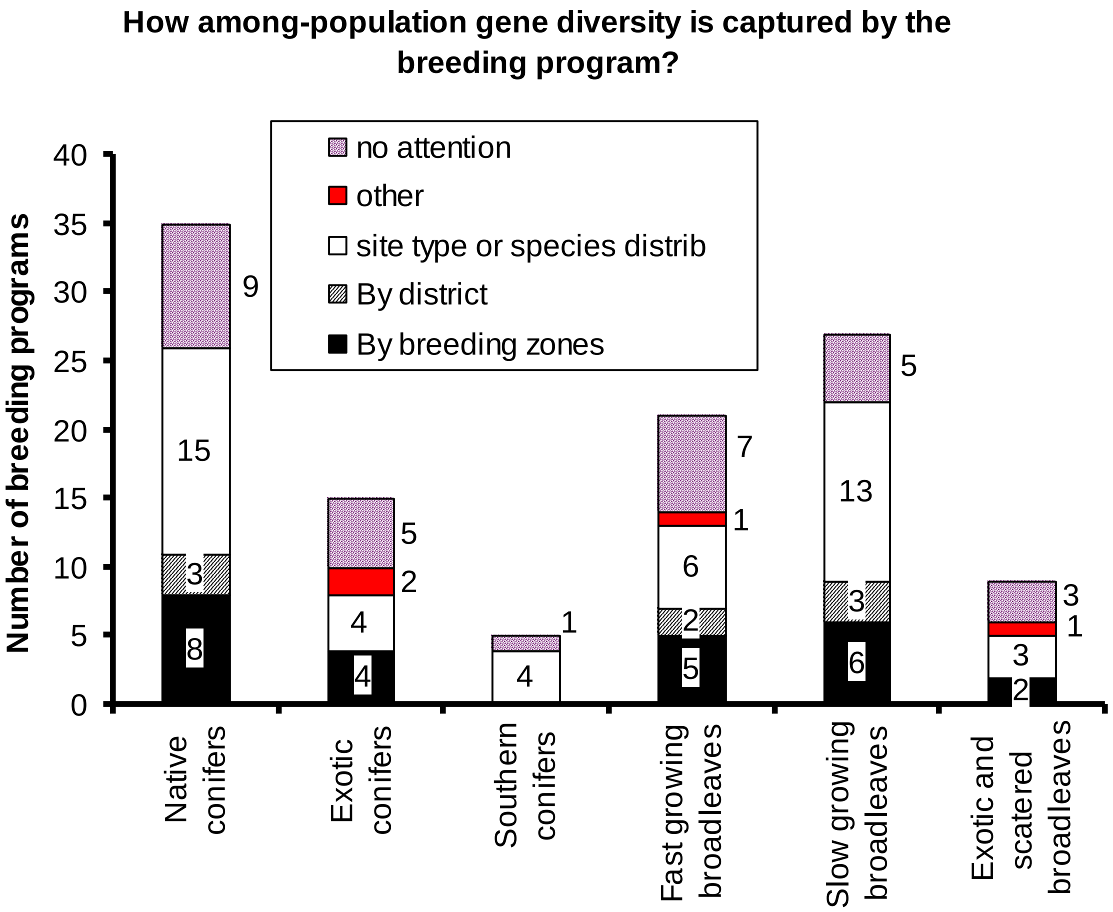

Fig. 3.3.3. Summary of answers to the question "How species gene diversity is captured by a breeding program?" by species groups.

The statistics of the answers is given in Fig.s 3.3.1 and 3.3.2. Multiple breeding populations based on site type or natural species range are dominating. What surprising is the high number of cases where the zones are not considered at all or are based on site type or species distribution. As regards species groups, for the widespread native conifers such as *Pinus sylvestris*, it would be a disadvantage to disregard the eco-climatic variation (breeding zone) in the range, nevertheless 8 programs of 35 does so and there are as much as 9 programmes where no attention is paid (Fig. 3.3.3).

Establishment of one breeding population in each adaptive environment is an efficient approach for all the high-input breeding strategies. It is not worth the risk to face the consequences of reduced adaptedness because of failure to consider the climatic variation, when investing much in breeding. However, this seems to be not the case as shown in Fig. 3.3.4. For, high-input programs only 9 out of 58 programs are using climatic data to delineate zones within which their breeding populations will be breed.

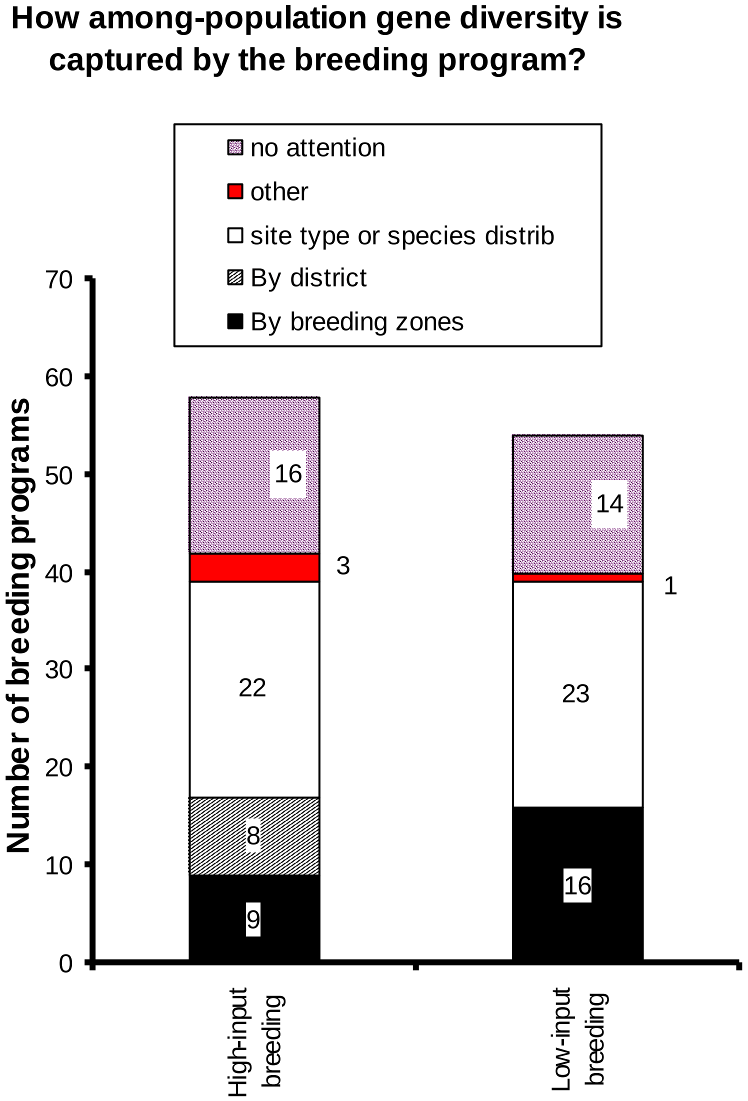

Fig. 3.3.4. Summary of answers to the question “How species gene diversity is captured by a breeding program?” by type of input into breeding program.

3.4. Dividing breeding population into intensively managed nucleus with top-ranking genotypes and less intensively managed main population.

Aim of this question and the interpretation of the results.

In case of long-term breeding, where the need to carry gene diversity load slows dawn the progress in genetic gain, such division allows to achieve higher gains for the near future and satisfy the stakeholders in faster returns.

This chapter summarises answers of the question number 4:

Do you divide breeding population into intensively managed nucleus with top-ranking genotypes and less intensively managed main population?

Possible answers:

1. Yes.

0. No.

For detailed answers by species see Table 3.1.

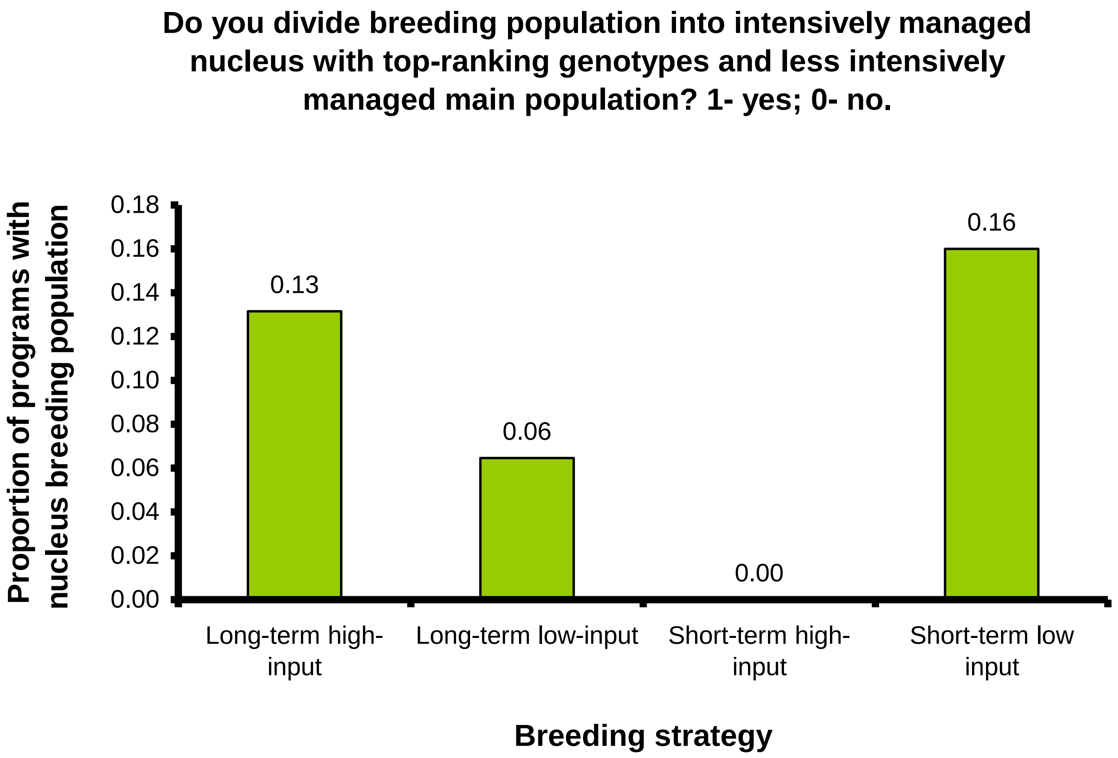
Do you divide breeding population into intensively managed nucleus with top-ranking genotypes and less intensively managed main population? 1- yes; 0- no.

Fig. 3.4.1. The answers grouped by the breeding strategies as regards their terms and input.

In general , separation of incisively managed nucleus is not widespread – 10% of the programs only. As discussed in the box above, it is most relevant for long-term high input breeding. However, it exists only in 13% of such programs (Fig. 3.4.1). It is mostly used for low input breeding, and it is rather surprising. We assume that the respondents treated the nucleus breeding as a smaller group with the aims are to do something more intensive with a better part of a larger material.

3.5. Strategy for maintenance of gene diversity within breeding population.

Aim of this question and the interpretation of the results.
There alternatives to maintain gene diversity within a breeding population, each having own advantages under specific cases. Are these methods appropriate for certain type of breeding? If one is planning for long-term breeding and makes no thinking on how to maintain gene diversity in long run, he is seriously mistaken. This chapter summarises answers of the question number 5: How is gene diversity maintained in (or planned) in the breeding population? Possible answers: 1. Open population, recurrent infusion of genetic material. 2. Closed population, no infusion of new material. 3. Other method (state which). 4. No long-term plans. For detailed answers by species see Table 3.1.

In the breeding populations, the gene diversity reserve could be provided by two main methods: (a) recurrent infusion of fresh genetic material presumably from the wild and therefore usually referred to as “open breeding population” or (b) using of a balanced selection and keeping track of the relatedness to prevent inbreeding, usually called “closed breeding population”. The results of the theoretical studies showed, that if high investment is given, closed population strategy with balanced selection” is superior over the open population strategy, because in advanced breeding cycles, the material from the wild will have too low breeding value to be included into breeding population and the closed nucleus with balanced selection can provide higher gains.

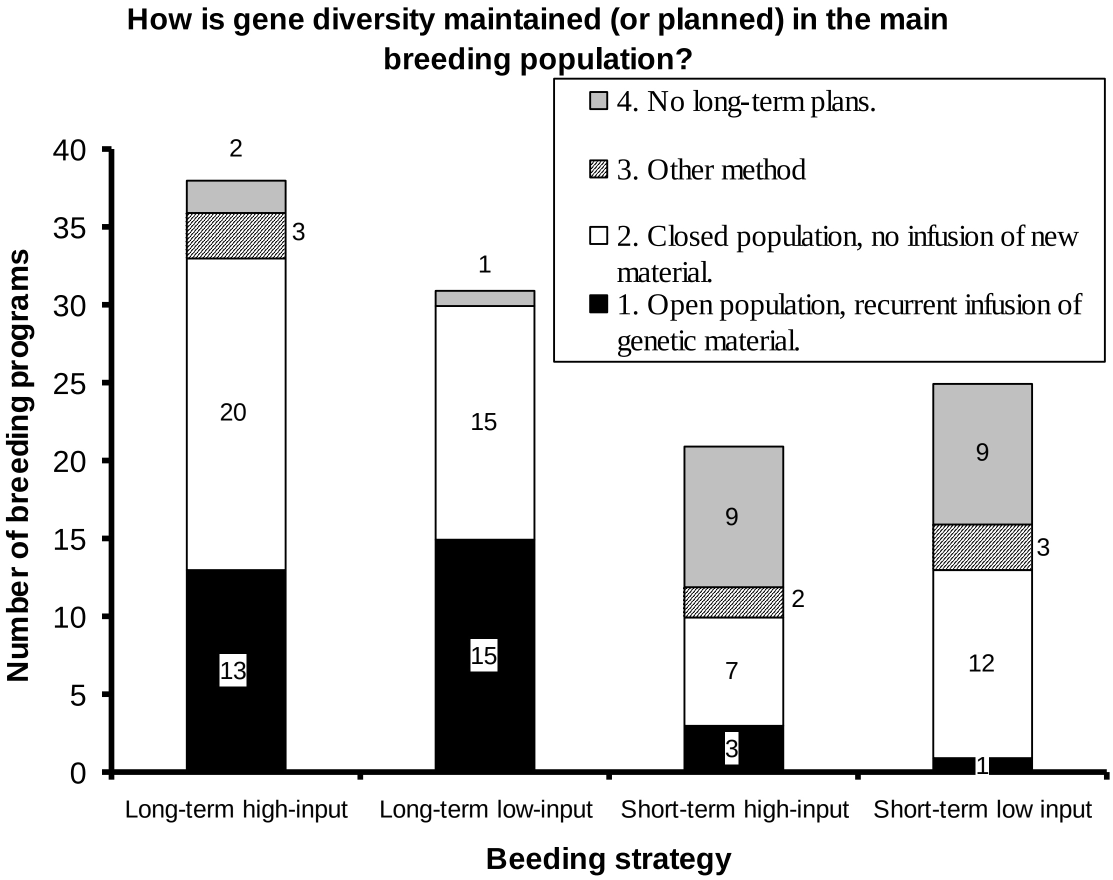

Fig. 3.5.1. How gene diversity is maintained within breeding populations for each breeding strategy.

There are 38 long-term high-input breeding programs, representing the greatest investment in breeding. In theory, this approach has two major concerns: how to faster provide high genetic gains and at the same time preserve genetic diversity for future breeding. In other words- how to return maximum genetic gain per unit of gene diversity lost. As explained above, for long-term high-input strategies (where resources are given to maximise genetic gain), closed populations with no infusion of less advanced genetic material is more beneficial than open population strategy. However, 13 of 38 long-term high-input breeding strategies still indent to use open population strategy (Fig. 3.5.1). Otherwise for long-term high-input strategies, the 3 answers of other methods and 4 answers stating no long term-plans certainly is a misinterpretation of the questions by the respondents.

There were 31 long-term low-input breeding strategies, where presumably the adaptation of forests to the climatic change, their ecological, protective and recreational values are more beneficial than the commercial values (which still could be exploited given no harm for ecology is made). Here, maintenance of high gene diversity is one of the major tasks. Therefore, open populations with recurrent infusion of fresh genetic material form the natural populations could be more economically beneficial than investing a lot in controlled matings and track of relatives. Our review showed that there still is 15 out of 31 long-term low-input strategies aiming at closed populations (Fig. 3.5.1).

For the short-term strategies, especially with low-input, gene diversity should not be a major concern and the reserves should be mainly directed to provide high gains as fast as possible.

3.6. Mating systems to create the candidates.

Aim of this question and the interpretation of the results.

Controlled pollination offers better control. In a situation with a pollen cloud from the forest CP has an important function to isolate the bred material from unimproved or less improved forests. CP is expensive, administrative demanding and may cause time delay for organising the crosses. Open pollination is simple and cheap. OP requires good pollen production of fathers and that may mean longer waiting times for recombination than CP. OP offers no control of the father and that may mean that parents will be inoptimally distributed in the breeding population with some fathers over represented and that inbreeding may occur in not foreseeable patterns. OP may introduce new genetic material in the breeding stock at early generations of breeding

This chapter summarises answers of the question number 6:
Which mating system among breeding population members is used to create the candidate population?
Possible answers:
1- Controlled pollination (CP).
0- Open pollination (OP).
For detailed answers by species see Table 3.1.

Note that here the candidate population is defined as the group of individuals that carry the recombined genes of the breeding population members and are considered as breeding population members for the next breeding cycle. Open pollination may be used for progeny testing, but the candidate population may still be created by controlled crosses and if so controlled crosses is the right answer.

The enquiry did not ask about development in time of the breeding population, it may be common to make selections in open pollinated progenies from selected plus trees pollinated in the forest, but in later stages of the breeding program switch to controlled pollination, thus the responses may overestimate the actual use of wind-pollination in advanced generation breeding. But it can be predicted to be more common to clear out pedigrees by molecular markers in open pollinated progenies and thus capture some of the advantages of CP, and thus the need of CP in advanced generation breeding may decrease in the future.

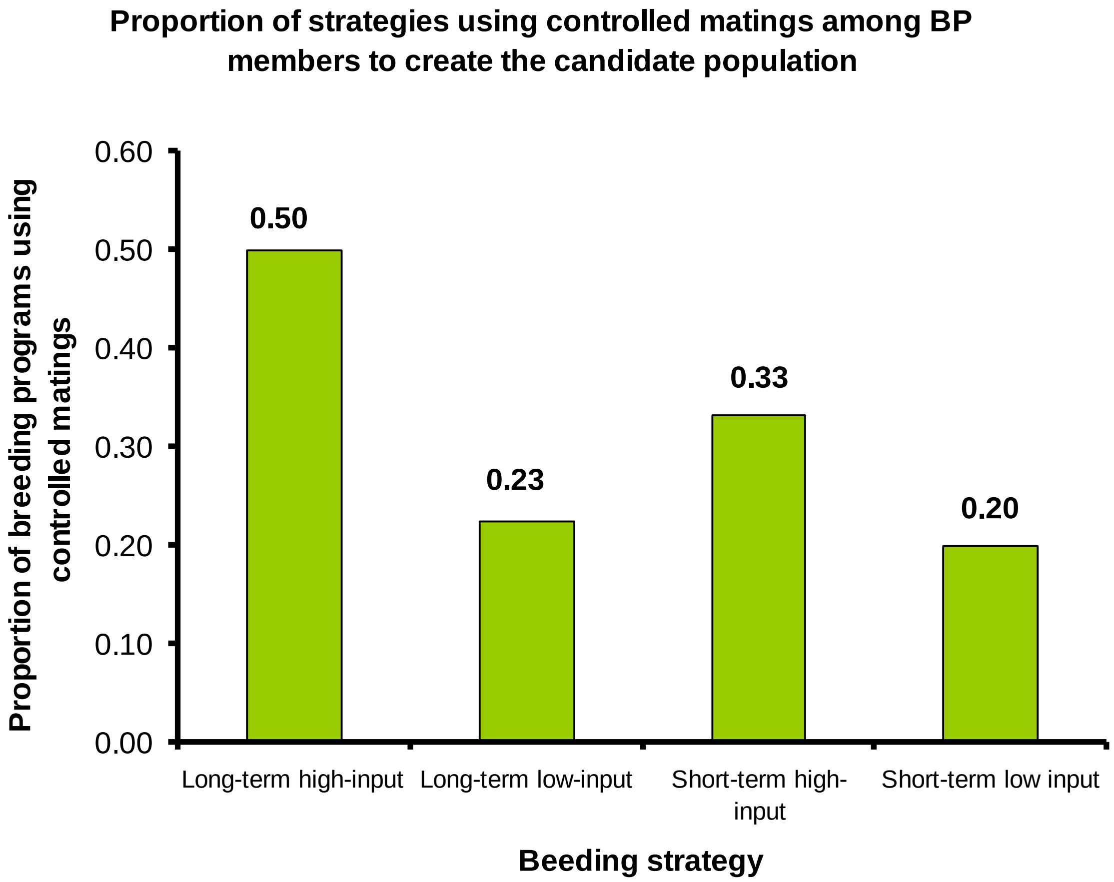

Fig. 3.6.1. Proportion of breeding programs using controlled pollination to create the candidate population given by breeding strategies.

Only 33 % of all strategies use controlled matings. The percentage was not higher for long term breeding, and even in high input long term it was only 50%. That includes native important wind-pollinated species, where OP can be expected to contaminate the breeding population by genes from unimproved forests. Controlled mating requires large investment (grafting archives, experienced staff) and the arrangements for crosses may mean a long unproductive timelag, but CP is efficient for the high-input strategies especially to those aimed for long-term, where appropriate control of relatedness and gain progress is important. But open pollination has the advantages that it carries on more combinations with parents than controlled crosses and within the same budget more mothers can be used. OP is used in 67% o the short-term high-input strategies, which seems high for well funded programs (Fig 2.6.1). For conifers CP is used more often that for broadleaves (especially slow growing broadleaves), but it is remarkable that Poplars is the major breeding object, which uses CP to the highest extent. An explanation maybe that it is the only species considered which has progressed most in advanced generations (Mertens enquiry Table 11).

OP in a closed long-term program will generate more problems with relatedness and coancestry will tend to raise faster in a rather uncontrolled way compared to CP. This can partly be compensated by using large breeding populations and intensifies the need for predictions what is likely to happen after five generations. The limited use of simulators is a bit surprising from that point of view. Simulators should probably give more attention to OP strategies.

In Finland, METLA for Scots pine uses SPM as the main method and 2PM and 3PM are used with the highest ranked BP trees. This also creates among family selection component and generates additional genetic gain.

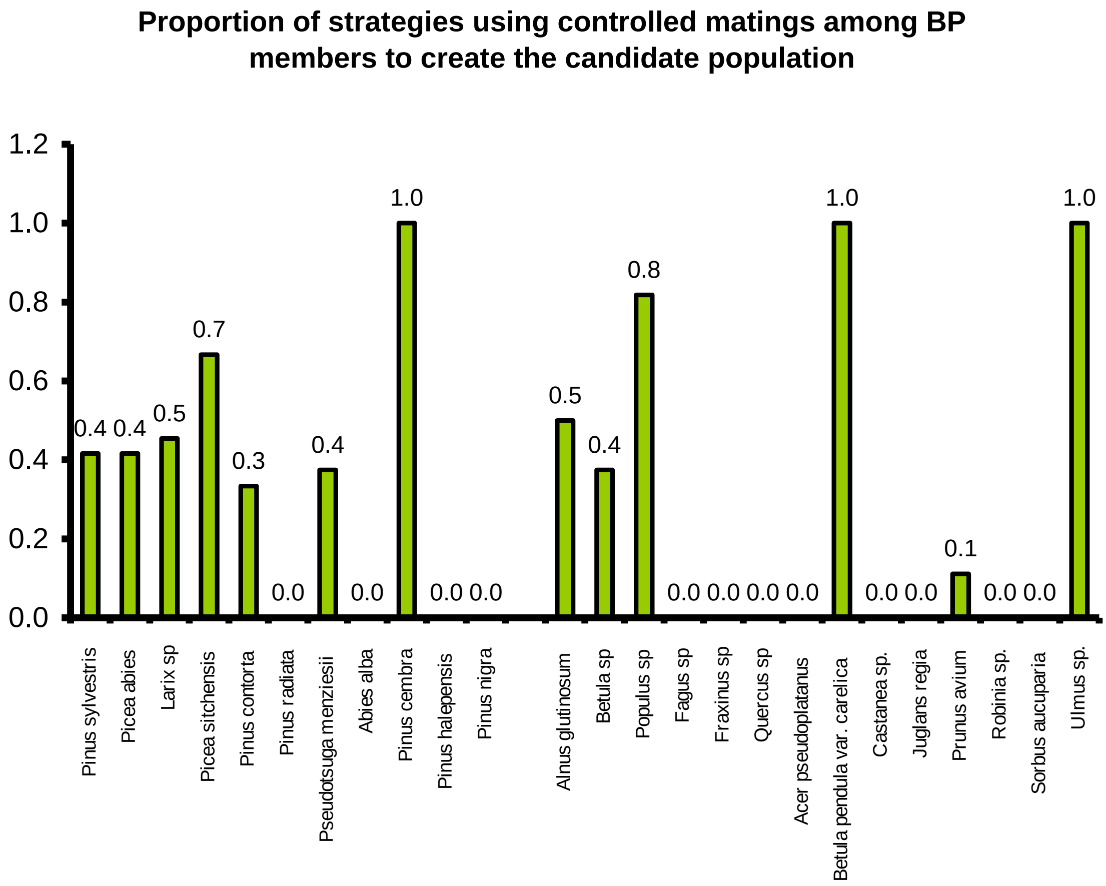

Fig. 3.6.2. Proportion of breeding programs using controlled pollination to create the candidate population given by species.

3.7. Are different testing strategies used for different traits?

Aim of this question and the interpretation of the results.
This question concerns testing strategy. There may exist sub-tests for specific important properties relevant to certain species. Aim was to investigate existence of such cases. Is such complex approach really efficient? An example of different: progeny testing for wood yield (low heritability) and phenotype testing for growth rhythm (high heritability). This chapter summarises answers of the question number 7: Are different testing strategies used for different traits? Possible answers: 1. Yes, different strategies. 0. No, the same strategies. For detailed answers by species see Table 3.1.

Minority of the programs (14 out of 115 programs surveyed) use different testing strategies for different traits, (Table 3.7.1). Such approach is mostly used for *Populus* sp. (3 programs) and mainly by the breeders in Czech Republic (VUHLM): 10 of the 14 programs using different strategies from different traits were form VUHLM (Table 3.7.1).

Table 3.7.1. Breeding programs using different testing strategies for different traits.

No.	Species	Institution	Treebreedex institution code
1	*Betula sp*	VULHM	5
2	*Castanea sp.*	XG-CIFAL	24
3	*Fagus sp*	VULHM	5
4	*Fraxinus sp*	VULHM	5
5	*Larix sp*	VULHM	5
6	*Picea abies*	VULHM	5
7	*Pinus contorta*	VULHM	5
8	*Pinus sylvestris*	VULHM	5
9	*Populus sp*	BFH	6
10	*Populus sp*	VULHM	5
11	*Populus sp*	BFW	2
12	*Prunus avium*	INRA	1
13	*Quercus sp*	VULHM	5
14	*Ulmus sp.*	VULHM	5

3.8 Separation of breeding population and multiplication populations.

Aim of this question and the interpretation of the results.

This question is important for an efficient deployment of the genetic gain. In case of long-term breeding, the breeding population must carry the load of preserving the gene diversity for the future. This diversity load slows dawn the progress in genetic gain. Because of this gene diversity load, it is a rather inefficient to keep whole breeding population in multiplication population, e.g. in one seed orchard. If breeding and multiplication populations are kept separate, it is possible to boost the genetic gain by deploying the very best into multiplication populations, which do not need such large gene diversity reserve as long-term breeding populations. The separation is also convenient for controlled matings when doing it in a top-grafted achieve. On the other hand, the separation requires greater and long-term investment. Therefore, this issue is especially relevant to log-term high-input breeding, where long-term funding commitment is possible. Breeding population is defined as the group of individuals that will carry the advancement of breeding into future generations. Multiplication (propagule) population is the group of individuals primarily aimed for sexual or vegetative multiplication of the genetically advanced material for commercial purposes (seed orchard, hedges for cloning). Example of geographic separation is when set of genotypes located in a crossing archive (breeding population) close to institute and the same set of their copies in a "milder" location to get more seeds. Example of genetic separation is family seed orchard thinned based on own performance or clonal orchard thinned on based on progeny test. Example of genetic and geographic separation is when certain number of the best genotypes located in a crossing archive (breeding population) is deployed in a seed orchard, established at another site. An example of not separated breeding and multiple populations is a clonal seed orchard with progeny of the clones under test but no thinning is planned. Or second generation seed orchard with backwards selected clones.

This chapter summarises answers of the question number 8:

Is breeding population and multiplication pop. separated from each other as regards location and genetic composition?

1. Yes, separated geographically.
2. Yes, separated genetically.
3. Yes, separated geographically and genetically.
4. No, not separated.

For detailed answers by species see Table 3.1.

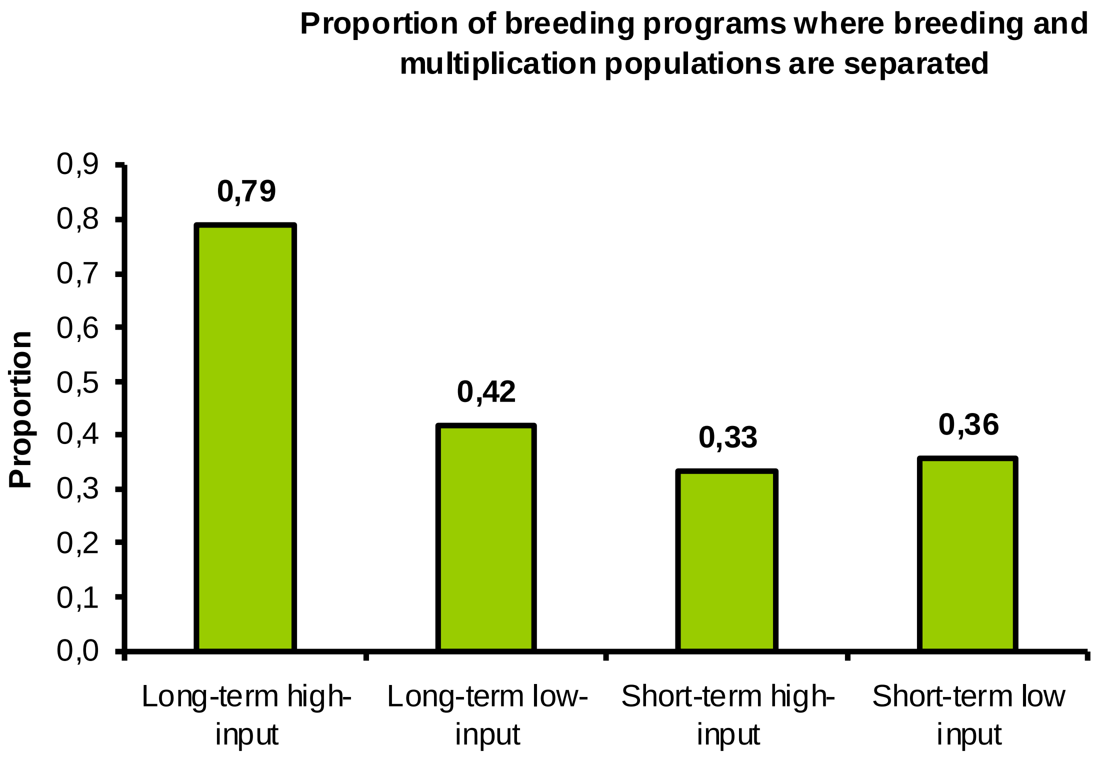

Fig. 3.8.1. Proportion of breeding programs with separate breeding and multiplication populations by the type of breeding.

Breeding and multiplication populations are separated in 51% of the surveyed programmes. As expected, this separation is used mainly in long-term high-input breeding programs, where it is motivated (possibility to generate higher gain) and financially feasible (high-input is provided) (Fig. 3.8.1). It is surprising, however, that in 42% and 36% of low-input breeding, where the idea is breeding at minimum cost, these populations are kept separate. Separation by species groups and species is given in Fig. 3.8.2, where a note is that species with the value of 0 or 1 are those having just 1 breeding program included in this survey. Separation of breeding and multiplication populations is a common practise for most of the species, except *Pinus cembra* and *Robinia* species and there is no clear leader among species groups nor among species. As regards the type of separation, the most common was the geographic separation (the same material in a milder for seed production environment) and least common genetic separation (thinning of seed orchards after testing). The simultaneous geographical and genetic separation, which is most efficient method for high-input breeding, is used in few programs only (Fig. 3.8.3).

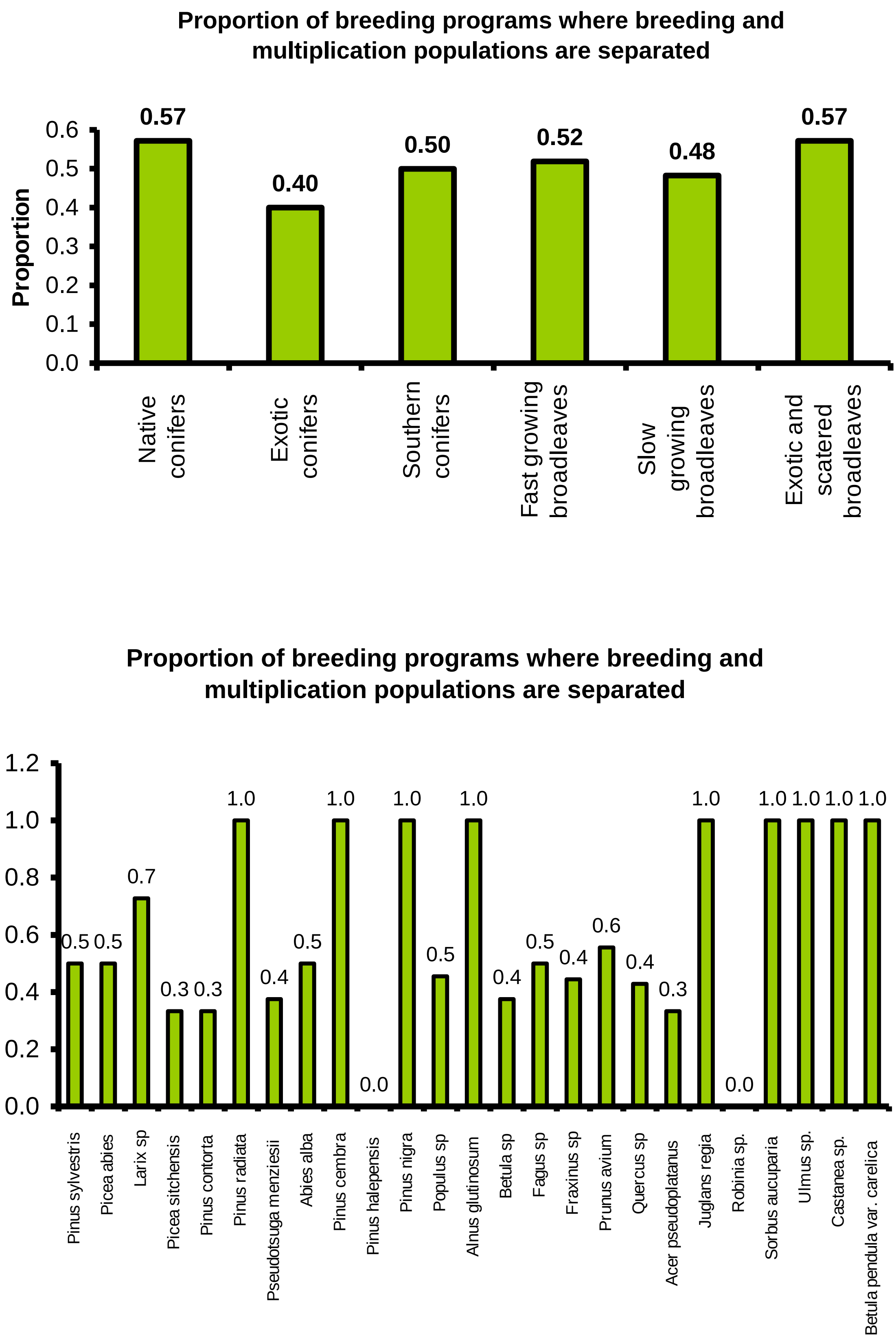

Fig. 3.8.2. Proportion of breeding programs with separate breeding and multiplication populations given by species groups (top) and species (bottom).

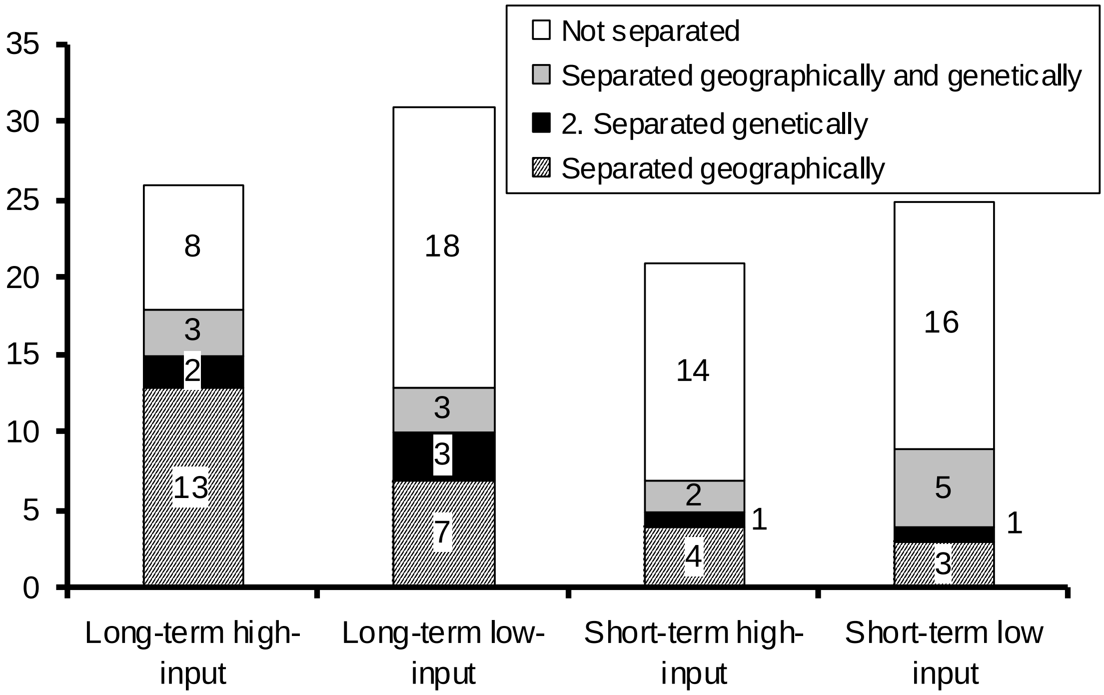

Fig. 3.8.3. Answers to the question are breeding and multiplication populations kept separated with specifying the type of separation.

3.9. Genetic level at which the breeding population members are selected.

Aim of this question and the interpretation of the results.

This question is important for finding optimum balance between the genetic gain and gene diversity in the breeding population and for controlling the coancestry in the breeding population. Within-family selection allows to efficiently preserve the gene diversity for the future breeding and is a necessity for long-term breeding with no infusion of genetic material from outside (closed breeding populations). However, within family selection does not allow generating such high genetic gain as among-family selection. If the there are no clear long term commitments then among-family selection could be more appropriate.

Breeding cycle the successive alternation of recruitment, candidate and breeding populations in one breeding generation. Note, when establishing breeding populations, the selection may be made among families, but later for each new breeding cycle, it could continue as within family selection. In such case the answer is "within families". In our survey, the cases of among-family selection and combined among- and- within-family selection were separated because by the among family selection alone we assume of the selection of whole families in breeding seed orchards and family bulk seeds are used for second breeding generation. Otherwise, if mating of individuals is made then among family selection automatically implies within family selection as well.

This chapter summarises answers of the question number 9: At which level is the selection of the new breeding population members made in each breeding cycle?

1. Within families
2. Among families
3. Among and within families
4. Other, free comment

For detailed answers by species see Table 3.1.

The most common method of selection is “among-and-within-family” selection (Fig. 3.9.1). It is the oldest method where the best individuals from the best families are selected. Note, that this refers to the breeding populations not to seed orchards, except for the programs where breeding population and seed orchard is combined into one plantation. There are only 12 breeding programs using within-family selection alone. Selection of family bulks (among family selection) is used in 21 breeding programs. 22 programs use other than family selection. The other methods than among or within family selection were the selection at the provenance or stand level and use of their bulk seeds. Also in several cases clonal testing and clonal deployment were used.

If comparing the types of breeding, within-family selection alone is mostly used in long-term breeding programmes (Fig. 3.9.1). The family bulk selection and selection of populations are mainly used in the short-term breeding programmes. Surprisingly little within-family selection is used in long-term breeding programmes. We have amplified the case where the long-term breeding populations are closed (means no infusion of material for outside) to see how many of these use within-family selection (Fig. 3.9.2). The result was astonishing: 5 out of 20 long-term breeding programs with closed breeding populations are using within family selection. How then they are going to maintain the gene diversity of uncertain future? Even with low intensity selection, among family will accumulate the coancestry fast and pending inbreeding depression will require infusion of less advanced material which is an inefficient approach in case of high input breeding. One exception of this case is in Finland, where a specific combination of among family and within family selection is used for Scots pine: selection occurs among the families of the top-ranking trees, which are mated more often than ordinary trees in the breeding population. Similarly, a possibility of balancing grandparents instead of parents is an efficient approach to generate the among family selection component while maintaining a balanced breeding strategy (Lindgren et al. 2008, Danusevicius and Lindgren 2010).

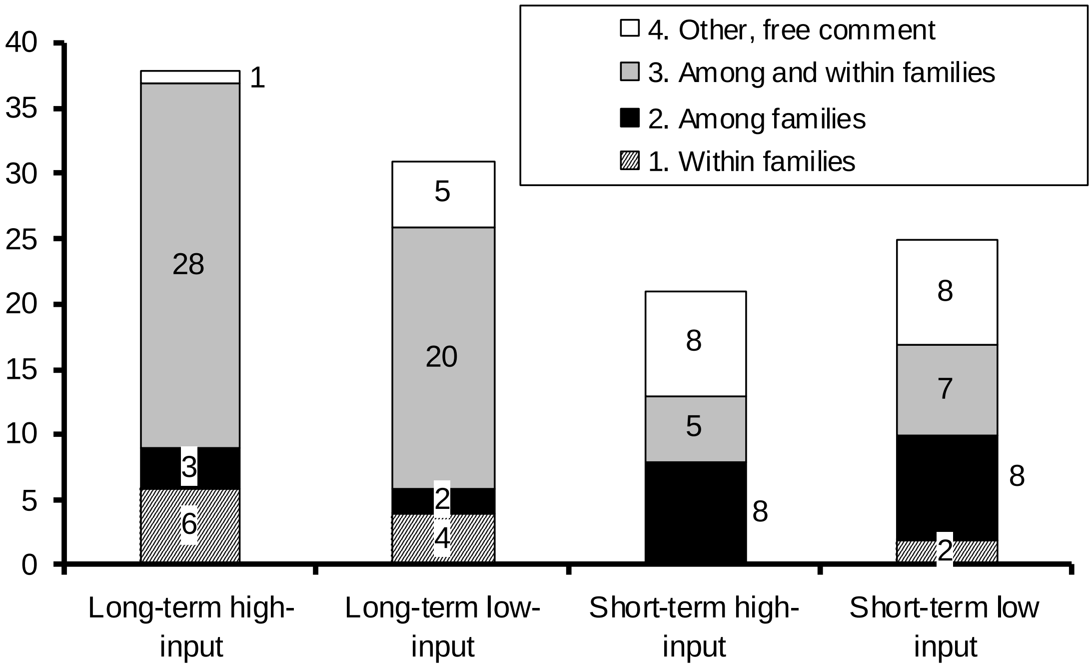

Fig. 3.9.1. The genetic level of the selection of the new breeding population members is made in each breeding cycle, given by the type of the breeding programmes.

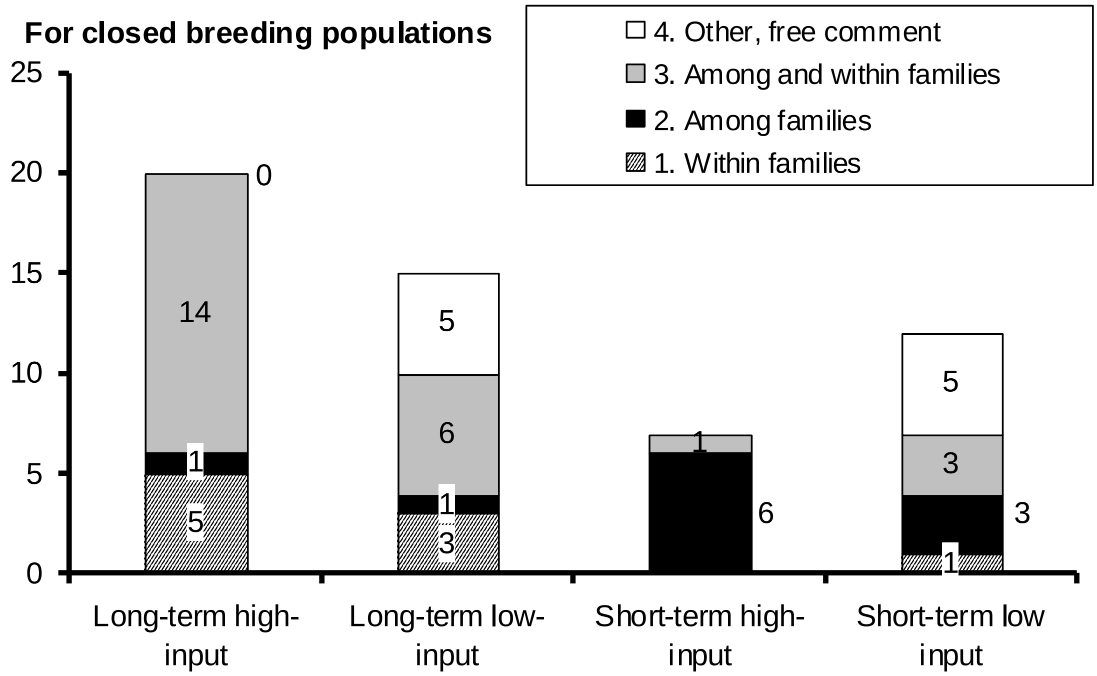

Fig. 3.9.2. The genetic level at which the selection of the new breeding population members is made in each breeding cycle, given only for these programmes where breeding populations are kept closed (see question 3).

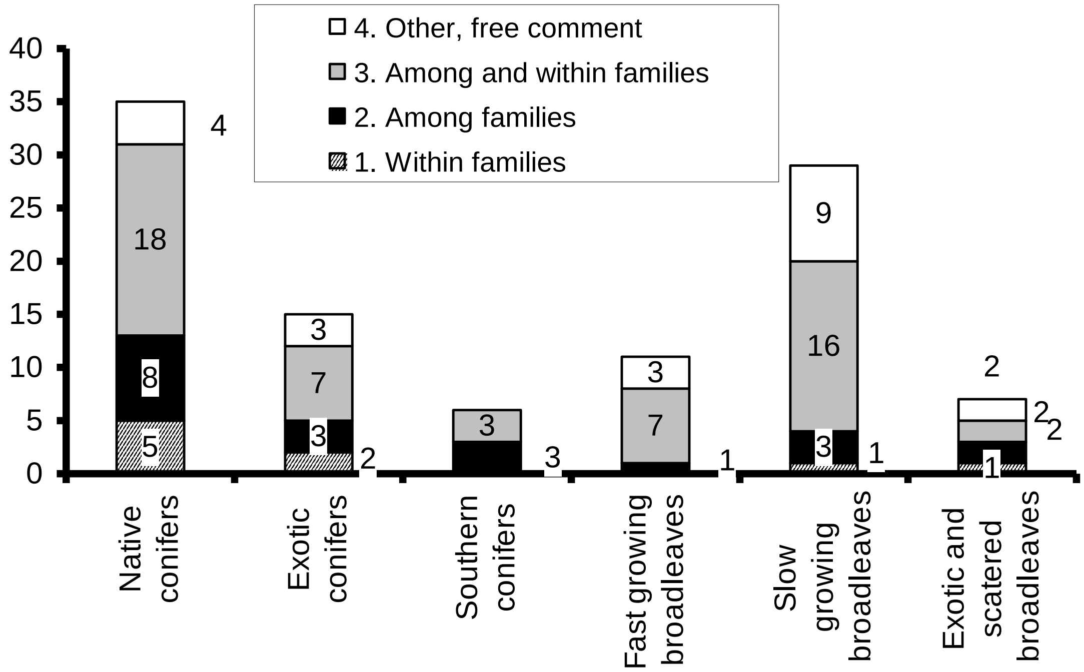

Fig. 3.9.3. The genetic level at which the selection of the new breeding population members is made in each breeding cycle, given by species groups.

3.10. Choice of the testing strategy.

Aim of this question and the interpretation of the results.
This question is aimed to survey the existing testing strategies and to discuss their efficiency given certain breeding strategy as regards its terms and input. Note, that choice of of the testing strategy depend snot only on gain generating efficiency but also on its time (duration) and costs. Only the index combining the genetic gain, costs and time could provide the complete estimate of the efficiency. For instance, waiting until selected candidates reach the sexual maturity rather inefficient when having possibility to clone them at an earlier age. This chapter summarises answers of the question number 10: What testing strategy is used/planned to select the BP members (pre-screening in nursery for growth rhythm or vitality may be considered as single-stage)? 1. Single-stage: phenotype testing . 2. Single-stage: clone testing . 3. Single-stage: progeny testing. 4. Two-stage: phenotype/progeny testing. 5. Two-stage: phenotype/clone testing. 6. Other, free comment. For detailed answers by species see Table 3.1.

Single-stage strategies are less precise in predicting the breeding values but are less time consuming and cheaper. Two-stage-strategies provide a better prediction of breeding values but are longer and require greater input. How to find the optimum? A short summary of up-to-date computer simulations indicates the following solutions. In case of long-term high input breeding, clonal testing is by far the most efficient approach combing both genetic gain, cost and time (Danusevičius and Lindgren 2002a). If cloning not possible the two-stage phenotype-progeny testing or single-stage phenotype testing (especially for the tait with higher heritability such as wood basic density) could be more appropriate (Danusevicius and Lindgren 2002b). Two-stage phenotype-clonal strategy does not add a significant improvement to the single-stage clonal testing (Danusevicius and Lindgren 2002b). The phenotype testing strategy was further amplified for the possibility to generate extra gain from an among family selection component, where the balance is made by the grandparents but not by the parents (Lindgren et al. 2009; Danusevicius and Lindgren 2010). As regards, low input breeding phenotype testing is the cheapest and could give optimum results given the inputs; a good overview is presented by Lindgren and Wei (2007) and also at http://www-genfys.slu.se/staff/dagl/Meetings/Antalya06/Antalya06.htm.

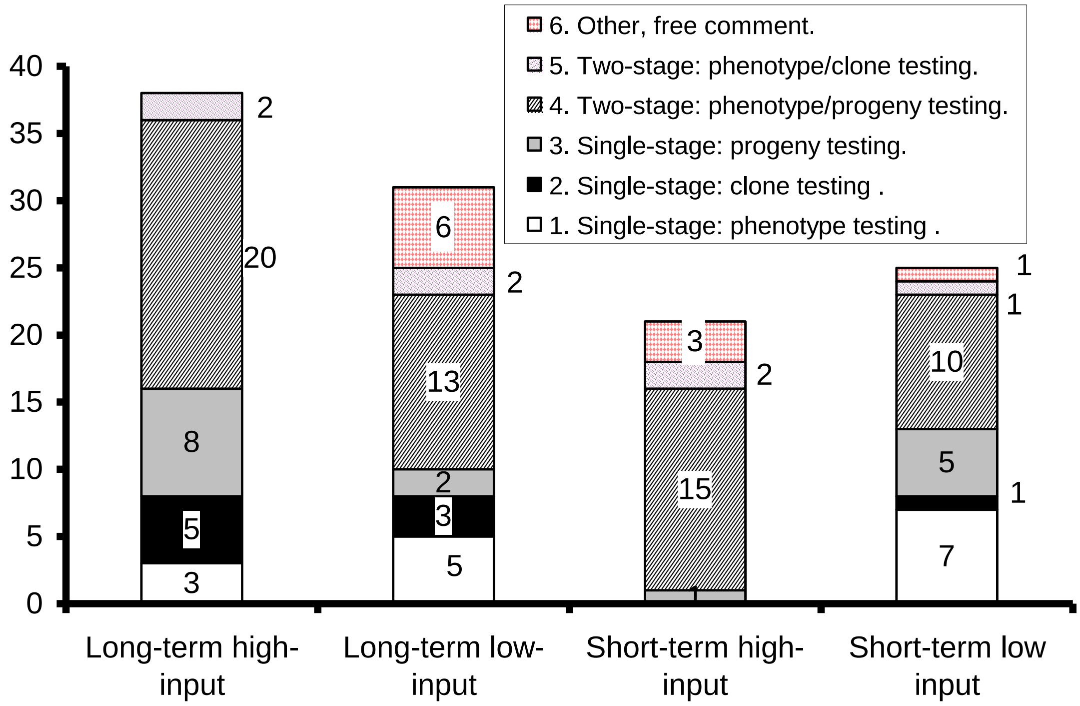

Fig. 3.10.1. Number of testing strategies used in each type of breeding.

Our survey indicates that two-stage phenotype/progeny testing is the most common testing strategy. It is also most common in each type of breeding, but most frequently used in long-term high-input breeding programs (Fig. 3.10.1). Even for low-input breeding majority of the programs use this testing method. Even though we have assumed that the nursery pre-screening does not qualify to be called the first stage of a two-stage strategy, there still is a possibility that it was understood so by the respondents (see the definition for the two-stage testing above). By the two-stage testing we assumed that the phenotypes are tested and pre-selected, then they are cloned or their seed are collected to establish a new test to be used for the second stage. In long-term high-input breeding, single stage progeny testing is the second ranking strategy. Surprising little of phenotype testing is used in the low-input breeding strategies. Also, noteworthy is that clonal testing is not used in any of the 21 short-term high-input breeding programs (Fig. 3.10.1). As mentioned above, the two-stage phenotype/clonal testing is not efficient, but still used in 7 programs.

Survey of testing type by species groups shows that two stage phenotype/progeny testing is common for each species group; single-stage phenotype testing use mostly used for slow growing broadleaves; clonal testing – for native conifers and fast growing broadleaves; single stage progeny testing- for native and exotic conifers; two stage phenotype/clonal testing for fast growing broadleaves (Fig. 3.10.2).

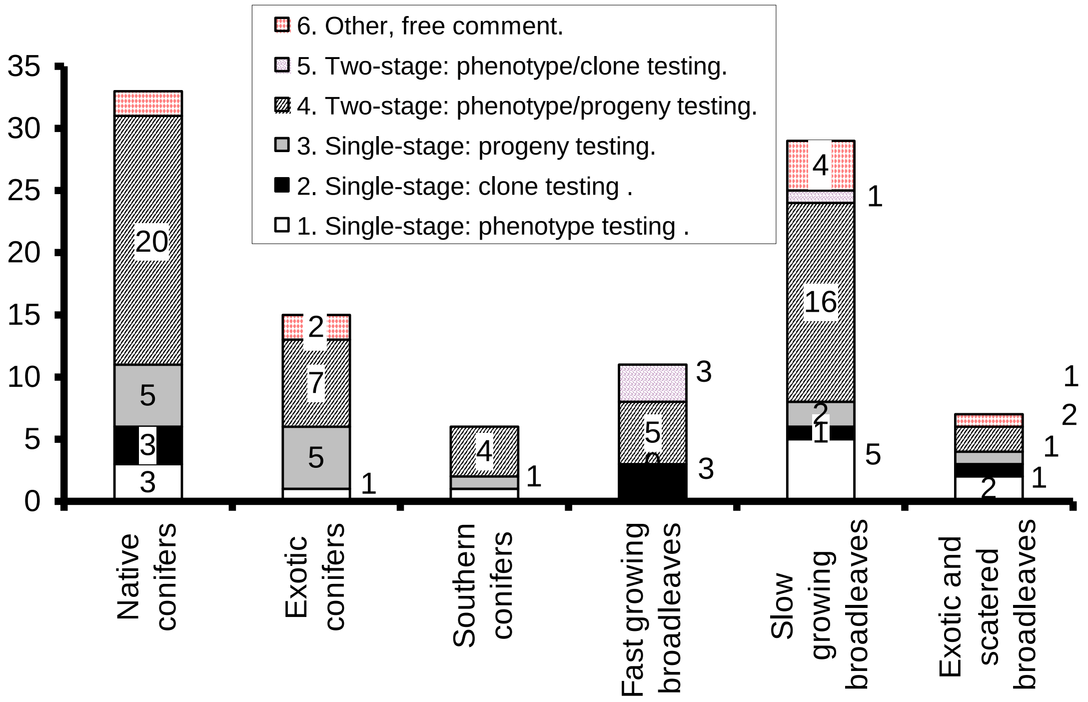

Fig. 3.10.2. Number of testing strategies used in each species group.

From the survey by species in Fig. 3.10.3, the flowing points worth emphasising. *Pinus sylvestris*, the most common conifer in Europe is mainly tested as by two-stage phenotype progeny testing strategy, which is in agreement with the theoretical findings discussed above. Surprising little clonal testing is used for the species which are could easily be cloned by rooting, e.g. *Picea abies, Picea sitchensis and Populus* sp. Phenotype testing is most common for *Fraxinus* and *Betula* species.

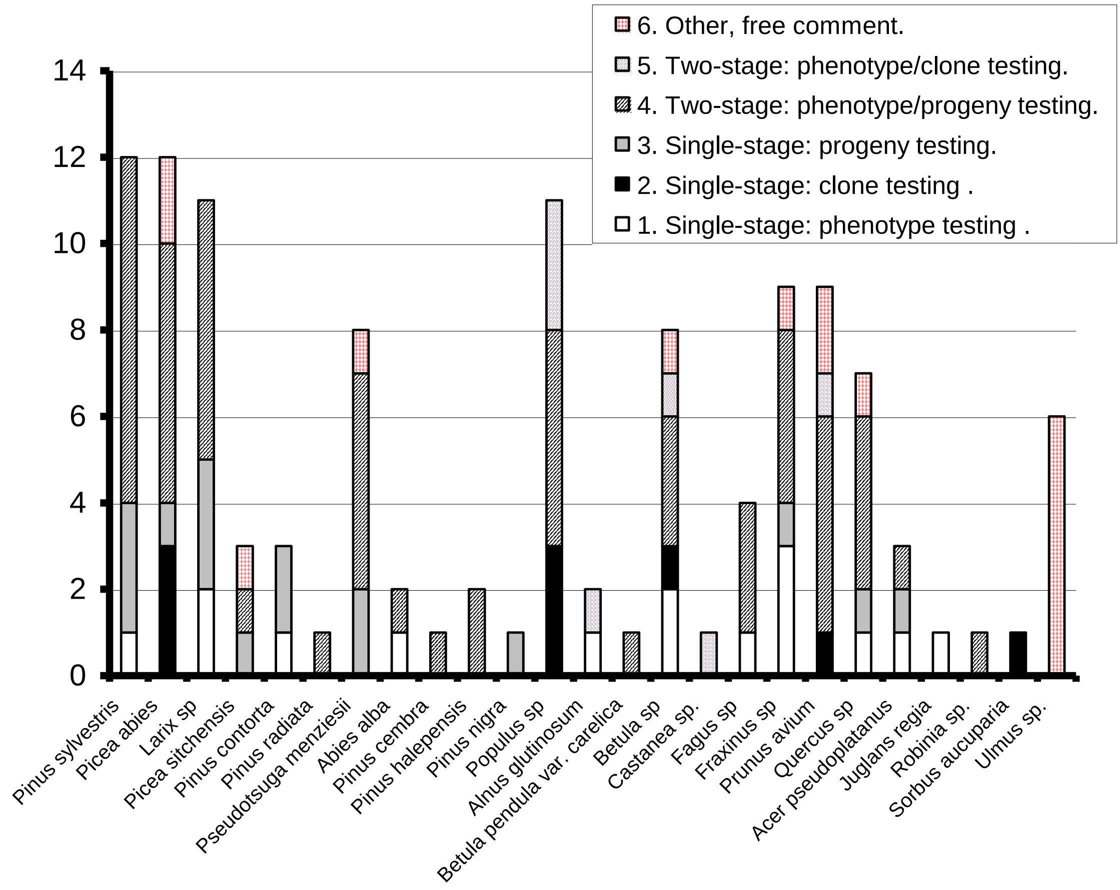

Fig. 3.10.3. Number of testing strategies used in each species group.

3. 11. Is information on molecular markers used to aid breeding?

Aim of this question and the interpretation of the results.

This question is aimed to survey what benefit the recent advance in forest genomics brought to practical tree breeding

This chapter summarises answers of the question number 11:

Is information on molecular markers used to aid breeding?

1. Yes.
2. No.

For detailed answers by species see Table 3.1.

Only 4 out of 114 breeding programmes use molecular markers to aid practical breeding. The users of MAS are listed in Table 3.11.1.

Table 3.11.1. Breeding programmes using MAS.

Institution	Treebreedex code	Species
SkogForsk	21	*Picea abies*
INRA	1	*Pseudotsuga menziesii*
University of Copenhagen	9	*Pseudotsuga menziesii*
XG-CIFAL	24	*Pinus radiata*

4. Simulations

Simulations are not much used to aid practical breeding- only 6 out of 28 partners use simulations. These were SLU & SkogForsk (Sweden), INTRA (Grance), LFRI (Lithuania), METLA (Finland), University of Copenhagen and TUZVO in Slovakia (Table 4.1). Most of the respondents stated that they are willing to use simulations.

The users and developers as well as the information on the simulators for forest tree breeding are summarised in Table 4.2. These manly are deterministic simulators. Most of the simulations were produced by the group of prof. Dag Lindgren in SLU, Sweden and are available free of charge at his WEB page http://www-genfys.slu.se/staff/dagl/Index.htm. The WEB side also contains literature list, presentations, and information important to tree breeding. This information is useful and worth preserving for the future.

Table 4.1. Short list of instituons using simulatiors to aid practivla breeding.

Use simulations	Species
INRA	*Pseudotsuga menziesii*
LFRI	*Picea abies*
LFRI	*Pinus sylvestris*
SkogForsk	*Picea abies*
University of Copenhagen	*Pseudotsuga menziesii*
TUZVO	*Pinus sylvestris*
XG-CIFAL	*Pinus radiata*

4.2. Short description of users of simulators and the simulation software available to optimise breeding.

TreeBreedex No.	Short name	Country	Tree species (for which the respondent is giving the answers)	Software name	user (or person who provided answer)	Author of the software	Author's TBX No	Type of simulator	Remarks (write who made the remark, Darius or someone else
1	INRA	France	Fraxinus	Yes , we are using a simulator, which we have bought or dawnloaded for free	dufour@orleans.inra.fr				They did not specify which simulator is in use , we may contact them
1	INRA	France	Pseudotsuga menziesii	Yes, I have created a software “Allele dropping”	leopoldo.sanchez@orleans.inra.fr and jean-charles.bastien@orleans.inra.fr	leopoldo.sanchez@orleans.inra.fr and jean-charles.bastien@orleans.inra.fr	1	Both stochastic and deterministic	Platform where stochastic and deterministic models are combined depending on needs

9	UoC	Denmark		Simulation programs are developed in SAS and ASReml - but not as standardised programs as e.g. POPSIM. Made simply for "home" use.	Jon K Hansen jkh@life.ku.dk			Stochastic	Simulation programs are developed in SAS and ASReml - but not as standardised programs as e.g. POPSIM. Made simply for "home" use.
10	METLA	Finland	Sc. pine, Norway sprice, birch sp.	Yes , we are using a simulator, which we have bought or dawnloaded for free	matti.haapanen@metla.fi	Dag Lindgren et al.	25	Deterministic; there are several versions to fit particular scenarios	"Seed Orchard Deployer by Dag Lindgren et al.) , we may contact Matti
15	LFRI	Lithuania	Simulator can be used for all species	Breeding Cycler	darius.danusevicius@akas.lt	Dag Lindgren in cooperation with Darius	25 & 15	Deterministic; there are several versions to fit particular scenarios	Can be dawlnloaded for free at http://www-genfys.slu.se/staff/dagl/Breed_Home_Page/
15	LFRI	Lithuania	Simulator can be used for all species	Seed Orchard Deployer	darius.danusevicius@akas.lt	Dag Lindgren in cooperation with Darius	25 & 15	Deterministic	Can be dawlnloaded for free at http://www-genfys.slu.se/staff/dagl/Breed_Home_Page/
17	NFLI	Norway	Picea abies	Yes , we are using a simulator, which we have bought or downloaded for free	oystein.johnsen@skogoglandskap.no				They did not specify which simulator is in use , we may contact them
19	IBL	Poland	Picea abies, Pinus sylvestris, Abies alba, Larix europea, Quercus spp., Betula spp., Fagus spp.,	Yes , we are using a simulator, which we have bought or downloaded for free	j.kowalczyk@ibles.waw.pl				They did not specify which simulator is in use , we may contact them
21	SKOGFORSK	Sweden	Pinus sylvestris, Picea abies, Betula sp. and Pinus contorta.	Popsim	gunnar.jansson@skogforsk.se	Tim Mullin	21	Stochastic	Can be purchased from Tim Mullin in NZ; Ola Rosvall is the person in Skogforsk who has used the software
24	XG - CIFAL	Spain	Pinus spp. , Prunus avium, Pseudotsuga, Castania	SYNCHRO.SAS	vcodesido.cifal@siam-cma.org	vcodesido.cifal@siam-cma.org and dr. Rafael Zas	24	Deterministic; there are several versions to fit particular scenarios	For seed orchards , flowering phenology
25	SLU	Sweden	Simulator can be used for all	Breeding Cycler	Dag.Lindgren@genfys.slu.se	Dag Lindgren in cooperation	25 & 15	Deterministic; there are several	Can be dawlnloaded for free at

			species			with Darius		versions to fit particular scenarios	http://www-genfys.slu.se/staff/dagl/Breed_Home_Page/
25	SLU	Sweden	Simulator can be used for all species	Seed Orchard Deployer	Dag.Lindgren@genfys.slu.se	Dag Lindgren in cooperation with Darius	25 & 15	Deterministic	Can be dawlnloaded for free at http://www-genfys.slu.se/staff/dagl/Breed_Home_Page/
25	SLU	Sweden	Simulator can be used for all species	GainPred	Dag.Lindgren@genfys.slu.se	Dag Lindgren	25	Deterministic	Can be dawlnloaded for free at http://www-genfys.slu.se/staff/dagl/Breed_Home_Page/
25	SLU	Sweden	Simulator can be used for all species	LinearDeployment	Dag.Lindgren@genfys.slu.se	Dag Lindgren	25	Deterministic	Can be dawlnloaded for free at http://www-genfys.slu.se/staff/dagl/Breed_Home_Page/
25	SLU	Sweden	Simulator can be used for all species	OrchardMananger	Dag.Lindgren@genfys.slu.se	Dag.Lindgren@genfys.slu.se and Kyu-Suk Kang	25	Deterministic	Can be dawlnloaded for free at http://www-genfys.slu.se/staff/dagl/Breed_Home_Page/
25	SLU	Sweden	Simulator can be used for all species	A number of small programs based on DOS and Excell (day lenght and temperature prediction from lat. long; status number calculation, conacestry calculation; finding optimum number of testing sitres; selelction intesity calculator)	Dag.Lindgren@genfys.slu.se	Dag.Lindgren@genfys.slu.se (main author and a number of co-authors-see the web site)	25	Deterministic	Can be dawlnloaded for free at http://www-genfys.slu.se/staff/dagl/Breed_Home_Page/
25	SLU	Sweden	Simulator can be used for all species	Popsim	Dag.Lindgren@genfys.slu.se	Tim.Mullin@biosylve.com and lstiburek@fle.czu.cz	25	Stochastic	Can be purchased from Tim Mullin in USA; there is a free demo version
25	SLU	Sweden	Simulator can be used for all species	StatusNumberCalculator	Dag.Lindgren@genfys.slu.se	lstiburek@fle.czu.cz	25	Deterministic	Free dawnload from http://fle.czu.cz/~lstibure

									k/
28	TUZVO	Slovakia	Pinus sylvestris	Yes, I have created a software (Darius note: he did not indicate name of the softw.)	gomory@vsld.tuzvo.sk	gomory@vsld.tuzvo.sk	28	Deterministic	No name but the simulator is Intended for Pinus sylvestris; Free, on demand by e-mail

5. Summarising remarks

The most common drawbacks of the existing breeding programmes are as follows:

Long term and high input breeding

1. Reduced breeding value because of the need to refresh gene diversity by introducing less genetically advanced breeding stock. We have amplified the case where the long-term breeding populations are closed (means no infusion of material for outside) to see how many of these use within-family selection. The result was astonishing: 15 out of 20 long-term breeding programs with closed breeding populations use among-family selection. How then they are going to maintain the gene diversity of uncertain future?
2. Open pollinating is used to often. This causes failure to control relatedness and reduces breeding efficiency. Even if the programme is referred as long term breeding programme it is clear that it does not allow to control relatedness among breeding population members in the future generations. If so such programme will be ineffective as at certain point there will be a need to enrich the diversity in BP by introducing less advanced genetic material and in the way waist of recourses by reducing the genetic gain. Or it will be necessary to redesign it or even start form the beginning if inbreeding depression will be expressed.
3. Not considering time component in breeding to target not just generic gain but genetic gain per unit of time. In this time-infective way, there are many programmes based on progeny testing and selection backwards where no thinking seems to be for the cases when the selections backwards will be made for the following cycles.
4. Ineffective deployment. In most of the programmes breeding and multiplication populations are merged. Merging breeding and production populations will (a) reduce gain generating capacity of production populations, because they will need to carry the genetic diversity necessary for future breeding. By serving only for deployment needs.
5. Inefficient testing strategies. Most of the long-term and high-input breeding programmes still relay on progeny testing and selection backward or forward, however, phenotype

testing and clonal testing is less considered as options. Surprising little clonal testing is used for the species which are could easily be cloned by rooting, e.g. *Picea abies, Picea sitchensis and Populus* sp.

6. Simulations are used little to aid practical breeding, which result sin the inefficiencies listed above. There is a strong need to promote their use.

5. Acknowledgments

Comments by Patrik are appreciated.

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Appendix 1. The answers summarised by each of the four breeding strategies.

Appendix 1. Answers summarised by each of the four breeding strategies: the top most low input breeding (answers form the 1st two questions are 0,0), plantation forestry breeding (short term, high input breeding), conservation forestry breeding (long-term, low-input breeding) and commercial forestry breeding (long-term and high-input breeding). For answer codes are explained in the first row (expent for Q10 the code are as follws: 1- Single-stage: phenotype testing; 2- Single-stage: clone testing ; 3- Single-stage: progeny testing ; 4- Two-stage: phenotype/progeny testing.

Country	Country	Participant name	Participant short name and number	Species code	Species name	1. Are there specific plans to maintain sufficient level of gene diversity in breeding populations for many breeding cycles? 1- yes, 0- no	2. Are you aiming at high intensity breeding to obtain high benefit at the cost of large investments? 1-yes, 0- no	3. How is among-pop gene diversity captured by the breeding program? 1- MPBS by breeding zone, 2-3 other MPBS, 4- other, 5- do not care	4. Do you divide breeding population into intensively managed nucleus with top-ranking genotypes and less intensively managed main population 1- yes, 2 no	5. How is gene diversity maintained (or planned) in the main breeding population? 1- open pop.s, 2- closed pop.s, 3- other, 4- no plans	6. Which mating system among breeding population members is used to create the candidate population? 1- controlled, 2- open.	7. Are different testing strategies used for different traits? 1- yes, 2- no.	8. Is breeding population and multiplication pop. separated from each other as regards location and genetic composition? 1-3- yes, 4- no.	9. At which level is the selection of the new breeding population members made in each breeding cycle? 1- within fams, 2-among fams, 3-both, 4-other	10. What testing strategy is used/planned to select the BP members? (pre-screening in nursery for growth rhythm or vitality may be considered as single-stage)	11. Is information on molecular markers used to aid breeding? 1-yes, 0- no	12. Have you used simulations to optimise breeding? (If "Yes" then go to part 2 in the next worksheet) 1-yes, 0- no
						Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12
ES	Spain	Centro de investigacion y Tecnologia Agroalimentaria de Aragon (CITA)	27	1	Pinus sylvestris	0	0	3	2	3	2	2	4	2	1	0	0

DE	DE	NW-FVA	7	1	Pinus sylvestris	0	1	3	2	2	2	2	4	2	4	0	0
NL	Holand	Alterra	16	1	Pinus sylvestris	0	1	5	2	4	2	2	4	4	4	0	0
DE	DE	BFH	6	1	Pinus sylvestris	1	0	5	2	1	1	2	1	3	4	0	0
IE	Irland	Coillte Teoranta- The Irish Forestry Board	13	1	Pinus sylvestris	1	0	5	2	1	1	2	1	3	4	0	0
PL	PL	IBL	19	1	Pinus sylvestris	1	0	3	2	1	2	2	4	3	4	0	0
SK	Slovakia	NCL	22	1	Pinus sylvestris	1	0	3	1	1	2	2	3	3	4	1	0
LT	LT	LFRI	15	1	Pinus sylvestris	1	0	1	2	4	2	2	4	3	3	0	1
CZ	Czech	VULHM	5	1	Pinus sylvestris	1	1	2	2	1	2	1	3	3	4	0	0
FI	FI	Metla	10	1	Pinus sylvestris	1	1	1	2	2	1	2	3	1	4	0	0
UK	UK	(FR)FC	11	1	Pinus sylvestris	1	1	5	2	2	1	2	3	2	3	0	0
SE	SE	SkogForsk	21	1	Pinus sylvestris	1	1	1	2	2	1	2	4	1	3	0	0
						0.75	0.50									0.08	0.08
SK	Slovakia	NCL	22	2	Picea abies	0	0	3	1	4	2	2	3	3	4	0	0
DE	DE	NW-FVA	7	2	Picea abies	0	1	3	2	2	1	2	4	2	6	0	0
NL	Holand	Alterra	16	2	Picea abies	0	1	5	2	4	2	2	4	4	4	0	0
DK	DK	University of Copenhagen	9	2	Picea abies	1	0	3	1	2	2	2	4	4	6	0	0
PL	PL	IBL	19	2	Picea abies	1	0	3	2	1	2	2	4	3	4	0	0
CZ	Czech	VULHM	5	2	Picea abies	1	1	2	2	2	1	1	3	3	4	0	0
DE	DE	SBS	8	2	Picea abies	1	1	3	2	2	2	2	1	3	2	0	0
FI	FI	Metla	10	2	Picea abies	1	1	1	2	2	1	2	3	1	2	0	0
LT	LT	LFRI	15	2	Picea abies	1	1	1	2	4	2	2	4	3	3	0	1
NL	Norway	Norwegian Forest and	17	2	Picea abies	1	1	3	1	1	1	2	3	3	4	0	0

		Landscape Institute															
RO	RO	ICAS 20	20	2	Picea abies	1	1	3	2	2	2	2	1	3	4	0	0
SE	SE	SkogForsk	21	2	Picea abies	1	1	1	2	2	1	2	4	1	2	0	1
						0.75	0.75									0.00	0.17
UK	UK	(FR)FC	11	6	Larix sp	0	0	5	2	2	1	2	3	2	3	0	0
LT	LT	LFRI	15	6	Larix sp	0	0	5	2	4	2	2	4	2	1	0	0
DE	DE	BFH	6	6	Larix sp	0	1	5	2	4	1	2	1	2	3	0	0
DE	DE	NW-FVA	7	6	Larix sp	0	1	3	2	2	2	2	4	2	4	0	0
NL	Holand	Alterra	16	6	Larix sp	0	1	5	2	4	1	2	3	4	4	0	0
PL	PL	IBL	19	6	Larix sp	1	0	3	2	1	2	2	4	3	4	0	0
FR	FR	INRA	1	6	Larix sp	1	1	3	2	2	1	2	1	3	4	0	0
CZ	Czech	VULHM	5	6	Larix sp	1	1	2	2	2	1	1	3	3	4	0	0
DE	DE	SBS	8	6	Larix sp	1	1	1	2	3	2	2	1	3	3	0	0
FI	FI	Metla	10	6	Larix sp	1	1	1	2	2	2	2	3	1	1	1	0
RO	RO	ICAS 20	20	6	Larix sp	1	1	3	2	2	2	2	1	3	4	0	0
Exotic conifers						0.55	0.73									0.09	0
CZ	Czech	VULHM	5	3	Pinus contorta	1	0	4	2	2	2	1	3	3	3	0	0
SE	SE	SkogForsk	21	3	Pinus contorta	1	0	1	2	2	1	2	4	1	3	0	0
LT	LT	LFRI	15	3	Pinus contorta	0	0	5	2	4	2	2	4	2	1	0	0
DK	DK	University of Copenhagen	9	16	Picea sitchensis	1	0	3	2	2	2	2	4	4	6	0	0
UK	UK	(FR)FC	11	16	Picea sitchensis	1	1	5	2	2	1	2	3	3	3	0	0
IE	Irland	Coillte Teoranta- The Irish Forestry	13	16	Picea sitchensis	1	1	5	1	1	1	2	4	1	4	0	0

		Board															
BE	Belgium	CRNFB	3	15	Pseudotsuga menziesii	0	0	1	2	2	2	2	4	4	4	0	0
DE	DE	NW-FVA	7	15	Pseudotsuga menziesii	0	1	3	2	2	2	2	4	2	4	0	0
NL	Holand	Alterra	16	15	Pseudotsuga menziesii	0	1	5	2	4	2	2	4	4	4	0	0
DK	DK	University of Copenhagen	9	15	Pseudotsuga menziesii	1	0	3	2	2	2	2	4	3	6	0	1
IT	IT	CRA SEL	12	15	Pseudotsuga menziesii	1	0	1	2	2	2	2	4	2	4	0	0
ES	Spain	XG-CIFAL	24	15	Pseudotsuga menziesii	1	0	1	2	1	1	2	1	3	4	0	0
FR	FR	INRA	1	15	Pseudotsuga menziesii	1	1	4	1	3	1	2	1	3	3	0	1
DE	DE	SBS	8	15	Pseudotsuga menziesii	1	1	3	2	2	1	2	1	3	3	0	0
						0.63	0.5									0	0.25
Southern conifers																	
ES	Spain	Centro de investigacion y Tecnologia Agroalimentaria de Aragon (CITA)	27	28	Pinus halepensis	0	0	3	2	3	2	2	4	2	4	0	0
UK	UK	(FR)FC	11	21	Pinus nigra	0	0	5	2	2	2	2	3	2	3	0	0

ES	Spain	XG-CIFAL	24	22	Pinus radiata	0	0	5	1	1	2	1	3	3	4	0	1
RO	RO	ICAS 20	20	20	Pinus cembra	1	1	3	1	2	1	2	1	3	4	0	0
PL	PL	IBL	19	27	Abies alba	1	0	3	2	1	2	2	4	3	4	0	0
IT	IT	CRA SEL	12	27	Abies alba	1	0	3	2	1	2	2	2	2	1	0	0
Fast growing deciduous																	
SK	Slovakia	NCL	22	11	Populus sp	0	0	5	1	2	1	2	4	3	4	0	0
ES	Spain	Centro de investigacion y Tecnologia Agroalimentaria de Aragon (CITA)	27	11	Populus sp	0	0	5	2	3	1	2	2	4	2	0	0
DE	DE	NW-FVA	7	11	Populus sp	0	1	3	2	3	2	2	1	2	4	0	0
DE	DE	NW-FVA	7	11	Populus sp	0	1	3	2	1	1	2	1	3	4	0	0
FI	FI	Metla	10	11	Populus sp	0	1	4	2	1	1	2	4	4	5	0	0
AT	AT	BFW	2	11	Populus sp	1	0	5	2	1	1	1	4	3	2	1	0
CZ	Czech	VULHM	5	11	Populus sp	1	1	2	2	1	2	1	3	3	4	0	0
DE	DE	BFH	6	11	Populus sp	1	1	5	2	1	1	1	1	3	5	0	0
DE	DE	SBS	8	11	Populus sp	1	1	3	1	2	1	2	4	3	4	0	0
LT	LT	LFRI	15	11	Populus sp	1	1	5	2	1	1	2	4	3	2	1	0
NL	Holand	Alterra	16	11	Populus sp	1	1	5	2	3	1	2	4	4	5	0	0
						0.55	0.73									0.18	0.00
FI	FI	Metla	10	18	Alnus glutinosum	1	0	1	2	2	1	2	3	1	5	0	0
LT	LT	LFRI	15	18	Alnus glutinosum	1	0	1	2	2	2	2	1	3	1	0	0
DE	DE	BFH	6	9	Betula sp	0	0	5	2	4	1	2	4	1	5	0	0

UK	UK	(FR)FC	11	9	Betula sp	0	0	3	2	4	2	2	4	4	1	0	0
DE	DE	NW-FVA	7	9	Betula sp	0	1	3	2	2	2	2	4	2	6	0	0
LT	LT	LFRI	15	9	Betula sp	1	0	1	2	2	2	2	1	3	1	0	0
PL	PL	IBL	19	9	Betula sp	1	0	3	2	1	2	2	4	3	4	0	0
SE	SE	SkogForsk	21	9	Betula sp	1	0	1	2	2	1	2	4	1	2	0	0
CZ	Czech	VULHM	5	9	Betula sp	1	1	2	2	1	2	1	3	3	4	0	0
FI	FI	Metla	10	9	Betula sp	1	1	1	2	2	1	2	3	3	4	0	0
						0.63	0.38									0.00	0.00
Slow growing deciduous																	
FR	FR	INRA	1	8	Fraxinus sp	0	0		2	4	2	2	4	4	3	0	0
DE	DE	SBS	8	8	Fraxinus sp	0	0	3	2	2	2	2	1	1	1	0	0
UK	UK	(FR)FC	11	8	Fraxinus sp	0	0	1	2	4	2	2	4	3	1	0	0
DE	DE	NW-FVA	7	8	Fraxinus sp	0	1	3	2	2	2	2	4	2	4	0	0
NL	Holand	Alterra	16	8	Fraxinus sp	0	1	5	2	4	2	2	4	4	4	0	0
DK	DK	University of Copenhagen	9	8	Fraxinus sp	1	0	3	2	2	2	2	4	4	6	0	0
LT	LT	LFRI	15	8	Fraxinus sp	1	0	1	2	2	2	2	1	3	1	0	0
CZ	Czech	VULHM	5	8	Fraxinus sp	1	1	2	2	1	2	1	3	3	4	0	0
RO	RO	ICAS 20	20	8	Fraxinus sp	1	1	3	2	2	2	2	1	3	4	0	0
						0.44	0.44										
BE	Belgium	CRNFB	3	7	Quercus sp	0	0	1	2	2	2	2	4	4	4	0	0
UK	UK	(FR)FC	11	7	Quercus sp	0	0	5	2	4	2	2	4	2	3	0	0
DK	DK	University of Copenhagen	9	7	Quercus sp	1	0	3	2	2	2	2	4	4	6	0	0
LT	LT	LFRI	15	7	Quercus sp	1	0	1	2	2	2	2	1	3	1	0	0
PL	PL	IBL	19	7	Quercus sp	1	0	3	2	1	2	2	4	3	4	0	0

CZ	Czech	VULHM	5	7	Quercus sp	1	1	2	2	1	2	1	3	3	4	0	0
RO	RO	ICAS 20	20	7	Quercus sp	1	1	3	2	2	2	2	1	3	4	0	0
						0.71	0.29										
BE	Belgium	CRNFB	3	13	Prunus avium	0	0	1	2	2	2	2	4	4	4	0	0
DE	DE	SBS	8	13	Prunus avium	0	0	3	2	2	2	2	1	3	6	0	0
FR	FR	INRA	1	13	Prunus avium	0	1	5	2	2	1	1	3	3	5	0	0
DE	DE	NW-FVA	7	13	Prunus avium	0	1	3	2	1	2	2	1	3	4	0	0
NL	Holand	Alterra	16	13	Prunus avium	0	1	5	2	4	2	2	4	4	4	0	0
ES	Spain	XG-CIFAL	24	13	Prunus avium	0	1		2	4	2	2	4	3	4	0	0
DK	DK	University of Copenhagen	9	13	Prunus avium	1	0	3	2	2	2	2	4	4	6	0	0
BE	Belgium	Research Institute for Nature and Forest	4	13	Prunus avium	1	1	5	2	1	2	2	1	3	4	1	0
IT	IT	CRA SEL	12	13	Prunus avium	1	1	3	2	1	2	2	2	2	2	1	0
						0.33	0.67										
BE	Belgium	CRNFB	3	10	Fagus sp	0	0	1	2	2	2	2	4	4	4	0	0
CZ	Czech	VULHM	5	10	Fagus sp	1	1	2	2	1	2	1	3	3	4	0	0
DE	DE	SBS	8	10	Fagus sp	1	1	3	2	2	2	2	1	3	1	0	0
PL	PL	IBL	19	10	Fagus sp	1	0	3	2	1	2	2	4	3	4	0	0
						0.75	0.5										
Decidous of limited distribution																	
NL	Holand	Alterra	16	19	Acer pseudoplatanus	0	1	5	2	4	2	2	4	4	4	0	0
DE	DE	SBS	8	19	Acer	0	0	3	2	2	2	2	1	2	1	0	0

					pseudoplatanus												
UK	UK	(FR)FC	11	19	Acer pseudoplatanus	0	0	5	2	4	2	2	4	3	3	0	0
BE	Belgium	CRNFB	3	14	Robinia sp.	0	0	1	2	2	2	2	4	4	4	0	0
SK	Slovakia	TUZVO	28	9.1	Betula pendula var. carelica	0	0	5	1	2	1	2	3	3	4	0	0
CZ	Czech	VULHM	5	24	Ulmus sp.	0	1	4	2	3	1	1	2	3	6	0	0
IT	IT	CRA SEL	12	25	Sorbus aucuparia	1	0	3	2	1	2	2	2	1	2	1	0
ES	Spain	XG-CIFAL	24	23	Castanea sp.	1	0	1	2	4	2	1	2	3	5	1	0
IT	IT	CRA SEL	12	26	Juglans regia	1	1	3	2	1	2	2	2	2	1	1	0

Appendix 2. Raw table of answers at the individual level.

(answer codes are explained in the table below).

Participant name	Participant short name and number	E-mail to contact you	Tree species:	1. Are there specific plans to maintain sufficient level of gene diversity in breeding populations for many breeding cycles? 1= yes, 2=No	2. Are you aiming at high intensity breeding to obtain high benefit at the cost of large investments?	3. How is among-population gene diversity captured by the breeding program?	4. Do you divide breeding population into intensively managed nucleus with top-ranking genotypes and less intensively managed main population	5. How is gene diversity maintained (or planned) in the main breeding population?	6. Which mating system among breeding population members is used to create the candidate population?	7. Are different testing strategies used for different traits?	8. Is breeding population and multiplication pop. separated from each other as regards location and genetic composition?	9. At which level is the selection of the new breeding population members made in each breeding cycle?	10. What testing strategy is used/planned to select the BP members? (pre-screening in nursery for growth rhythm or vitality may be considered as single-stage)	11. Is information on molecular markers used to aid breeding?	12. Have you used simulations to optimise breeding? (If "Yes" then go to part 2 in the next worksheet)
Research Center on Nature, Forests and Wood	CRNFB (n°3)	p.mertens@mrw.wallonie.be	12	2	2	1	2	2	2	2	4	4	4	2	2
Research Center on Nature, Forests and Wood	CRNFB (n°3)	p.mertens@mrw.wallonie.be	8	2	2	1	2	2	2	2	4	4	4	2	2
Research Center on Nature, Forests and Wood	CRNFB (n°3)	p.mertens@mrw.wallonie.be	7	2	2	1	2	2	2	2	4	4	4	2	2
Research Center	CRNFB	p.mertens@mrw.	12	2	2	1	2	2	2	2	4	4	4	2	2

on Nature, Forests and Wood	(n°3)	wallonie.be													
Research Center on Nature, Forests and Wood	CRNFB (n°3)	p.mertens@mrw.wallonie.be	12	2	2	1	2	2	2	2	4	4	4	2	2
Matti Haapanen	?		1	1	1	1	2	2	1	2	3	1	4	2	2
Matti Haapanen	?	matti.haapanen@metla.fi	11	2	1	4	2	1	1	2	4	4	5	2	2
Matti Haapanen	?	matti.haapanen@metla.fi	9	1	1	1	2	2	1	2	3	3	4	2	2
Matti Haapanen	?	matti.haapanen@metla.fi	2	1	1	1	2	2	1	2	3	1	2	2	2
Matti Haapanen	?	matti.haapanen@metla.fi	12	1	2	1	2	2	1	2	3	1	5	2	2
Matti Haapanen	?	matti.haapanen@metla.fi	6	1	1	1	2	2	2	2	3	1	1	1	2
INRA	1	paques@orleans.inra.fr	6	1	1	3	2	2	1	2	1	3	4	2	2
inra	1	dufour@orleans.inra.fr, santi@orleans.inra.fr	12	2	1	5	2	2	1	1	3	3	5	2	2
inra	1	dufour@orleans.inra.fr	8	2	2		2	4	2	2	4	4	3	2	2
Alterra	16	sven.devries@wur.nl	6	2	1	5	2	4	1	2	3	4	4	2	2

Alterra	16	sven.devries@wur.nl	2	2	1	5	2	4	2	2	4	4	4	2	2
Alterra	16	sven.devries@wur.nl	11	1	1	5	2	3	1	2	4	4	5	2	2
Alterra	16	sven.devries@wur.nl	12	2	1	5	2	4	2	2	4	4	4	2	2
Alterra	16	sven.devries@wur.nl	8	2	1	5	2	4	2	2	4	4	4	2	2
Alterra	16	sven.devries@wur.nl	12	2	1	5	2	4	2	2	4	4	4	2	2
Alterra	16	sven.devries@wur.nl	12	2	1	5	2	4	2	2	4	4	4	2	2
Alterra	16	sven.devries@wur.nl	1	2	1	5	2	4	2	2	4	4	4	2	2
Norwegian Forest and Landscape Institute	NFLI, P17	oystein.johnsen@skogoglandskap.no	2	1	1	3	1	1	1	2	3	3	4	2	2
Instytut Badawczy Leśnictwa	IBL	j.kowalczyk@ibles.waw.pl	1	1	2	3	2	1	2	2	4	3	4	2	2
Instytut Badawczy Leśnictwa	IBL	j.kowalczyk@ibles.waw.pl	2	1	2	3	2	1	2	2	4	3	4	2	2
Instytut Badawczy Leśnictwa	IBL	j.kowalczyk@ibles.waw.pl	6	1	2	3	2	1	2	2	4	3	4	2	2

Instytut Badawczy Leśnictwa	IBL	j.kowalczyk@ibles.waw.pl	7	1	2	3	2	1	2	2	4	3	4	2	2
Instytut Badawczy Leśnictwa	IBL	j.kowalczyk@ibles.waw.pl	9	1	2	3	2	1	2	2	4	3	4	2	2
Instytut Badawczy Leśnictwa	IBL	j.kowalczyk@ibles.waw.pl	10	1	2	3	2	1	2	2	4	3	4	2	2
Instytut Badawczy Leśnictwa	IBL	j.kowalczyk@ibles.waw.pl	12	1	2	3	2	1	2	2	4	3	4	2	2
National Forest Centre & Technical University Zvolen	NLC 22 and TUZVO 28	bruchanik@lesy.sk	1	1	2	3	1	1	2	2	3	3	4	1	2
Technical University Zvolen	TUZVO 28	paule@vsld.tuzvo.sk	12	2	2	5	1	2	1	2	3	3	4	2	2
National Forest Centre & Technical University Zvolen	NLC 22	roman.longauer@nlcsk.org	2	2	2	3	1	4	2	2	3	3	4	2	2
National Forest Centre	NLC 22	roman.longauer@nlcsk.org	11	2	2	5	1	2	1	2	4	3	4	2	2
Gunnar Jansson	Partner 21 Skogforsk	gunnar.jansson@skogforsk.se	9	1	2	1	2	2	1	2	4	1	2	2	2

Gunnar Jansson	Partner 21 Skogforsk	gunnar.jansson@skogforsk.se	3	1	2	1	2	2	1	2	4	1	3	2	2
Gunnar Jansson	Partner 21 Skogforsk	gunnar.jansson@skogforsk.se	2	1	1	1	2	2	1	2	4	1	2	2	1
Gunnar Jansson	Partner 21 Skogforsk	gunnar.jansson@skogforsk.se	1	1	1	1	2	2	1	2	4	1	3	2	2
Coillte Teoranta-The Irish Forestry Board	Coillte Partner No. 13	david.thompson@coillte .ie	12	1	1	5	1	1	1	2	4	1	4	2	2
Coillte Teoranta-The Irish Forestry Board	Coillte Partner No. 13	david.thompson@coillte .ie	1	1	2	5	2	1	1	2	1	3	4	2	2
Johann Heinrich von Thuenen-Institute, Federal Research Institute for Rural areas, Forestry and Fisheries, Institute of Forest Genetics	vTI (former BFH), P 6	volker.schneck@vti.bund.de	1	1	2	5	2	1	1	2	1	3	4	2	2
Johann Heinrich von Thuenen-Institute, Federal Research Institute for Rural areas, Forestry and	vTI (former BFH), P 6	volker.schneck@vti.bund.de	6	2	1	5	2	4	1	2	1	2	3	2	2

Fisheries, Institute of Forest Genetics															
Johann Heinrich von Thuenen-Institute, Federal Research Institute for Rural areas, Forestry and Fisheries, Institute of Forest Genetics	vTI (former BFH), P 6	volker.schneck@vti.bund.de	9	2	2	5	2	4	1	2	4	1	5	2	2
Johann Heinrich von Thuenen-Institute, Federal Research Institute for Rural areas, Forestry and Fisheries, Institute of Forest Genetics	vTI (former BFH), P 6	volker.schneck@vti.bund.de	11	1	1	5	2	1	1	1	1	3	5	2	2
Nordwestdeutsche Forstliche Versuchsanstalt	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	11	2	1	3	2	3	2	2	1	2	4	2	2
Nordwestdeutsche Forstliche Versuchsanstalt	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	1	2	1	3	2	2	2	2	4	2	4	2	2
Nordwestdeutsche Forstliche	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	2	2	1	3	2	2	1	2	4	2	6	2	2

Versuchsanstalt															
Nordwestdeutsche Forstliche Versuchsanstalt	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	6	2	1	3	2	2	2	2	4	2	4	2	2
Nordwestdeutsche Forstliche Versuchsanstalt	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	8	2	1	3	2	2	2	2	4	2	4	2	2
Nordwestdeutsche Forstliche Versuchsanstalt	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	9	2	1	3	2	2	2	2	4	2	6	2	2
Nordwestdeutsche Forstliche Versuchsanstalt	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	11	2	1	3	2	1	1	2	1	3	4	2	2
Nordwestdeutsche Forstliche Versuchsanstalt	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	12	2	1	3	2	1	2	2	1	3	4	2	2
Nordwestdeutsche Forstliche Versuchsanstalt	NW-FVA (07)	helmut.grotehusmann@nw-fva.de	12	2	1	3	2	2	2	2	4	2	4	2	2
Staatsbetrieb Sachsenforst	SBS; 8	doris.krabel@smul.sachsen.de	12	2	2	3	2	2	2	2	1	3	6	2	2
Staatsbetrieb Sachsenforst	SBS; 8	doris.krabel@smul.sachsen.de	12	1	1	3	2	2	1	2	1	3	3	2	2
Staatsbetrieb Sachsenforst	SBS; 8	doris.krabel@smul.sachsen.de	10	1	1	3	2	2	2	2	1	3	1	2	2
Staatsbetrieb	SBS; 8	doris.krabel@smu	8	2	2	3	2	2	2	2	1	1	1	2	2

Sachsenforst		l.sachsen.de													
Staatsbetrieb Sachsenforst	SBS; 8	doris.krabel@smul.sachsen.de	6	1	1	1	2	3	2	2	1	3	3	2	2
Staatsbetrieb Sachsenforst	SBS; 8	doris.krabel@smul.sachsen.de	2	1	1	3	2	2	2	2	1	3	2	2	2
Staatsbetrieb Sachsenforst	SBS; 8	doris.krabel@smul.sachsen.de	11	1	1	3	1	2	1	2	4	3	4	2	2
Staatsbetrieb Sachsenforst	SBS; 8	doris.krabel@smul.sachsen.de	12	2	2	3	2	2	2	2	1	2	1	2	2
Austria BFW	2	Berthold	11	1	2	5	2	1	1	1	4	3	2	1	2
Forest Research and Management Institute	ICAS 20	gh_parnuta@icas.ro	2	1	1	3	2	2	2	2	1	3	4	2	2
Forest Research and Management Institute	ICAS 20	gh_parnuta@icas.ro	6	1	1	3	2	2	2	2	1	3	4	2	2
Forest Research and Management Institute	ICAS 20	gh_parnuta@icas.ro	7	1	1	3	2	2	2	2	1	3	4	2	2
Forest Research and Management Institute	ICAS 20	gh_parnuta@icas.ro	8	1	1	3	2	2	2	2	1	3	4	2	2
Forest Research and Management Institute	ICAS 20	gh_parnuta@icas.ro	12	1	1	3	1	2	1	2	1	3	4	2	2
INRA	INRA 1	leopoldo.sanchez	12	1	1	4	1	3	1	2	1	3	3	2	1

		@orleans.inra.fr and jean-charles.bastien@orleans.inra.fr													
Jason Hubert		jason.hubert@forestry.gsi.gov.uk	9	2	2	3	2	4	2	2	4	4	1	2	2
Jason Hubert		jason.hubert@forestry.gsi.gov.uk	12	2	2	5	2	4	2	2	4	3	3	2	2
Jason Hubert		jason.hubert@forestry.gsi.gov.uk	7	2	2	5	2	4	2	2	4	2	3	2	2
Jason Hubert		jason.hubert@forestry.gsi.gov.uk	8	2	2	1	2	4	2	2	4	3	1	2	2
Forest Research	FR 11	steve.lee@forestry.gsi.gov.uk	1	1	1	5	2	2	1	2	3	2	3	2	2
Forest Research	FR 11	steve.lee@forestry.gsi.gov.uk	12	2	2	5	2	2	2	2	3	2	3	2	2
Forest Research	FR 11	steve.lee@forestry.gsi.gov.uk	6	2	2	5	2	2	1	2	3	2	3	2	2
Forest Research	FR 11	steve.lee@forestry.gsi.gov.uk	12	1	1	5	2	2	1	2	3	3	3	2	2
Centro de Información Ambiental de Lourizán	XG-CIFAL, Partner 24	ffina.cifal@siam-cma.org	12	2	2	5	1	1	2	1	3	3	4	2	1
Centro de Información	XG-CIFAL,	ffina.cifal@siam-cma.org	12	2	1		2	4	2	2	4	3	4	2	2

Ambiental de Lourizán	Partner 24														
Centro de Información Ambiental de Lourizán	XG-CIFAL, Partner 24	ffina.cifal@siam-cma.org	12	1	2	1	2	1	1	2	1	3	4	2	2
Centro de Información Ambiental de Lourizán	XG-CIFAL, Partner 24	ffina.cifal@siam-cma.org	12	1	2	1	2	4	2	1	2	3	5	1	2

Decoding of the answer codes

Species	1. Pinus sylvestris
	2. Picea abies
	3. Pinus contorta
	4. Juniperus sp.
	5. Taxus bocata
	6. Larix sp.
	7. Quercus sp.
	8. Fraxinus sp.
	9. Betula sp.
	10. Fagus sp.
	11. Populus sp.

	12. Other species (fill the cell to the right)
1. What type of breeding program is used/planned as regards gene diversity	1. Yes (long term breeding)
	2. No (short term breeding)
2. What type of breeding program is used/planned as regards costs	1. Yes (high input breeding)
	2. No (low input breeding)
3. How among-population gene diversity is captured by the breeding program?	1. Multiple breeding populations, one in each breeding zone
	2. Multiple breeding populations, established by administrative districts
	3. Multiple breeding pops. based on sitetype or natural species range
	4. Other, state which
	5. No attention is paid: all range is one breeding zone
4. Is nucleus breeding system used? (separation of a smaller group of genetically advanced trees within the breeding population)?	1. Yes
	2. No
5. How is gene diversity maintained in (or planned) in the breeding population (BP)?	1. Open population, recurrent infusion of genetic material.
	2. Closed population, no infusion of new material.
	3. Other method (state which)
	4. No long-term plans,

6. Which mating system among breeding population members is used (or planned) to create the candidate population?	1. Controlled pollination (SPM, DPM, diallel, factorials, polycross, other)
	2. Open pollination
7. Are different testing strategies used for different traits	1. Yes, different strategies (indicate which for which)
	2. No, the same strategies
8. Is breeding population and multiplication population separated from each other as regards location and genetic composition?	1. Yes, separated geographically
	2. Yes, separated genetically
	3. Yes, separated geographically and genetically
	4. No, not separated
9. Level of selection	1. Within families
	2. Among families
	3. Among and within families
	4. Other, free comment
10. What testing strategy is used/planned to select the BP members (pre-screening in nursery for growth rhythm or vitality may be considered as single-stage):	1. Single-stage: phenotype testing
	2. Single-stage: clone testing
	3. Single-stage: progeny testing
	4. Two-stage: phenotype/progeny testing
	5. Two-stage: phenotype/clone testing
	6. Other, free comment
11. Is information on molecular markers used to aid the selection?	1. Yes (list the traits)
	2. No

12. Have you used simulations?	1. Yes
	2. No