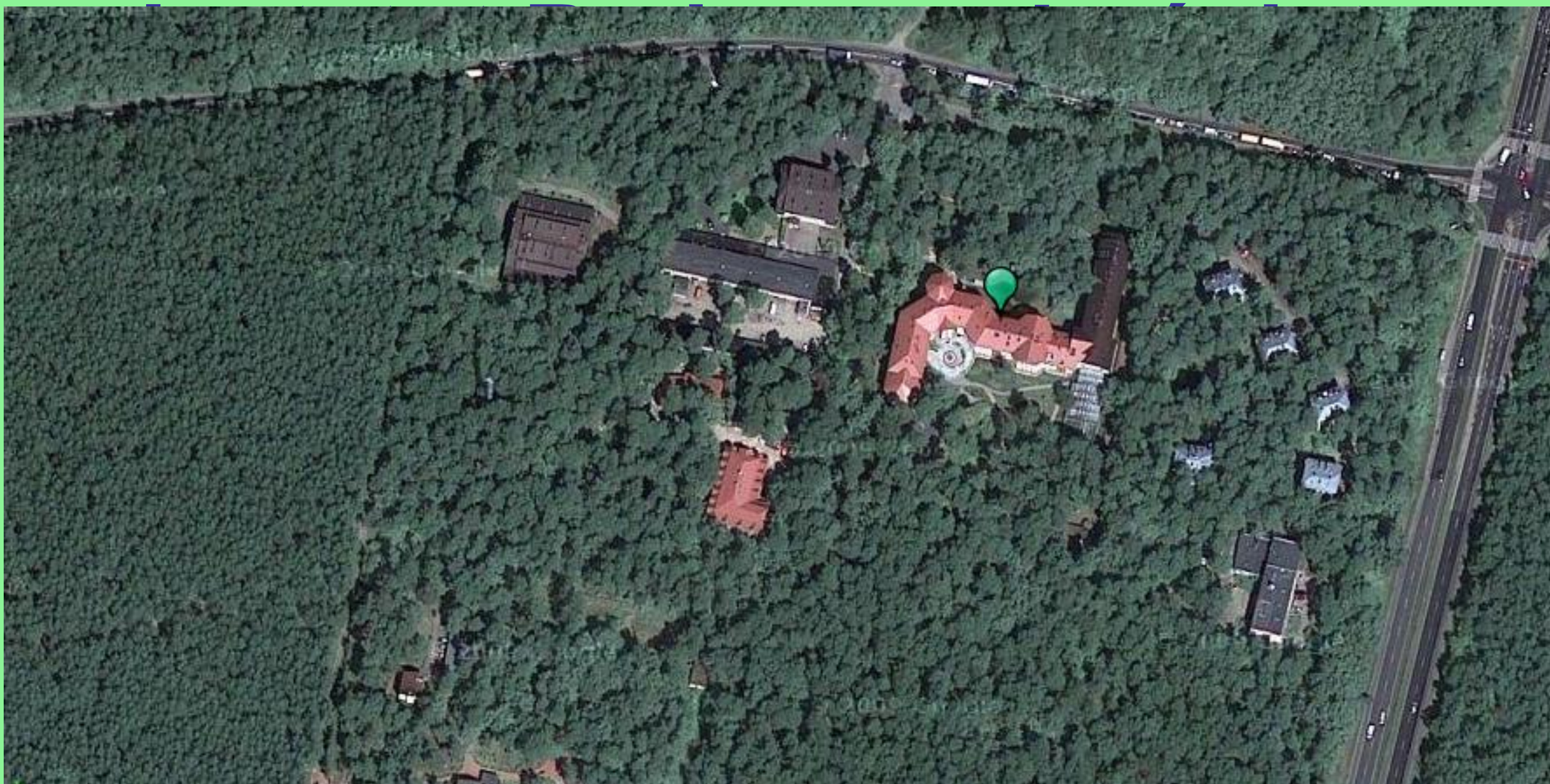
FOREST RESEARCH INSTITUTE



www.ibles.pl

Jan Teodor HAUSBRANDT
first director of IBL
(1895-1940)

The Forest Research Institute

• was established in **1930** as an Experimental Station of the State Forests,

• in **1934** it has been transferred into Forest Research Institute of the State Forests,

• since **1945** it has been acting as the Forest Research Institute, subordinated to the **Minister of Environment**.

Sękocin Stary

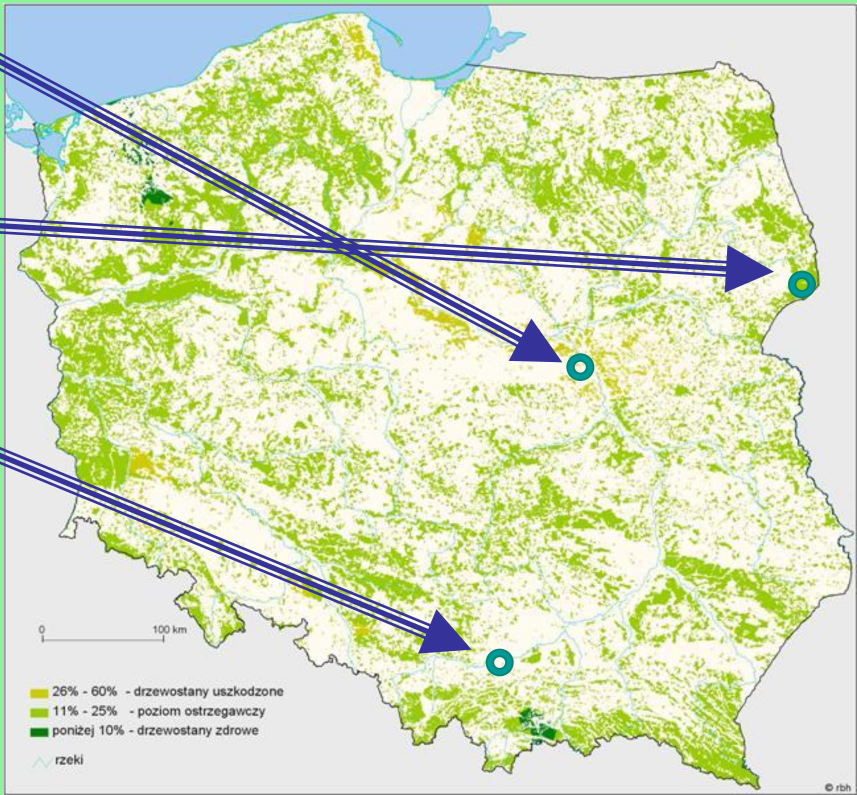
- Department of Forest Ecology
- Department of Sylviculture, Genetics and Tree Physiology
- Department of Forest Protection
- Departmant of Forest Fires
- Department of Forest Management
- Department of Scientific Information
- Laboratory of Chemistry of Forest Environment
- Ph.D. study program
- PEFC Office

Białowieża

- European Center for Natural Forests

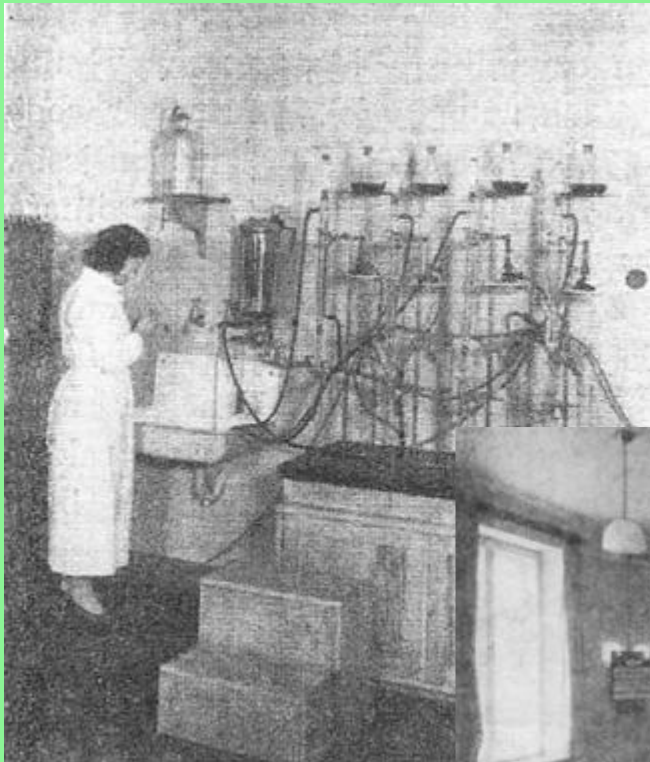
Kraków

- Department of of Mountain Forestry



- *203 persons employed including 21 professors and 56 doctors.*

80 years IBL



POLSKIE CENTRUM AKREDYTACJI
POLISH CENTRE FOR ACCREDITATION

PCA

Sygnatariusz EA MLA
EA MLA Signatory

CERTYFIKAT AKREDYTACJI
LABORATORIUM BADAWCZEGO
ACCREDITATION CERTIFICATE OF TESTING LABORATORY
Nr AB 740

Potwierdza się, że: / This is to confirm that:

INSTYTUT BADAWCZY LEŚNICTWA
PRACOWNIA CHEMII ŚRODOWISKA LEŚNEGO
ul. Braci Leśnej 3, Sękocin Stary, 05-090 Raszyn

spełnia wymagania normy PN-EN ISO/IEC 17025:2005
meets requirements of the PN-EN ISO/IEC 17025:2005 standard

Akredytowana działalność jest określona w Zakresie Akredytacji Nr AB 740
Accredited activity is defined in the Scope of Accreditation No AB 740

Akredytacja pozostaje w mocy pod warunkiem przestrzegania
...jącej określonych w kontrakcie Nr AB 740
...e in force provided the Laboratory observes
...itation Body defined in the Contract No AB 740

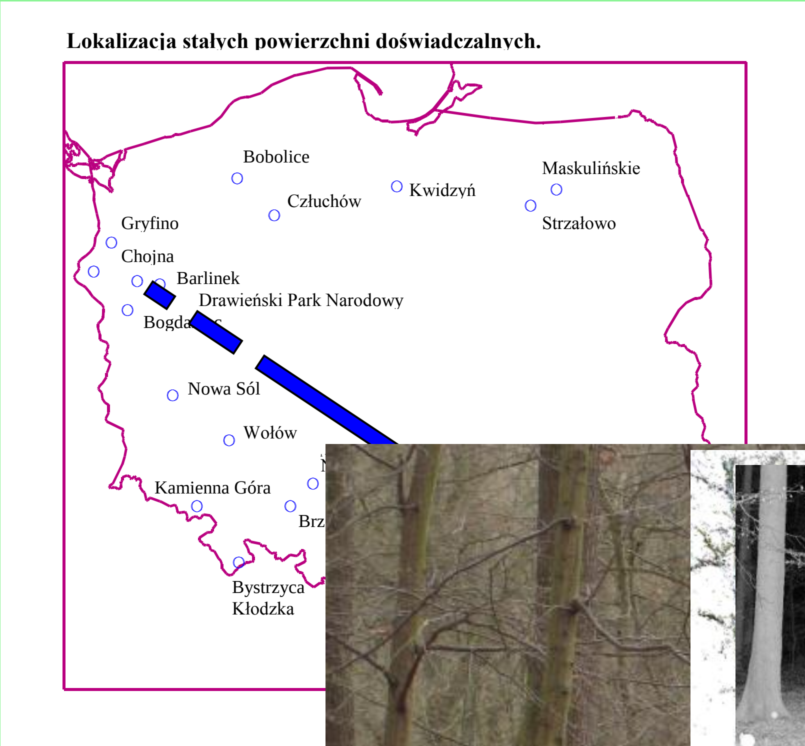
...cji ważny do dnia 22.06.2010 r.
...ccreditation is valid until 22.06.2010

...dzielono dnia 23.06.2006 r.
...on was granted on 23.06.2006

DYREKTOR
POLSKIEGO CENTRUM AKREDYTACJI
KAROL HAUPTMANN

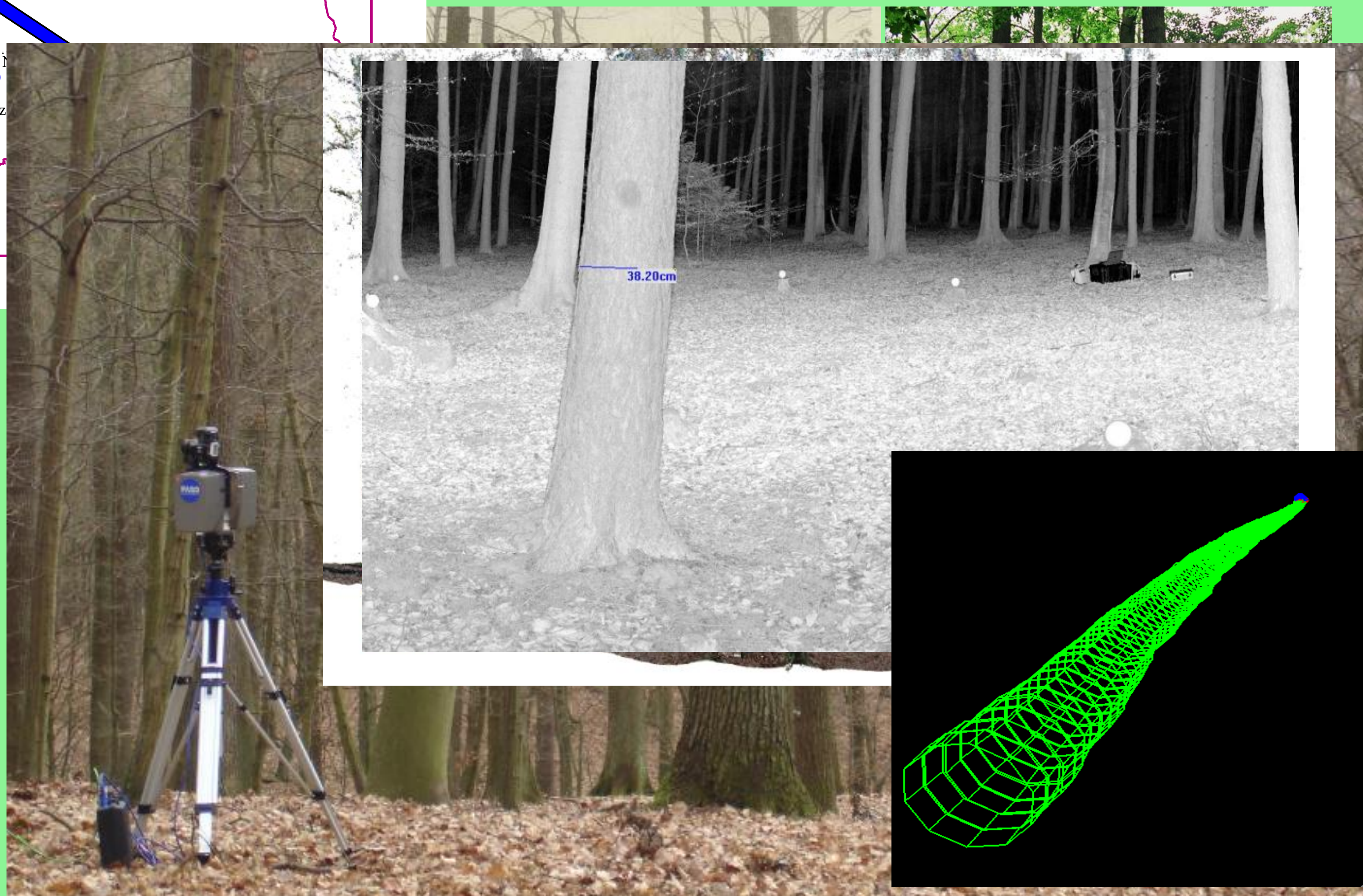
..., dnia 4 maja 2007 roku

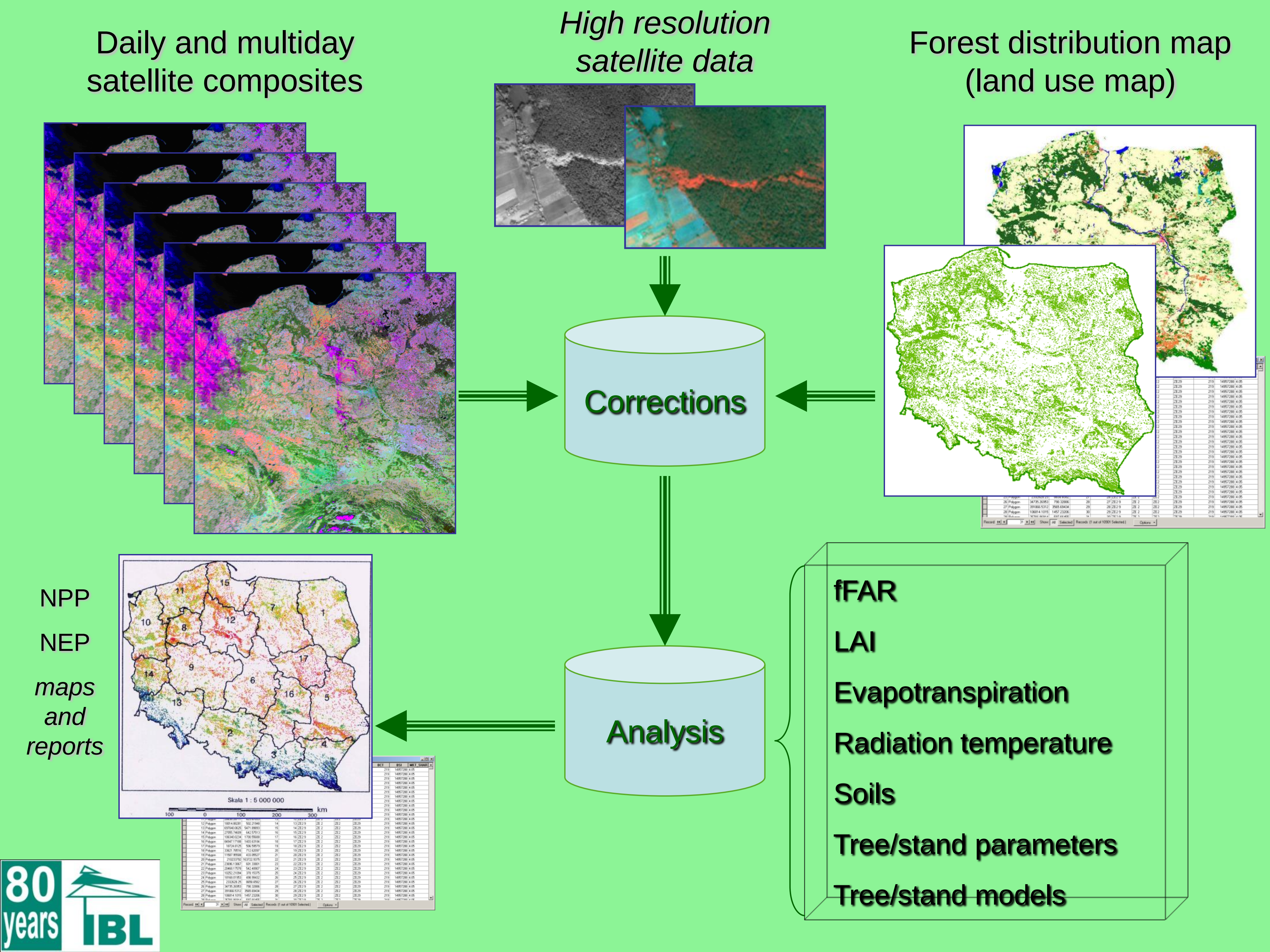
80 years IBL



Permanent plots

- By Adam Schwappach (since 1886) and Eilhard Wiedemann (since 1927)
- The oldest - 1874
- The oldest in Poland - 1895 (till know 67 plots)




Daily and multiday satellite composites
High resolution satellite data
Forest distribution map (land use map)
Corrections
Analysis
fFAR
LAI
Evapotranspiration
Radiation temperature
Soils
Tree/stand parameters
Tree/stand models
NPP
NEP
maps and reports
Skala 1 : 5 000 000
100 0 100 200 300 km
80 years
IBL

IUFRO

Certificate of Membership

Member Organization: Poland - 125.00.00

Forest Research Institute

The International Union of Forest Research Organizations (IUFRO) was founded in 1892 and has become the advocate of forest science on a world-wide scale. It promotes coordination of and international cooperation in research and science synthesis, and application of science in management and policy, in all areas related to forests and trees. IUFRO is a voluntary, non-profit, non-governmental scientific body open to organizations and individuals involved in forestry research and forest-related sciences.

Membership in IUFRO means that the researchers at the Forest Research Institute can enjoy a wide range of services and benefits and cooperate in a global network for forest science.

IUFRO Headquarters
Secretariat, Hauptstrasse 7
A-1140 Vienna-Hadersdorf
Austria

IUFRO President

Tel.: +43-1-8770151-0
Fax: +43-1-8770151-50
E-mail: office@iufro.org
Web: http://iufro.boku.ac.at

- member since 1936 r.

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FIRE PARADOX

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eea grants norway grants

FlexWood
Flexible Wood Supply Chain

Treebreedex

polska pomoc

EUROPEAN FOREST INSTITUTE

Certificate of Associate Membership

This is to certify that

Forest Research Institute, Poland

is one of the twelve founding member organizations of the EFI Association founded in 1993.

Risto Päivinen,
Director

www.efi.int

80 years IBL


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Kwartalnik Instytutu Badawczego Leśnictwa
Leśne Prace Badawcze
Vol. 71 (1)
Marzec 2010
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Folia Forestalia Polonica
Series A - Forestry
Stan różnorodności biologicznej lasów w Polsce
na podstawie powierzchni obserwacyjnych monitoringu
pod redakcją
Janusza Czerepko
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PRACE INSTYTUTU BADAWCZEGO LEŚNICTWA
ROZPRAWY I MONOGRAFIE
10
Jan Tyszka
Hydrologiczne funkcje lasu w małych nizinnych zlewniach rzecznych
PRACE INSTYTUTU BADAWCZEGO LEŚNICTWA
ROZPRAWY I MONOGRAFIE
7
Jan Głaz
Zasady funkcjonowania zrównoważonego gospodarstwa leśnego na przykładzie regionu uprzemysłowionego
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Poradnik dla Właścicieli Lasów Prywatnych
pod redakcją
Piotra Gołosa
PRACE INSTYTUTU BADAWCZEGO LEŚNICTWA
ROZPRAWY I MONOGRAFIE
9
Justyna Anna Nowakowska
Zmienność genetyczna polskich wybranych populacji sosny zwyczajnej (Pinus sylvestris L.) na podstawie analiz polimorfizmu DNA
ZIMOWA SZKOŁA LEŚNA
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– stan obecny i przyszłość
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Sękocin Stary, 17–19 marca 2009 r.
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streszczenia referatów i doniesień
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Sękocin Stary, 16–18 marca 2010 r.
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Instytut Badawczy Leśnictwa
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Sękocin Stary 2009
Axel Schwerk
Model of the rate of succession of epigeic carabid beetles (Coleoptera: Carabidae) on degraded areas
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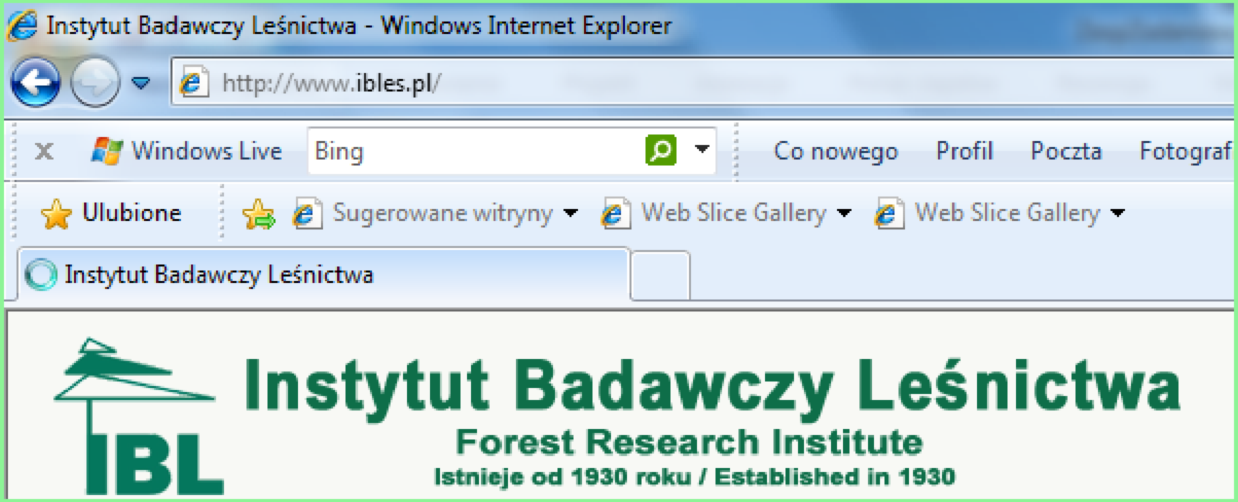
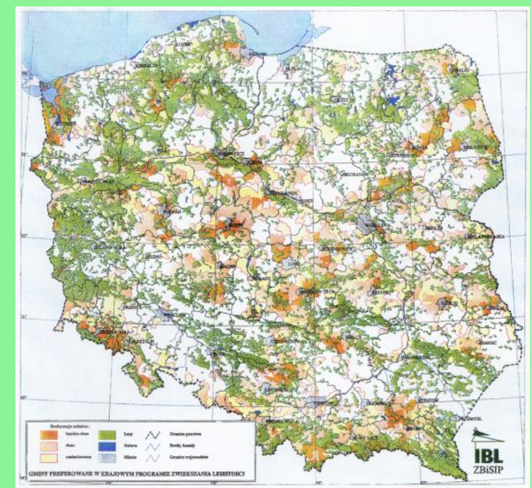
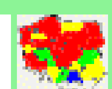
Forests and Forestry in European Union Countries
The guide
to forests and forest issues
THE STATE FORESTS INFORMATION CENTRE
75 years IBL
FOREST RESEARCH INSTITUTE
80 years IBL





Nowości Piśmiennictwa Leśnego 

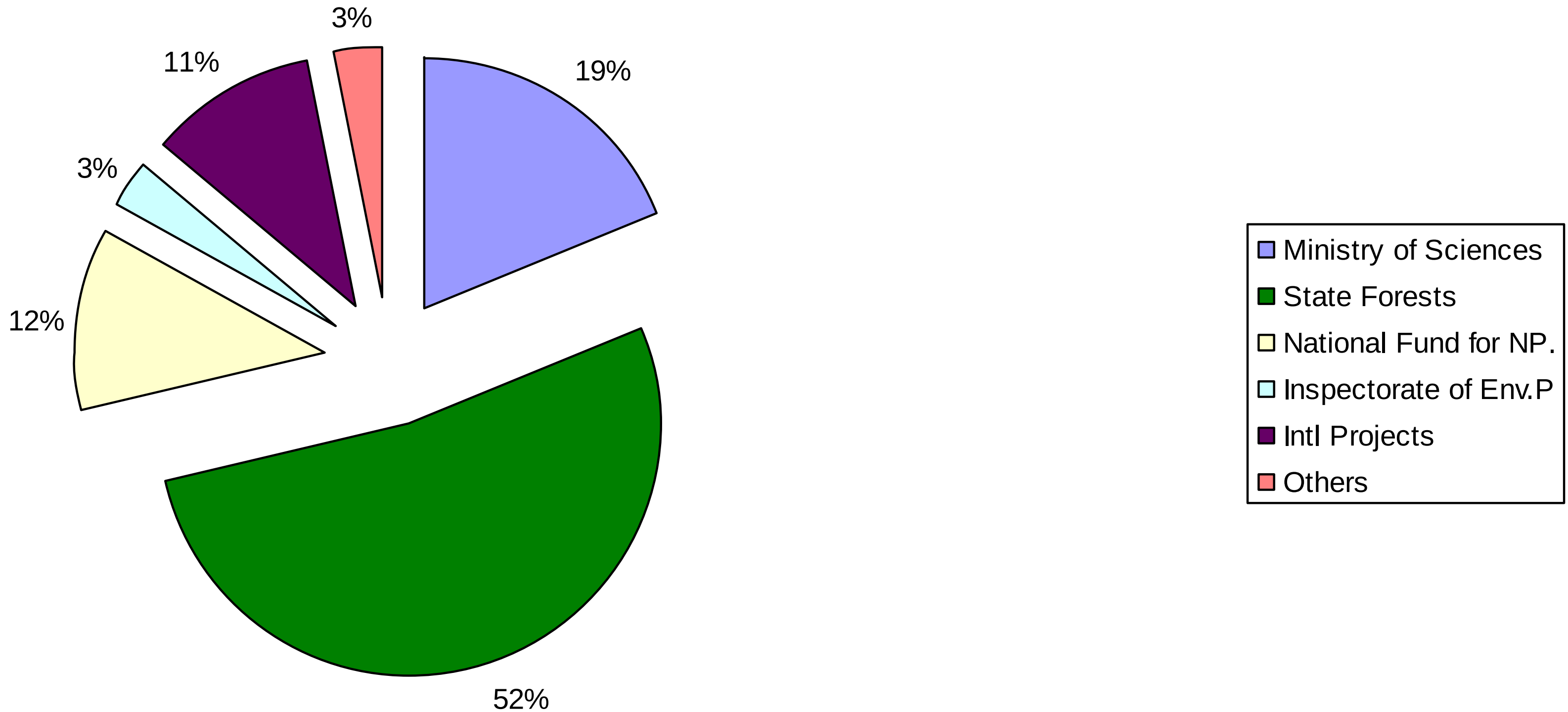
Monitoring Lasu 

Mapa zagrożenia pożarowego lasu 

Krajowy System Informacji o Pożarach Lasów 

80 years IBL

Our main clients



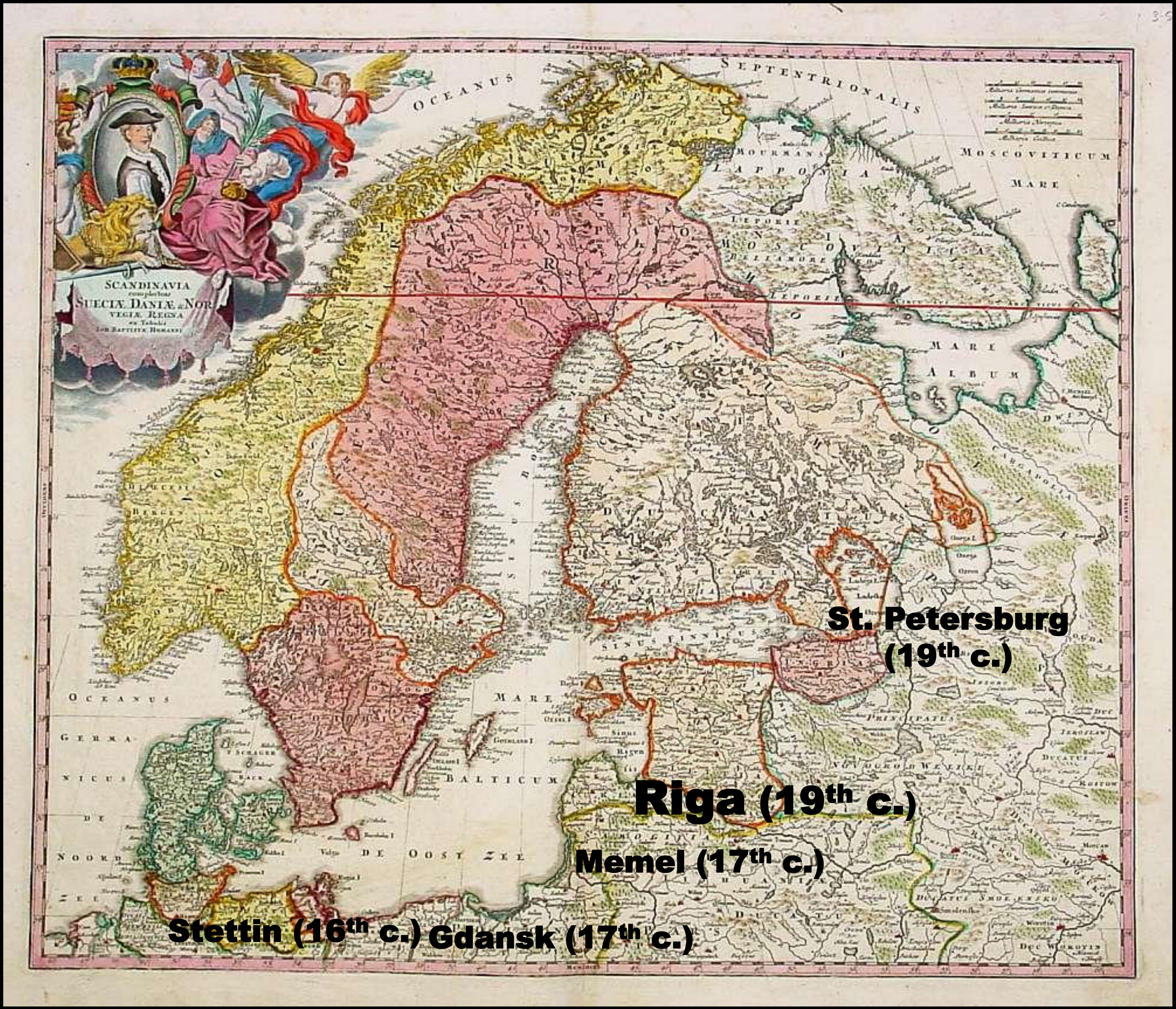
Thank you….

Usefulness of the genetic field experiments for biological sciences

Jacek Oleksyn

Polish Academy of Sciences
Institute of Dendrology

HMS Victory (104 guns)


SCANDINAVIA complectens SUECIÆ, DANIÆ & NORVEGIÆ REGNA
OCEANUS SEPTENTRIONALIS
MOSCOVITICUM MARE
MARE ALBUM
SINUS FINNICUS
MARE BALTICUM
DE OOST ZEE
OCEANUS GERMANICUS DE NOORD ZEE
St. Petersburg (19th c.)
Riga (19th c.)
Memel (17th c.)
Stettin (16th c.)
Gdansk (17th c.)

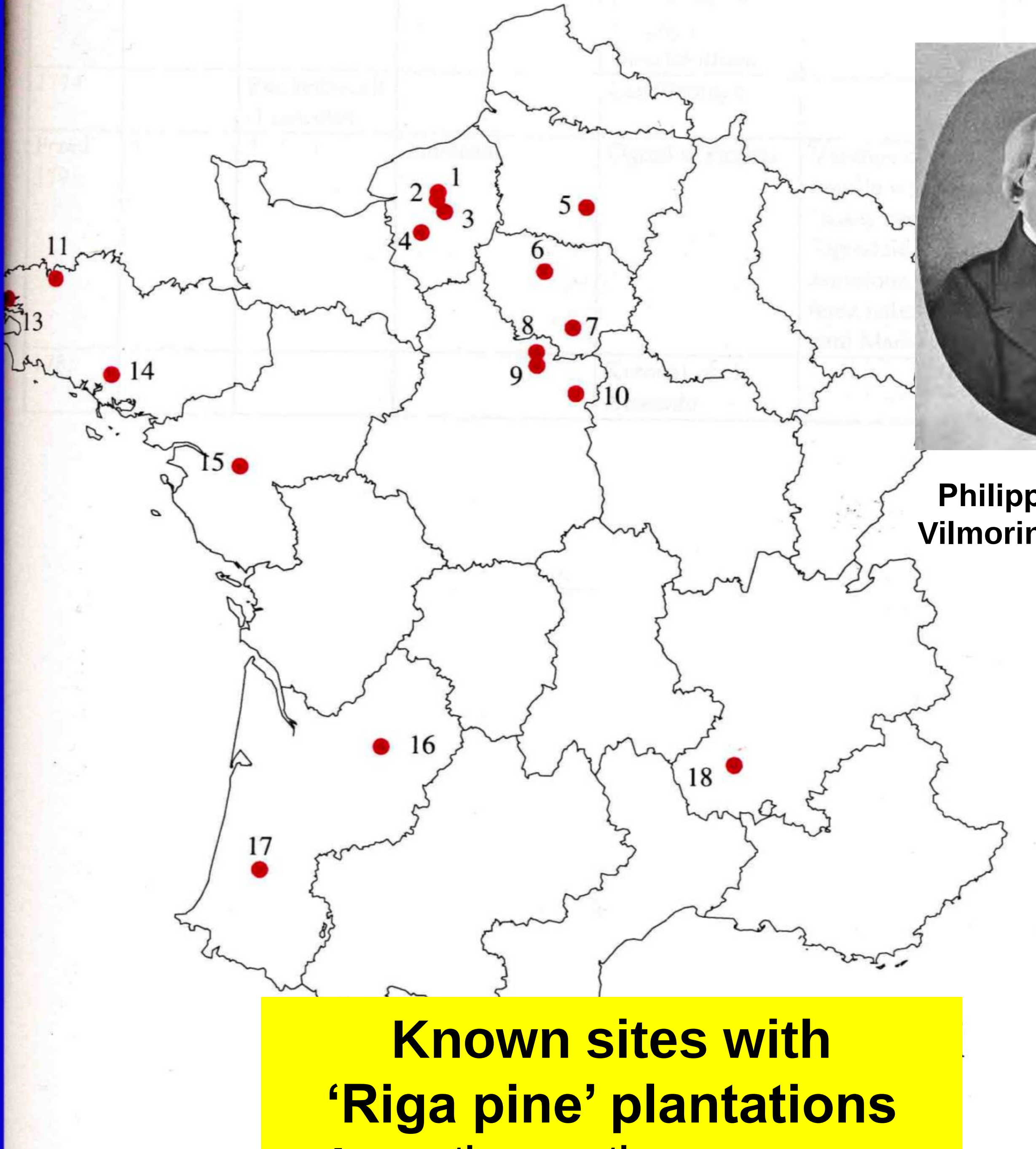
Dvina river, S.M. Prokudin-Gorskii (1912)

Mariinskii channel, S.M. Prokudin-Gorskii (1912)

Mariinskii channel, S.M. Prokudin-Gorskii (1912)

Volga near Kostroma, S.M. Prokudin-Gorskii (1912)

Piotr Daszkiewicz
Muséum national d'Histoire naturelle



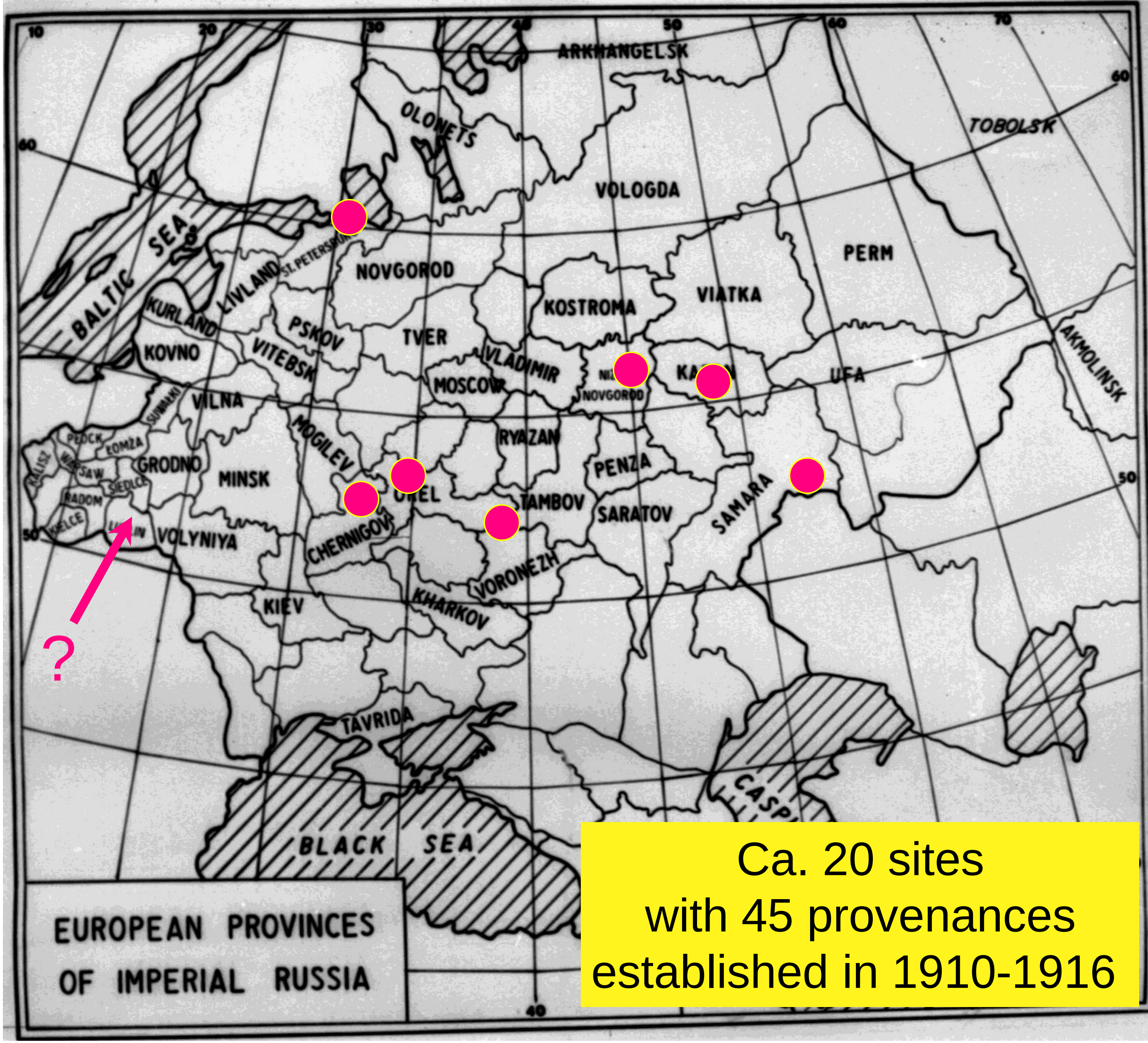
Philippe André de Vilmorin (1776-1862)

Known sites with ‘Riga pine’ plantations in 18th – 19th c. France

IUFRO Scots pine provenance experiments

- 1907
- 1938-1939
- 1982

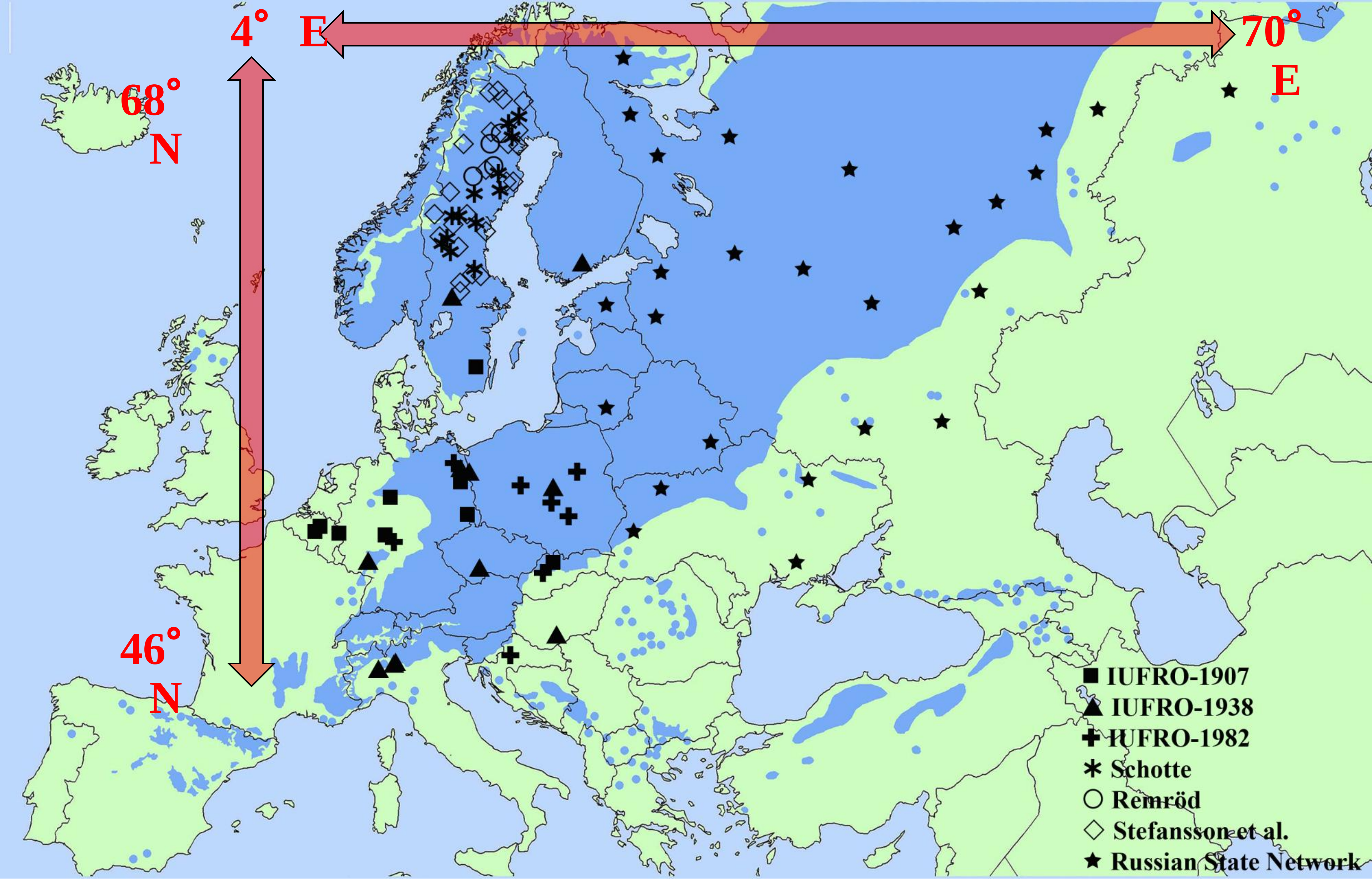
V.D. Ogievskii, 1909 г.



Ca. 20 sites
with 45 provenances
established in 1910-1916

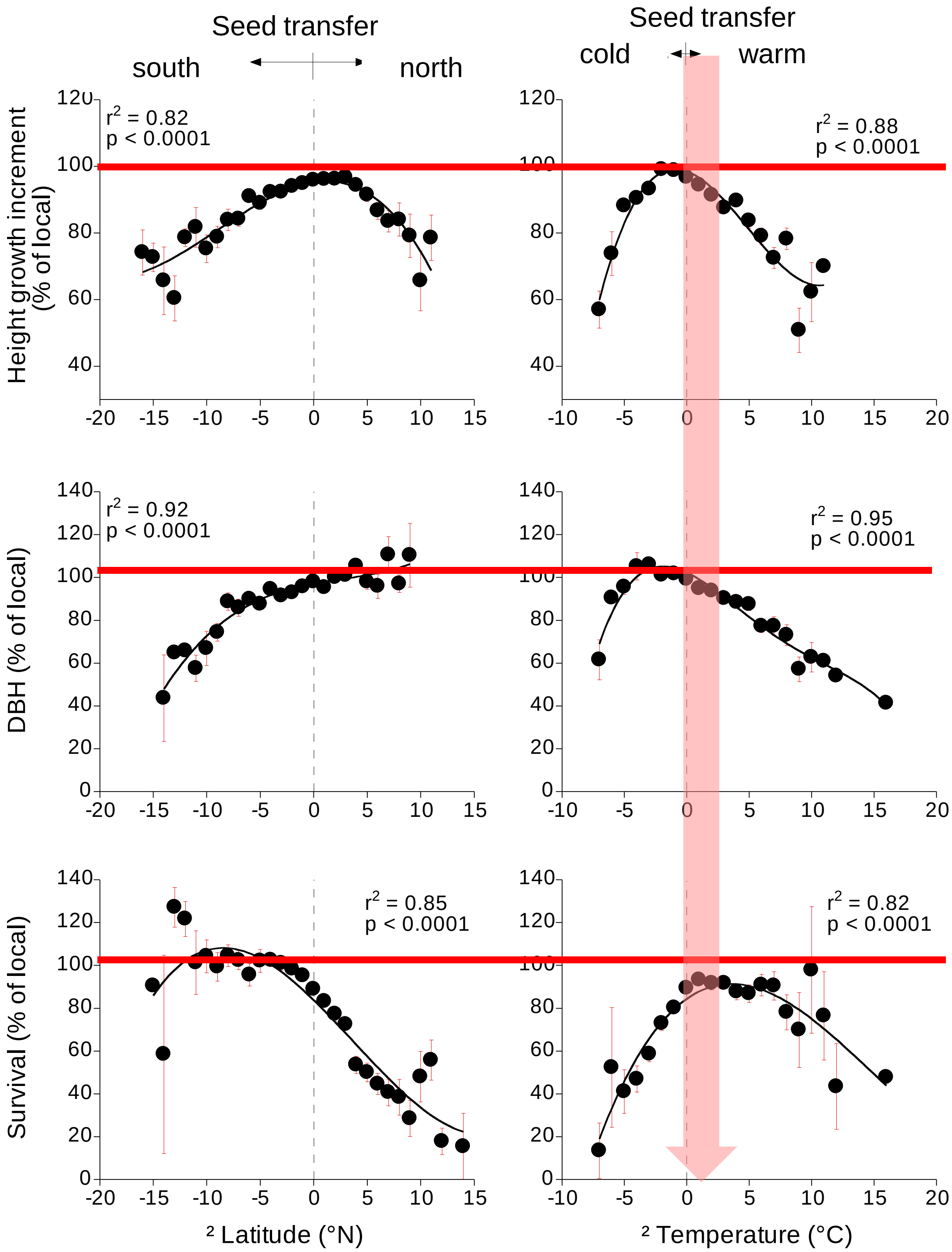
Salomon Z. Kurdiani, *ca*. 1930


29 14:32

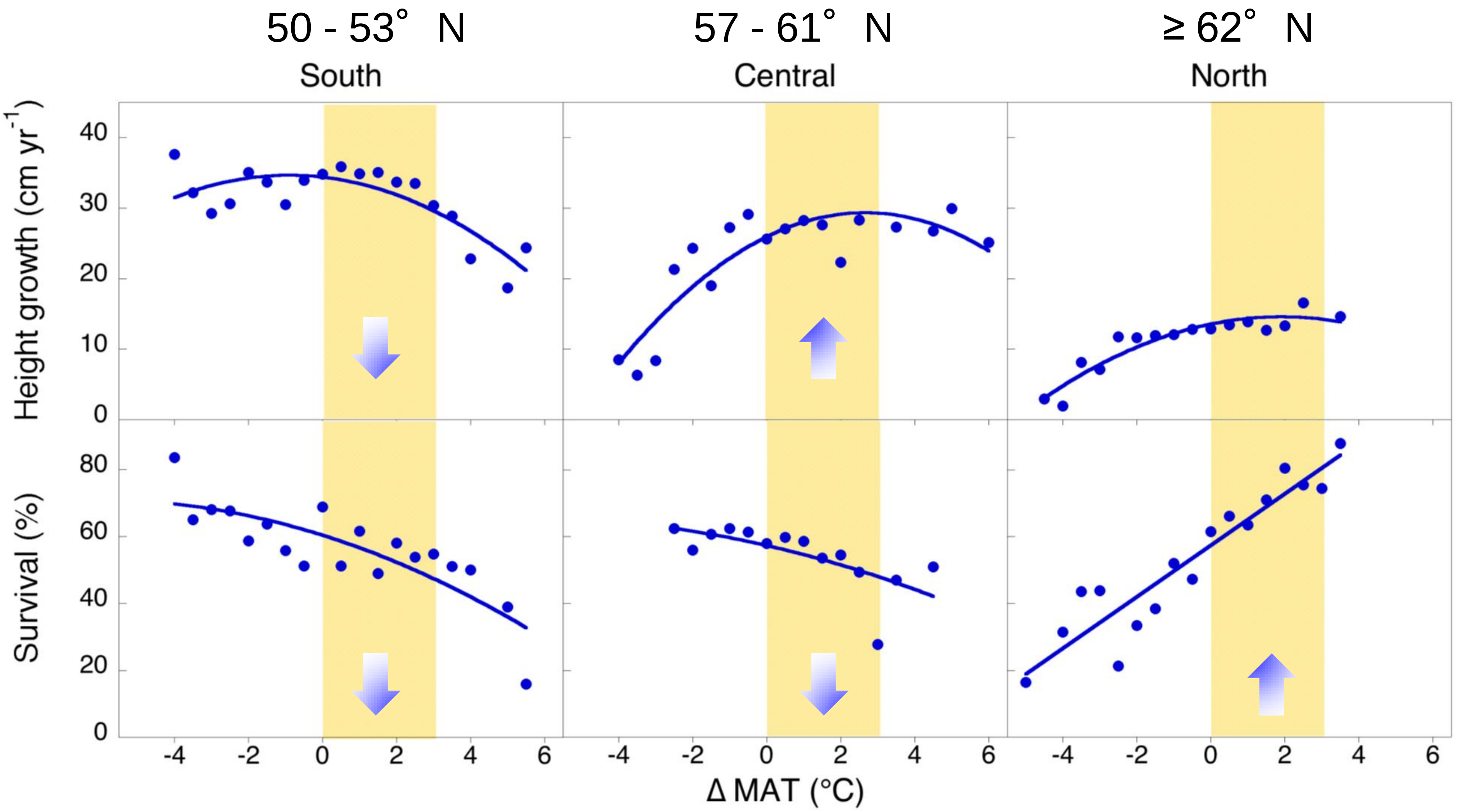


95 sites, 295 seed sources of Scots pine

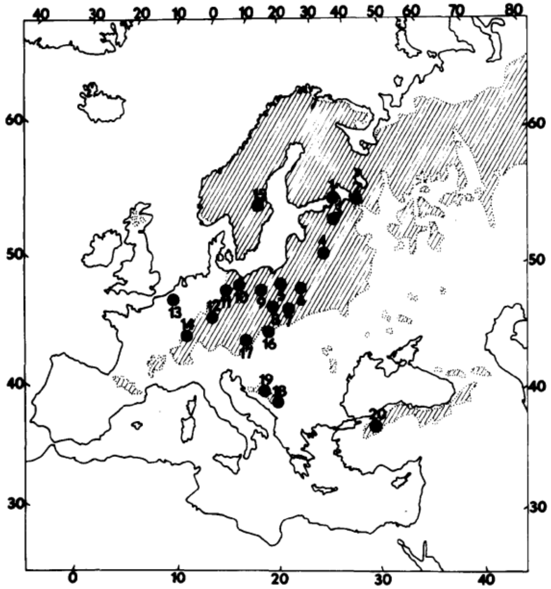
Mean annual temperature -1.7 to 14° C, precipitation from 294 to 698 mm, growing season length from 124 to 224 days. Plantation age - 17±10 yrs.



Seed transfer
south
north
Seed transfer
cold
warm
r2 = 0.82
p < 0.0001
r2 = 0.88
p < 0.0001
Height growth increment (% of local)
r2 = 0.92
p < 0.0001
r2 = 0.95
p < 0.0001
DBH (% of local)
r2 = 0.85
p < 0.0001
r2 = 0.82
p < 0.0001
Survival (% of local)
Δ Latitude (°N)
Δ Temperature (°C)



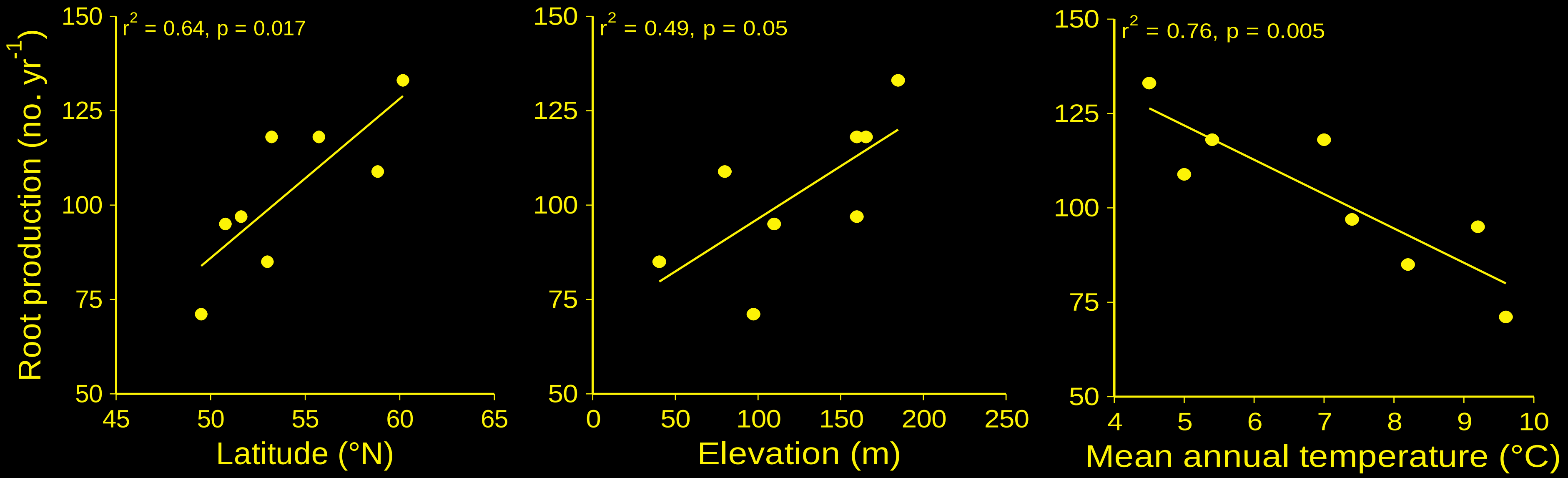
Climate transfers equivalent to warming by 1-3 ° C markedly increased the survival of populations in northern Europe (≥ 62° N, < 2 ° C MAT) and modestly increased height growth ≥ 57° N but decreased survival at < 62° N and modestly decreased height growth at < 54° N latitude in Europe. Thus, even modest climate warming will likely influence Scots pine survival and growth, but in distinct ways in different parts of the species range.



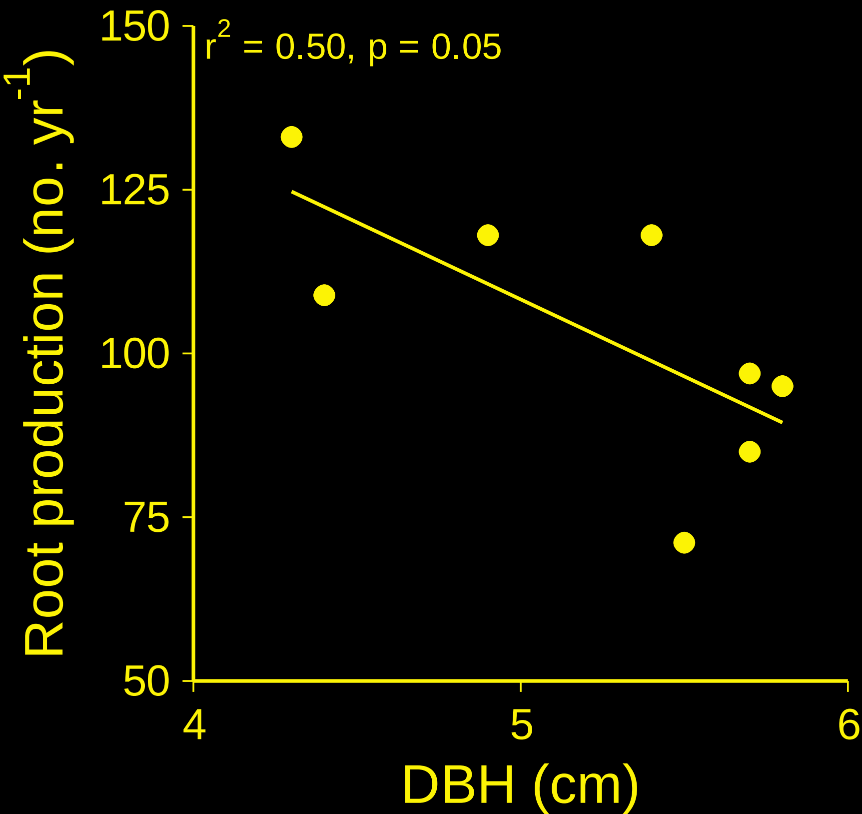
IUFRO – Scots pine-1982

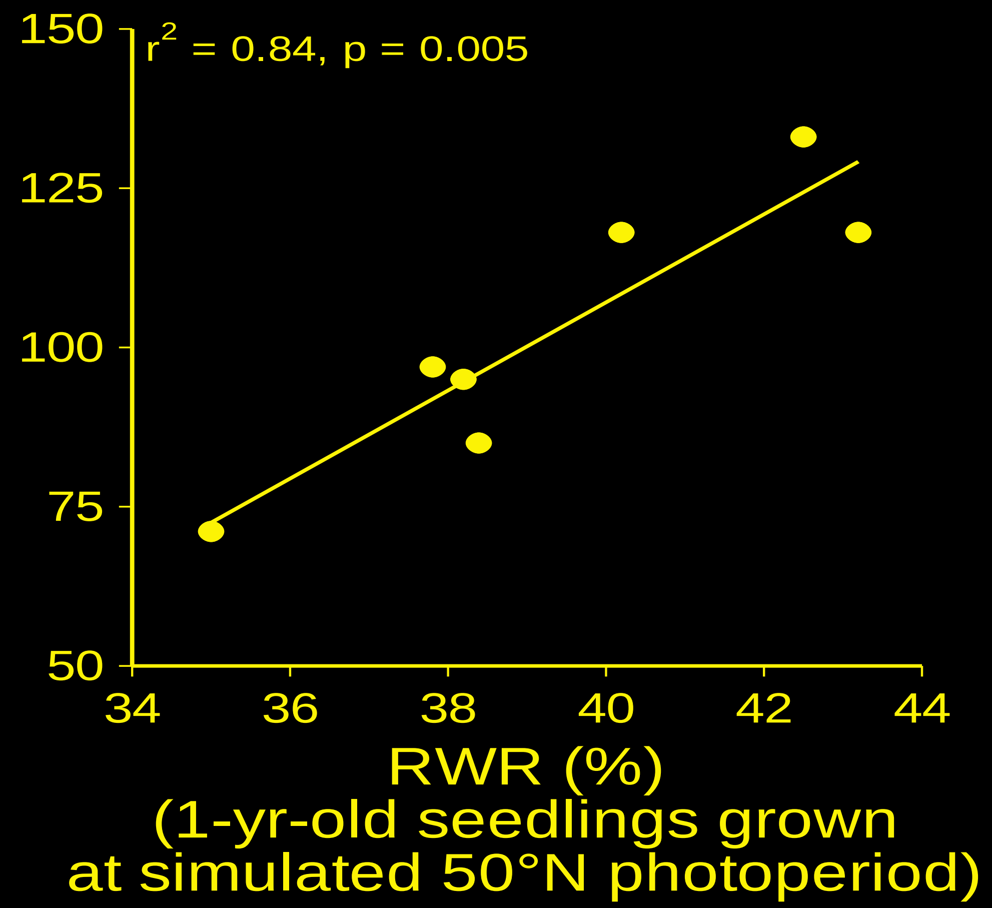
Provenance experiment

IUFRO – Scots pine-1982
Provenance experiment

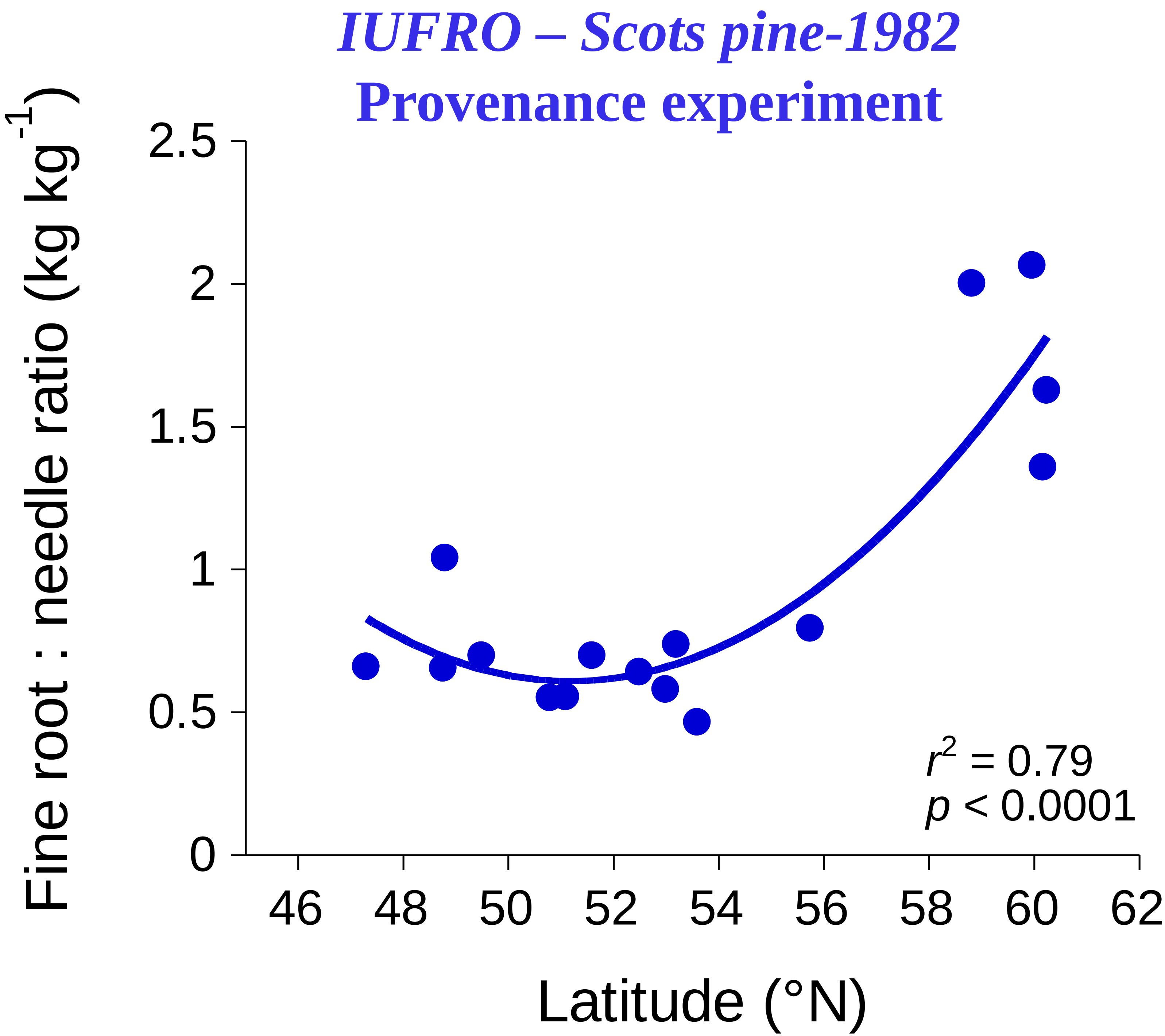


IUFRO – Scots pine-1982
Provenance experiment



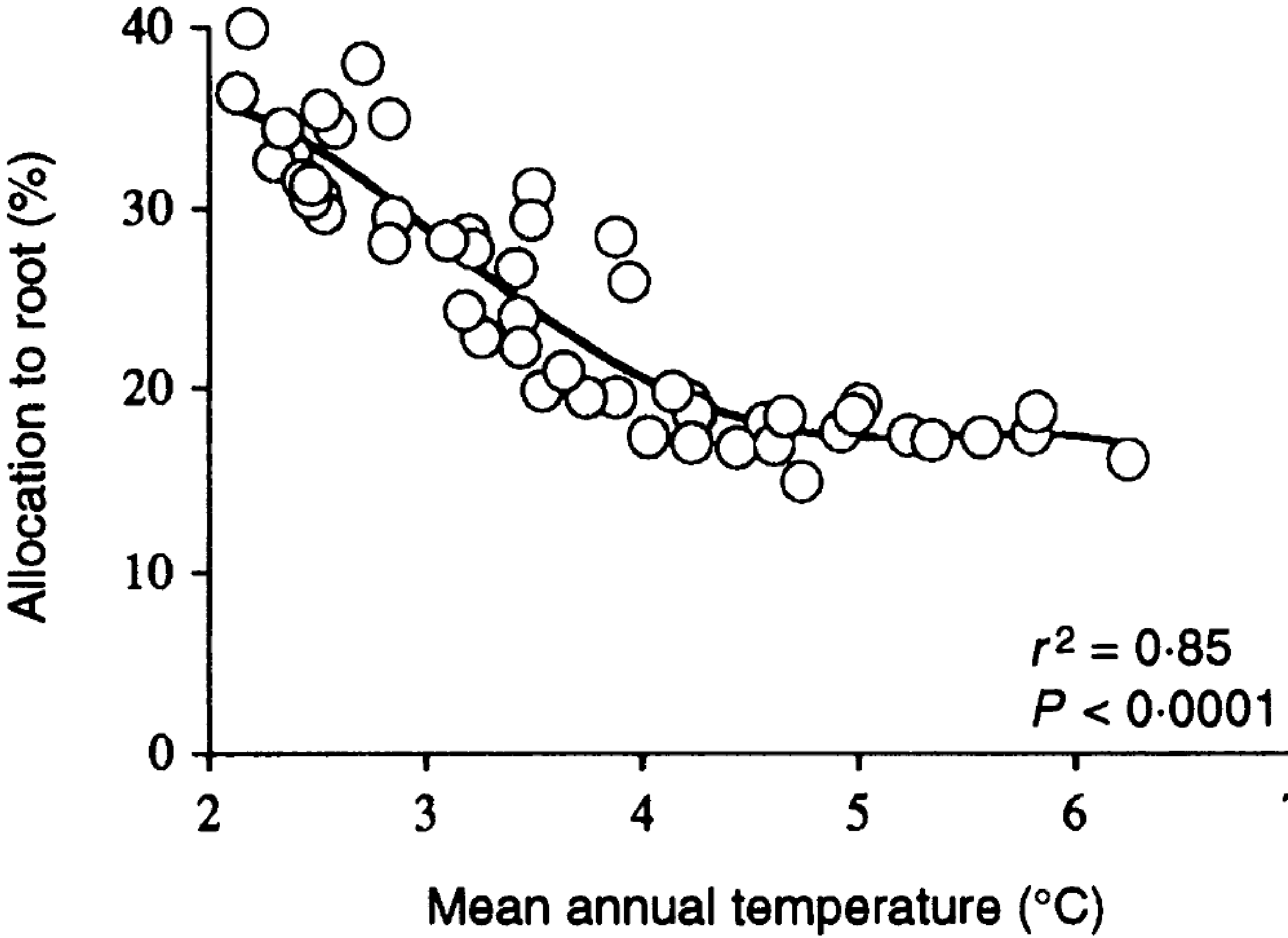


IUFRO – Scots pine-1982
Provenance experiment

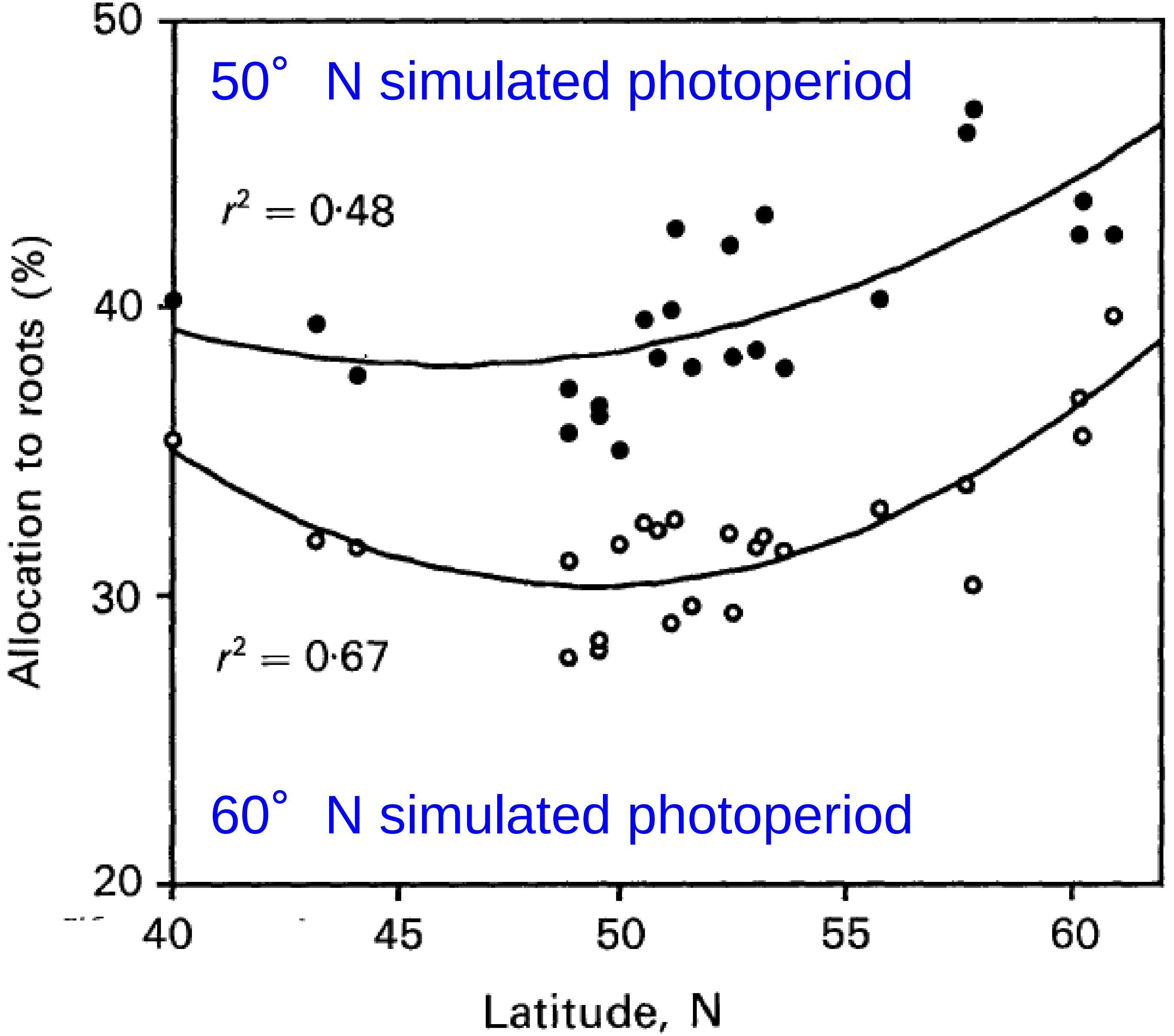


IUFRO – Scots pine-1982
Provenance experiment
Fine root : needle ratio (kg kg^{-1})
2.5
2
1.5
1
0.5
0
46
48
50
52
54
56
58
60
62
Latitude (°N)
r^2 = 0.79
p < 0.0001

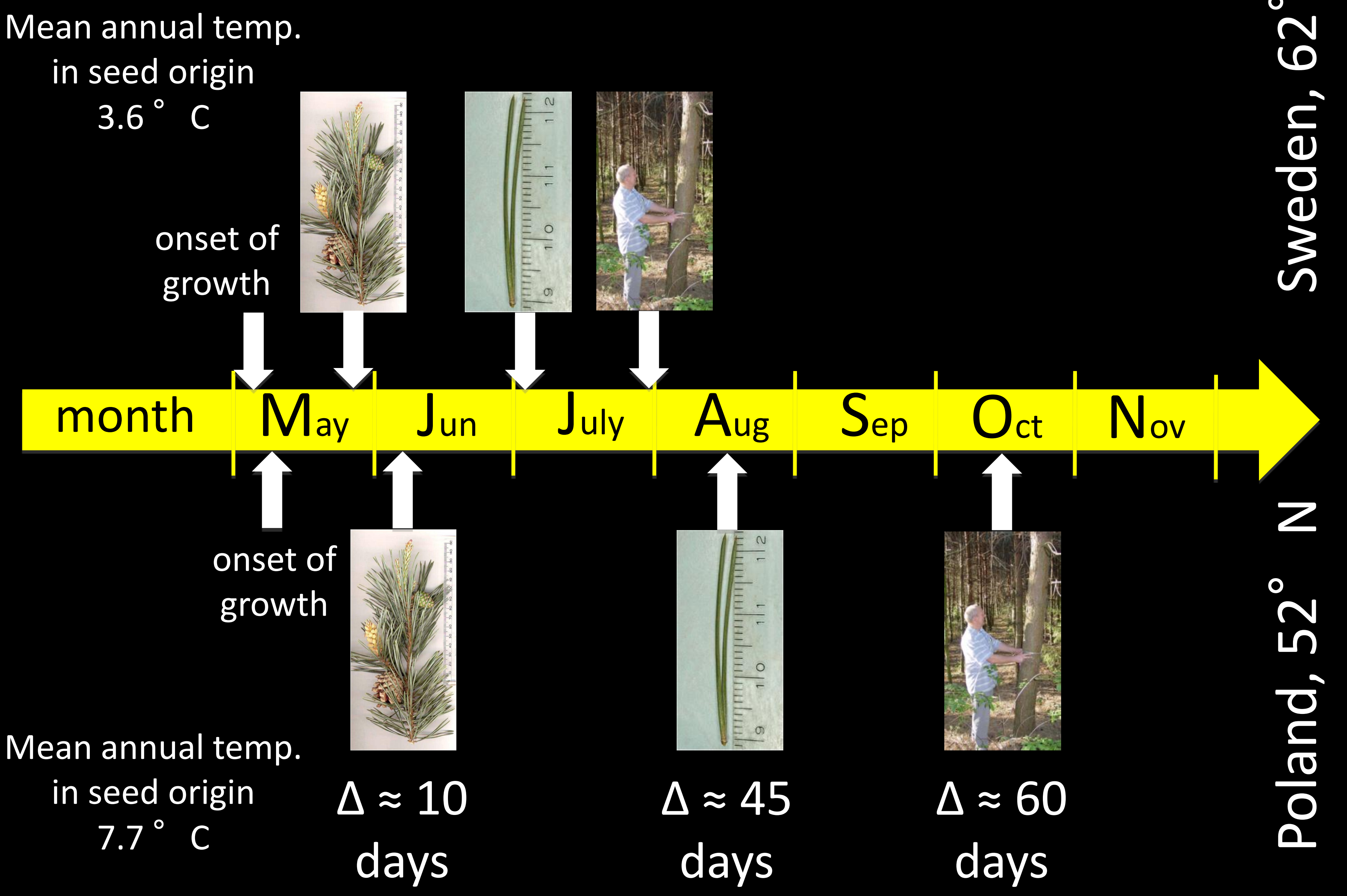
2-yr-old *seedlings*
Picea abies
provenance experiment



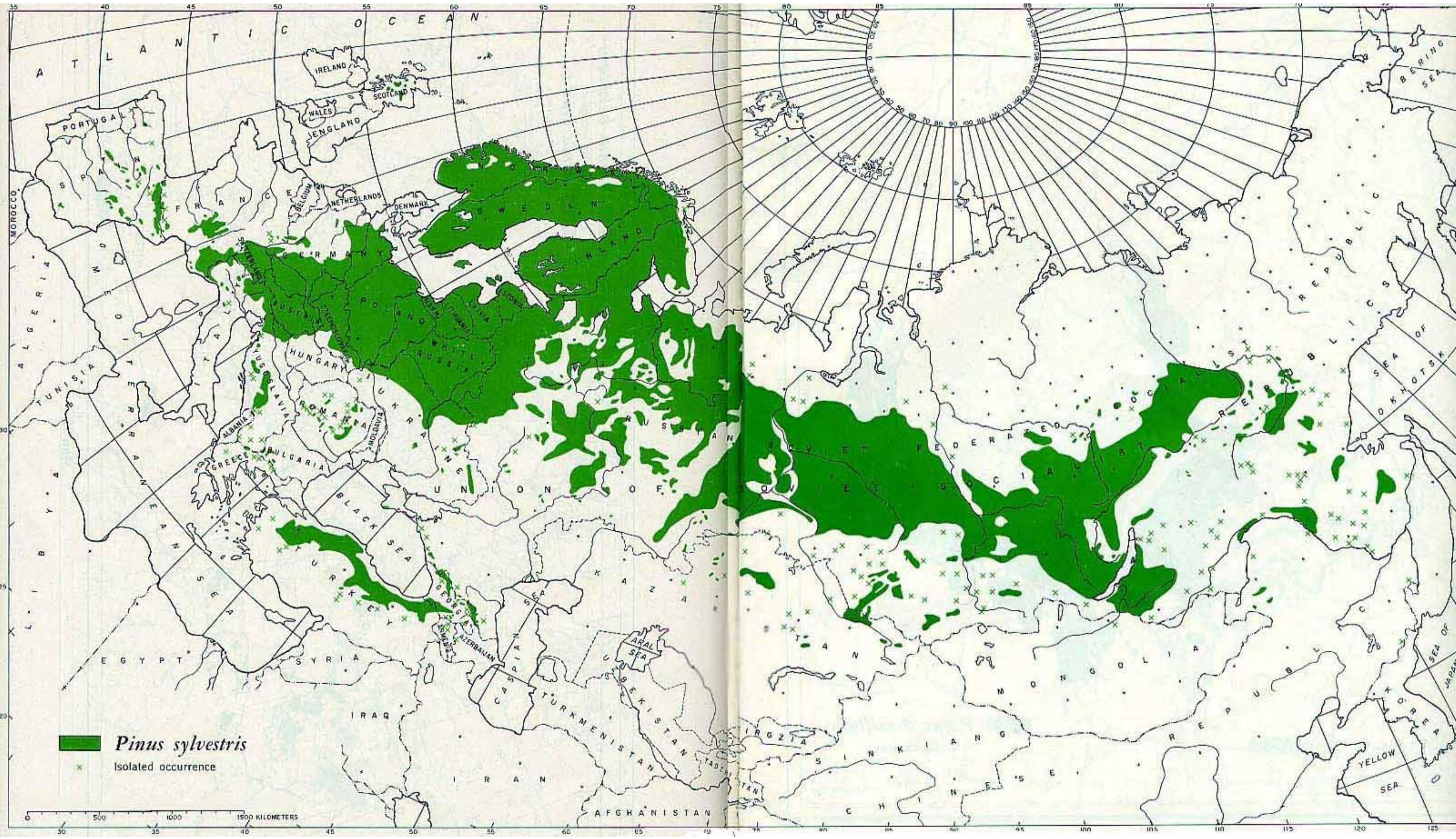
1-yr-old seedlings
IUFRO – Scots pine-1982
Provenance experiment



Growth phenology, Scots pine (*Pinus sylvestris*)

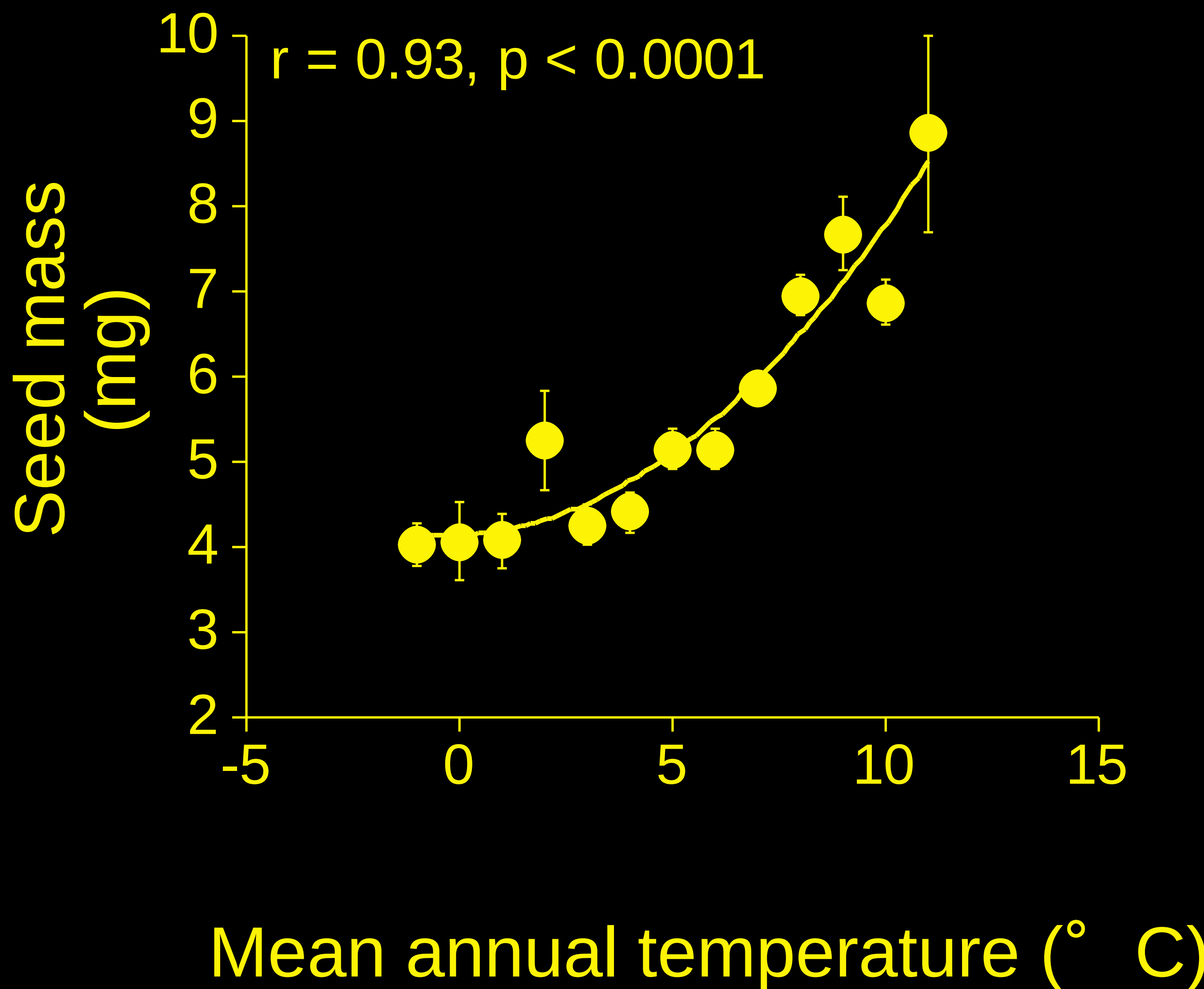


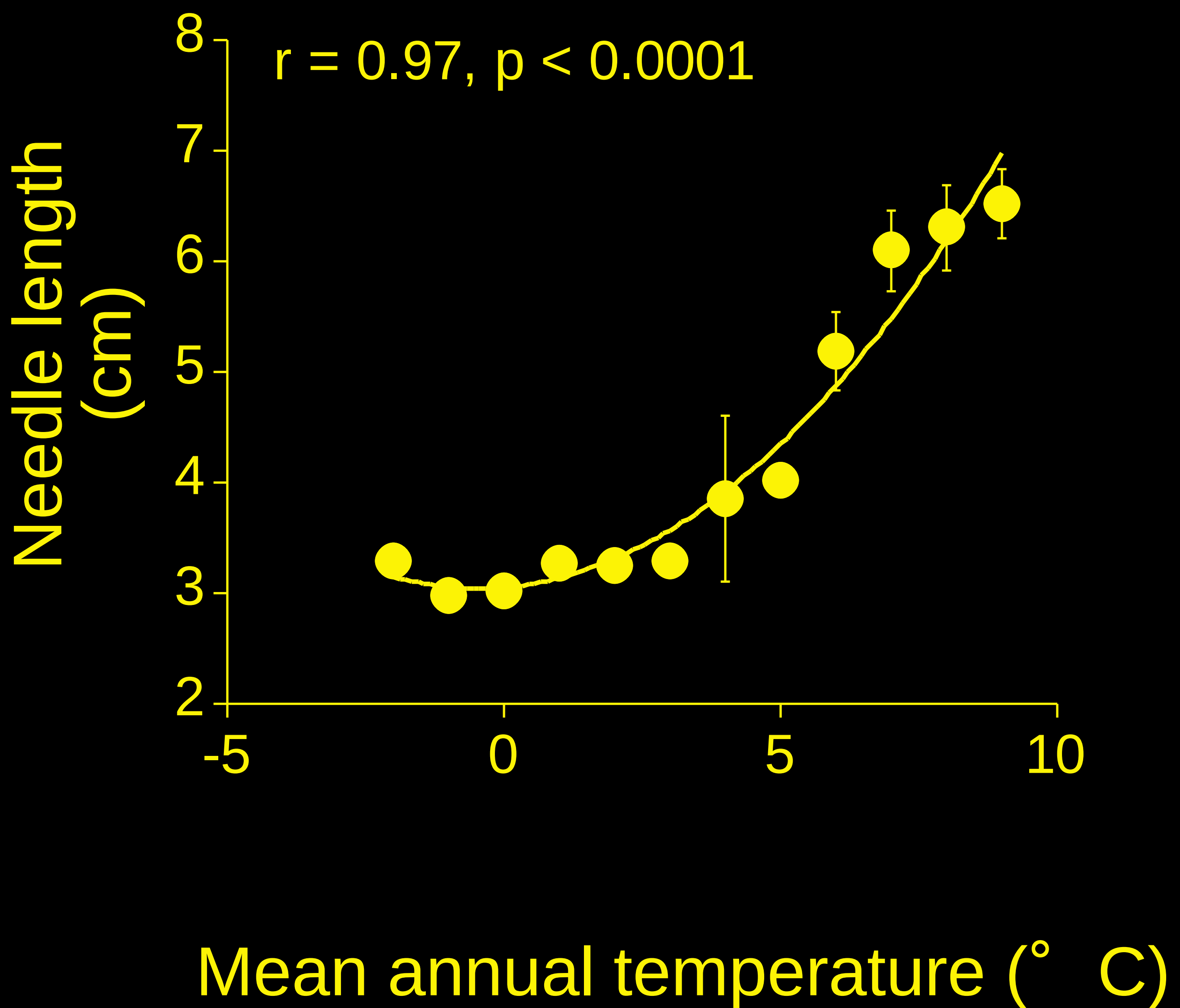

Sweden, 62° N
Poland, 52° N



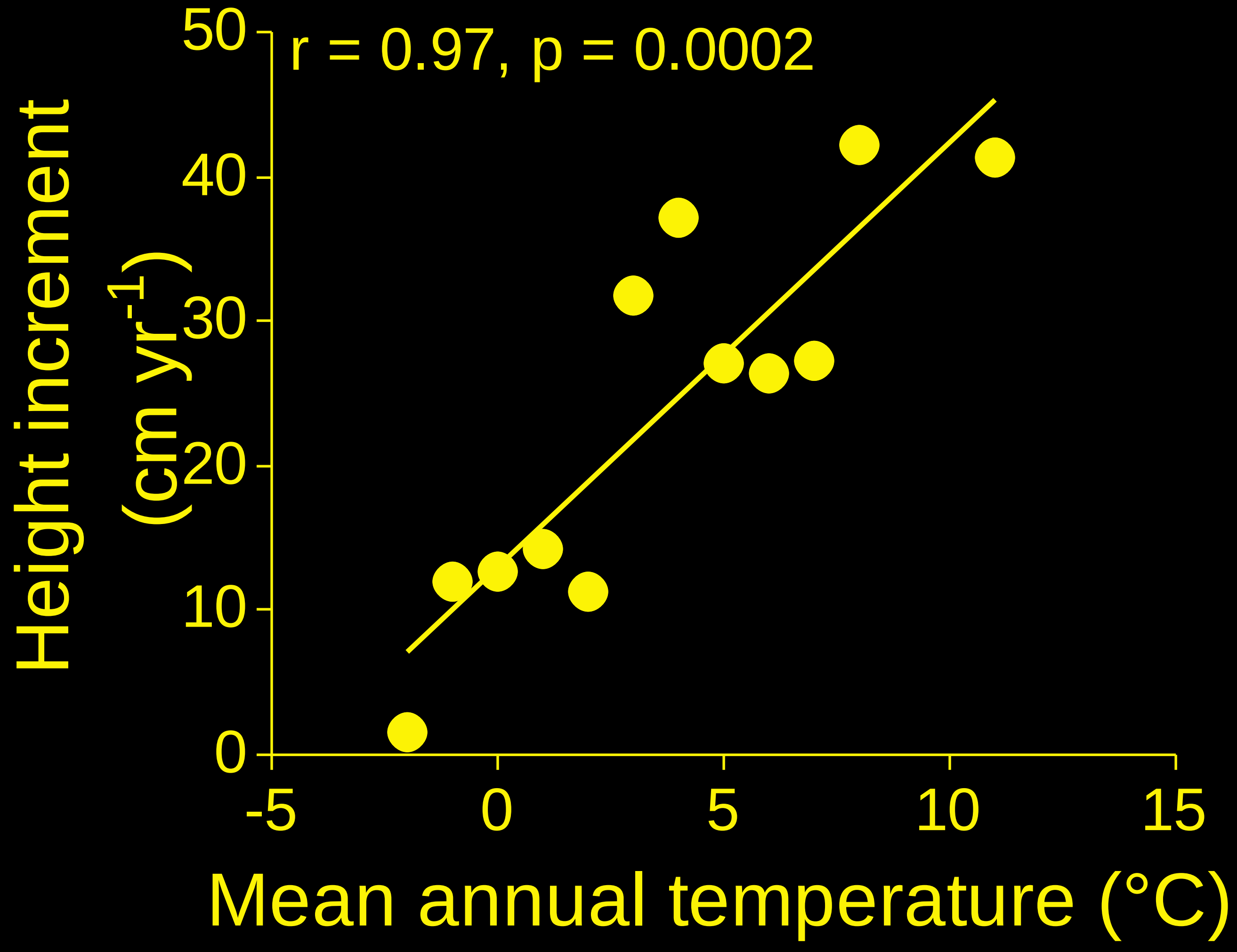
Pinus sylvestris
Isolated occurrence
0
500
1000
1500 KILOMETERS
ATLANTIC OCEAN
IRELAND
SCOTLAND
WALES
ENGLAND
PORTUGAL
SPAIN
FRANCE
BELGIUM
NETHERLANDS
DENMARK
GERMANY
SWEDEN
FINLAND
POLAND
WHITE RUSSIA
HUNGARY
ROMANIA
MOLDAVIA
BULGARIA
ALBANIA
GREECE
UKRAINE
BLACK SEA
TURKEY
GEORGIA
AZERBAIJAN
SYRIA
IRAQ
IRAN
EGYPT
LIBYA
TUNISIA
ALGERIA
MOROCCO
MEDITERRANEAN SEA
CASPIAN SEA
ARAL SEA
TURKMENISTAN
UZBEKISTAN
AFGHANISTAN
KAZAKHSTAN
UNION OF SOVIET SOCIALIST REPUBLICS
RUSSIAN SOVIET FEDERATED SOCIALIST REPUBLIC
MONGOLIA
MONGOLIAN PEOPLE'S REPUBLIC
SINKIANG
CHINESE
KOREA
YELLOW SEA
SEA OF JAPAN
SEA OF OKHOTSK
BERING SEA

Pinus sylvestris
(*in situ* data)

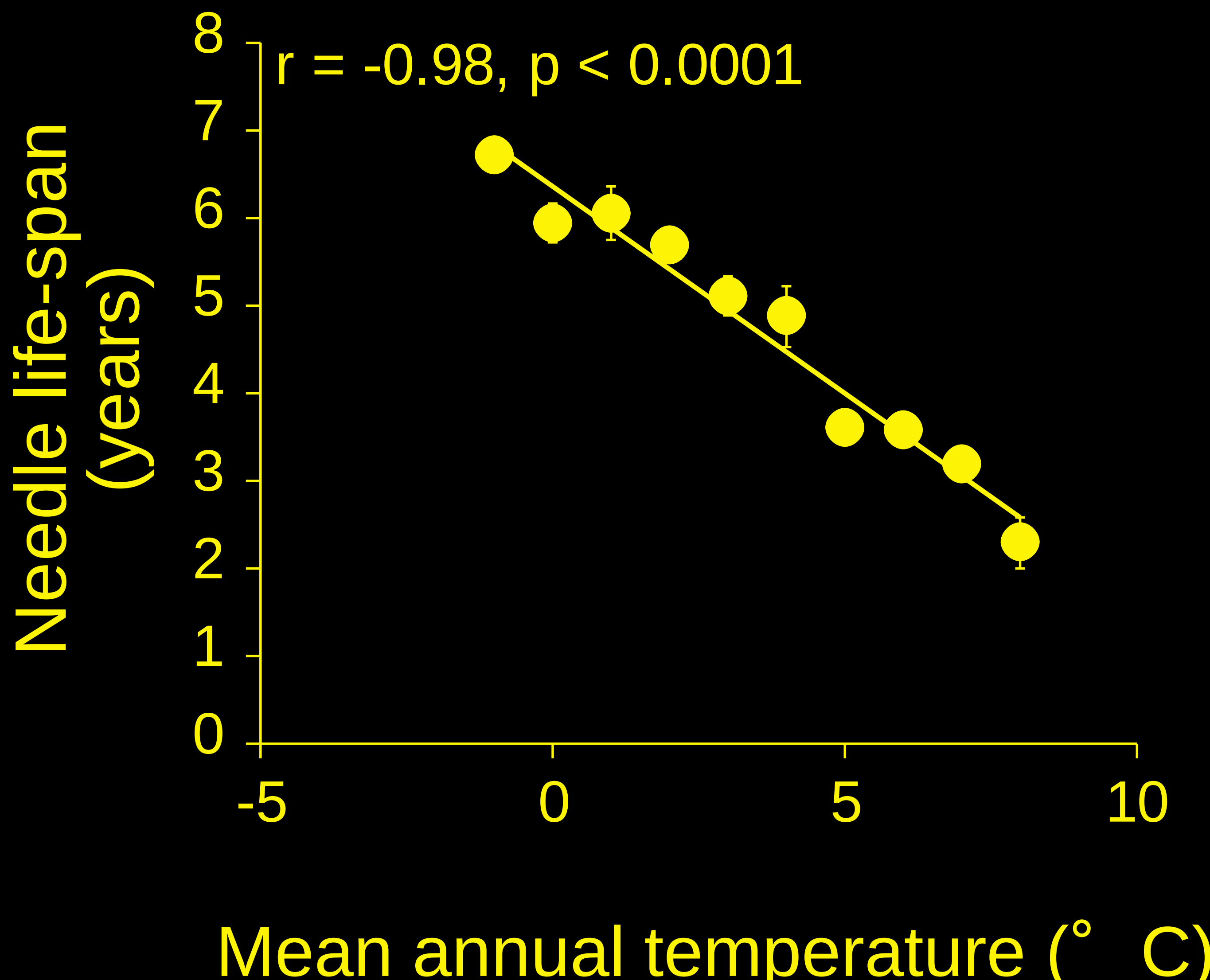




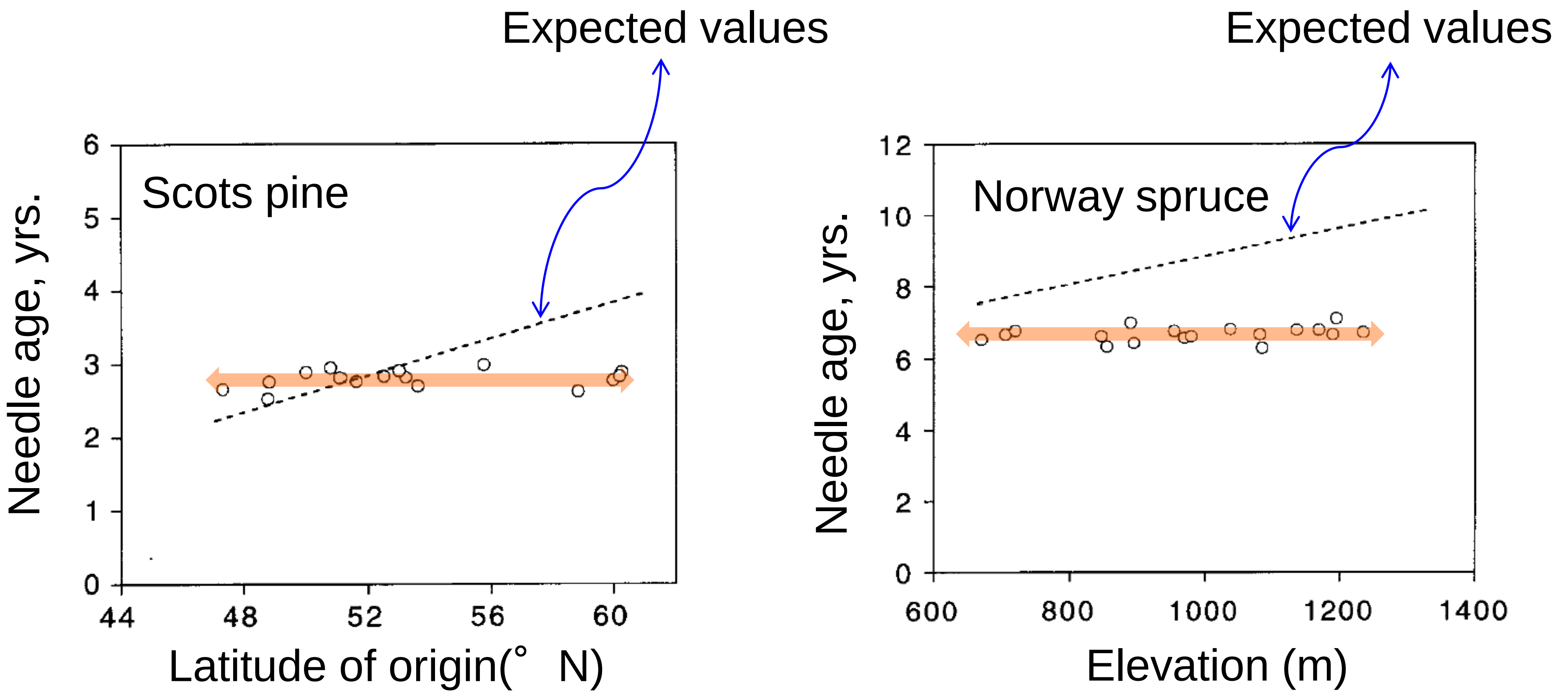
r = 0.97, p < 0.0001
Needle length (cm)
Mean annual temperature (° C)
8
7
6
5
4
3
2
-5
0
5
10

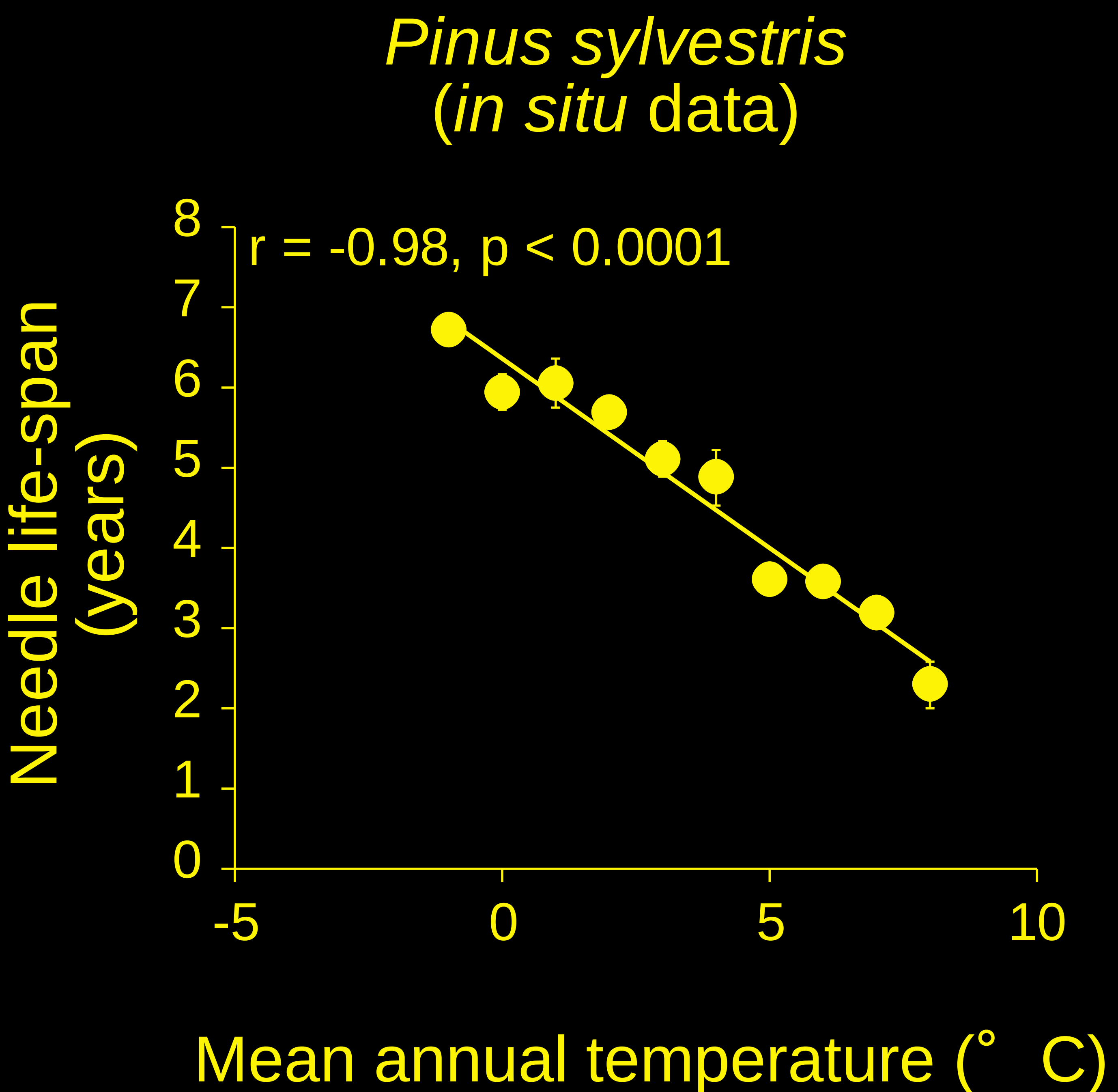

r = 0.97, p = 0.0002
Height increment (cm yr-1)
50
40
30
20
10
0
-5
0
5
10
15
Mean annual temperature (°C)

Pinus sylvestris (*in situ* data)



Provenance experiments





Pinus sylvestris
(in situ data)
r = -0.98, p < 0.0001
Needle life-span (years)
Mean annual temperature (° C)
0
1
2
3
4
5
6
7
8
-5
0
5
10

Picea abies 7-yr-old provenance experiment

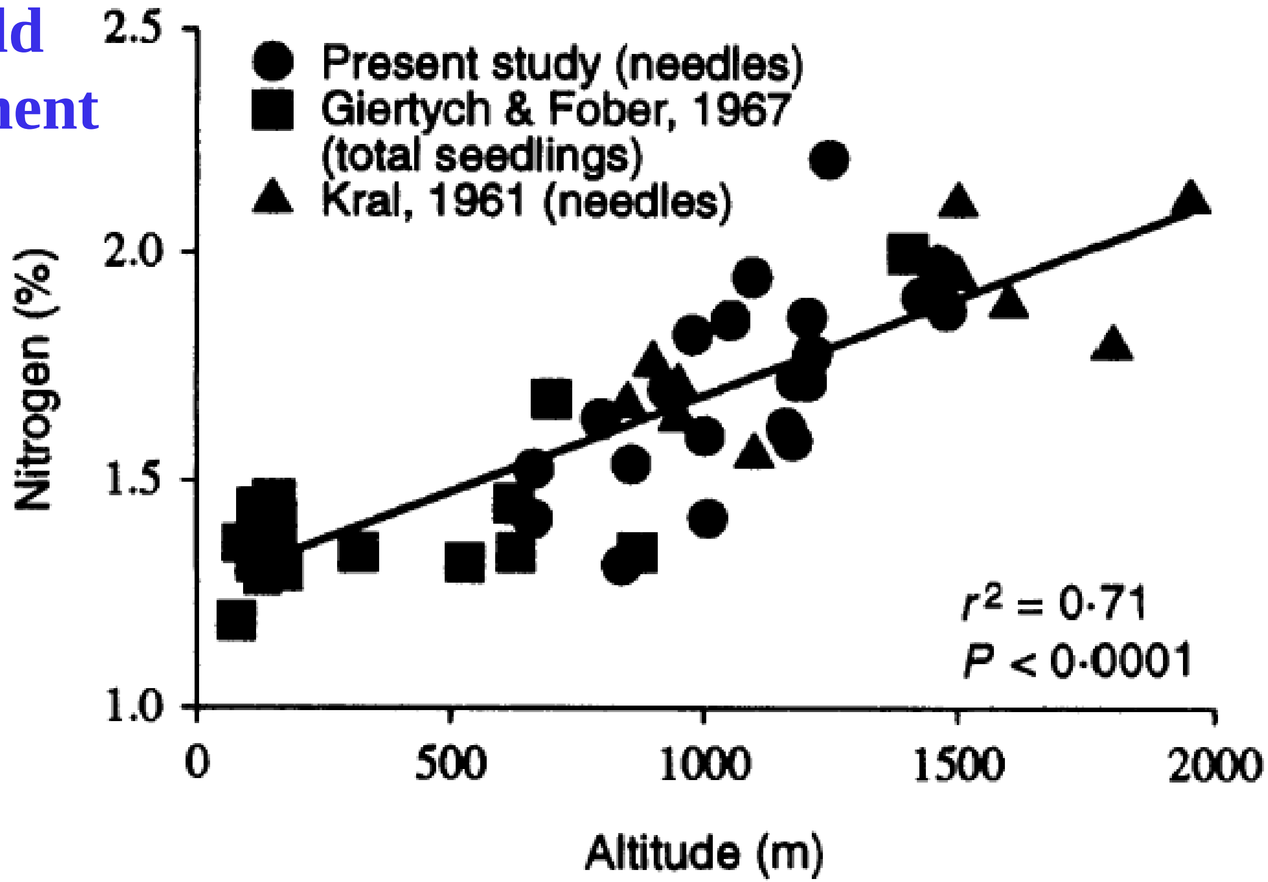
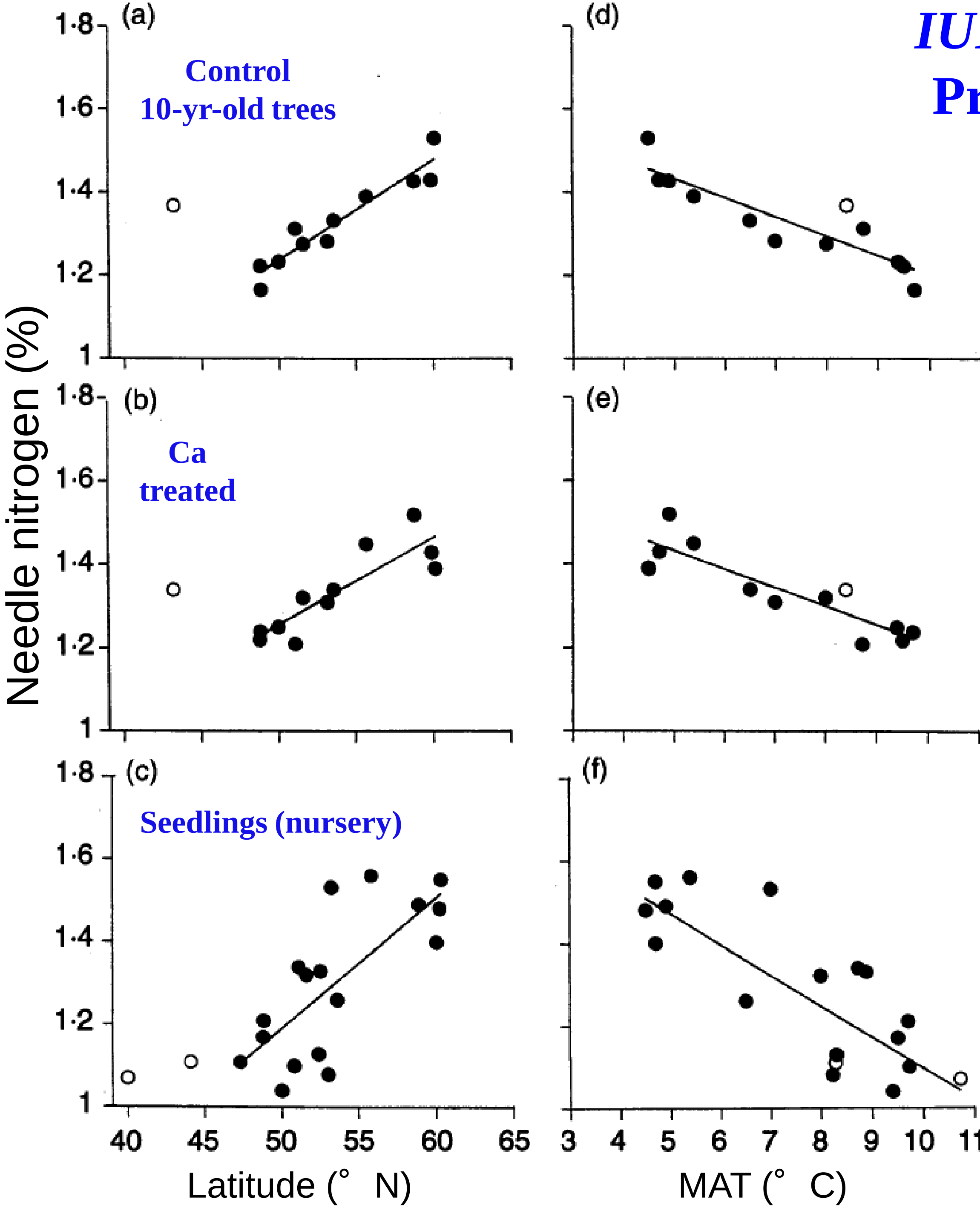
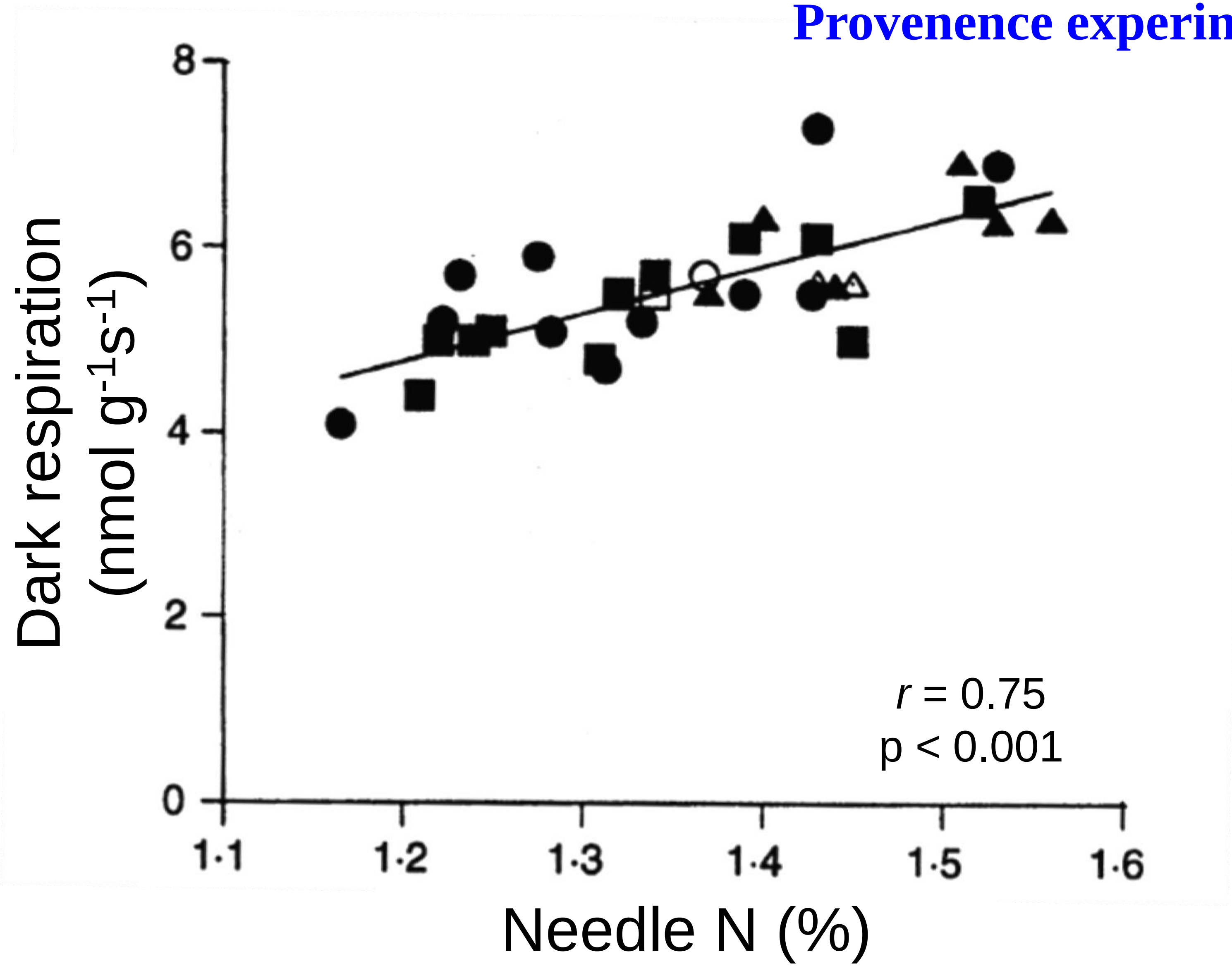


Fig. 8. Needle or total plant nitrogen concentrations in Norway spruce populations in a common garden in the present study and those of Kral (1961) and Giertych & Fober (1967) in relation to the population's altitude of origin. Relationship between altitude of seed stand and needle or plant %N were significant for each study ($r^2 \geq 0{\cdot}48$, $P \leq 0{\cdot}01$).

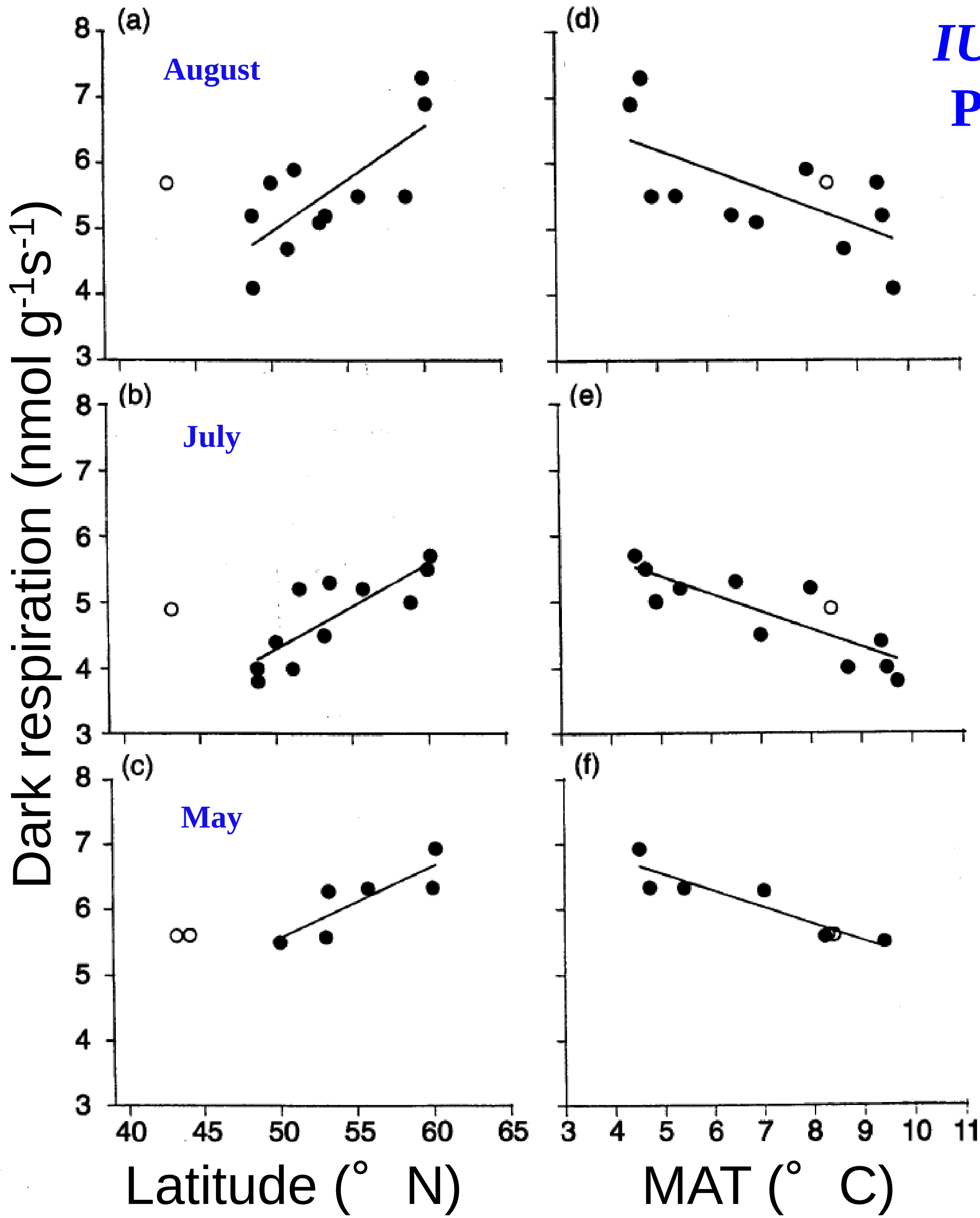
IUFRO – Scots pine-1982
Provenance experiment



IUFRO – Scots pine-1982
Provenence experiment



IUFRO – Scots pine-1982
Provenance experiment



Picea abies
Provenence experiment

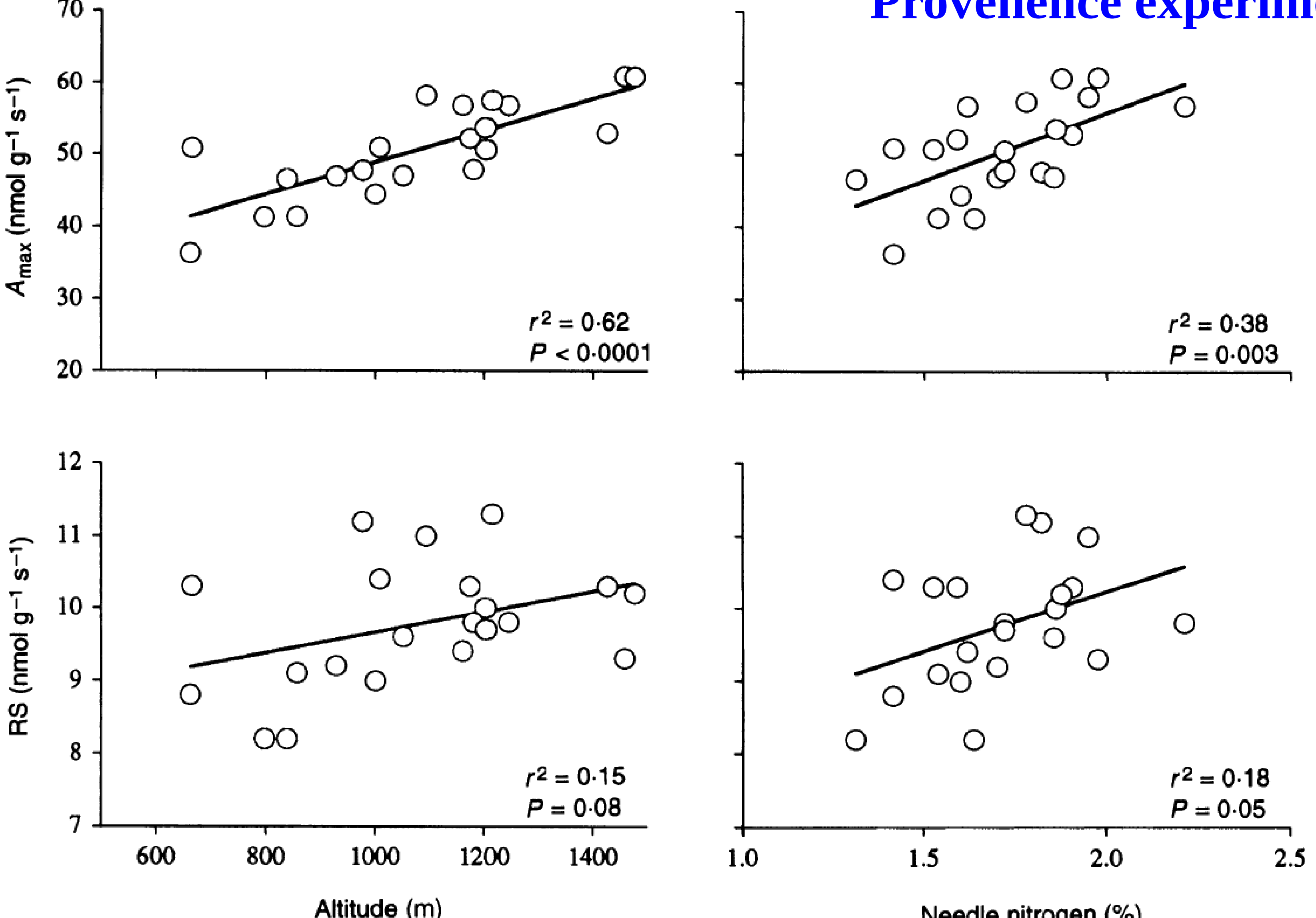
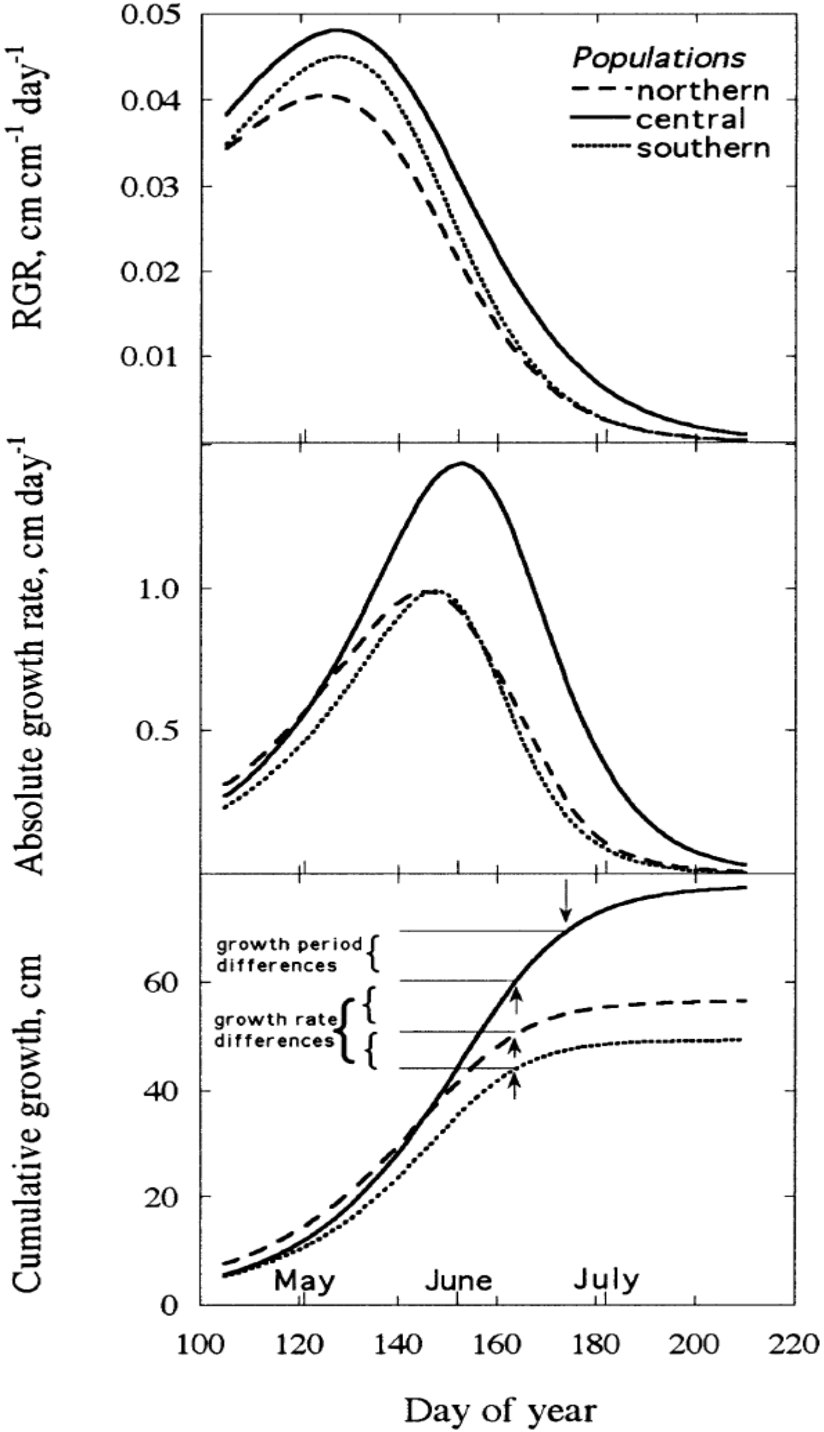
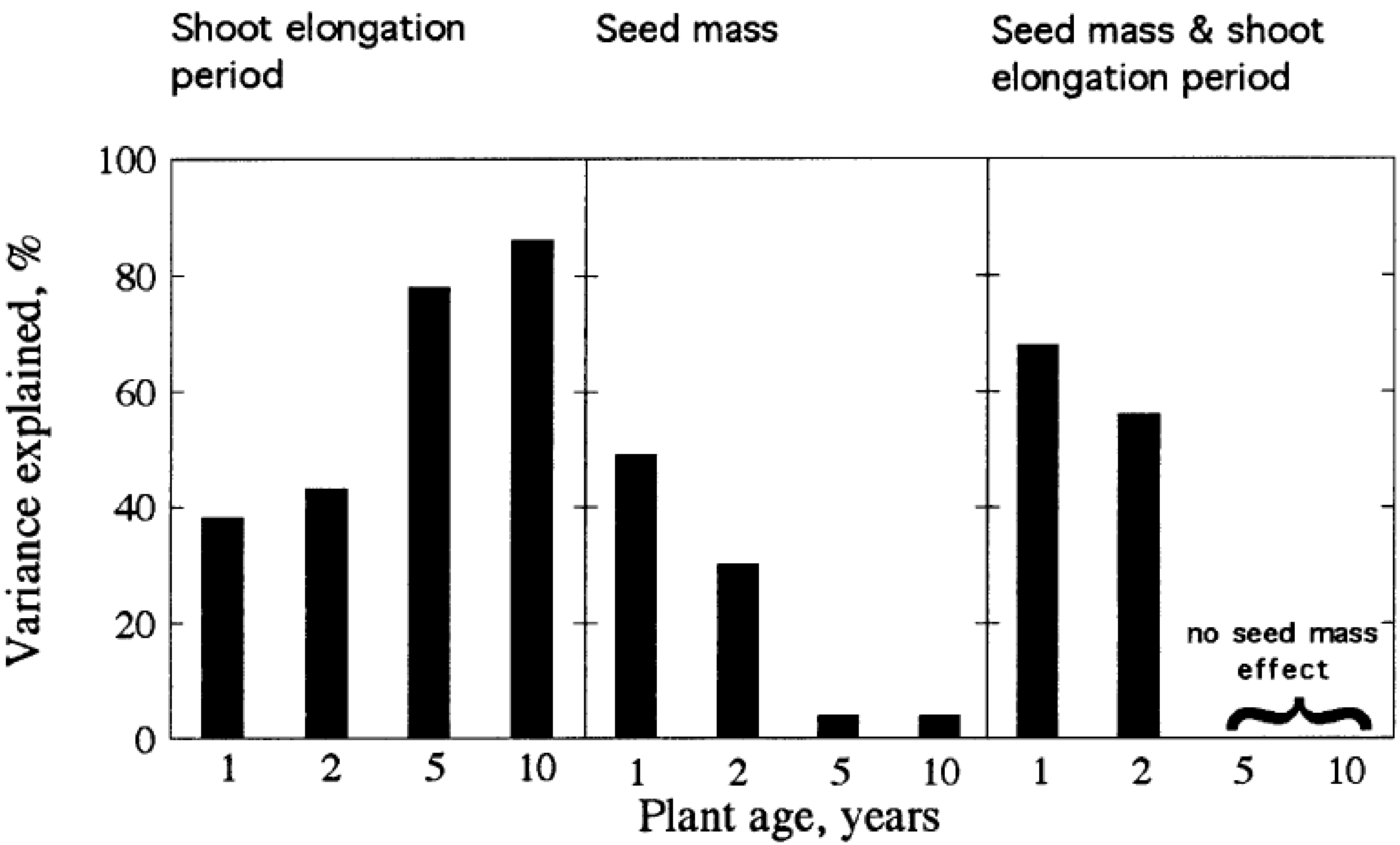


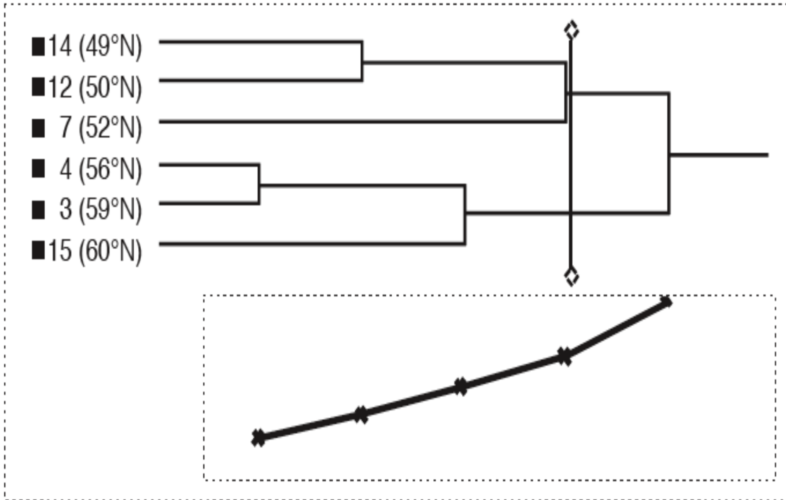
Fig. 7. Mean needle light-saturated net photosynthesis (A_{max}) and respiration (RS) rates in Norway spruce populations growing in common-garden conditions in relation to the altitude of origin or needle nitrogen concentration of each population.

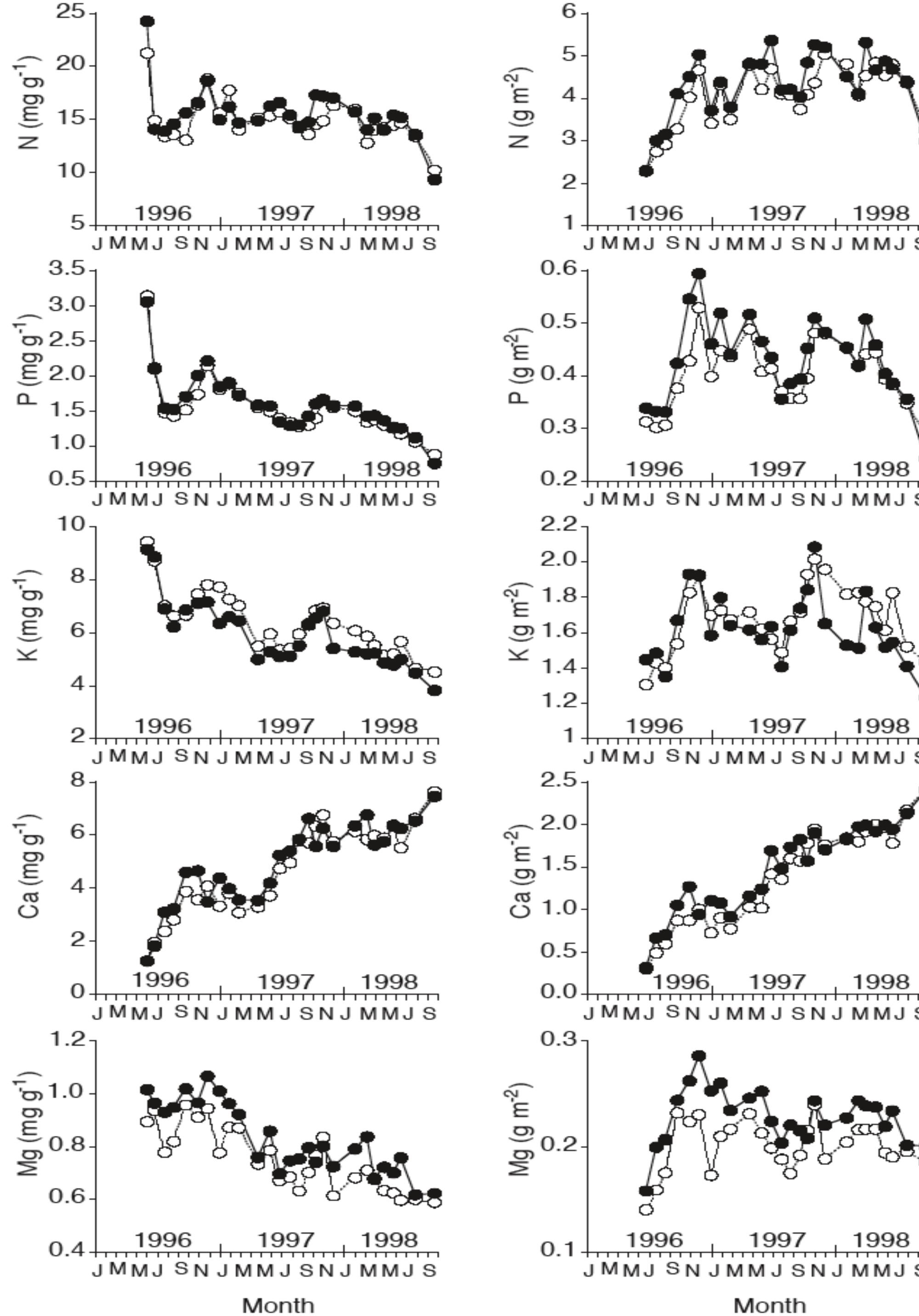
IUFRO – Scots pine-1982
Provenance experiment



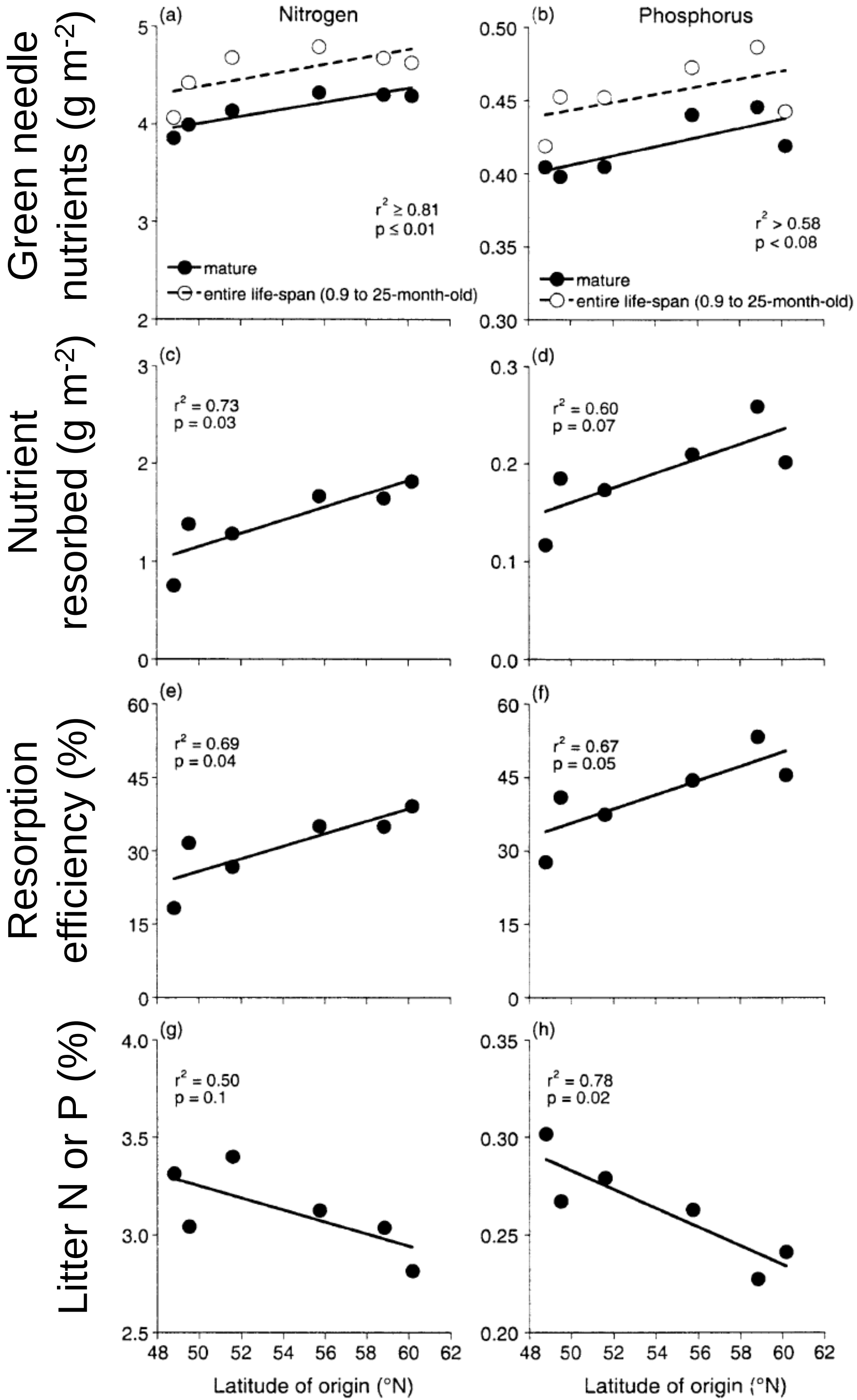
IUFRO – Scots pine-1982
Provenance experiment




14 (49°N)
12 (50°N)
7 (52°N)
4 (56°N)
3 (59°N)
15 (60°N)

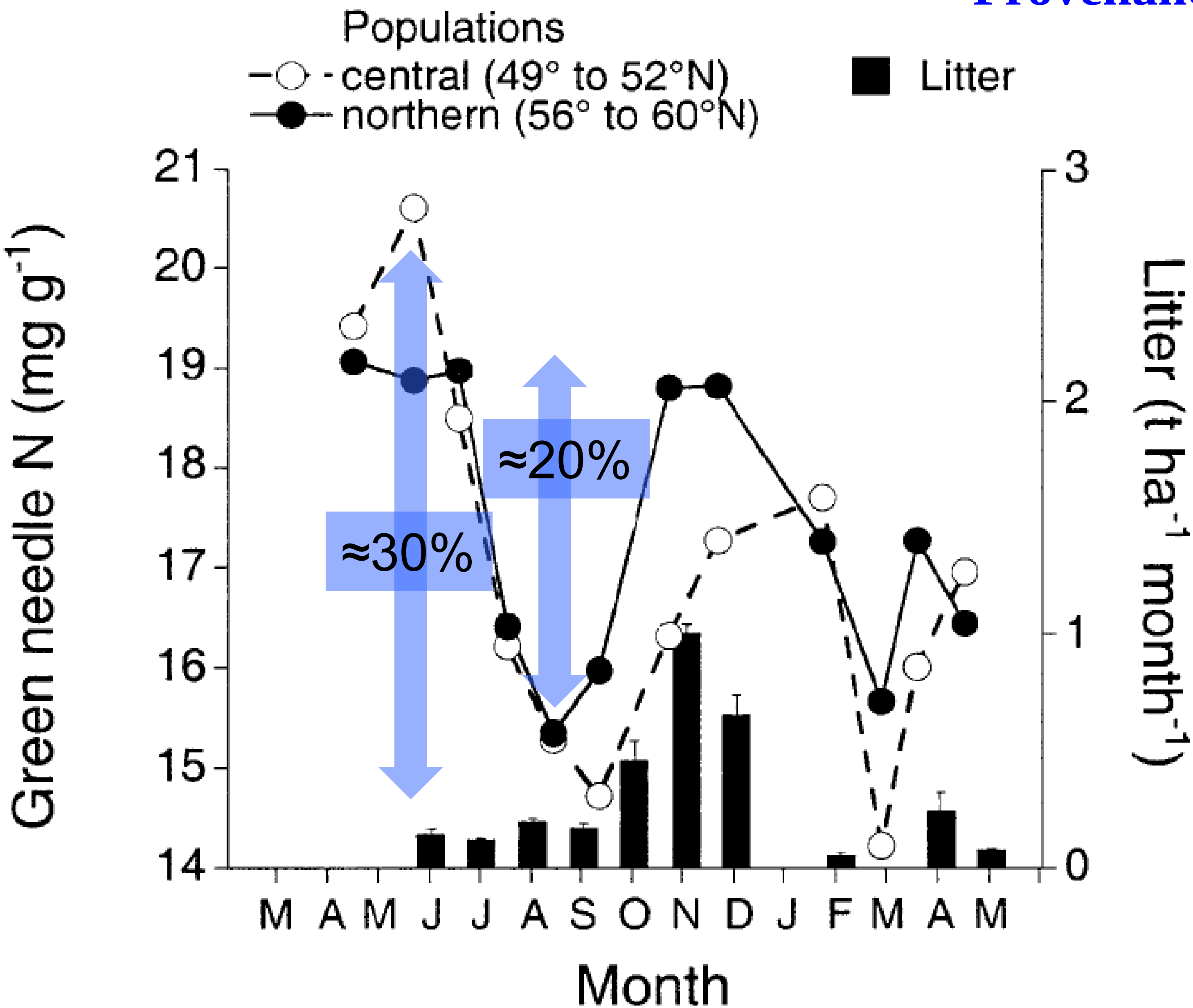

N (mg g-1)
N (g m-2)
P (mg g-1)
P (g m-2)
K (mg g-1)
K (g m-2)
Ca (mg g-1)
Ca (g m-2)
Mg (mg g-1)
Mg (g m-2)
1996
1997
1998
J M M J S N J M M J S N J M M J S
Month

IUFRO – Scots pine-1982
Provenance experiment



IUFRO – Scots pine-1982

Provenance experiment



The Role of Common Garden Studies in Adapting Forests to Climate Change in the Northwestern United States

Daniel J. Chmura, Glenn Howe, Brad St.Clair, Paul Anderson

TAFCC

Taskforce on Adapting Forests to Climate Change

Taskforce on Adapting Forests to Climate Change

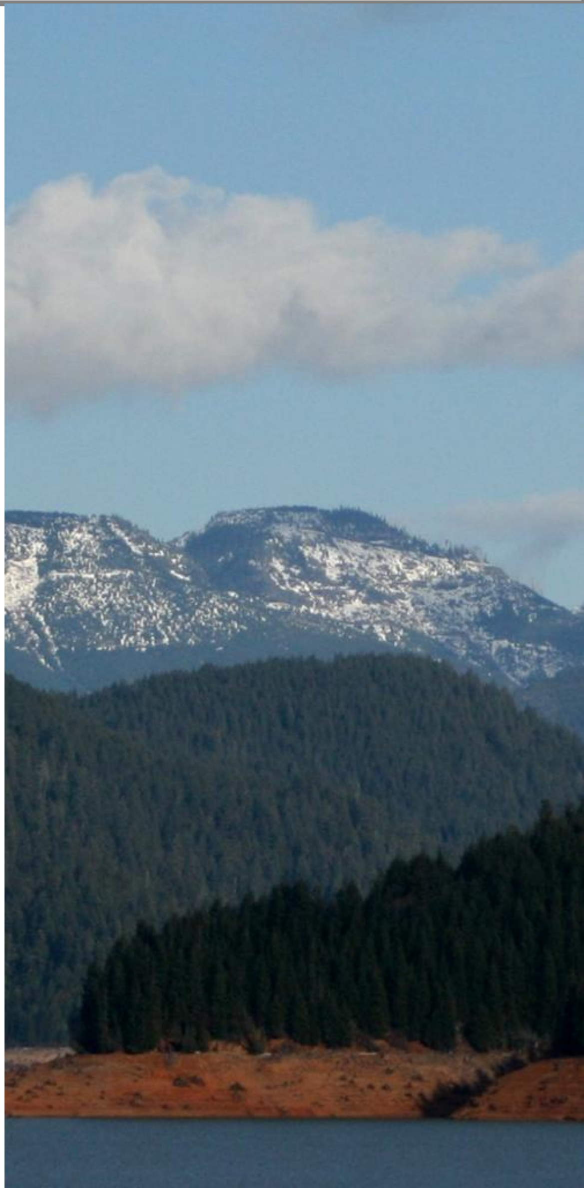
The TAFCC is a group of scientists and land managers interested in:

- Understanding the potential effects of climate change on forests in the western U.S.
- Providing forest landowners with science-based management options suitable for meeting diverse management objectives under alternative climate change scenarios

TAFCC Taskforce on Adapting Forests to Climate Change

Outline

- The role of genetic variation in forest adaptation to climate change
- How to approach management of genetic resources to help forests adapt to future climates
- Tools for decision support
- Closing remarks



TAFCC Taskforce on Adapting Forests to Climate Change

Trees

- Are key components of forest ecosystems
- Are economically important and provide multiple other ecosystem services
- Long-lived - many of today's trees will be exposed to the climate of the end of the century
- Have long generation intervals, meaning that adaptation is slow

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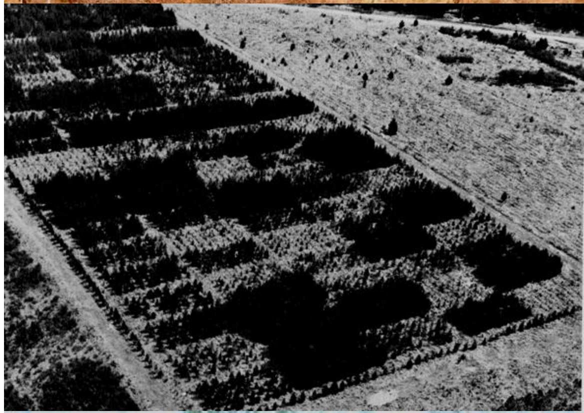
Genetic Variation Cannot Be Ignored

- Trees are genetically adapted to their local environments
- Therefore populations, not the species as a whole, should be the management units

Provenance tests

Douglas-fir in Spain (Hernandez et al 1993)



Lodgepole pine in New Zealand (Wright 1976)

Lodgepole pine in Finland

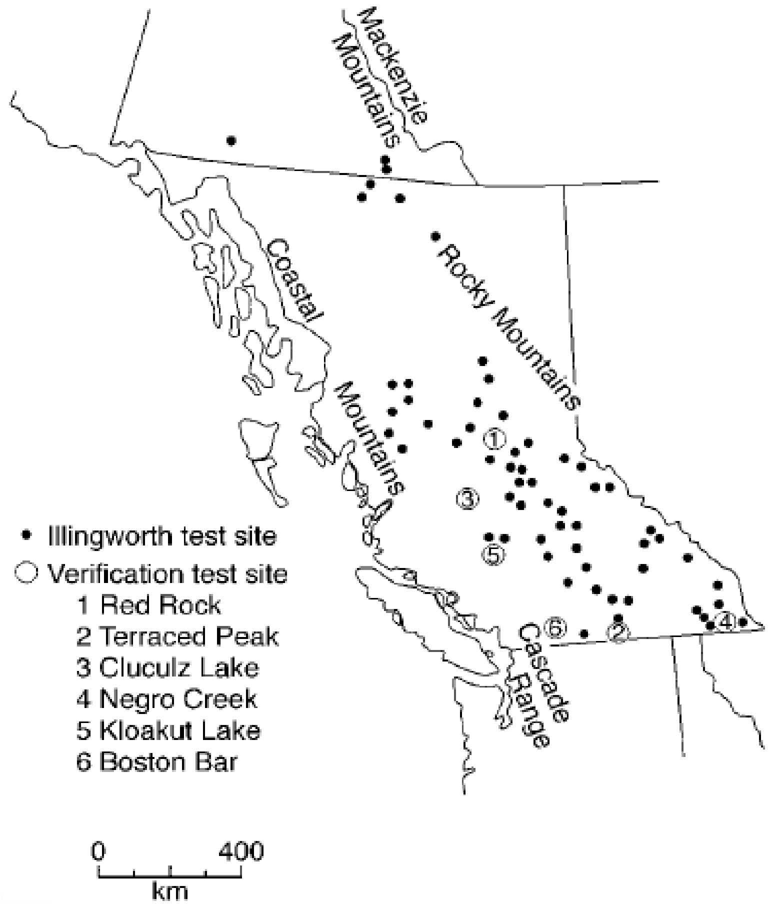
Finnish Forest Research Institute

Using Provenance Data to Project Impact of Climate Change on Forest Trees

Lodgepole pine provenance test in BC

Illingworth series

- 60 sites
- 142 populations



Rehfeldt et al. 1999. *Ecol. Monogr*. 69: 375-409

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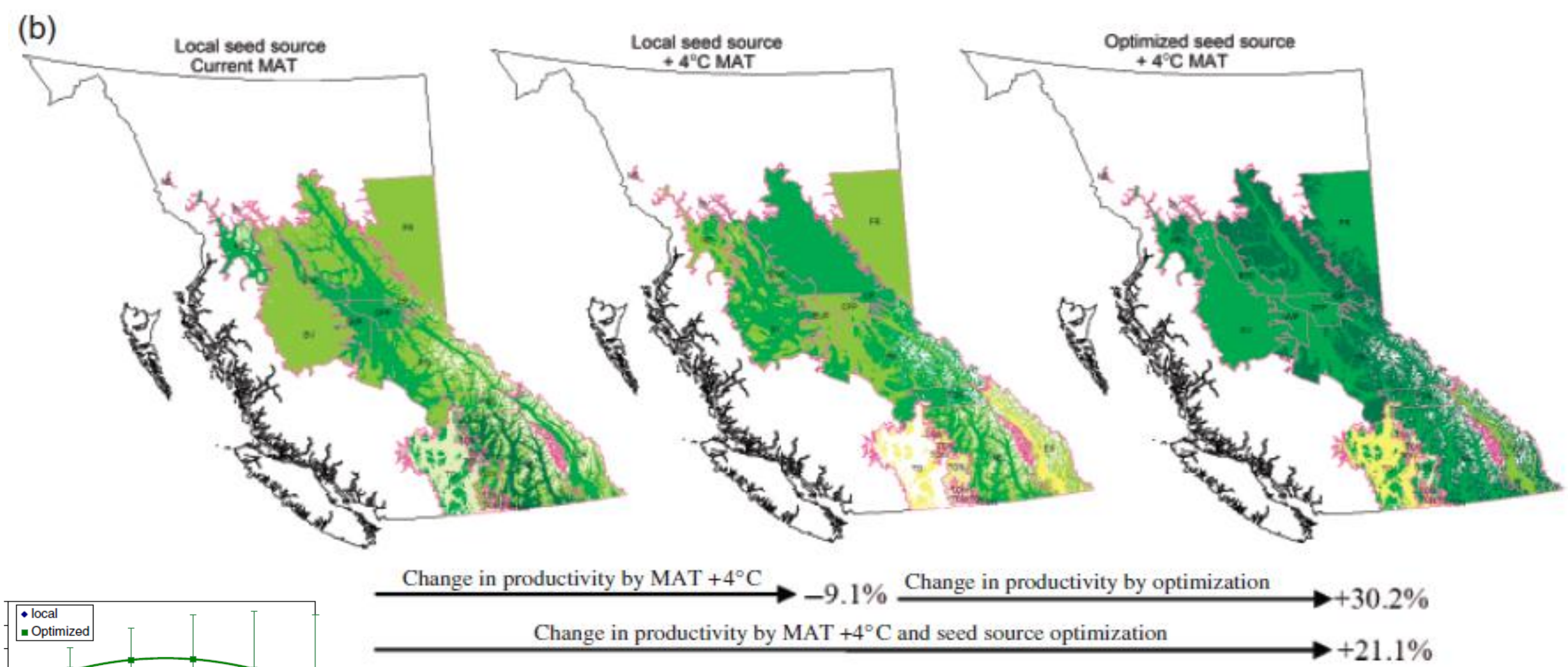
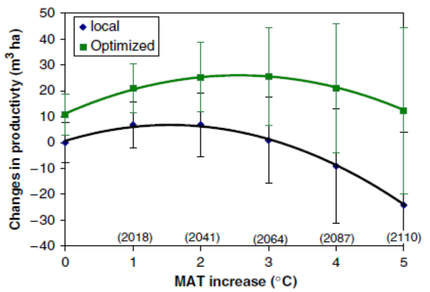
Using Provenance Data to Project Impact of Climate Change on Forest Trees





Wang et al. 2006. *Glob. Change Biol*. 12: 2404-2416

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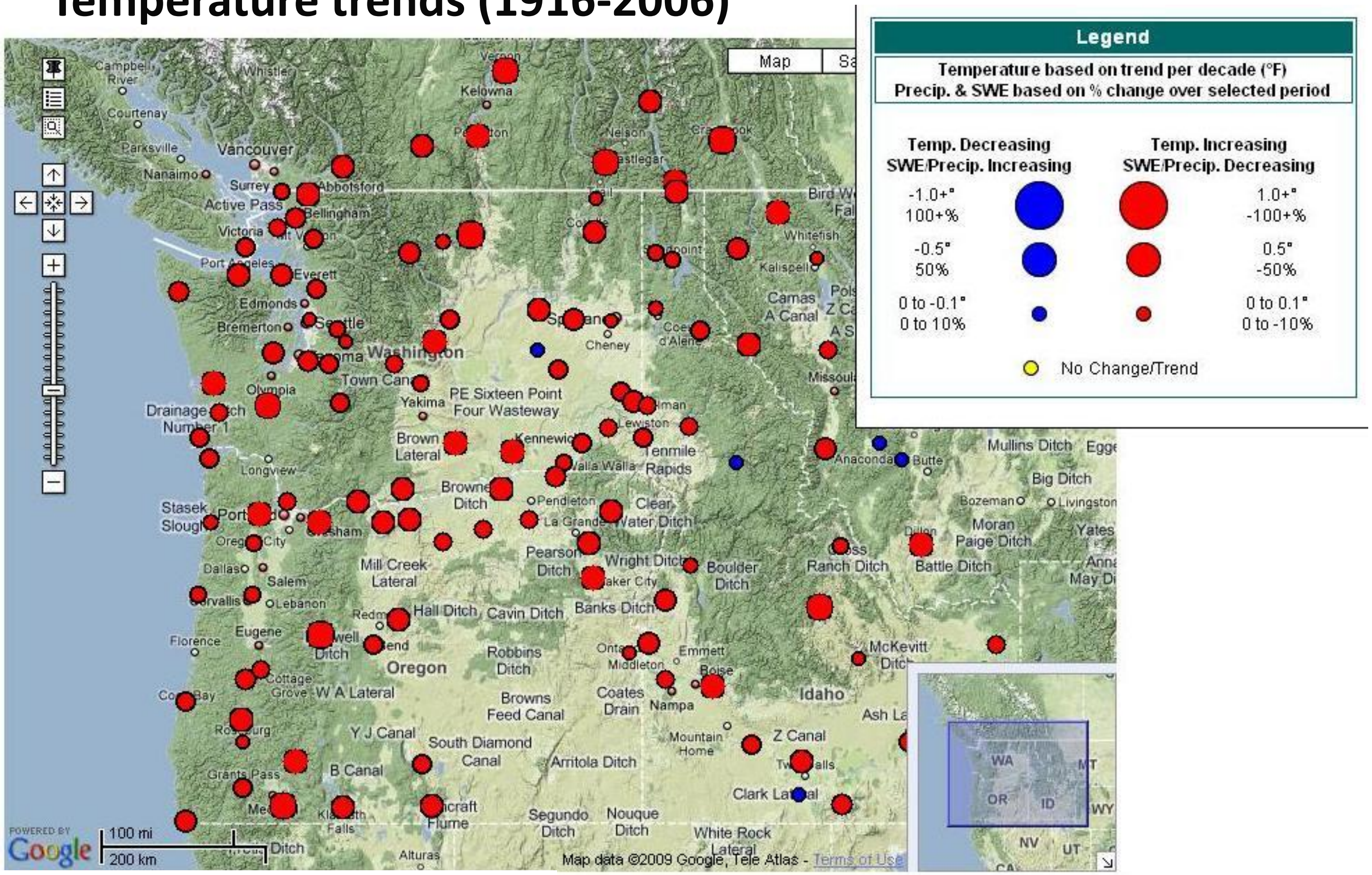
The Climate in the Pacific Northwest is Changing

Temperature trends (1916-2006)



Office of the Washington State Climatologist

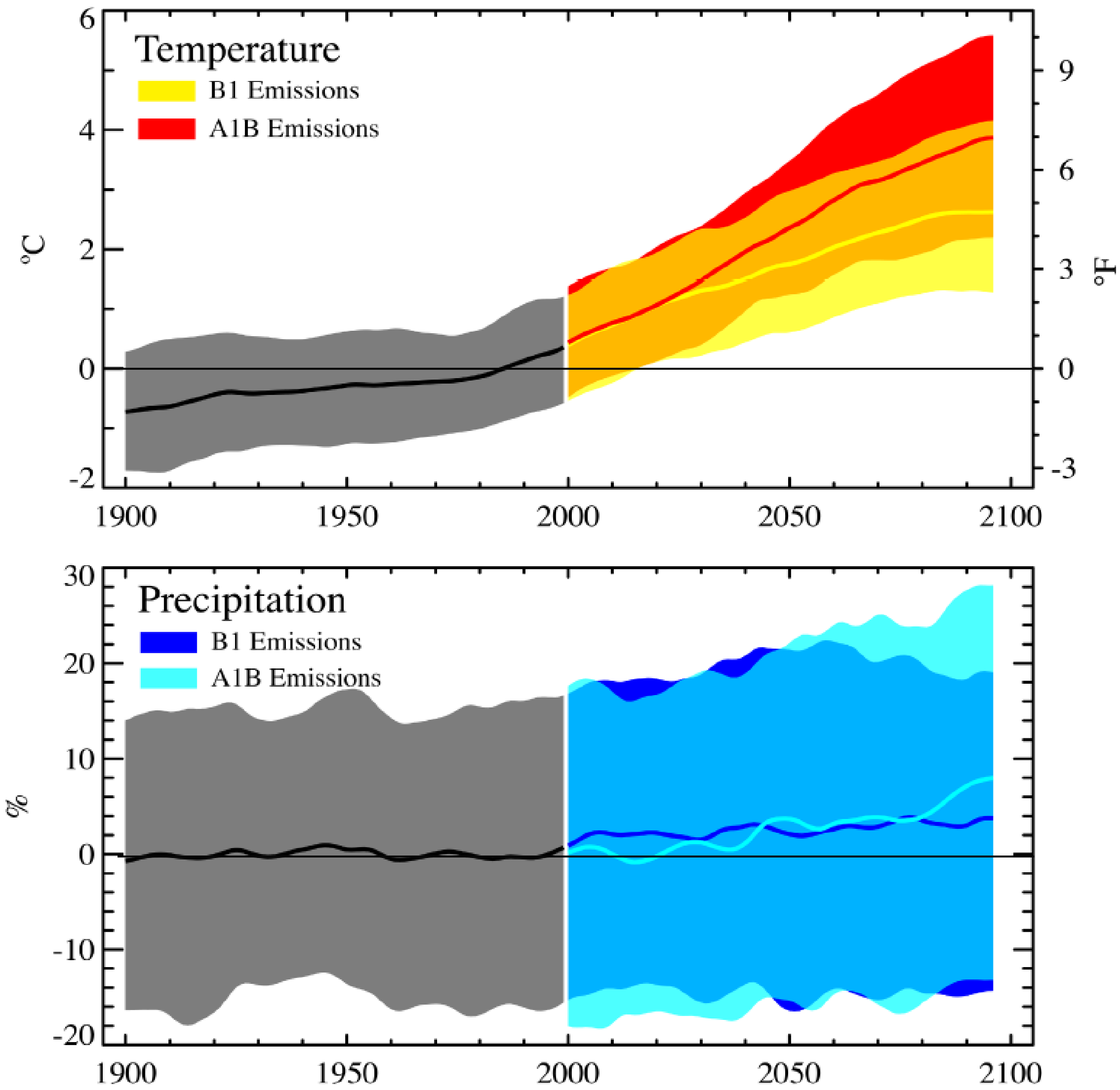
http://climate.washington.edu/trendanalysis/

Is the Pacific Northwest Climate Going to Change Further? – Yes

Relative to the 1970-1999 mean, at the end of the 21st century:

- Annual temperatures are likely to be warmer
- Annual precipitation may slightly increase

There is substantial variability associated with these projections.



Mote and Salathé (2009)

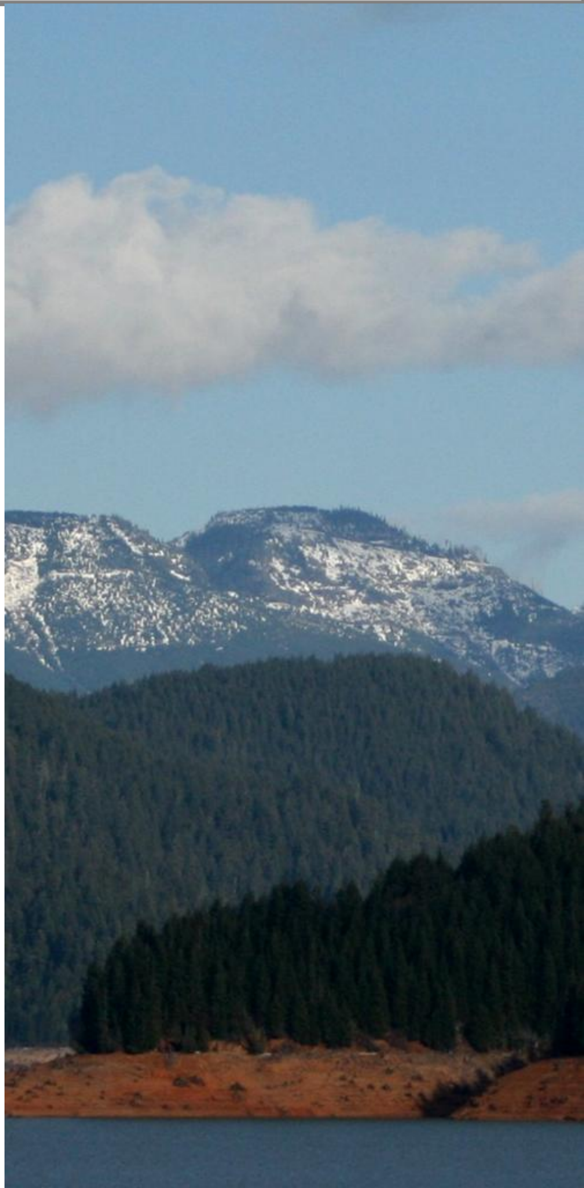
Trees and Forests Will be Challenged by Climate Change

- **Abiotic stressors**
  - Wildfires
  - Summer droughts
  - Summer heat
  - Warm winters
  - Spring and fall frosts – even with general warming
- **Biotic stressors**
  - Insects and pathogens
  - Competition, including invasive exotic species

TAFCC Taskforce on Adapting Forests to Climate Change

What Can We Do?

- Understand climate variability and climate change
- Understand climate change impacts on forests
- Help forests adapt to climate change – use Genetic Options for adaptation



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Genetic Options for Adaptation

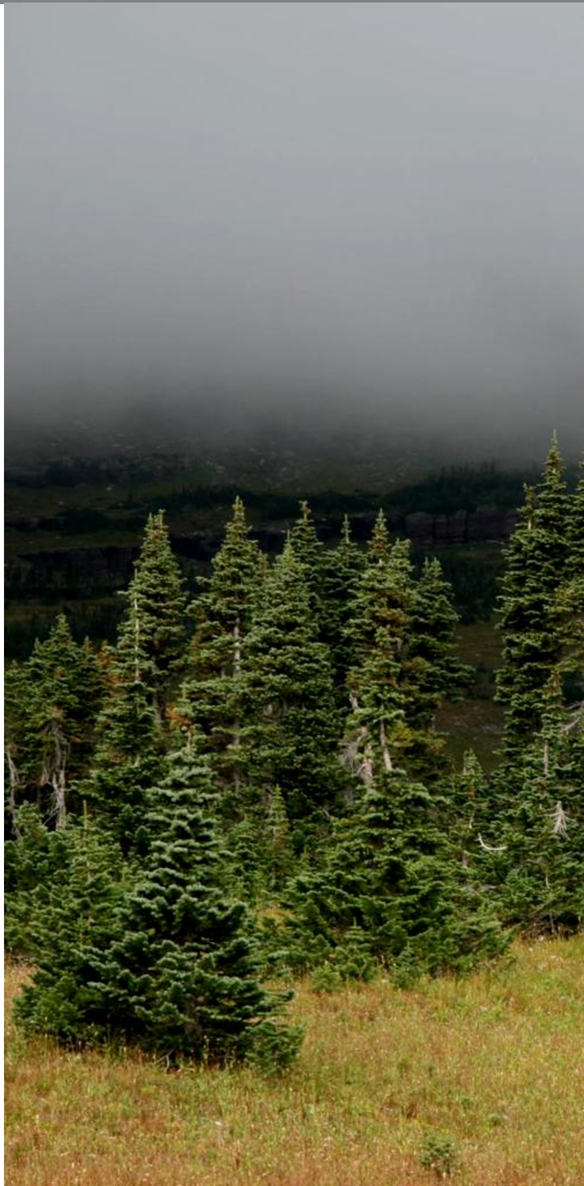
- Conserve genetic diversity
  - In situ (on site)
  - Ex situ (outside)
- Understand and manage populations within the species
  - Seed zones
  - Breeding zones
- Help populations migrate
  - Natural migration
  - Assisted migration
- Develop improved genotypes
  - Selection and breeding
  - Genetic engineering

TAFCC Taskforce on Adapting Forests to Climate Change

Conserve Genetic Diversity

Maintain species diversity and within-species variation

- *In situ* (on site) reserves
  - Valuable populations
  - Areas of high environmental and genetic diversity
- *Ex situ* (outside) reserves
  - Endangered populations
  - Seed and tissue collections for long-term storage
  - Assisted migration
  - **Provenance tests** – provided enough variation is represented



TAFCC Taskforce on Adapting Forests to Climate Change

Promote Migration

Natural migration

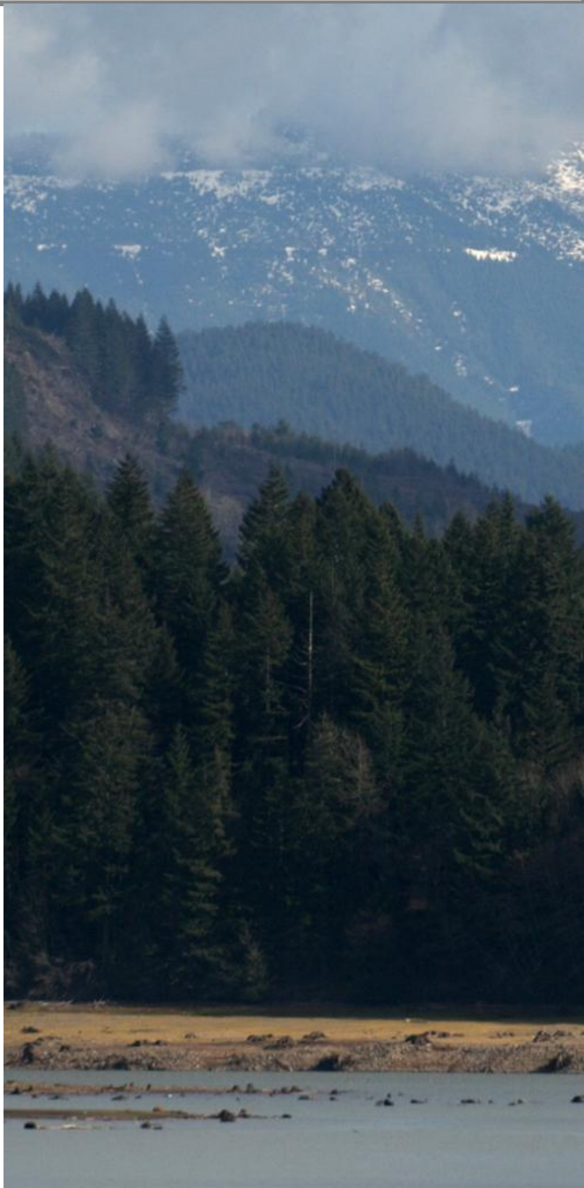
- Avoid landscape fragmentation to facilitate migration via pollen and seed
- Maintain forests in all succession stages (age classes) across the landscape

Assisted migration - planting

- Facilitate migration of populations within the species to help track the climate

Applications

- Seedlot Selection Tool
- Center for Forest Provenance Data



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Seedlot Selection Tool

On-line seed transfer decision-support tool:

- helps foresters select seedlots that are adapted to current and future climates at their sites
- works for multiple species with a user choice of ***multiple climatic variables*** and ***various climate change scenarios***

http://sst.forestry.oregonstate.edu/

Contact Glenn Howe or Ron Beloin at OSU for details

Home About Instructions Related Sites Contact Us

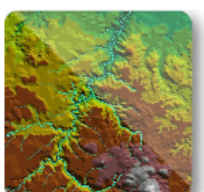
Find seedlots for my planting site Go!

Find planting sites for my seedlot Go!

Seedlot Selection Tool

Planting Healthy Forests

The seedlot selection tool (SST) is a GIS mapping program designed to help forest managers match seedlots with planting sites based on climatic information. The tool can be used to map current climates, or future climates based on selected climate change scenarios. Although it is tailored for matching seedlots and planting sites, it can be used by anyone interested in mapping present or future climates defined by temperature and precipitation.



⊕ See Example Map

Purpose

Forest managers can use this tool to help choose **seedlots** that are appropriate for planting on a particular site, or planting sites that are appropriate for a particular seedlot. This can be done using **current climate models** (i.e., ignoring potential climate change) or by choosing a **climate change model**, **emissions scenario**, and **future target year**. Because of the uncertainty in climate change projections, the tool is really a planning and educational tool. It can be used to explore alternative future conditions, assess risk, and plan potential responses, but cannot tell the user exactly which seedlots will be optimally adapted to a particular planting site in the future. The tool allows the user to control many input parameters so the results are appropriate for the management practices, climate change assumptions, and risk tolerance of the user.

Background

Populations of trees, such as those from native stands or **seed orchards**, are genetically different from one another, and are adapted to different climatic conditions. Therefore, forest managers must match the

How the tool works

1. Select Your Goal
Choose to find seedlots for your planting site or planting sites for your seedlot.

2. Login
The optional login feature allows you to store your inputs.

3. Enter Location
You can use Google Maps or coordinates to show the location of your seedlot or planting site.

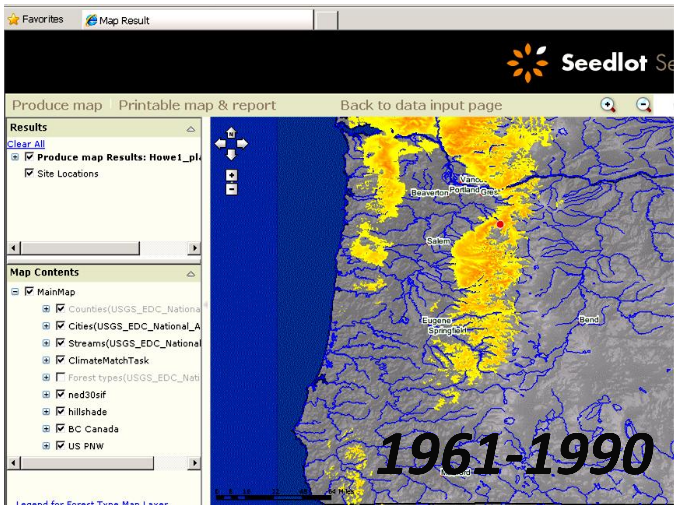
4. Select Species
You can use species-specific or generic zones and transfer limits.

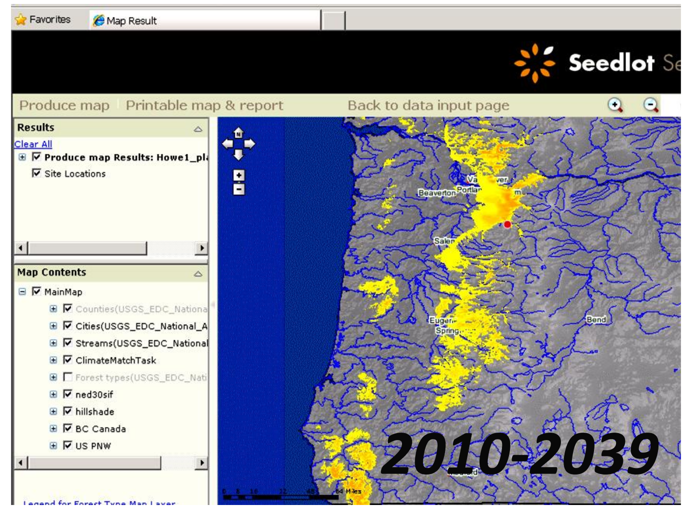
5. Determine Transfer Limit
Use one of our recommended limits, enter your own limit, or use an existing zone to calculate a limit.

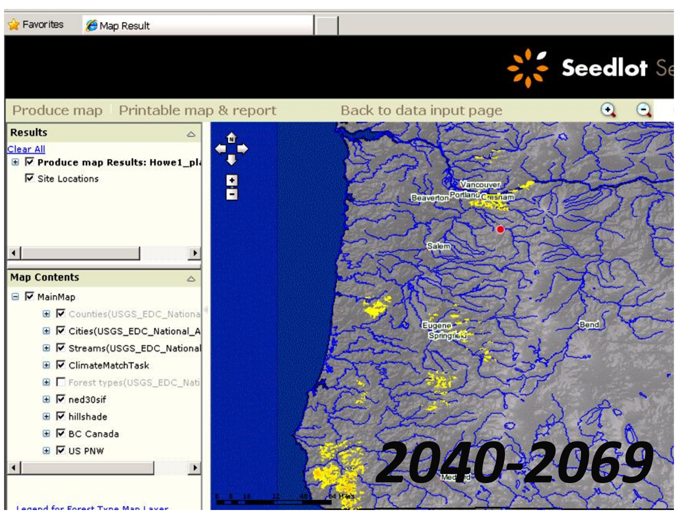
6. Select Climate Models
Use present climate only, or present and future climates by selecting an emissions scenario, future climate model, and year.

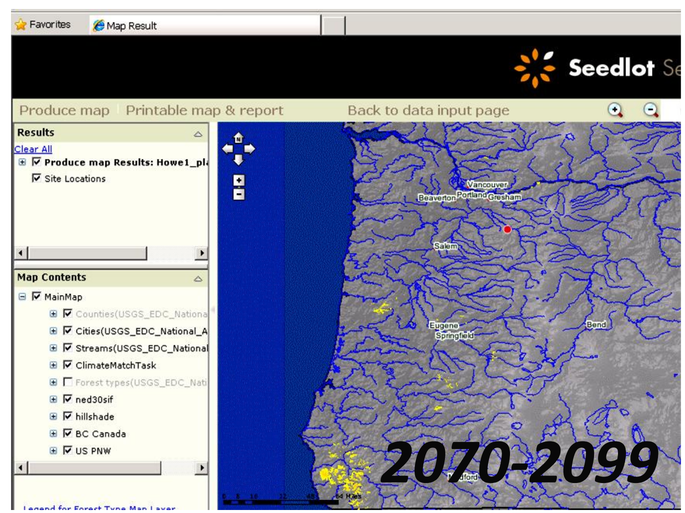
Internet 100%

Seedlot Selection Tool
Find Seedlots for My Planting Site

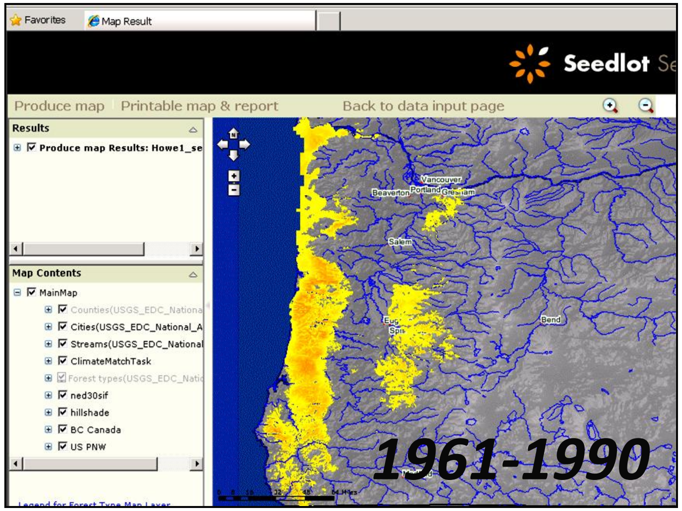


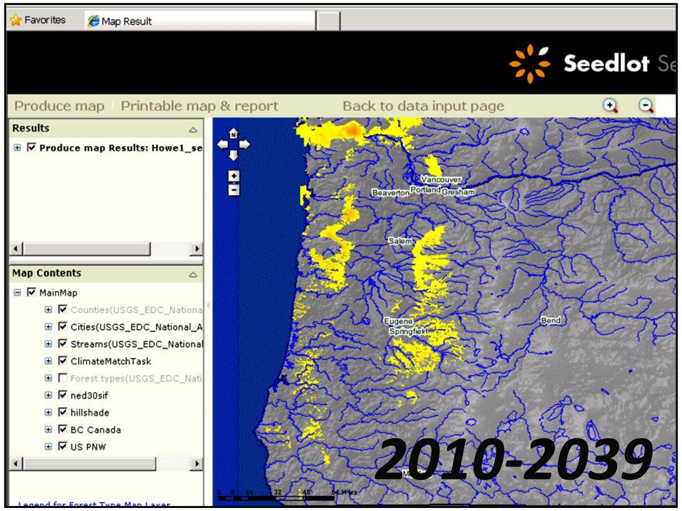


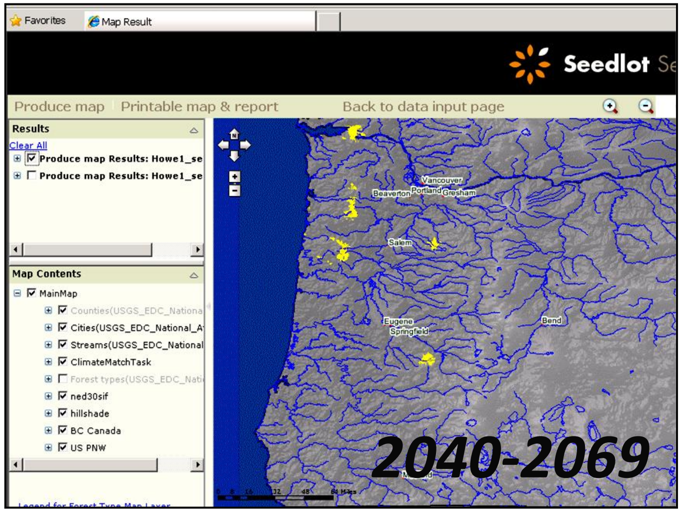


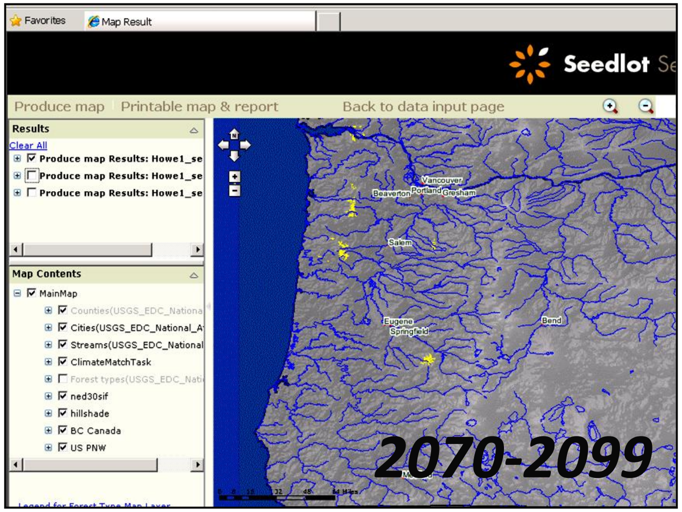


Seedlot Selection Tool
Find Planting Sites for My Seedlot









Center for Forest Provenance Data

- A centralized data and information management system to archive, maintain, and distribute forest genetics data
- Data will be available to researchers for promoting national and international collaboration to study forest genetics, plant adaptation, and responses to climate change
- Hardware and software has been configured to ensure that the data are safely archived and accessible now and in the long term

http://cenforgen.forestry.oregonstate.edu/

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Center for
Forest Provenance Data

Retrieve Data

Search for and download datasets from forest provenance studies

Submit Data

Upload data from long-term provenance tests and seedling genecology tests

Healthy forests for a changing world

The Center for Forest Provenance Data is a place for researchers to go to archive their data from provenance and genecology studies of forest trees and make those data available for collaboration with other researchers.

Provenance and genecology studies consider genetic variation among forest trees from different source locations by growing them in replicated tests in a common environment such that observed differences are primarily due to genotype and not the environment. Consistent differences among sources that are associated with environmental gradients are indicative of adaptively significant variation. Provenance and genecology studies are important for understanding adaptive variation across the landscape and managing genetic resources for reforestation, restoration, gene conservation, and responding to climate change.

The Center for Forest Provenance Data has sections for submitting and retrieving data from the database. There is also a search tool for determining studies that are currently in the database.

To submit or retrieve data, you will be asked to create a profile including a username and password for logging onto the site. Creating a profile provides us with contact information that will allow us contact you with questions or updates. The contact information will not be used for any purposes not related to managing the database.

Learn More

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Retrieve Data | Submit Data

Center for
Forest Provenance Data

Search and Retrieve Studies

View study with ID# [ ] Go!

Retrieve Data

Use the search tools to the right to find the study of interest. You can either search the database using keywords that are part of a study or you can search the database by species names (scientific or common). The species drop-down menu includes only those species that are currently in the database. You can view all studies in the database by clicking on the View All Studies button.

If you download data, we strongly encourage you to contact the primary contact to discuss collaboration. It is important to recognize people who conducted these experiments and made the data available (Sieber 2005*), and they may have important insights into data quality, analysis, and interpretation. Please use these data in a spirit of appreciation and open collaboration.

* Sieber, J.E. 2005. Ethics of sharing scientific and technological data: a heuristic for coping with complexity and uncertainty. Data Science Journal 4: 165-170.

Keyword Search | Species Dropdown Menu

View All Studies

Douglas-fir | Search

Internet 100%

Home Overview Species Codes Related Sites Contact Us | Login Join

Retrieve Data Submit Data

Center for Forest Provenance Data

Search and Retrieve Studies

View study with ID# Go!

Search Results

Search

Sort by Project Name Sort

1 result(s) found for 'Douglas-fir'

STUDY ID
1

Provenance Study of Douglas-fir in the Pacific Northwest Region

The purpose of this study was to detect genetic variations of this widely distributed species and to correlate the existence of distinct races if any, with geographical variables such as latitude and altitude.

SCIENTIFIC NAME	Pseudotsuga menziesii
COMMON NAME	Douglas-fir
STUDY TYPE	field
CONTACT	Glenn Howe
ESTABLISHED BY	Kim K. Ching

 Disclaimer and Privacy Contact Us

http://cenforgen.forestry.oregonstate.edu/retrieve/DataRetrieve.php?study_id=1 Internet 100%

Retrieve Data | Submit Data | Forest Provenance Data

Search and Retrieve Studies

View study with ID# [ ] Go!

STUDY ID
1

SCIENTIFIC NAME	Pseudotsuga menziesii
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Provenance Study of Douglas-fir in the Pacific Northwest Region

The purpose of this study was to detect genetic variations of this widely distributed species and to correlate the existence of distinct races if any, with geographical variables such as latitude and altitude.

View Data

Tables may be viewed for each component of the study. If only the header appears for that set of records, it means there are no records for that particular study component.

Study Information [View Data]

Accession / Provenance Information [View Data]

Test Site Information [View Data]

Response Data [View Data]

Contact Information [View Data]

Download Data

Alternatively, you may download the tables for this study in an Excel workbook. Check the components you would like to include and hit submit.

- [ ] **Study Information**
- [ ] **Accession / Provenance Information**
- [ ] **Test Site Information**
- [ ] **Response Data**
- [ ] **Contact Information**

Name your file [ ]

File Format ( ) xls (Excel 2003) ( ) xlsx (Excel 2007)

Done | Internet | 100%

Submit Data

Contributing data from your provenance study to the Center for Forest Provenance Data consists of three steps:

Download
the Excel templates from this web site
Download Templates

Enter
the data from your study into the Excel files

Upload
your Excel files back to this web site
Upload Files

Downloading the Five Template Files

Information from provenance tests is submitted to the Center for Forest Provenance Data in five parts. To contribute data from your provenance study, you must download and complete an Excel file for each of the five components of the database. Each Excel file will be used to fill in the corresponding tables in the database. The spreadsheet program used is Microsoft Excel version 2003.

The five components of the database are described below:

1. Study Information. General information about the study including a name for the study, the type of study (field, nursery, greenhouse, or controlled-environment), the species involved, the overall number of accessions, provenances and test sites, general information about the geographic range of

Entering Your Data

Data for your specific provenance study is entered into each of the five template files. The Study Information template is an Excel file that is in the format of a form for which you enter general information about the study. The other four templates involve inserting your Excel worksheet into the first worksheet of the template, then indicating the variables that are in each column in the second worksheet of the template (the "Metadata"). The second worksheet includes a list of variables that might be expected for each component of the database, along with descriptions of the variables, formatting rules, and a place to indicate the units used. Not everyone will use every variable suggested in the metadata worksheet. Some variables, however, are a necessary part of a provenance study (e.g.,

Uploading Your Files

To submit files (or retrieve files from the database), you must create a profile using an email address and password. The email address and password are used to log-in on subsequent visits when submitting or updating files. Creating a profile provides us contact information in case we need to contact you with questions or updates. The contact information will not be used for any purposes not related to managing the database. Once you have logged-in, submitting your data is simply a matter of choosing the files from your computer and clicking Submit.

The submission process allows users to enter all or part of the data at one time, and return to enter additional data in the future. You may enter:

- Only the study information

Needs

- Better projections of local climate
- Information on population responses to climate – especially for non-commercial species
- Information to populate database
- Resolve ownership issues – credits to original scientists, proprietary datasets, data release, etc.

TAFCC Taskforce on Adapting Forests to Climate Change

Conclusions

- Common garden studies play a profound role in advancing our understanding of population's responses to climate
- Information generated in this kind of tests have been used to develop the information-sharing tools and decision support tools
- These tools can and should be used to help adapt forest to future climates

TAFCC Taskforce on Adapting Forests to Climate Change

Acknowledgements

Ron Beloin SST http://sst.forestry.oregonstate.edu/
Denise Cooper CFPD http://cenforgen.forestry.oregonstate.edu/

Support to the TAFCC comes from:

- Oregon State University
- Oregon Forest Resources Institute
- USDA Forest Service Pacific Northwest Research Station
- Bureau of Land Management
- Oregon Department of Forestry
- USDA Forest Service Western Wildlife Environmental Threat Assessment Center
- USDA Forest Service Region 6
- Washington Department of Natural Resources
- USDI National Park Service

SST is a joint project by: OSU and USDA Forest Service PNW Research Station
CFPD is a joint project by: OSU, USDA Forest Service PNW Research Station, and USDA Forest Service PSW Research Station

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Thank You

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Taskforce on Adapting Forests to Climate Change

Population variability of *Fagus sylvatica* leaves - a preliminary study

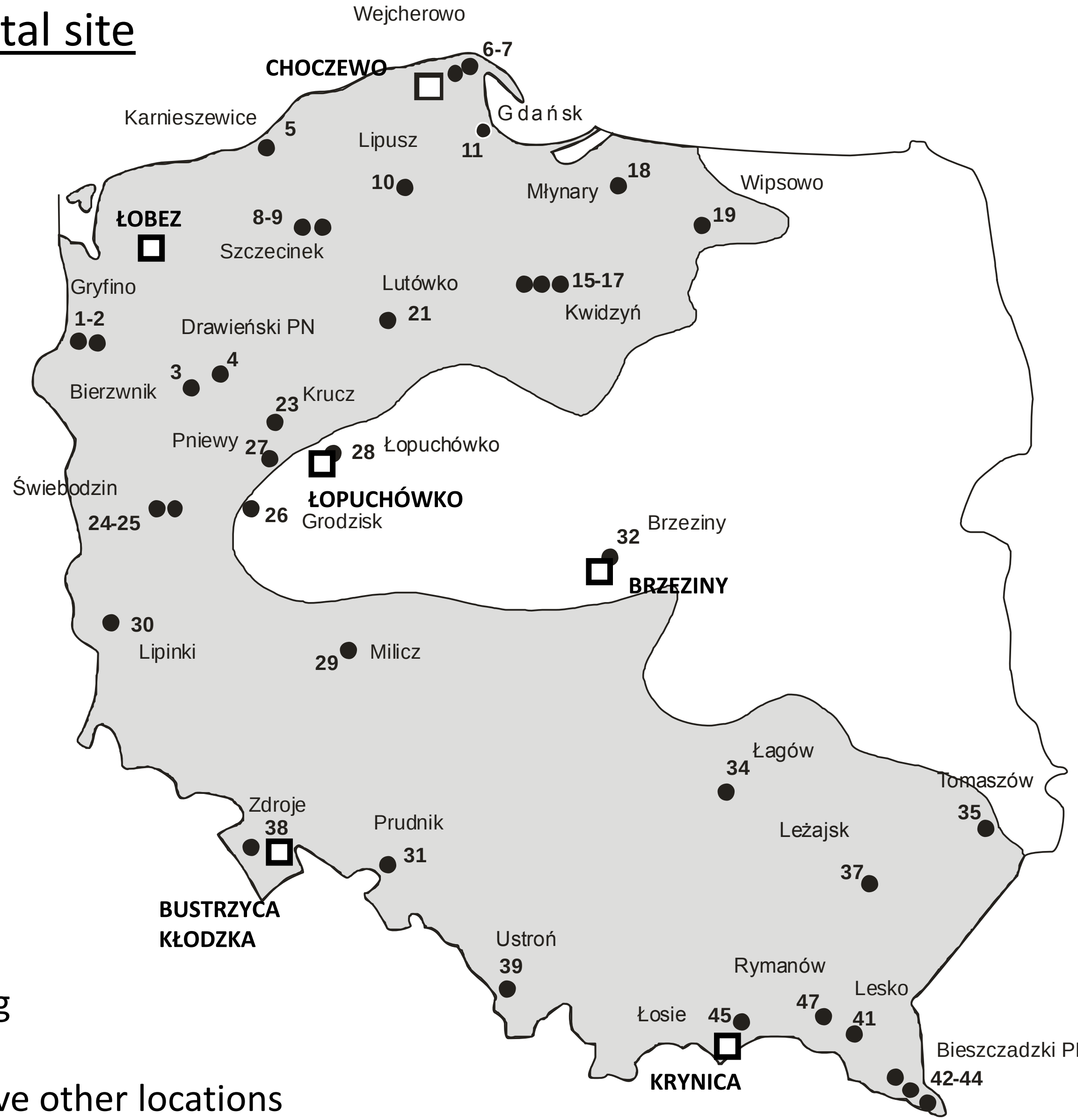
Marzenna Guzicka & Roman Rożkowski
Institute of Dendrology
Partner no. 18

Beech provenances in the Choczewo experimental site

38 provenances of beech from its natural distribution range in Poland

The experiment site was established in April 1996 with three-year-old seedlings

Each provenance is represented by 100 or 50 trees (1.5×1.3 m spacings) in plots in 1 to 6 replications



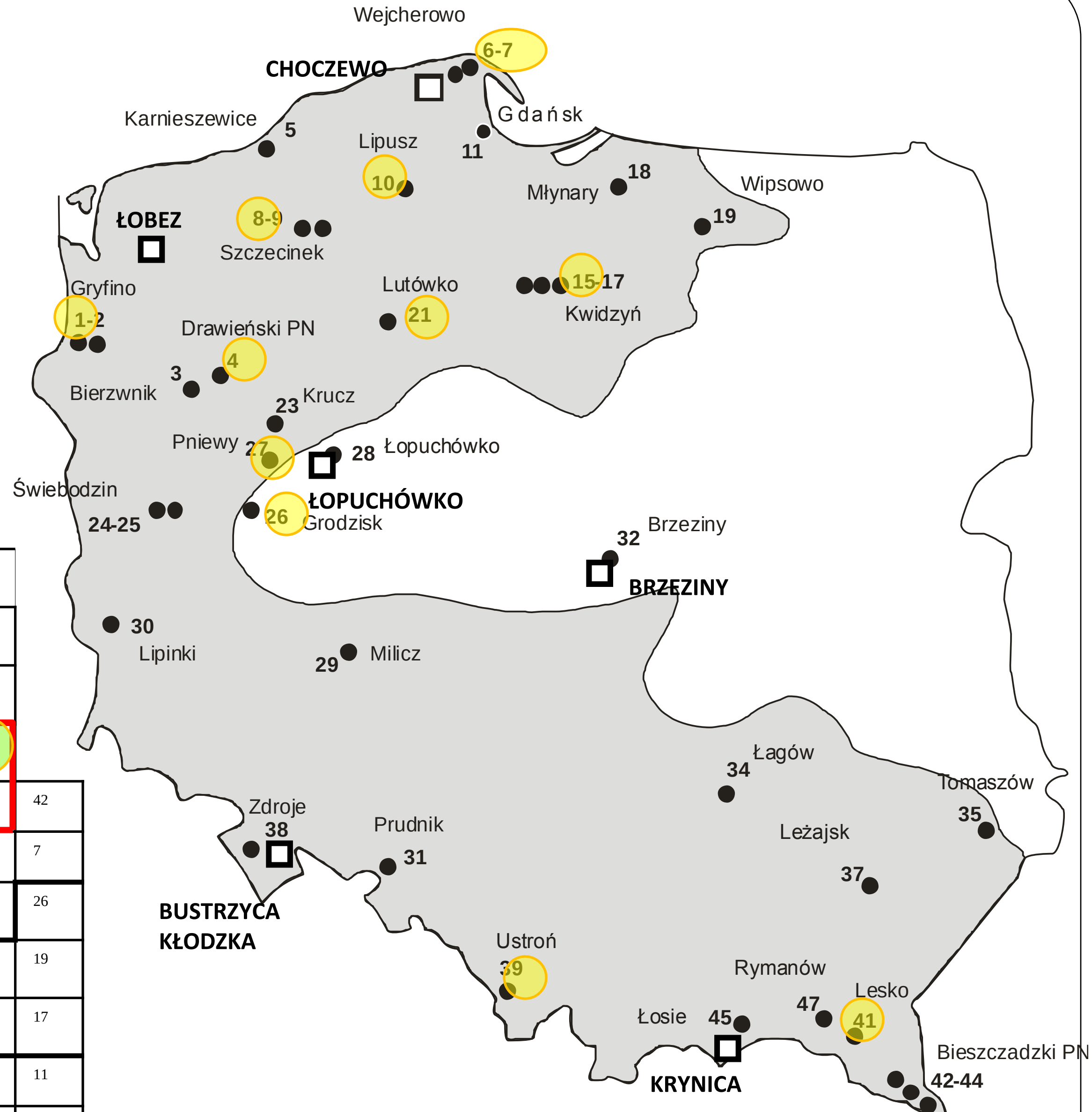
This site is a part of a project testing diversity of beech in Poland.
Similar trials were planted also in five other locations (Łobez, Łopuchówko, Brzeziny, Bystrzyca Kłodzka, and Krynica)

The experiment was established to investigate:

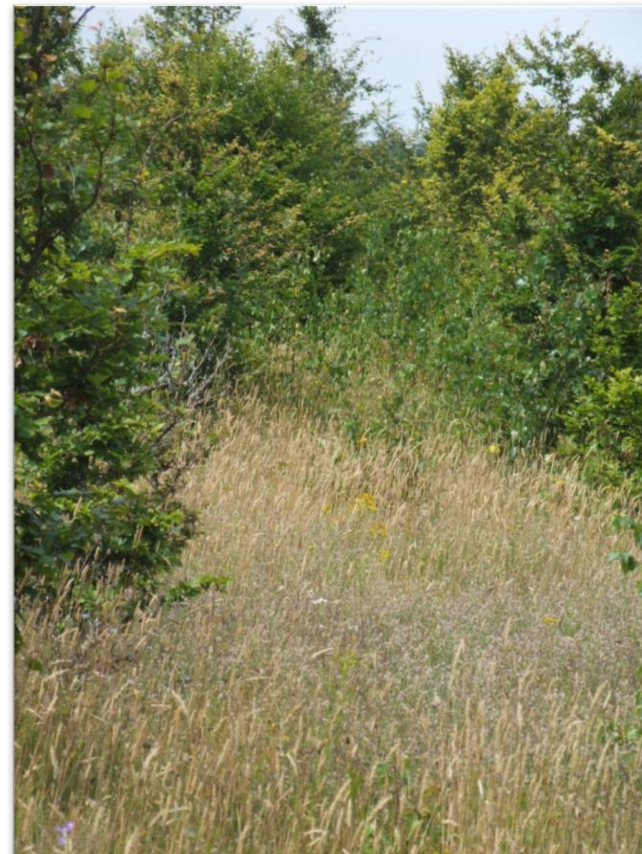
- genetic variability of common beech
- resistance of the particular populations to negative environmental factors (frost, ground frosts, drought, high temperature)
- interaction genotype × environment
- productivity
- to create the gene bank

12 provenances
for the study of variability
of leaf morphology

8	11	3	29	9	17	35	19	10	39	
7	31	4	6	7	16	41	38	47	24	
18	2	25	28	37	44	43	26	1	42	
32	34	45	21	15	30/ 18	5	30	19	39	
10	41	31	26	32	43	18	4	23	24	42
38	37	11	30	21	15	1	17	34	25	7
3	28	2	5	6	9	27	8	47/44	16	26
15/7	4	41	5	34	8	18	32	23	27	19
28	39	38	26/21	47	10	30	6	11	31	17
2	25	42	3	1	9	34	42	18	6	11
26	41/31	8	32	47	25	9	5	3	23	39
1	10	17/ 27	30	2	9	8	26	10	2	11
5	6	1	18	25	30	3	34	32/39	42	23

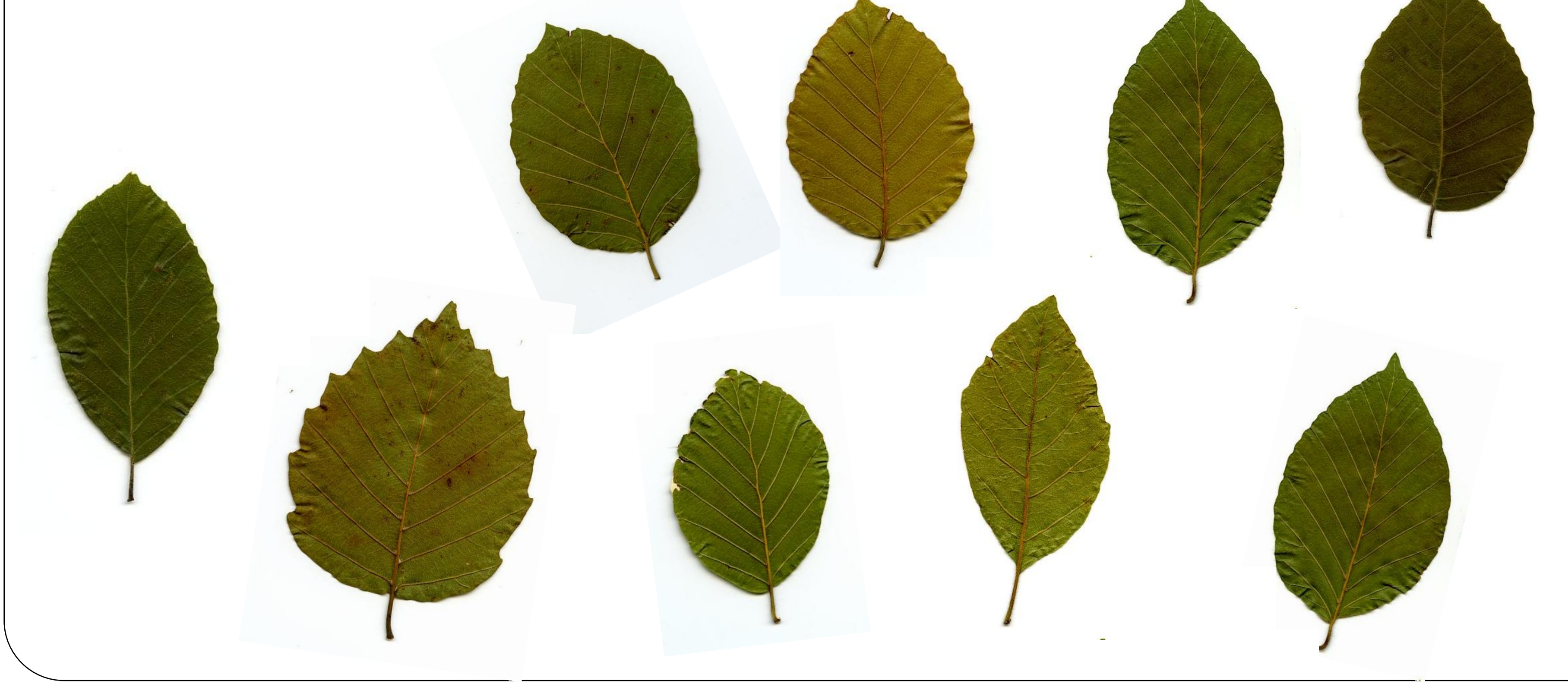


Differences between
block 1 and block 2



Morphological parameters of leaves were analysed using Winfolia:

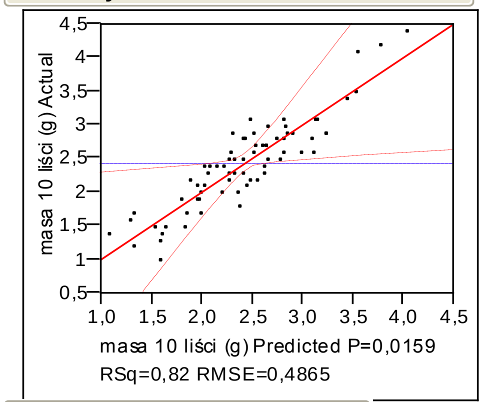
Perimeter
Area
Total holes area
Leaf length
Blade length
Blade width (maximum, in 50% and 90% of length)
Mass of 10 leaves
SLA [cm^2/g]



Response mass of 10 leaves

Whole Model

Actual by Predicted Plot



Summary of Fit

RSquare	0,817101
RSquare Adj	0,458924
Root Mean Square Error	0,486545
Mean of Response	2,434722
Observations (or Sum Wgts)	72

Analysis of Variance

Source	DF	Sum of Square:	Mean Square	F Ratio
Model	47	25,381766	0,540038	2,2813
Error	24	5,681429	0,236726	Prob > F
C. Total	71	31,063194		0,0159

Lack Of Fit

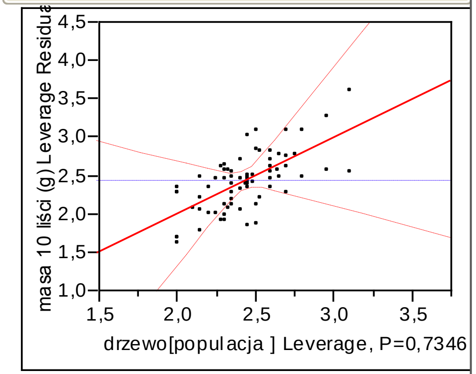
Source	DF	Sum of Square:	Mean Square	F Ratio
Lack Of Fit	23	5,5564286	0,241584	1,9327
Pure Error	1	0,1250000	0,125000	Prob > F
Total Error	24	5,6814286		0,5208
				Max RSq
				0,9960

Effect Tests

Source	Nparm	DF	Sum of Square:	F Ratio	Prob > F
Tree [population]	24	24	4,385238	0,7719	0,7346
Block	1	1	0,005606	0,0237	0,8790
Population	11	11	13,094248	5,0285	0,0005
Population x block	11	11	7,477015	2,8714	0,0149

drzewo[populacja]

Leverage Plot



LSMeans Differences Tukey HSD

Alpha=0,050 Q=3,60563

Level			Least Sq Mean
7	A		3,1333333
15	A		3,1333333
4	A	B	2,6833333
6	A	B	2,6833333
8	A	B	2,5833333
10	A	B	2,5761905
21	A	B	2,3333333
26	A	B	2,2333333
41		B	2,0333333
1		B	2,0333333
27		B	1,9833333
39		B	1,7500000

Levels not connected by same letter are significantly different

Response Perimeter

Whole Model

Summary of Fit

RSquare	0,392045
RSquare Adj	0,34822
Root Mean Square Error	2,297212
Mean of Response	19,86891
Observations (or Sum Wgts)	700

Analysis of Variance

Source	DF	Sum of Square:	Mean Square	F Ratio
Model	47	2218,7811	47,2081	8,9457
Error	652	3440,7246	5,2772	Prob > F
C. Total	699	5659,5057		<.0001

Lack Of Fit

Source	DF	Sum of Square:	Mean Square	F Ratio
Lack Of Fit	22	707,0715	32,1396	7,4069
Pure Error	630	2733,6531	4,3391	Prob > F
Total Error	652	3440,7246		<.0001
				Max RSq
				0,5170

Effect Tests

Source	Nparm	DF	Sum of Square:	F Ratio	Prob > F
Block	1	1	7,9997	1,5159	0,2187
Tree [population]	24	24	365,2190	2,8836	<.0001
Population	11	11	1015,2992	17,4904	<.0001
Population x block	11	11	743,8378	12,8140	<.0001

Blok

Least Squares Means Table

Level	Least Sq Mean	Std Error	Mean
1	19,964965	0,12601753	19,9473
2	19,745543	0,12601753	19,7905

Popul

Popul*Blok

LSMeans Differences Tukey HSD

Alpha=0,050 Q= 3,28

Level						Least Sq Mean
7	A					21,678022
6	A					21,081770
10	A	B				20,877100
15	A	B				20,752503
4	A	B	C			20,552096
8	A	B	C			20,447772
1		B	C	D		19,379006
21			C	D		19,370258
41			C	D		19,138223
27				D		19,013683
26				D		18,685078
39					E	17,287538

Levels not connected by same letter are significantly different

Response Area

Whole Model

Summary of Fit

RSquare	0,506156
RSquare Adj	0,470556
Root Mean Square Error	4,899515
Mean of Response	24,26817
Observations (or Sum Wgts)	700

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	47	16041,594	341,311	14,2182
Error	652	15651,421	24,005	Prob > F
C. Total	699	31693,014		<.0001

Lack Of Fit

Source	DF	Sum of Squares	Mean Square	F Ratio
Lack Of Fit	22	3500,861	159,130	8,2508
Pure Error	630	12150,559	19,287	Prob > F
Total Error	652	15651,421		<.0001
				Max RSq
				0,6166

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Block	1	1	2,2657	0,0944	0,7588
Tree [population]	24	24	2195,5204	3,8108	<.0001
Population	11	11	7373,2684	27,9229	<.0001
Population x block	11	11	5529,4453	20,9403	<.0001

Blok

Least Squares Means Table

Level	Least Sq Mean	Std Error	Mean
1	24,211232	0,26877130	24,1178
2	24,328006	0,26877130	24,4185

Popul

LSMeans Differences Tukey HSD

Alpha=0,050 Q= 3,28

Level		Least Sq Mean
7	A	29,679330
6	A B	27,768410
15	A B C	26,788745
10	B C	26,483043
4	B C	26,163196
8	B C D	25,016915
21	C D E	24,298873
1	D E	22,448657
41	E	21,944640
26	E	21,663980
27	E	21,372357
39	F	17,607280

Levels not connected by same letter are significantly d

Response BladeLength

Whole Model

Summary of Fit

RSquare	0,462218
RSquare Adj	0,423451
Root Mean Square Error	0,621688
Mean of Response	6,93801
Observations (or Sum Wgts)	700

Analysis of Variance

Source	DF	Sum of Square:	Mean Squar	F Ratio
Model	47	216,58739	4,60824	11,9231
Error	652	251,99574	0,38650	Prob > F
C. Total	699	468,58313		<.0001

Lack Of Fit

Source	DF	Sum of Square:	Mean Squar	F Ratio
Lack Of Fit	22	65,44910	2,97496	10,0469
Pure Error	630	186,54665	0,29611	Prob > F
Total Error	652	251,99574		<.0001
				Max RSq
				0,6019

Effect Tests

Source	Nparm	DF	Sum of Square:	F Ratic	Prob > F
Block	1	1	2,824512	7,3080	0,0070
Tree [population]	24	24	46,822947	5,0478	<.0001
Population	11	11	80,316506	18,8915	<.0001
Population x block	11	11	79,380450	18,6713	<.0001

Blok

Least Squares Means Table

Level	Least Sq Mean	Std Error	Mean
1	6,9951857	0,03410379	6,99810
2	6,8648040	0,03410379	6,87792

Popul

Popu

LSMeans Differences Tukey HSD

Alpha=0,050 Q= 3,28

Level		Least Sq Mean
7	A	7,4774400
6	A	7,3469933
15	A B	7,2049017
4	A B C	7,1570342
10	A B C	7,1084067
8	B C D	6,9520083
41	B C D	6,9510233
21	C D E	6,8023867
1	C D E	6,7258358
27	D E F	6,6603017
26	E F	6,4745933
39	F	6,2990133

Levels not connected by same letter are significantly different

Response LSA

Whole Model

Summary of Fit

RSquare	0,675544
RSquare Adj	-0,01761
Root Mean Square Error	16,70258
Mean of Response	101,3328
Observations (or Sum Wgts)	70

Analysis of Variance

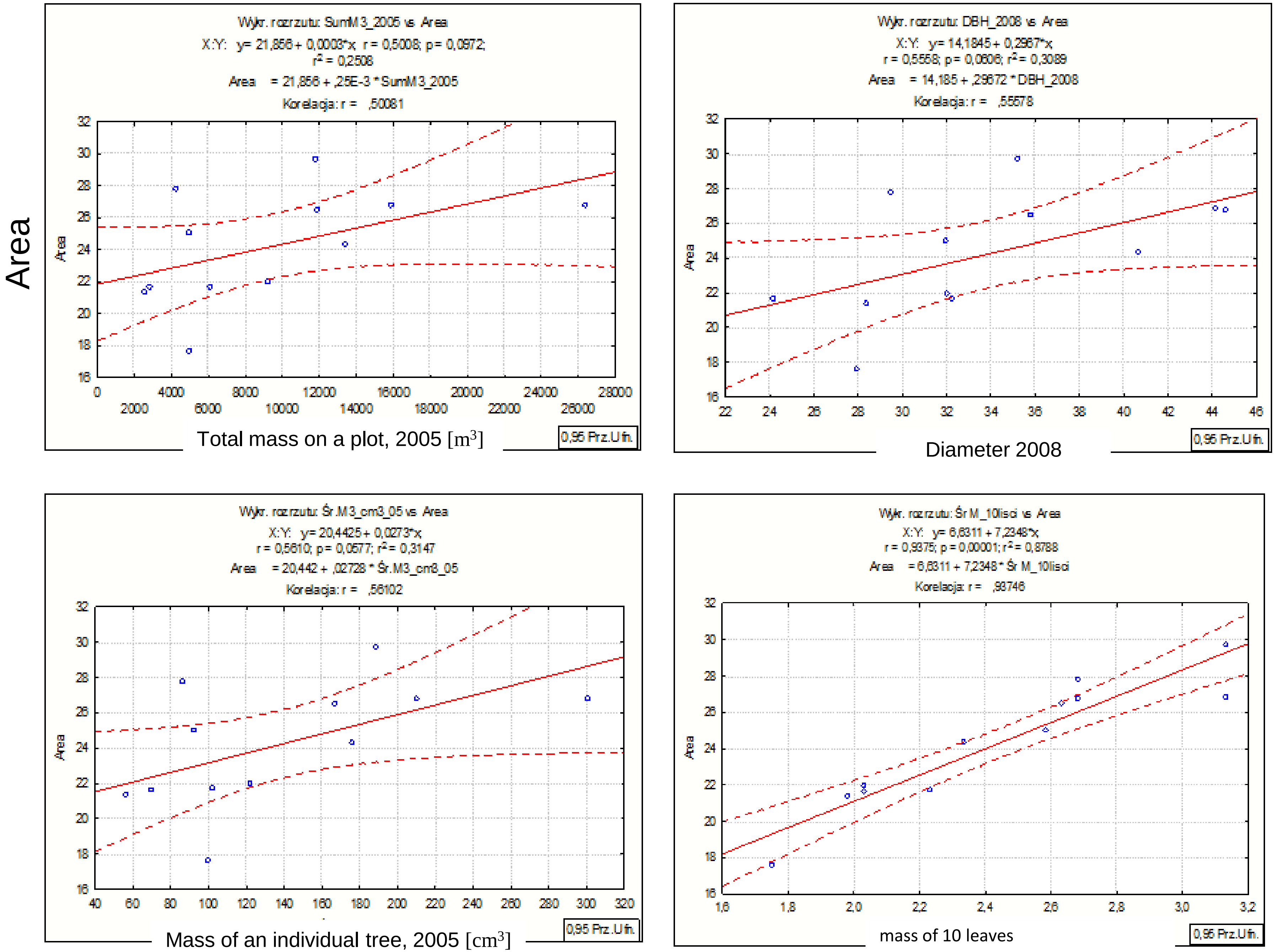
Source	DF	Sum of Square:	Mean Squar	F Ratio
Model	47	12778,722	271,888	0,9746
Error	22	6137,479	278,976	Prob > F
C. Total	69	18916,200		0,5455

Lack Of Fit

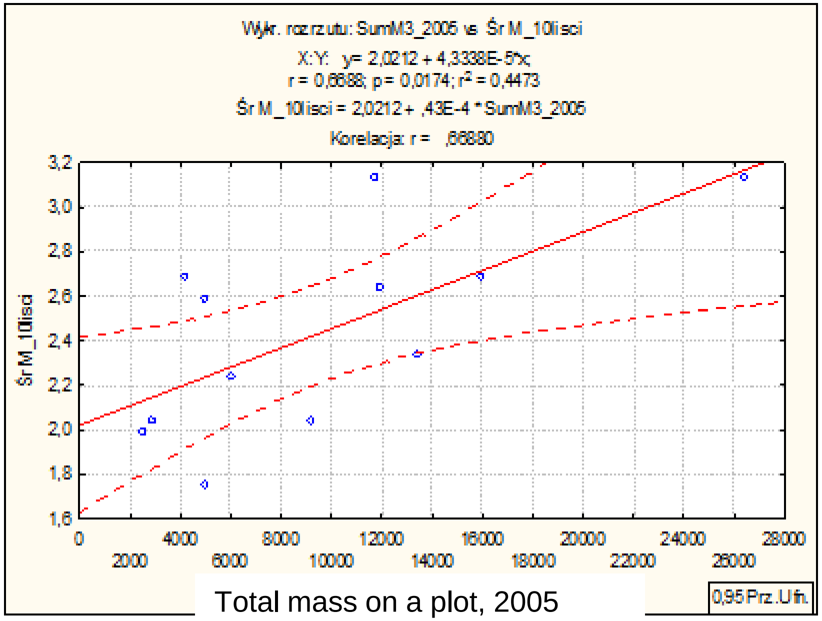
Source	DF	Sum of Square:	Mean Squar	F Ratio
Lack Of Fit	21	6079,1684	289,484	4,9645
Pure Error	1	58,3104	58,310	Prob > F
Total Error	22	6137,4788		0,3418
				Max RSq
				0,9969

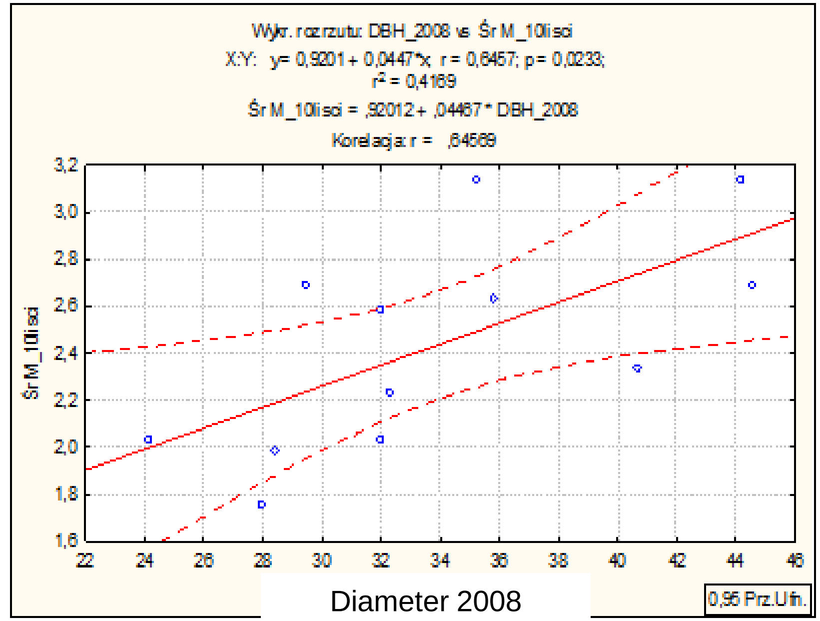
Effect Tests

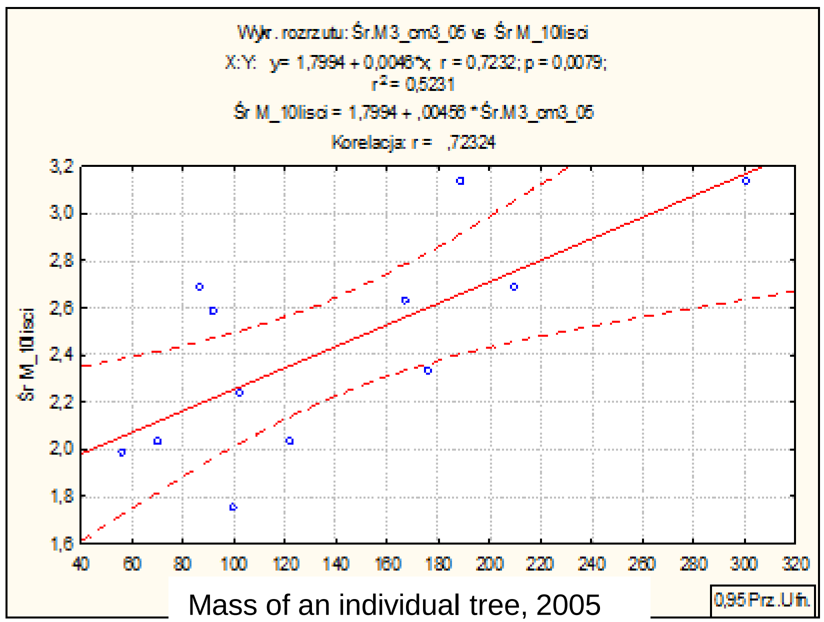
Source	Nparm	DF	Sum of Square:	F Ratic	Prob > F
Block	24	24	7766,8466	1,1600	0,3650
Tree [population]	11	11	3437,6784	1,1202	0,3921
Population	11	11	2068,2919	0,6740	0,7477
Population x block	1	1	32,2676	0,1157	0,7370


Area
Wykr. rozrzutu: SumM3_2005 vs Area
X:Y: y= 21,856+ 0,0003*x; r = 0,5008; p= 0,0972; r² = 0,2508
Area = 21,856 + ,25E-3 * SumM3_2005
Korelacja: r = ,50081
Area
Total mass on a plot, 2005 [m³]
0,95 Prz.Ufn.
Wykr. rozrzutu: DBH_2008 vs Area
X:Y: y= 14,1845+ 0,2967*x; r = 0,5558; p= 0,0606; r² = 0,3089
Area = 14,185 + ,29672 * DBH_2008
Korelacja: r = ,55578
Area
Diameter 2008
0,95 Prz.Ufn.
Wykr. rozrzutu: Śr.M3_cm3_05 vs Area
X:Y: y= 20,4425+ 0,0273*x; r = 0,5610; p= 0,0577; r² = 0,3147
Area = 20,442 + ,02728 * Śr.M3_cm3_05
Korelacja: r = ,56102
Area
Mass of an individual tree, 2005 [cm³]
0,95 Prz.Ufn.
Wykr. rozrzutu: Śr M_10lisci vs Area
X:Y: y= 6,6311 + 7,2348*x; r = 0,9375; p = 0,00001; r² = 0,8788
Area = 6,6311 + 7,2348 * Śr M_10lisci
Korelacja: r = ,93746
Area
mass of 10 leaves
0,95 Prz.Ufn.

mass of 10 leaves

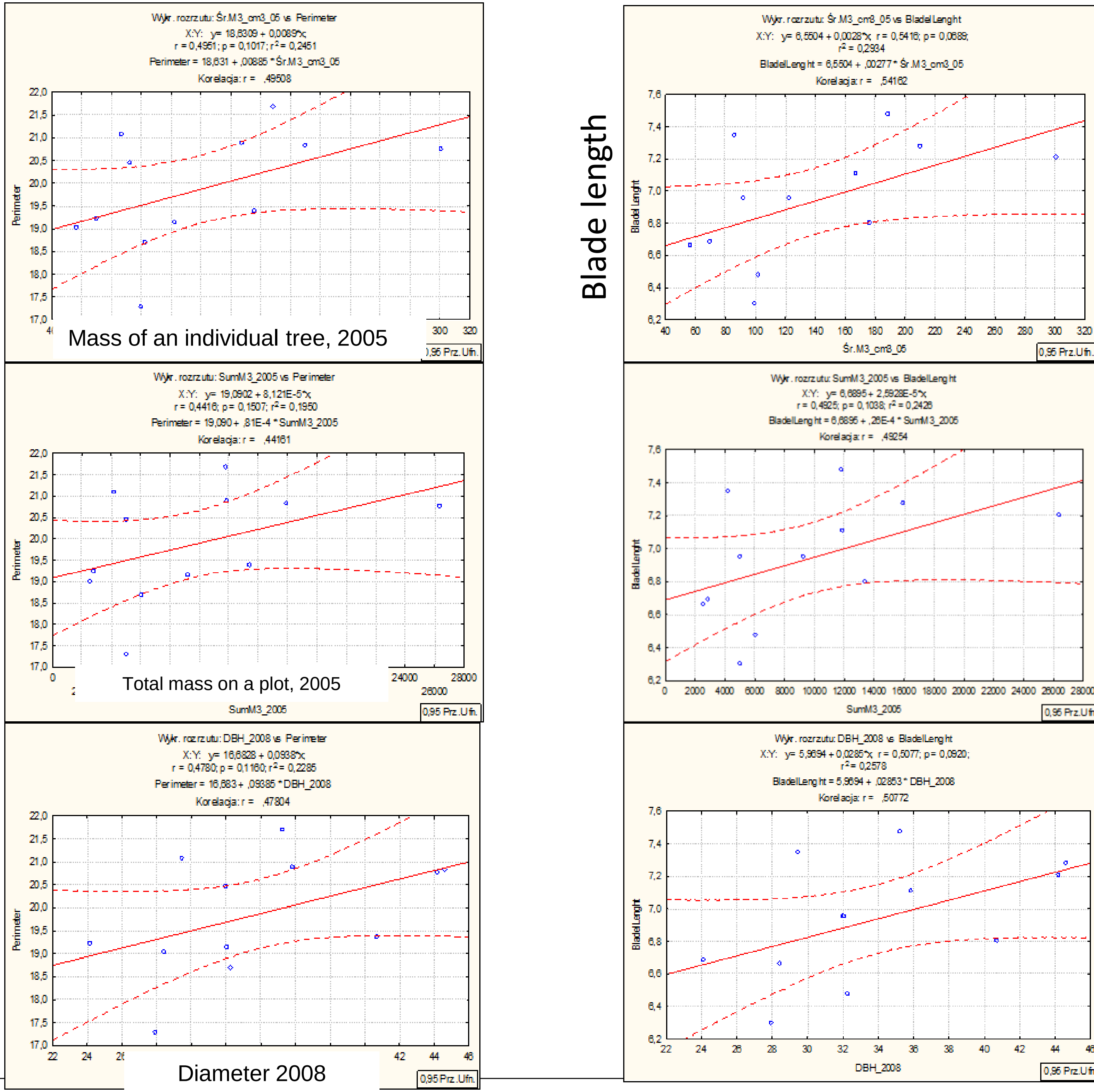


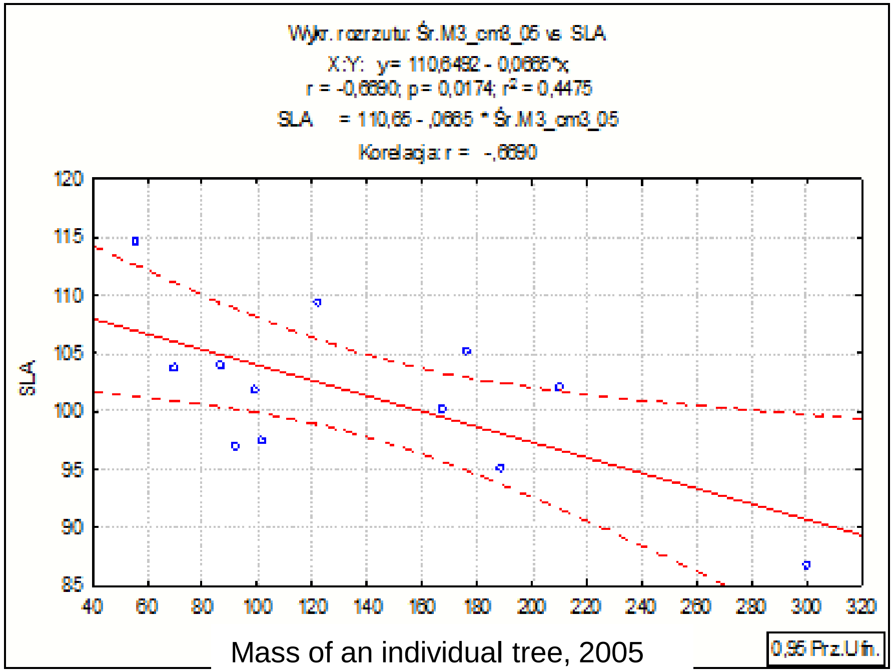




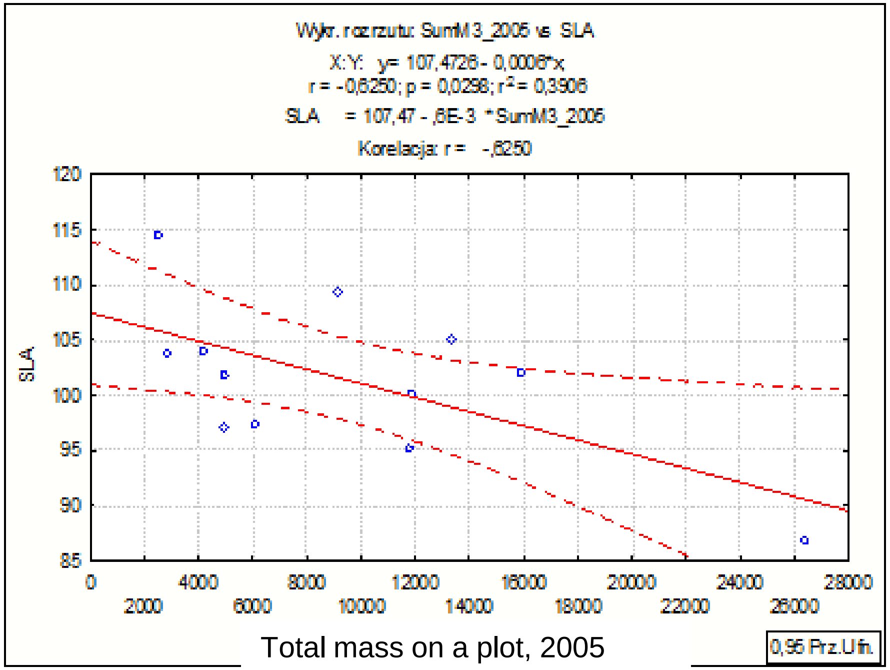
Perimeter

Blade length





Mass of an individual tree, 2005



Total mass on a plot, 2005

our hypothesis:

Morphological parameters of leaves can be an indicator of productivity

Acknowledgement

- Prof. Władysław Chałupka
- Prof. Jacek Oleksyn

- Miss Henryka Przybył

- This research was financially supported by the Institute Dendrology
- and the Polish State Forests


Thank you for your attention!
Kórnik invites you!

What do genetic field trials tell about the future use of forest reproductive material?

Prof. Csaba Mátyás
West Hungarian University, Sopron

Sękocin Stary 2010

Waldzukunft Report (Freiburg 2008)

Delphi interview, over 1000 forest experts

Out of 12 forecasts for 2050:

- Forests hit by climate change
- Genetic diversity declining
- GMOs unwanted but progressing

out of 5 unclear problems:

- Adaptation strategies?
- Risk management?

FRM use review → Climate change!

Problems, conventional forecasting of climate change effects

- limits assumed exclusively climatic
- vegetation supposed to move in community
- spontaneity of vegetation adjustment assumed
- human impact on European landscapes unconsidered: NO EMPTY SPACES!

→**no forestry imput?**

- Intraspecific adaptability differentiation of forest trees left unnoticed: “monolithic species?”

→**no genetic input?**

– ***role of forestry & genetics in internat’l climate mitigation: formal to nonexistent!***

Adaptability and tolerance are genetically set

Quantitative genetic knowledge is needed for:

- forecasting adaptive response
- formulating strategy of mitigation
- ***actively supporting adaptation***

(reprod. material trade, resource use & conservation)

Quantitative (growth , yield) forecasting needs field observations and tests!

Why are answers not ready?- 1

- Basic paradigm appropriate? (equilibrium and optimation as attainable goals?)
- Evolutionary change potential unclear
- Unsatisfactory coupling of quant. genetics with ecology, genomics
- Skewed approach to genetic processes: random vs directed →

Why are answers not ready?- 2

	Effect on response	Ease of investigation
(neutral) variation of the genome	?	xxxx
Past migration and drift	x	xxxx
Current selection, adaptation	xxxx	xx
Plasticity, epigenetics	xxxx	x

„The existence of climatic races within species is probable but it is not worth to follow further"

(Dengler 1935)

Can we offer anything beyond this?

„The existence of climatic races within species is probable but it is not worth to follow further”

(Dengler 1935)

Can we offer anything beyond this?

There are answers in common gardens since Ph. Vilmorin, 1840 à Madame de Vilmorin

Catalogue général des Arbres.

Composant les

Plantations des Barres.

Exemplaire à conserver portant les existences au 23 Juin 1858. Les n° 2 nos n'ont point existé sur le terrain.

1ère Partie.

Arbres résineux.

Pin Sylvestre, P. Sylvestris.

I. Graines de Russie.

1. Pin de Riga, gr. de Riga, par Mr. Zigra.

2. — — —, par Mr. Helmund.

3. — de Smolensk, par Mr. Wagner.

Common gardens

Provenance tests: probably the most important contribution of forestry to biology

- the only true simulation possibility for estimating adaptive response
- ***New use of tests***: assessment of response to changed conditions
- ***Transfer analysis*** (Matyas 1987): growth and health across test sites interpreted as response to changed climate

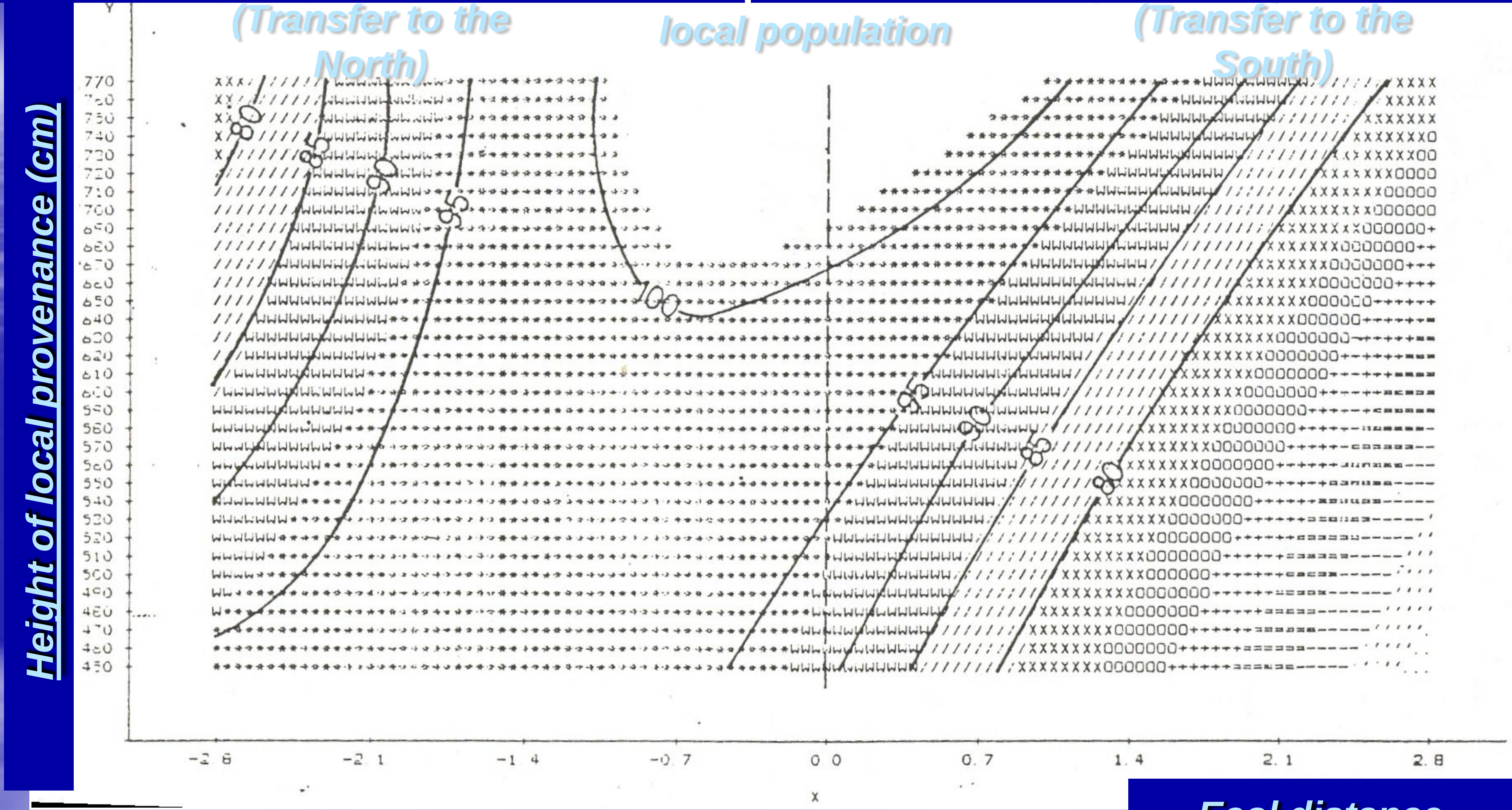
cooling

(Transfer to the North)

local population

warming

(Transfer to the South)



Transfer analysis *P. banksiana in: Mátyás – Yeatman 1992*

What are the genetic options to cope with climate change ?

- **Present generation:**

Plasticity/ acclimation: response tailored to environment

Selection (differentiation, mortality): survival of the fittest

- **Succeeding generations** :

Migration to friendlier places: dispersal

Inheritance of traits of the fittest: adaptation

Random replenishment of genet. resources: gene flow

Superscript over genetic codes: epigenetics


Climate selection, plasticity
and their interaction, consequences


This process is genetic-driven!
Photo: K. Kovács

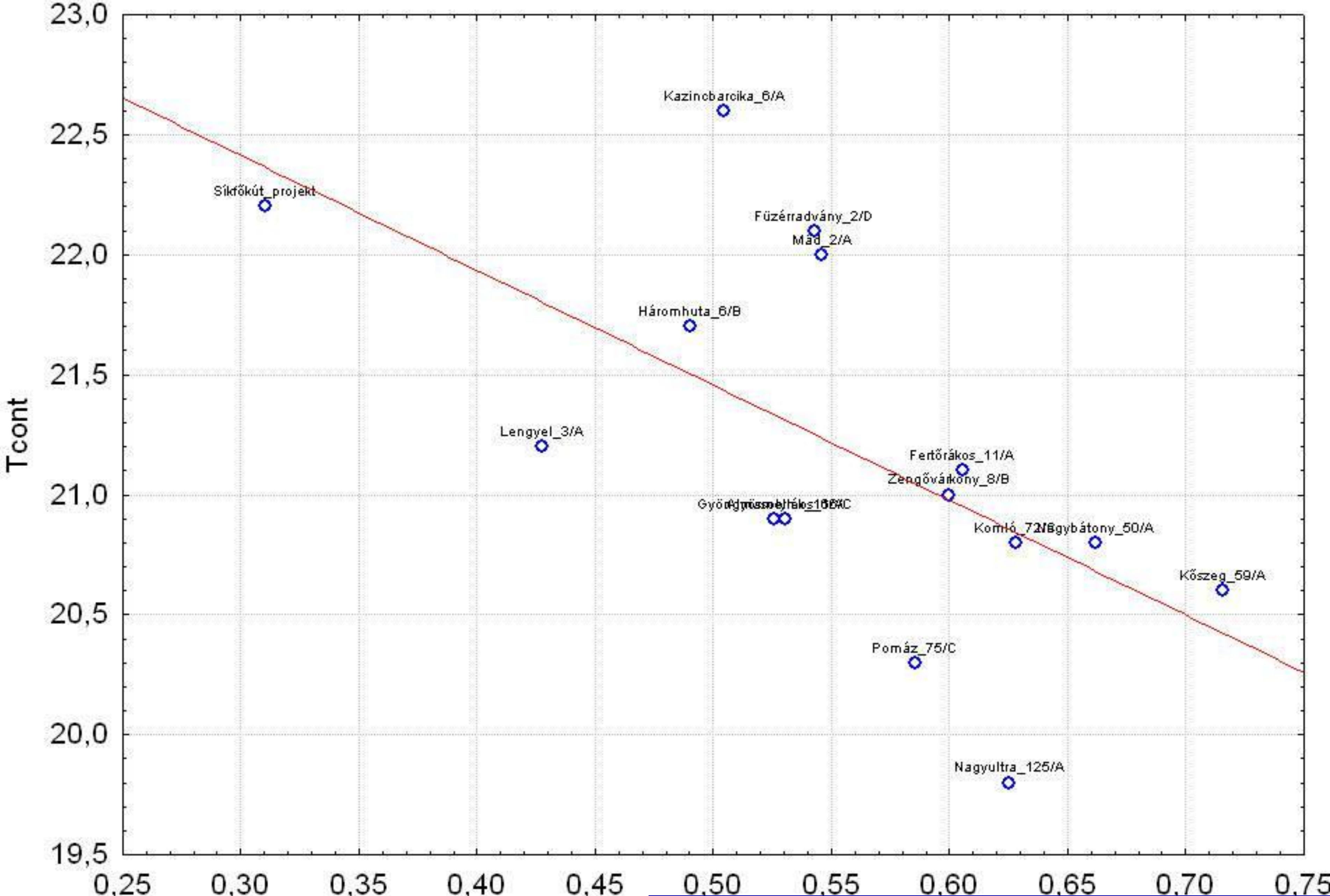
Effect of climate selection on allelic diversity:

Spring precipitation vs allelic frequency of ADH alleles:

(data for sessile oak by A. Borovics)

Allele type	Correlation with P_{spring}
ADH-3	+ 0,67 *
ADH-4	non sign.
ADH-5	- 0,73 * *
ADH-6	- 0,65 *

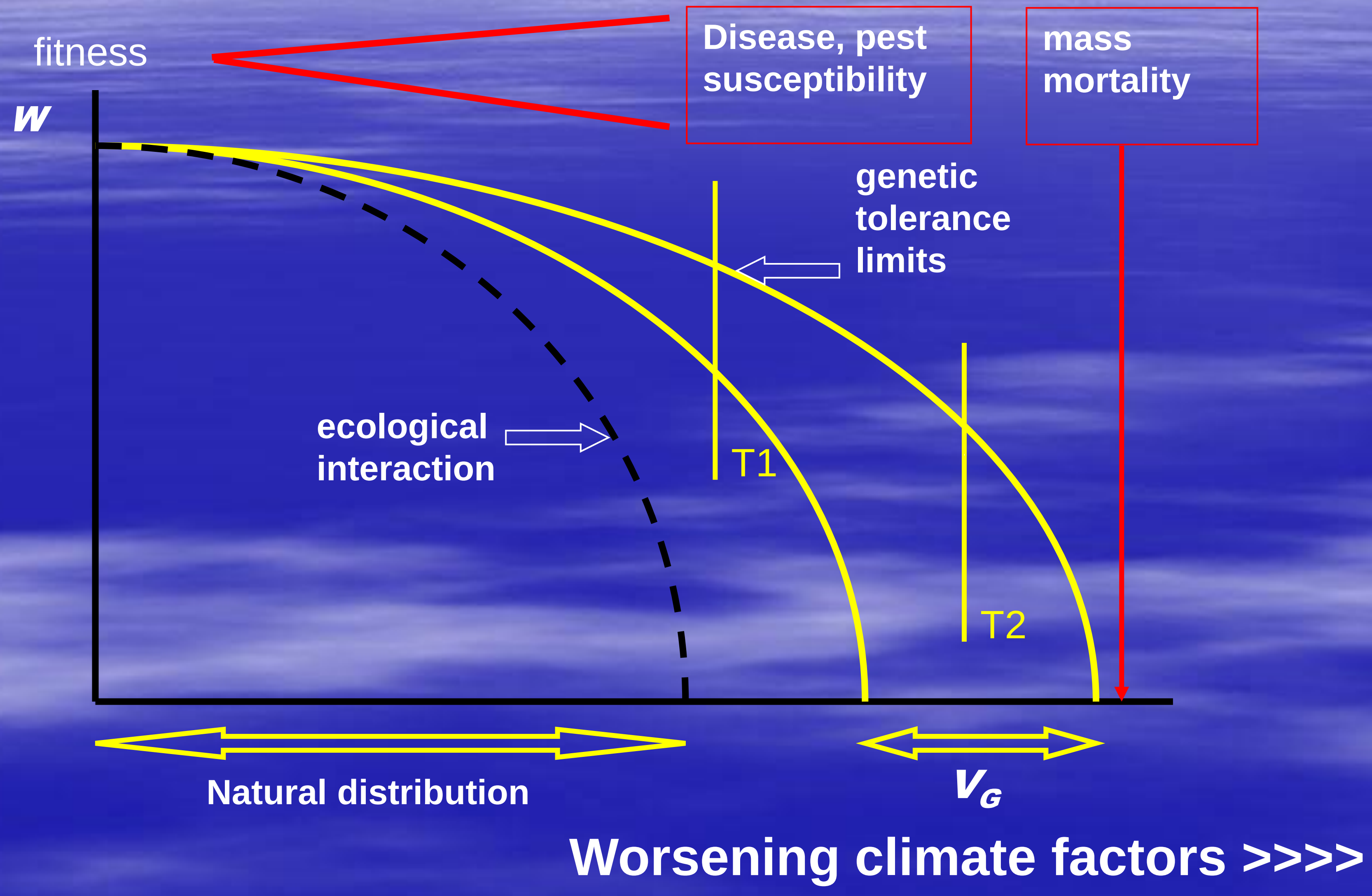
Continentality of temp. vs. exp. heterozygosity at EST-A



EST-A:Tcont: r = -0,6143, p = 0,0148

Data for sessile oak by A. Borovics

Ecological-genetic concept of population response to climatic changes



Scots pine provenances, age 6, Kámon Arboretum

Mass mortality, beyond the limits of tolerance

Test site: Kamon (Hungary) nr. ffd: 180, ann. prec.: 700 mm

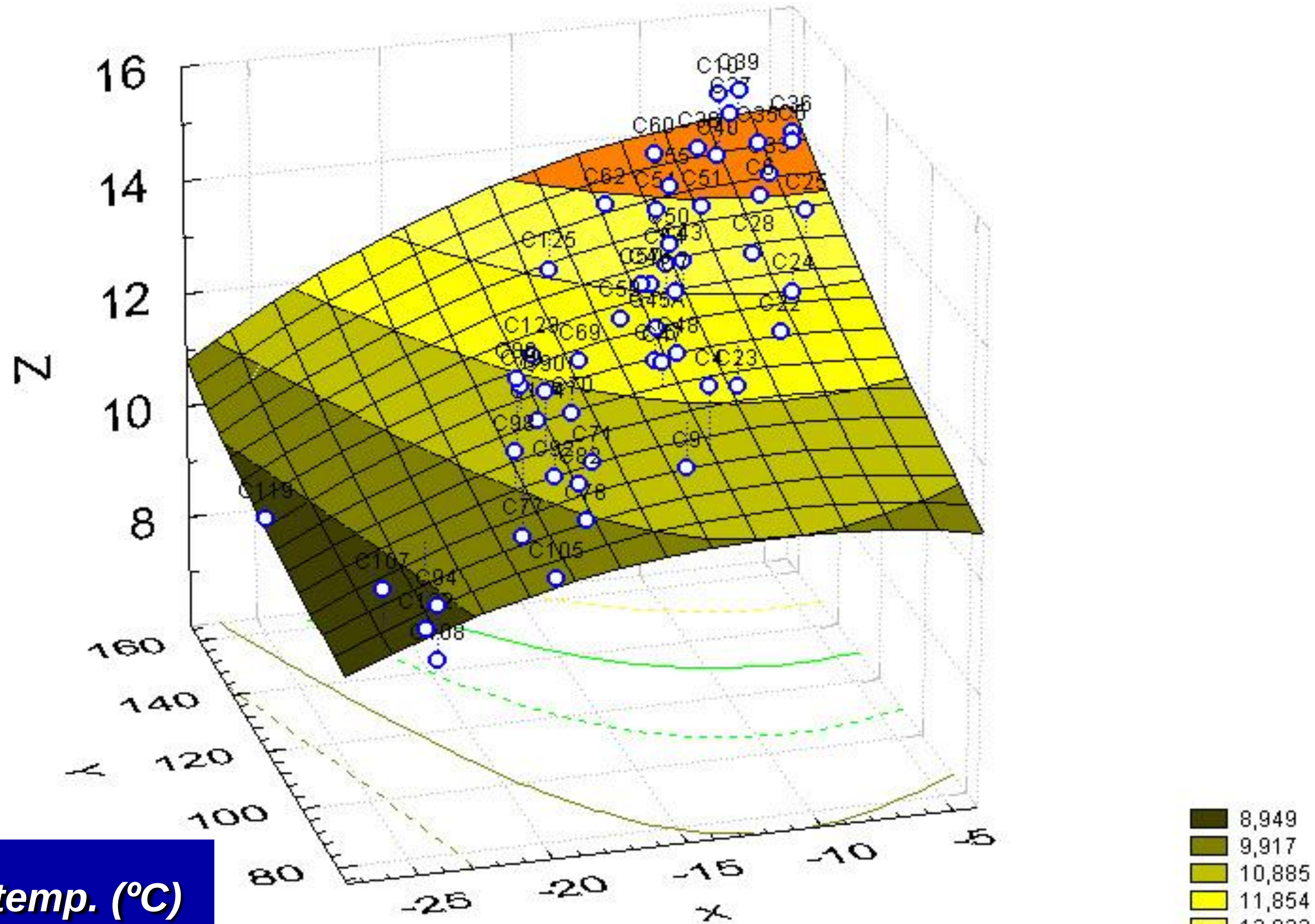
Provenance: Ayan, Yakutia (Russia)

Number of frostfree days: 107, annual precipitation: 890 mm

Height response of provenances in the VNIILM test Recsk, Hungary, age 15

$$Z = 6.753 - 0.267x - 0.007x^2 + 0.019y + 0.0001y^2 + 0.001xy$$

$$R = 0,907 ; R^2 = 0,824$$

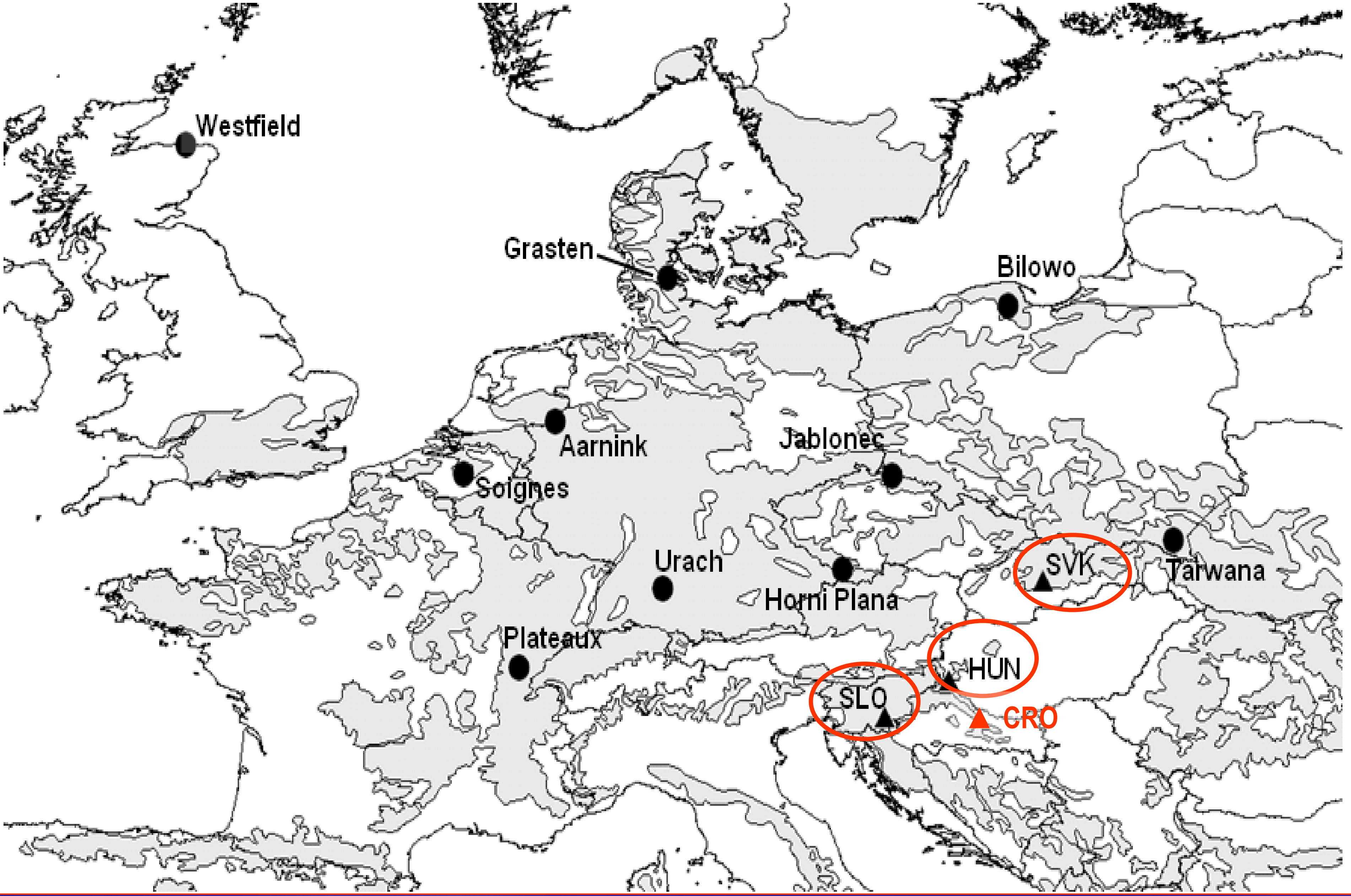


X: Mean January temp. (ºC)
Y: Number of frost days
Z: $D_{1.3}$

52. M.egregy (H) H: 3,13 m

13. Soignes (B) H: 2,62 m

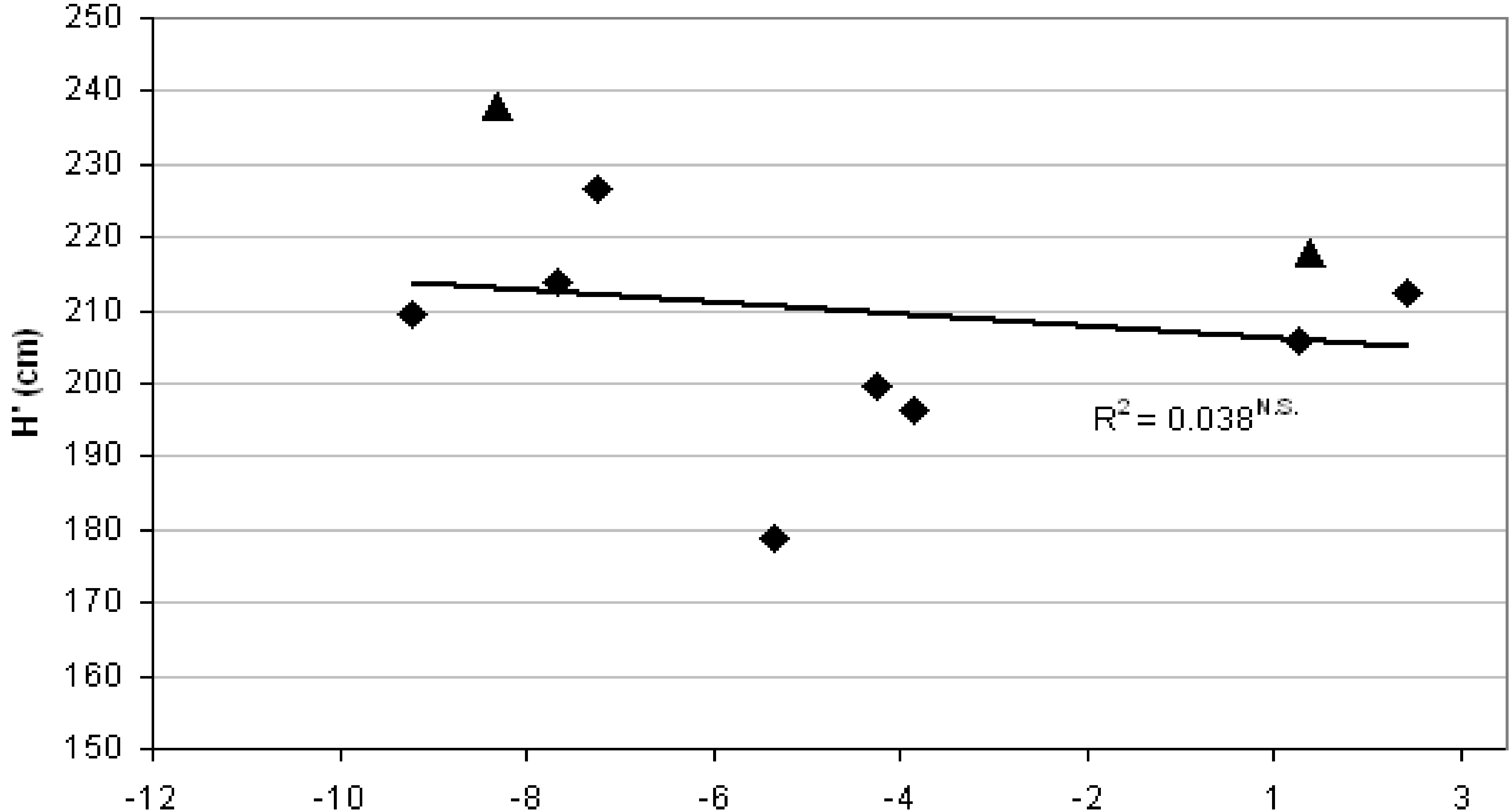

Gramatikovo, BG



Common provenances at SE European test sites

Response of juvenile height growth (*H'*) of beech to changed climate at the humid cool site Straza, SLO (*EQ:* 15.3)

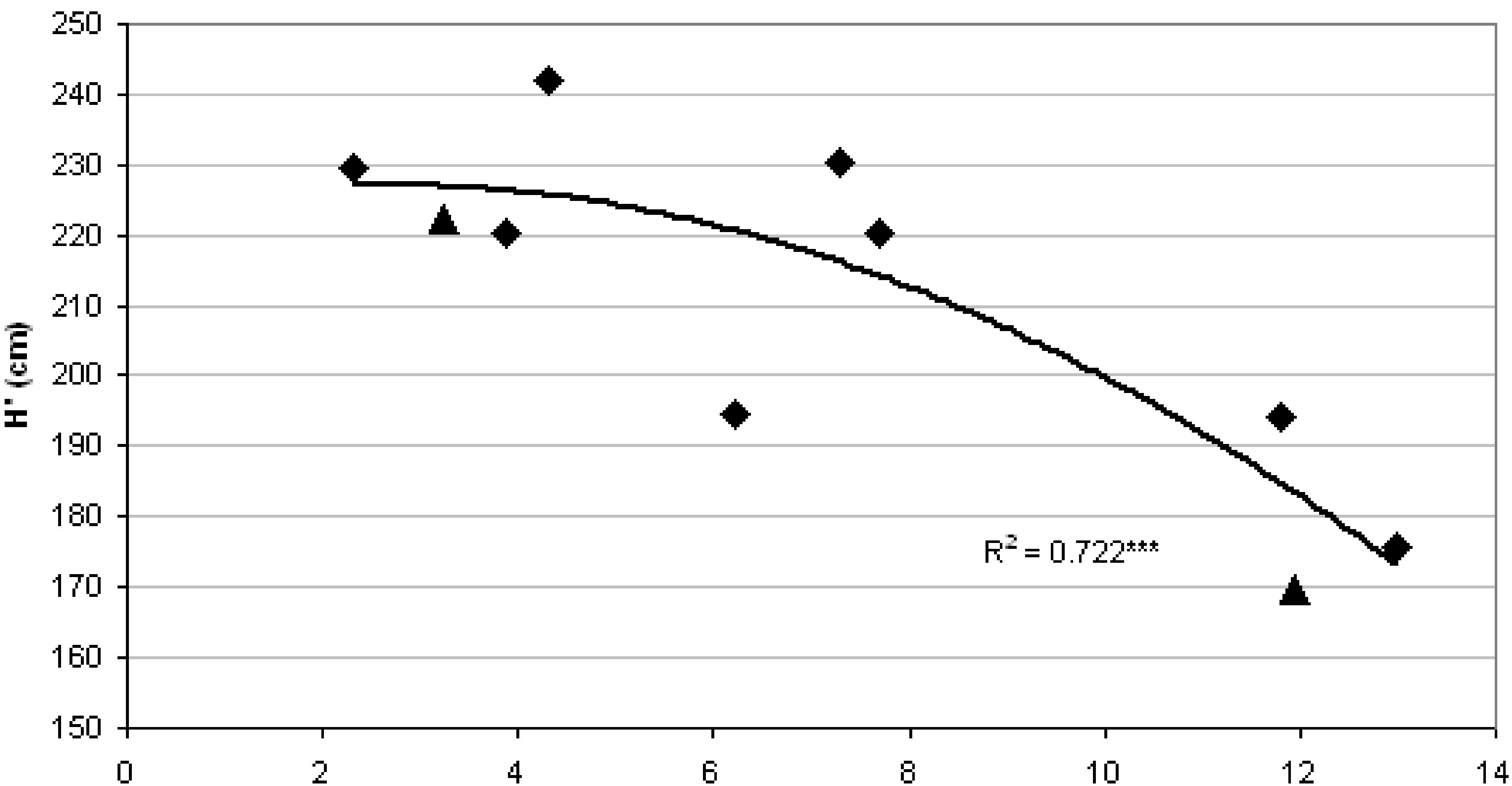
▲ interaction: Tarnawa (POL, left) and Plateaux (FRA, right).



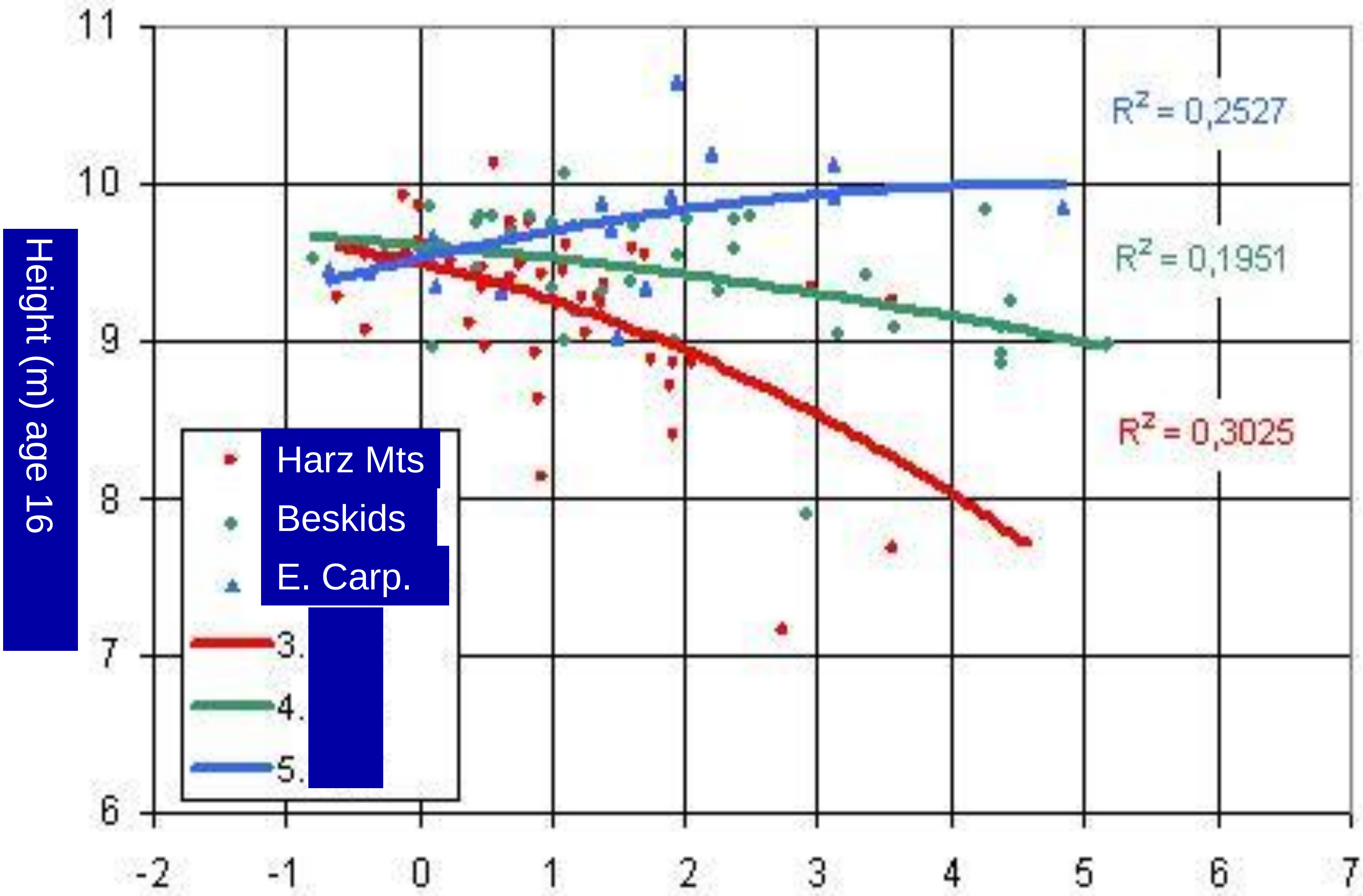
Change of Ellenberg's drought index, unit: Δ Cº/mm

Response of juvenile height growth (*H'*) of beech to changed climate at the warm, xeric limit in Bucsuta, H (*EQ:* 26.3)

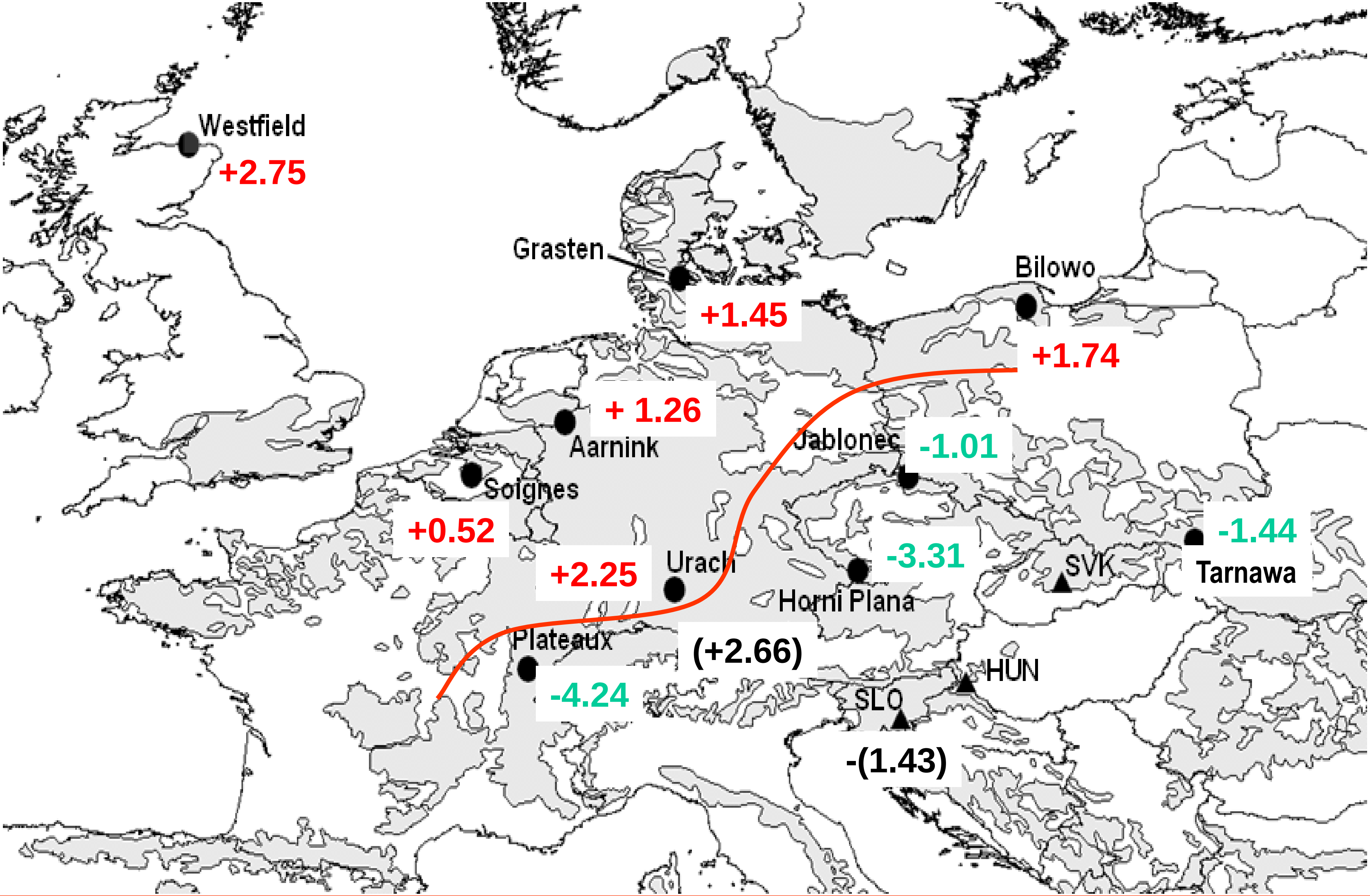
▲ interaction: Tarnawa (POL, left) and Plateaux (FRA, right).



Change of Ellenberg's drought index, unit: Δ Cº/mm

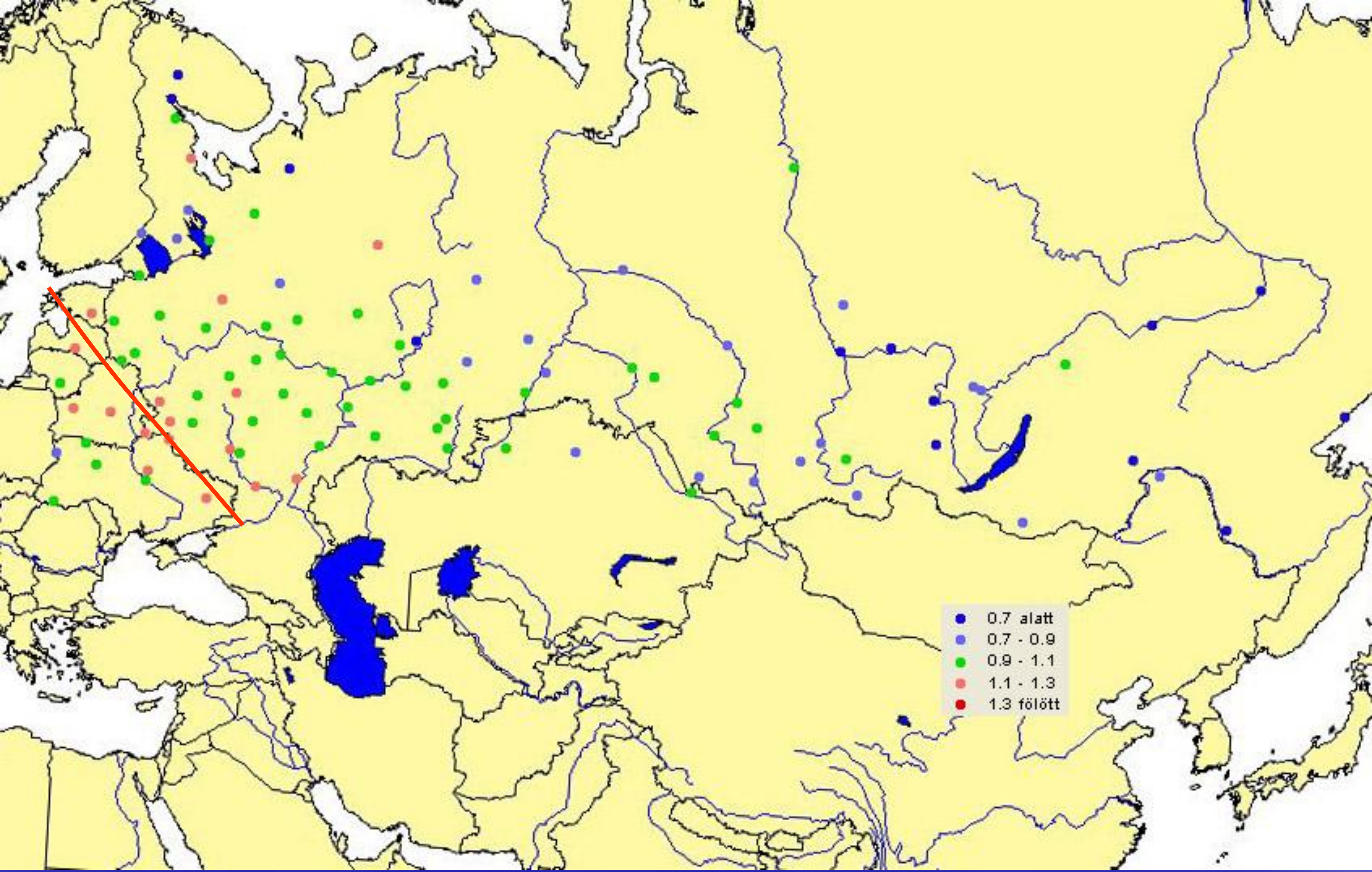


Height age 16 versus change of annual temp. change in plasticity differences in the IUFRO Norwa spuce trial (data É. Ujvari-Jarmai)

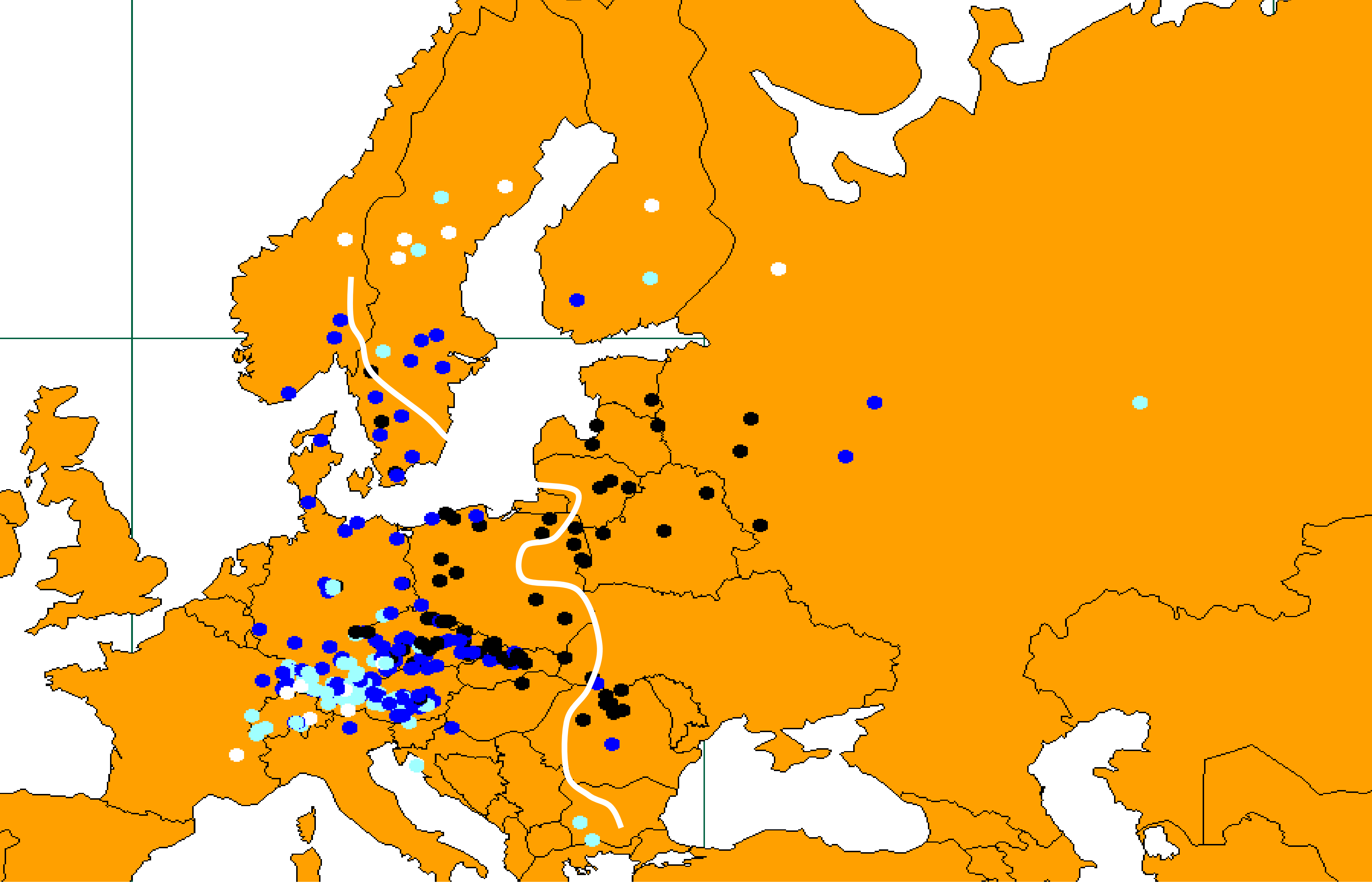


Response regression slopes indicating phenotypic plasticity

Juvenile beech populations tested in SE Europe (SVK, HUN, SLO)



Responsiveness (plasticity) of Scots pine provenances in Russian tests
(trait. juvenile height: L. Nagy unpubl.)



Responsiveness of Norway spruce in 5 IUFRO trials

Relative performance: black 100-120%, blue 90-100%, light blue 80-90%, white: 50-80% (Mátyás, Ujvári unpubl.)

Evolutionary optimisation thru **adaptive disequilibrium**

Paradigm of non-equilibrium state of ecosystems

valid also at the genetic level of adaptation to the (climatic) environment

- (genetic) selection and phenotypic plasticity are acting jointly,
- plasticity counterbalances the effect of natural selection= adaptation lag,
- "perfectly adapted": in reality under constant strain = better performance in more favourable environments.

Silviculture: adaptive optimization implicitely assumed:

- **Basic dogma of FRM use**

Consequences of adaptive non-equilibrium

Corollaries

"Decoupling" of local populations? →fitness loss and extinction risk across the whole range following fast changes?

- Reality: depend on location, may lead even to growth acceleration

Prediction models: → assume equilibrium

- models predict responses too pessimistic
- the genetic/physiological possibilities for persistence are not instantly exhausted under changing conditions

Revision of principles of FRM use necessary

Caveats: conclusions based on juvenile test responses!


Conclusions

General (descriptive) result of tests

- Differences between populations in all traits confirmed…
- Although effect of climate traceable, adaptability is broad,
- Between-population differences in phenotypic plasticity,
- Local is not necessarily best,
- Differences between species in adaptation pattern

not particularly exciting …

Predictive results

- **Macroclimatic adaptation + (simulated) climatic change** explains a significant part of response
- Response depends on change direction and limiting factors: **predictable**
- **Plasticity: a key factor in adaptation to fast climate change!**
- Natural populations not in adaptive optimum;
- Plasticity seems to be linked to climate selection: plastic zones?
- Extreme conditions → genetic depletion: special management needed

Prediction of growth response (considering only macroclimate)

Growth response depends on

- **macroclimatic adaptation** (at origin),
- the climatic **environment** where the population is growing/tested
- **climatic distance** of change,
  respectively: by which the population was moved
- **plasticity!**

Plasticity:

Role of plasticity in adaptation and speciation

- selection effects buffered
- acts for stasis of species, against isolation, speciation
- Result: local genetic inequilibrium

Questions directly related to FRM use:

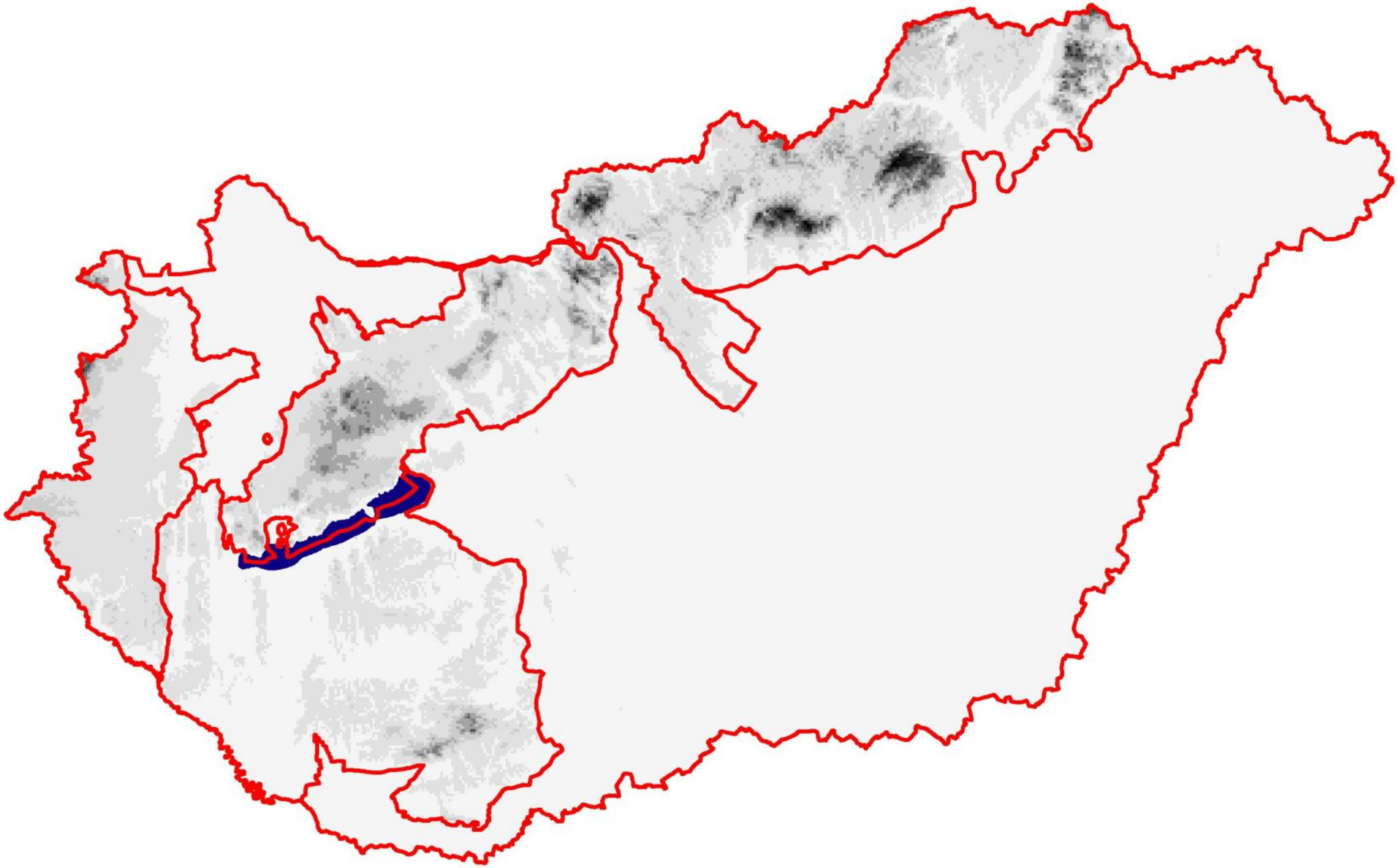
Value of autochthonity?

Width of plasticity?

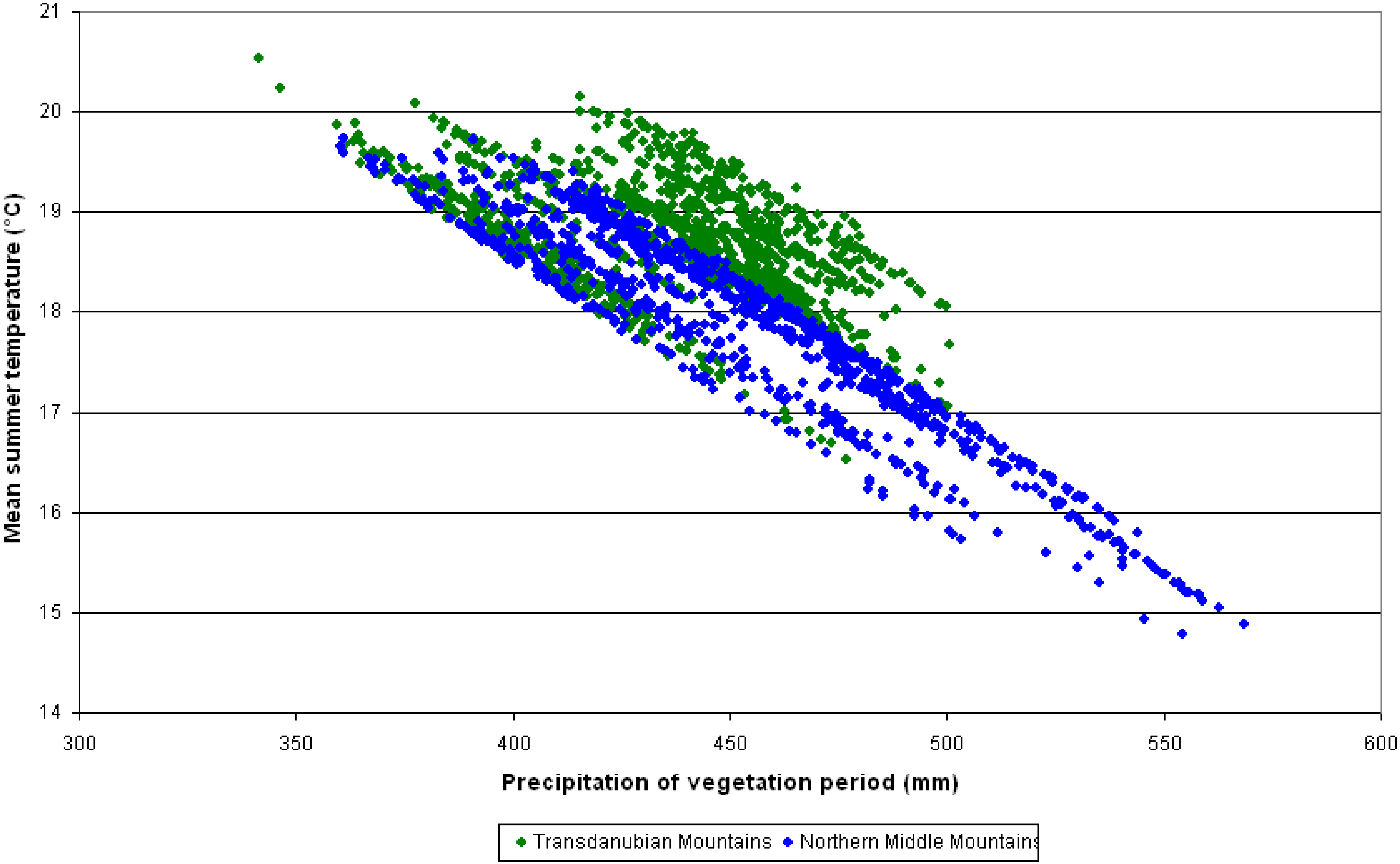
Speed of acclimation?

Unresolved: epigenetics??

Beech seed zones, Hungary



Climatic niche of beech stands in two seed zones in Hungary



Populations at the extremes

1.Effectivity of selection at extremes:

Severe selection depletes→plasticity loss

Effect may be very fast

2. Rethinking of forest management rules

Seed zones: pops at margins resemble each other better than geogr. adjacent ones

Special rules for exposed regions?

3. Conservation / management strategy

Marginal populations less valuable?

Spontaneous processes disrupted: interference unavoidable


Consequences, FRM use

Consequences for deployment of reproductive material

FRM policy: risk minimalization - ecology first

- leave more room for selection: plant higher numbers, prefer seeding, etc.
- reinterpretation of autochthony principle
- Preference for plastic, adaptable populations
- provenance regions to be redrawn – at least for extreme zones? (for optimum, northern: less urgent)
- novel bases for prop. material
- evacuation of threatened gene pools
- FRM serves „human supported migration"

Conclusions, FRM transfers

- apply ecological criteria instead of geographic-based ones to define recommended directions and limits of transfer;
- transfer effects are not similar in different part of the distribution area, in particular:
- in the range of the climatic optimum, in the area centre, and towards the thermal limit (north- upward) transfers are less critical;
- in (macro)climatical sense, local superiority is mostly not valid;

Conclusions: differentiated use of FRM

- individual („ecotypic") differentiation of pops in growth and plasticity, further support the use of selected sources, (seed) stands;

Reconsidering seed zones

- proposed separate treatment of higher elevation populations is supported by the deviating behaviour of provenances from above 1000m;
- stressful and uncertain conditions at the lower (xeric) limit of the species: more rigorous rules for use and conservation;

Again: seed zones and epigenetics???

General policy recommendations

- Concept of adaptation and appropriate use of FRM to be incorporated in **national forest strategies**
- Flexible pan-European guidelines to be developed
- Orienting research in adaptive response **(further field tests with specified aims)**

Priorities

- threatened extreme limit populations (mostly south-continental, mediterranean)
- phenotypically plastic populations
- rare species at xeric tolerance limit

Common plan of action

- crossborder collaboration
- sharing of responsibilities

References

- Mátyás C., Nagy L., Ujvari-Jármai É., 2008. Genetic background of response of trees to aridification at the xeric forest limit. In: Strelcova, Matyas *et al.*(eds.): Bioclimate and natural hazards, 2008, Springer
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End of (spontaneous) evolution?

Why human interference is indispensable

- Changes too fast!
- Human-dominated landscapes : slow or missing spontaneous adjustment
- Genetic adaptation unreliable
- Natural processes constrained at (lower) ecological limits (flowering, regeneration)
- ***SE continental Europe especially threatened***

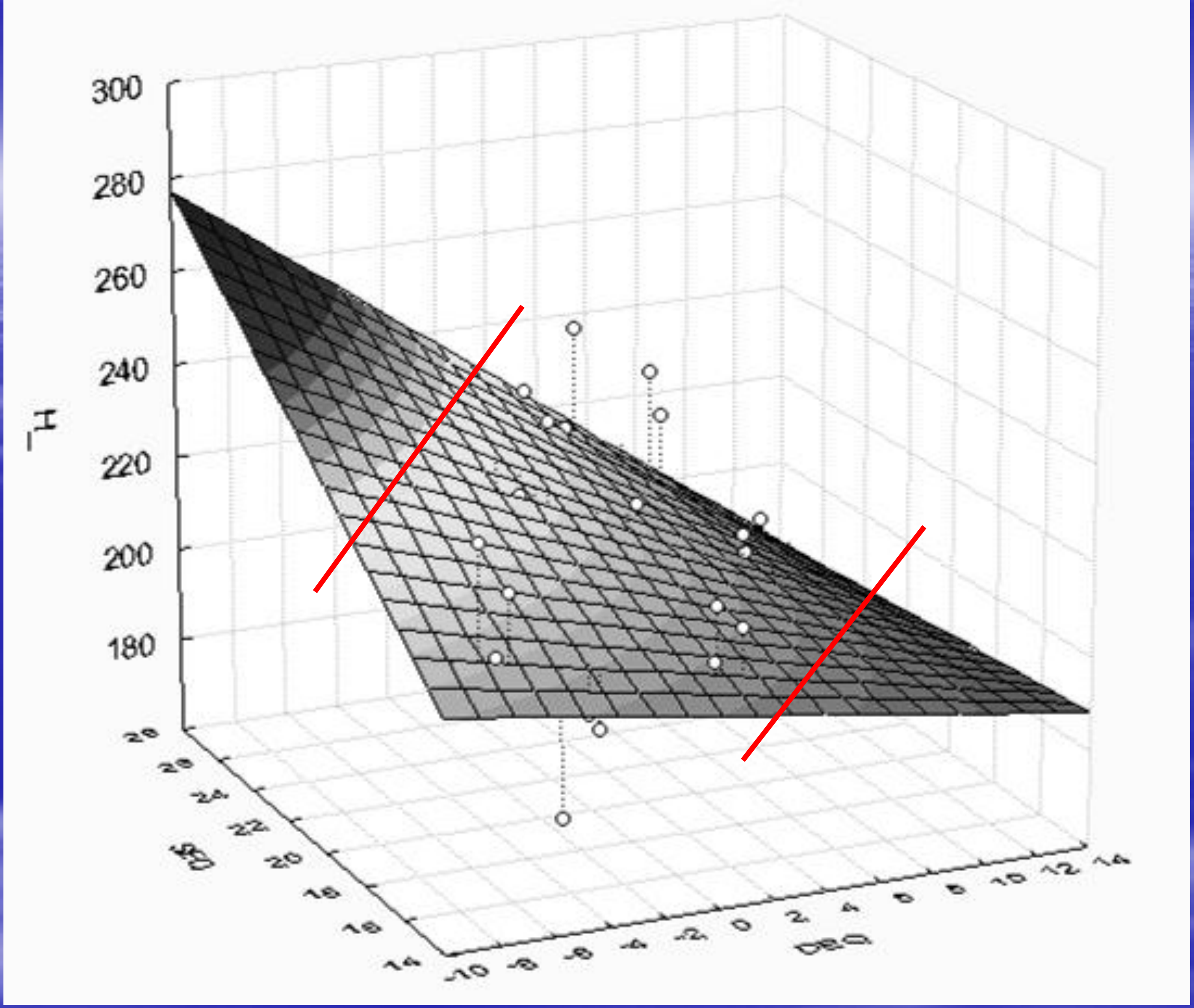
Method

Ecodistance approach:

Phenotypic response to climate depends:

- on the **climatic conditions** where the population is actually grown or tested, and
- on the **ecodistance of transfer**, i.e. on the magnitude and direction of environmental change experienced due to the transplanting to the test site

Selected variable: of ecological (not geographical!) relevance



Height response: thermic vs xeric limit

corrected height (*H'*) vs. climatic shift in EQ (*DEQ,* right) and test site climate in *EQ* (*SEQ, left)*

Width of plasticity / Autochthony:

Importance of autochtony determined by:

- Species level: genetic system and distributional pattern of species
- Within species: local selection pressure, local level of plasticity
- Planting site: severity of selection on site; ecological risks and constraints
- Genetic quality of population (human effects) and surrounding stands
- Policy level: priority of production vs conservation

How will trees respond *within a generation?*

- **How much climatic (site) change is tolerated?**
- Are available genetic resources sufficient?
- Speed of adaptation/evolution?
- Limits to genetic adjustment?
- Acting of natural (spontaneous) evolution?

In forestry/conservation practice:

- **Which populations to plant, where?**
- **How to conserve, what?**

Genetic reactivity of Norway spruce to climate change based on experimental results from IPTNS-IUFRO 1964/68 test in Poland

Prof. dr hab. Janusz Sabor

Department of Forest Tree Breeding
Faculty of Forestry, Agricultural University
Kraków

Treebreedex Activity 5 seminar
June 22-24.2010, Sękocin Stary (Poland)

Tuesday, 19th September 2006

Janusz Sabor, prof.. dr hab.

Organization:

Agricultural University of Cracow, Faculty of Forestry

Department of Forest Trees Breeding

Head

Akademia Rolnicza im. Hugona Kollataja w Krakowie

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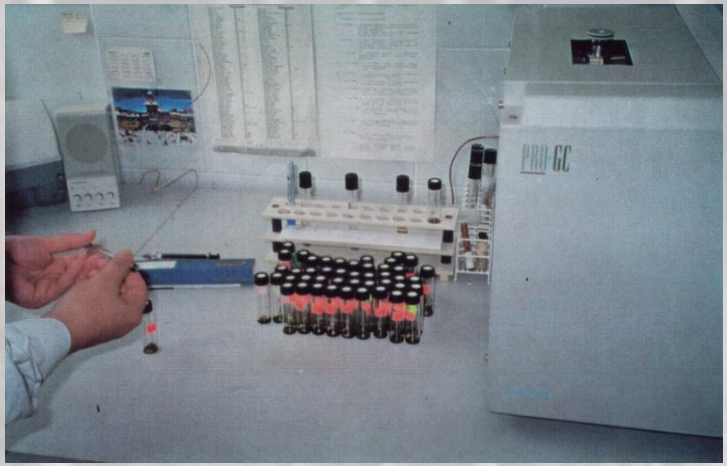
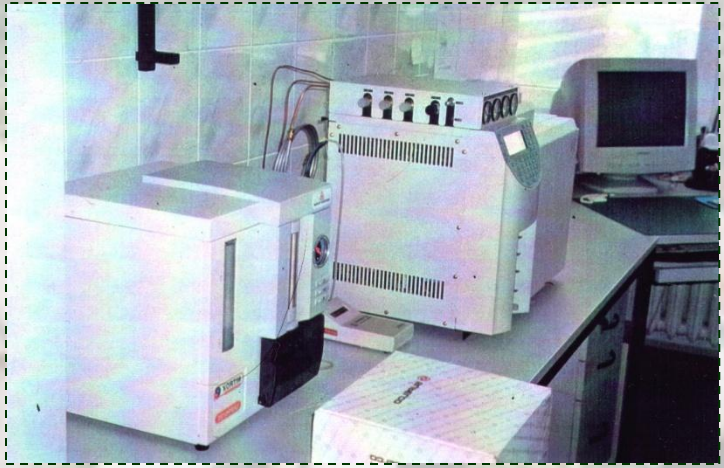




Research interests:

- national progeny test program in Poland and in Europe (specialy for Norway spruce, Silver fir and European beech)
- conservation of gene resources (specialy in the Carpathian Mts.)
- forest reproductive material
- gene markers for provenances of Norway spruce

Genetic reactivity of Norway spruce to climate change based on experimental results from IPTNS-IUFRO 1964/68 test in Poland

IUFRO 1964/68 - History

In 1959 Professor Olaf Langlet from the Stockholm Faculty of Forestry proposed that an international inventory provenance trial of Norway spruce be established. Prof. Langlet offered to establish such a trial. By 1964 Langlet already collected 1614 seed samples and an extensive international interest in the experiment developed. Langlet chose from his collection 1300 seed lots and these were sown in a nursery of the Institut für Forstgenetik in Schmalenbeck near Hamburg under the control of Professors Wolfgang Langner and Klaus Stern. In 1966 the seedlings were transplanted to a commercial nursery of Pein & Pein in Halstenbeck, near Hamburg. There, under the supervision of Dr Walter Neugebauer, the seedlings were grown till 1968 when each one was individually supplied with a label and prepared for transport to wherever the experimental areas were to be established. From the Institute at Schmalenbeck this work was co-ordinated by Dr E. Masching. Up to that stage there were no replicates. Finally 1100 populations were qualified for the experiment. For each of the populations there was a sufficient number of transplants needed by co-operators to include them in all of the planned 20 experimental areas. The populations were divided into 11 groups of 100 populations each, with a maximally even representation of the whole range of the species in each group. As a result each group in itself is already an experiment encompassing the whole range of the species. **In all, 20 trial areas were established, 3 in Germany and Sweden, 2 in Belgium and Norway and one each in Austria, Canada, Czech Republic, England, Finland, France, Hungary, Ireland, Poland and Scotland.**

The experimental design was proposed by Prof. Klaus Stern. As a result the experiment includes 1100 populations each represented by 25 trees on each trial area, treated as single-tree plots. Since each of the 11 groups of populations covers the whole range of spruce, it was assumed that blocks with populations from different groups would have similar means and variances. No 2.02.11 Norway Spruce Provenances, under the leadership of Jon Dietrichson and Peter Krutzsch, which took over responsibility for the international co-ordination of efforts pertaining to the 1964/68 experiment.

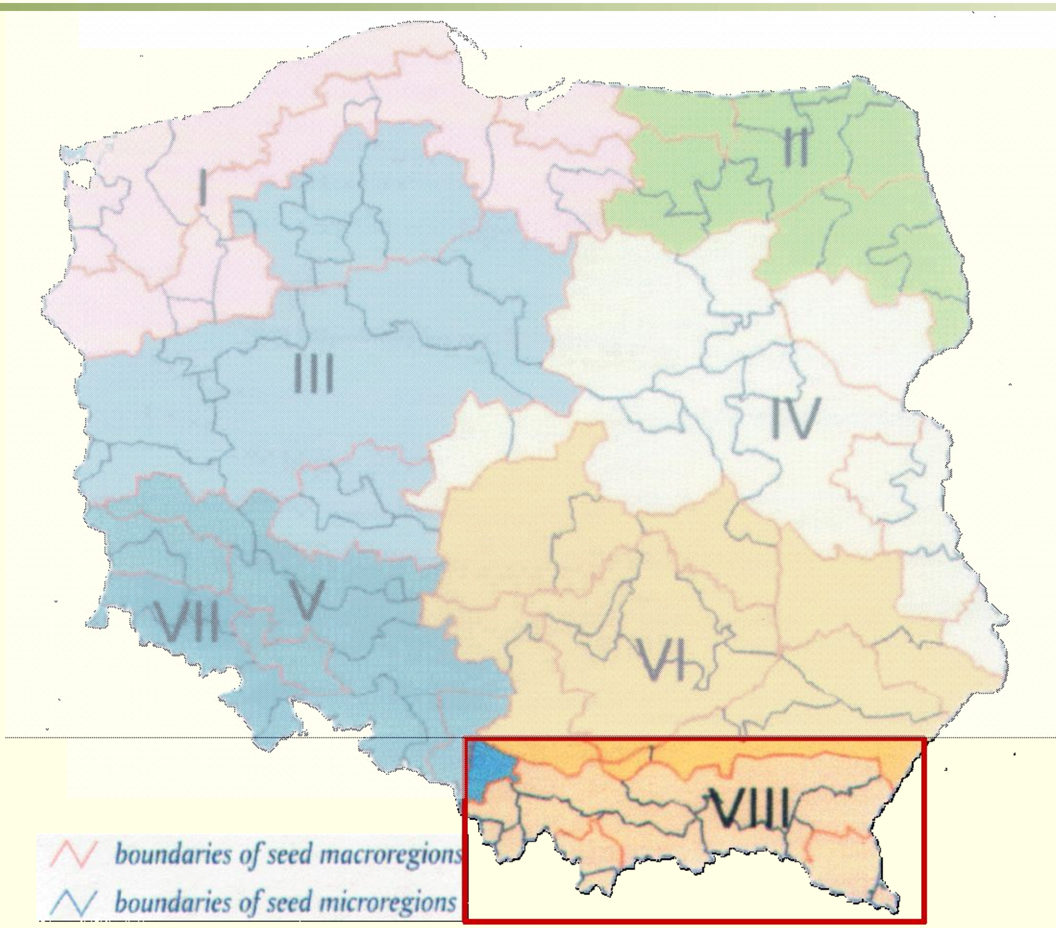
The Polish trial area was established by Prof. Stanisław Bałut in the Experimental Forest of the Cracow Agricultural University in Krynica.

The trial has a full set of 1096 provenances. It is the most elevated planting site (750 m) for the whole experiment. The experiment covers provenances from the natural range of the species and from the area where spruce was introduced by man. Poland is represented by 92 provenances. Among all the provenances considered, 528 have a strictly defined (accurate to a stand) location, so they can be reproduced and used in practice. The material is thus representative of the whole Picea abies species to the degree that has no parallel in any previous research.

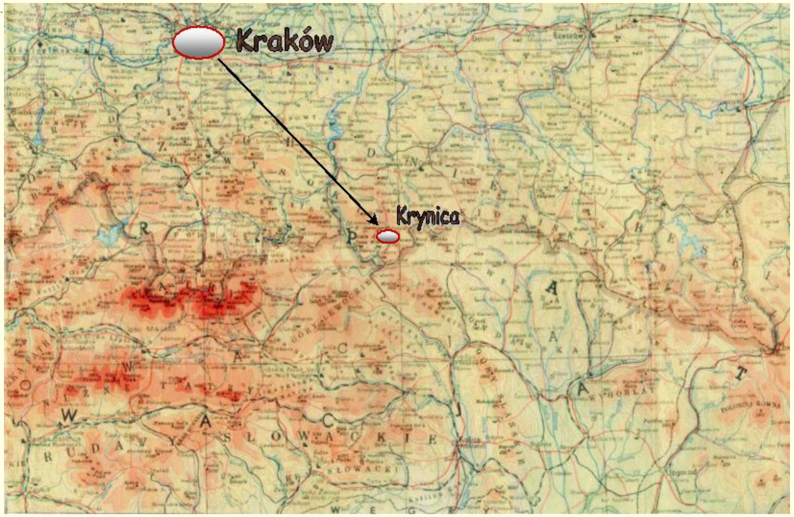
To avoid the effect of crown closure for as long as possible, a 2 × 2 m spacing was employed. As a result each block covers 1 ha. The specimens representing individual provenances are randomly distributed over the block area.

(prof. M. Giertych)

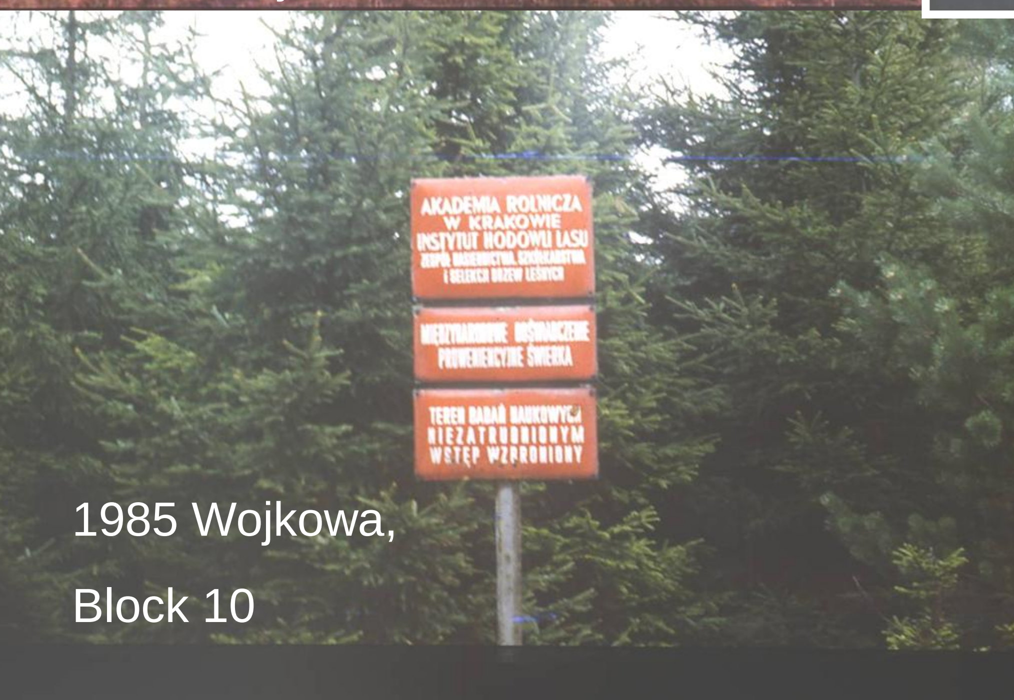
Division of Poland into seed regions againt the backround of natural-forest regions (I-VIII)



I. Baltic natural forest region
II. Mazury-Podlasie region
III. Great-Pomeranian region
IV. Mazowsze-Podlasie region
V. Silesian region
VI. Region central Polish
VII. Sudeten region
VIII. Carpathian region



1970 Wojkowa, Block 02



1985 Wojkowa,

Block 10

Location of blocks of the international provenance test of Norway spruce (area No 19 Poland). Krynica Experimental Forest Station

Forest Range	Block No	Geographical coordinates		Altitude (m)
		Longitude	Latitude	
Kopciowa	05	21°01'	49°28'	705
Wojkowa	02	20°58'	49°21'	795

Records from 1956–1965 (after Baliński, 1974)

Attitude	Average of temerature in year [°C]	Percipation [mm]	Period wit average tejmperature above 5°C	Snow covering period [date]	Period without frosts [days]	Period of snow covering in year [days]
800	*4,3*	*1000*	*179*	*2.XI – 15.IV*	*170*	*120*

Records from 1969–1988. Data base for belt 600 a 850 m abave sea level (Beskid Sądecki Mts) According to Dep. of Forest Protections and Forest Climatology. Forestry Faculty in Cracow

Years	Temp. Average (°C)	St. deviation	Precipitation (Mm)	St. deviation	Wegetation (days above 5°C)	Snow covering Days
1969	4,9	7,0	990	49	190	128
1972	5,6	6,9	885	55	180	85
1975	5,9	7,3	1020	45	187	126
1978	4,2	6,9	1190	55	181	124
1983	6,1	7,7	1175	57	198	134
1988	5,3	7,6	1117	53	184	133

Investigations

Investigations

Investigations:

Height in age 6, 9, 12, 15, 20, 25 (1969, 1972, 1975, 1978, 1983 and 1988)

The observations and measurements of the tree height were carried out in 11 blocks of the IPTNS-IUFRO test 1964/68 in Krynica. Each block contained 100 provenances of 25 young trees each on average. The measurements were carried out in the years 1969, 1972, 1975, 1978, 1983 and 1988.

The mean heights in blocks, locations and years were converted into values expressed in units of the standard deviation for the given year and block.

Methods of statistical analysis

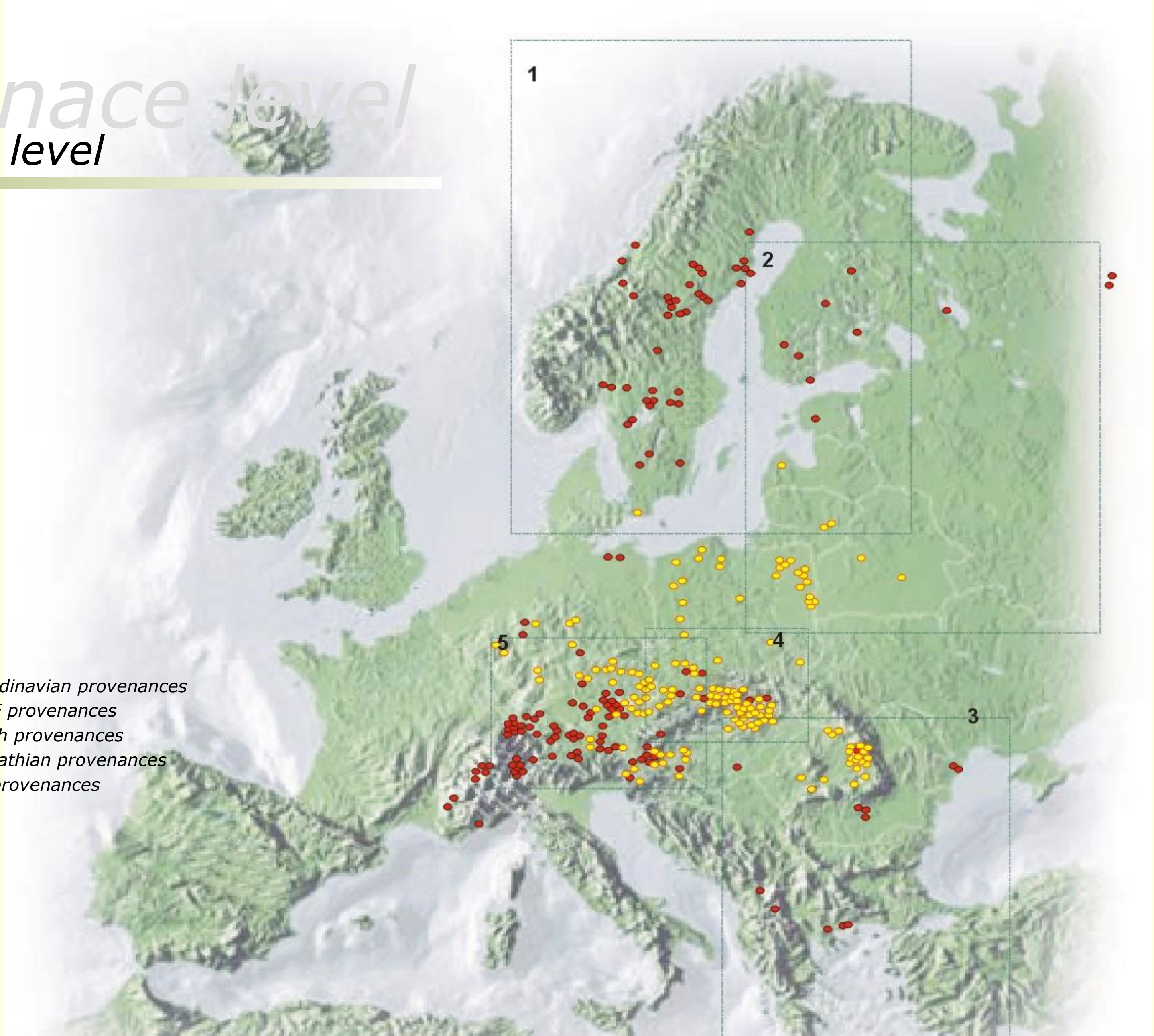
In evaluating the variability between the regions and between the years analysis of variance was applied with repetitions.

Cluster analysis with Euclidean distance was used for grouping similar regions.

The calculations were carried out in the STATISTICA software package.

Provenace level

Provenance level



REGIONS:

1 – Scandinavian provenances
2 – N-NE provenances
3 – South provenances
4 – Carpathian provenances
5 – Alp provenances

Distribution of Norway spruce provenances with high and short tree height (based on measurments of 1978, tree age 15 years)
Provenance test of Norway spruce IPTNS – IUFRO 1964/68 in Krynica

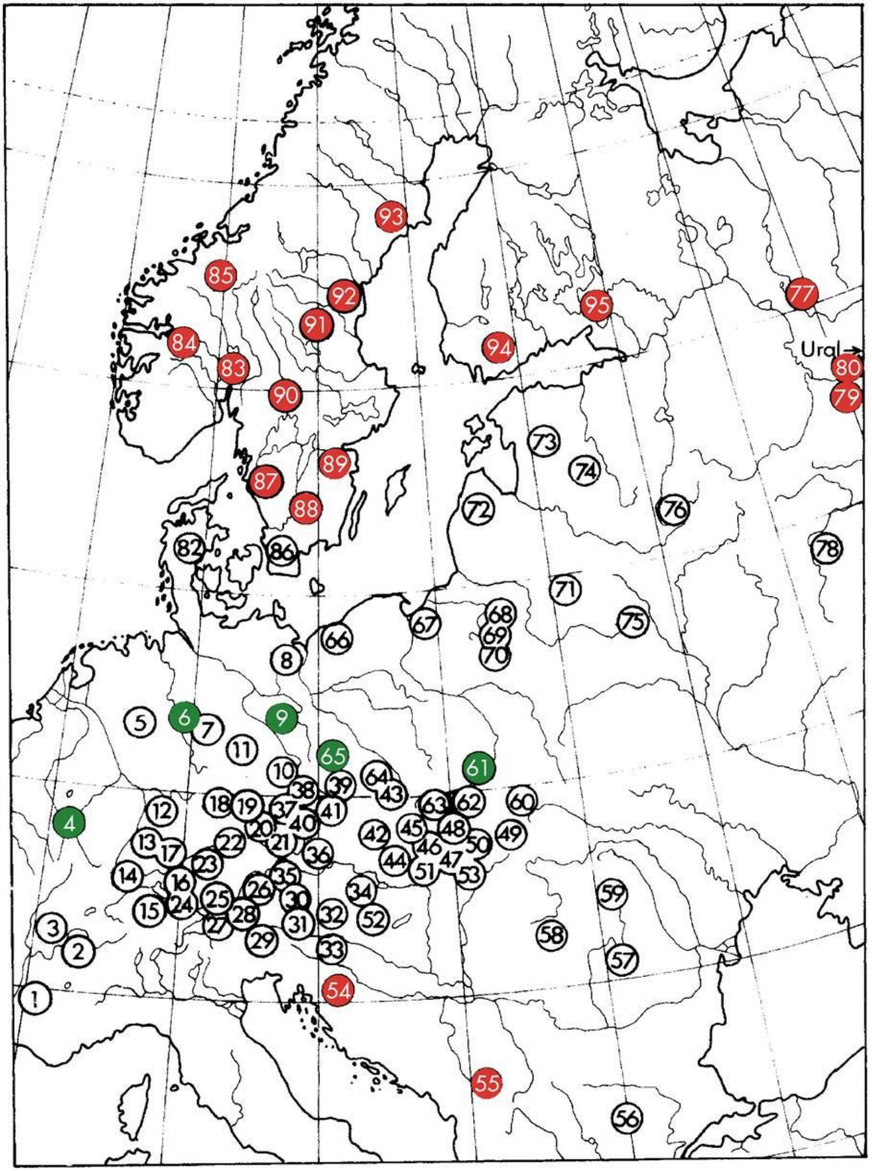
Differentation of average height of spruce provenances in relationship with attitude. (IPTNS-IUFRO 1964-68)

<table>
<tr><th rowspan="2">Altitude</th><th colspan="3">Mean height in unit of standard deviation. Age 25 years</th></tr>
<tr><th>100 m</th><th>200 m</th><th>300 m</th></tr>
<tr><td>Powyżej 1700</td><td>-</td><td rowspan="2">-0,87</td><td rowspan="2">-0,95</td></tr>
<tr><td>1601-1700</td><td>-0,87</td></tr>
<tr><td>1501-1600</td><td>-1,04</td><td rowspan="2">-0,32</td><td>-0,95</td></tr>
<tr><td>1401-1500</td><td>-0,29</td><td>-0,34</td></tr>
<tr><td>1301-1400</td><td>-0,55</td><td rowspan="2">-0,36</td><td rowspan="2">-0,34</td></tr>
<tr><td>1201-1300</td><td>-0,17</td></tr>
<tr><td>1101-1200</td><td>-0,29</td><td rowspan="2">-0,20</td><td rowspan="2">-0,09</td></tr>
<tr><td>1001-1100</td><td>-0,07</td></tr>
<tr><td>901-1000</td><td>0,10</td><td rowspan="2">0,14</td><td>-0,09</td></tr>
<tr><td>801-900</td><td>0,20</td><td>0,23</td></tr>
<tr><td>701-800</td><td>0,04</td><td rowspan="2">0,24</td><td rowspan="2">0,23</td></tr>
<tr><td>601-700</td><td>0,49</td></tr>
<tr><td>501-600</td><td>0,41</td><td rowspan="2">0,26</td><td rowspan="2">0,19</td></tr>
<tr><td>401-500</td><td>0,15</td></tr>
<tr><td>301-400</td><td>-0,27</td><td rowspan="2">-0,44</td><td>0,19</td></tr>
<tr><td>201-300</td><td>-0,61</td><td>-0,26</td></tr>
<tr><td>101-200</td><td>-0,14</td><td rowspan="2">-0,21</td><td rowspan="2">-0,26</td></tr>
<tr><td>0-100</td><td>-0,29</td></tr>
</table>

Krutzsch regions level

Location of provenance regions of Krutzsch (1–95) after Schmidt-Vogt (1977)
Mean height of Norway spruce provenances in different years of observation.
Height is given in units of standard deviation from the block mean, IPTNS-IUFRO 1964/68, Krynica 1969

Age 6 years



$\overline{H}_{1969} \leq \bar{x} - 1S$ (red) $\overline{H}_{1969} \geq \bar{x} + 1S$ (green)

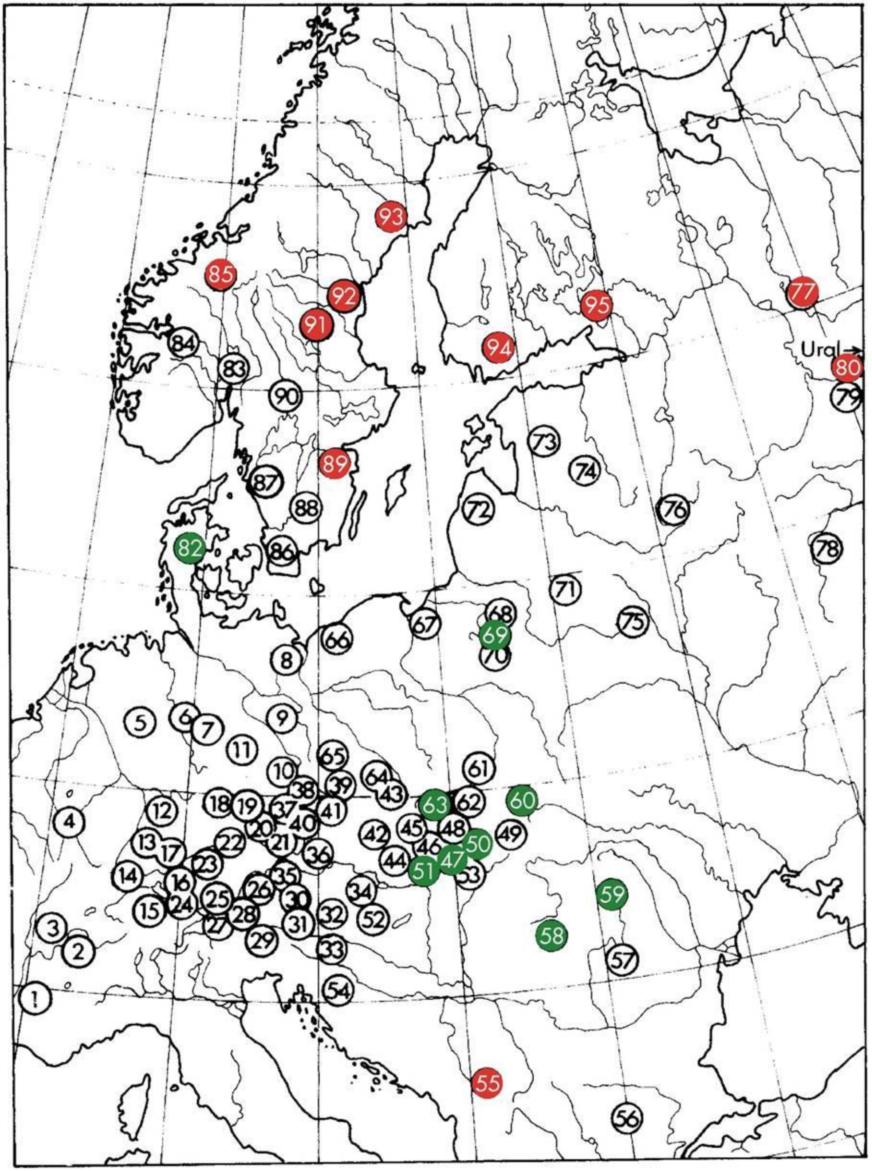
No	Provenance	1969
1	Massif Central, Dauphine; France	0.86
2	West Alps: France	-0.58
3	Jura; France	-0.07
4	Ardennes, Vosges, Eifel; Belgium, France, Germany	1.04
5	Rheinisches Schiefergebirge, Hessian, Foothills; Germany	0.59
6	Harz Mts 1; Germany	1.30
7	Harz Mts 2 (Westerhof); Germany	0.52
8	Mecklenburg Lakeland, Schwerin, Rostock; Germany	0.18
9	Lausitz; Germany	1.18
10	Erzgebirge; Czech Republic	0.11
11	Thuringerwald; Germany	0.09
12	Odenwald; Germany	0.76
13	Schwarzwald (Baden-Wurttemberg); Germany	0.26
14	Breisgau; Germany	-0.28
15	West (Lepontine) Alps; Switzerland	-0.51
16	Swabian Upland (Wurttemberg); Germany	0.19
17	Swabian Jura; Germany	0.49
18	Franconian Jury; Germany	0.93
19	Franconia, Upper Palatinate; Germany	0.83
20	Bavarian Forest; Germany	-0.11
21	Bohemian Forest; Czech Republik, Germany	-0.10
22	Swabian-Bavarian Upland (Bavaria) 1; Germany	0.92
23	Swabian-Bavarian Upland (Swabia) 2; Germany	0.67
24	Swabian-Bavarian Upland (Swabia) 3; Germany	0.04
25	Bavarian Alps; Germany	-0.28
26	East Alps; Germany	0.15
27	Tyrol; Austria	-0.15
28	Tyrol-Salzburg; Austria	0.17
29	East Alps; Italy	-0.27
30	Niedrige Tauern, Styria; Austria	0.20
31	Carinthia-Styria; Austria	0.07
32	Styria (N-E) 1; Austria	0.11
33	Styria (S-E) 2; Austria	0.49
34	Styria (E) 3; Austria	-0.10
35	Upper Austria; Austria	0.12
36	Bohemian Upland, Lower Austria; Czech Republic, Austria	0.69
37	West Bohemia; Czech Republic	0.63
38	Central Bohemia; Czech Republic	0.42
39	Sudetes (Krkonose, Tafelgebirge); Czech Republic	-0.03
40	South Bohemia; Czech Republic	0.73
41	Bohemia; Czech Republic	0.53
42	South Bohemia, Moravia; Czech Republic	0.41
43	Moravia 1; Czech Republic	0.74
44	Moravia 2; Czech Republic	0.40
45	Moravia 3; Czech Republic	0.20
46	Velka Fatra, Mala Fatra, Slovakia	0.85
47	Nizke Tatry; Slovakia	0.19
48	Tatras; Slovakia, Poland	-0.62

No	Provenance	1969
49	East Slovakia (Spis); Slovakia	0.44
50	Slovenske Rudohorie; Slovakia	0.19
51	Stiavnicke Pohorie; Slovakia	0.73
52	West Hungary; Hungary	0.14
53	North Hungary; Hungary	-0.81
54	Dalmatia; Croatia	-1.01
55	Montenegro; Yugoslavia	-1.44
56	Rhodope Mts; Bulgaria	-0.75
57	Southern Carpathians, Transylvanian Upland; Romania	-0.66
58	Bihor Mts,Transylvanian; Romania	0.12
59	East Carpathians; Romania	-0.12
60	East Beskids (Tarnawa); Poland	0.21
61	Little Poland Upland; Poland	1.16
62	Babia Góra, Beskid Sądecki; Poland	0.25
63	Beskid Śląski, Beskid Żywiecki;Poland	-0.10
64	Kłodzko Valley; Poland	0.59
65	Silesian Lowland, Great poland Lowland; Poland	1.31
66	West-Pomeranian Lakeland; Poland	0.46
67	East-Pomeranian Lakeland, Warmia, Masuria; Poland	0.24
68	Masurian Lakeland; Poland	0.29
69	Augustów Lakeland, Podlasie; Poland	0.49
70	Białowieża Primeval Forerst; Poland	-0.14
71	Vilnius Lakeland, Belarus Lakeland; Lithuania, Belarus	-0.13
72	Latvia, Estonia, 1	-0.70
73	Latvia, Estonia, 2	-0.54
74	Latvia, Estonia, 3	-0.69
75	Belarus	-0.25
76	East Russia (Valdai Hills); Russia	-0.91
77	Russia 1	-1.78
78	Russia 2 (Central Russian Upland, Smolensk-Moscow Heights)	-0.55
79	Udmurtsk (Upper Kama Upland); Russia	-1.52
80	West Siberia; Russia	-1.63
81	Knusk; Russia	0.23
82	Jutland,(Denmark)	0.32
83	Bogstad (Ostland); Norway	-1.18
84	S-E Norway; Norway	-1.67
85	Central Norway; Norway	-2.13
86	Scania; Sweden	-0.68
87	Gotland, Smaland (S-E Sweden); Sweden	-1.18
88	Gotland; Sweden	-1.42
89	Sondermanland (S-E Sweden); Sweden	-1.53
90	Central Sweden; Sweden	-1.47
91	Norrland; Sweden	-1.72
92	Madelpad, Angermanland; Sweden	-2.26
93	S-E Sweden Cost; Sweden	-2.38
94	South Finland; Finland	-1.35
95	Karelian; Finland, Russia	-1.99
96	Hudson, Ontario; Canada	0.20

Krutzsch regions level

Location of provenance regions of Krutzsch (1–95) after Schmidt-Vogt (1977)
Mean height of Norway spruce provenances in different years of observation.
Height is given in units of standard deviation from the block mean, IPTNS-IUFRO 1964/68, Krynica 1978

Age 15 years



No	Provenance	1978
1	Massif Central, Dauphine; France	-0.70
2	West Alps: France	-0.78
3	Jura; France	-0.48
4	Ardennes, Vosges, Eifel; Belgium, France, Germany	0.64
5	Rheinisches Schiefergebirge, Hessian, Foothills; Germany	-0.06
6	Harz Mts 1; Germany	0.16
7	Harz Mts 2 (Westerhof); Germany	0.16
8	Mecklenburg Lakeland, Schwerin, Rostock; Germany	-0.57
9	Lausitz; Germany	0.04
10	Erzgebirge; Czech Republic	0.57
11	Thuringerwald; Germany	-0.09
12	Odenwald; Germany	0.17
13	Schwarzwald (Baden-Wurttemberg); Germany	-0.36
14	Breisgau; Germany	-0.74
15	West (Lepontine) Alps; Switzerland	-0.77
16	Swabian Upland (Wurttemberg); Germany	-0.27
17	Swabian Jura; Germany	-0.26
18	Franconian Jury; Germany	0.22
19	Franconia, Upper Palatinate; Germany	0.66
20	Bavarian Forest; Germany	-0.15
21	Bohemian Forest; Czech Republik, Germany	-0.35
22	Swabian-Bavarian Upland (Bavaria) 1; Germany	-0.24
23	Swabian-Bavarian Upland (Swabia) 2; Germany	-0.19
24	Swabian-Bavarian Upland (Swabia) 3; Germany	-0.26
25	Bavarian Alps; Germany	-0.20
26	East Alps; Germany	0.02
27	Tyrol; Austria	-0.64
28	Tyrol-Salzburg; Austria	-0.19
29	East Alps; Italy	-0.30
30	Niedrige Tauern, Styria; Austria	-0.08
31	Carinthia-Styria; Austria	-0.09
32	Styria (N-E) 1; Austria	-0.01
33	Styria (S-E) 2; Austria	0.39
34	Styria (E) 3; Austria	-0.39
35	Upper Austria; Austria	-0.49
36	Bohemian Upland, Lower Austria; Czech Republic, Austria	0.40
37	West Bohemia; Czech Republic	0.29
38	Central Bohemia; Czech Republic	0.37
39	Sudetes (Krkonose, Tafelgebirge); Czech Republic	0.70
40	South Bohemia; Czech Republic	0.59
41	Bohemia; Czech Republic	0.73
42	South Bohemia, Moravia; Czech Republic	0.29
43	Moravia 1; Czech Republic	0.63
44	Moravia 2; Czech Republic	0.31
45	Moravia 3; Czech Republic	0.55
46	Velka Fatra, Mala Fatra, Slovakia	0.41
47	Nizke Tatry; Slovakia	1.04
48	Tatras; Slovakia, Poland	0.57

No	Provenance	1978
49	East Slovakia (Spis); Slovakia	0.90
50	Slovenske Rudohorie; Slovakia	1.14
51	Stiavnicke Pohorie; Slovakia	1.36
52	West Hungary; Hungary	0.68
53	North Hungary; Hungary	0.47
54	Dalmatia; Croatia	-0.60
55	Montenegro; Yugoslavia	-1.38
56	Rhodope Mts; Bulgaria	-0.55
57	Southern Carpathians, Transylvanian Upland; Romania	-0.86
58	Bihor Mts, Transylvanian; Romania	1.27
59	East Carpathians; Romania	1.20
60	East Beskids (Tarnawa); Poland	1.50
61	Little Poland Upland; Poland	0.75
62	Babia Góra, Beskid Sądecki; Poland	-0.07
63	Beskid Śląski, Beskid Żywiecki;Poland	1.19
64	Kłodzko Valley; Poland	0.03
65	Silesian Lowland, Great poland Lowland; Poland	0.67
66	West-Pomeranian Lakeland; Poland	0.48
67	East-Pomeranian Lakeland, Warmia, Masuria; Poland	0.44
68	Masurian Lakeland; Poland	0.87
69	Augustów Lakeland, Podlasie; Poland	1.20
70	Białowieża Primeval Forerst; Poland	0.69
71	Vilnius Lakeland, Belarus Lakeland; Lithuania, Belarus	0.59
72	Latvia, Estonia, 1	0.11
73	Latvia, Estonia, 2	-0.17
74	Latvia, Estonia, 3	0.21
75	Belarus	0.88
76	East Russia (Valdai Hills); Russia	-0.05
77	Russia 1	-1.29
78	Russia 2 (Central Russian Upland, Smolensk-Moscow Heights)	-0.32
79	Udmurtsk (Upper Kama Upland); Russia	-0.86
80	West Siberia; Russia	-1.74
81	Knusk; Russia	0.83
82	Jutland,(Denmark)	1.12
83	Bogstad (Ostland); Norway	-0.41
84	S-E Norway; Norway	-0.57
85	Central Norway; Norway	-1.70
86	Scania; Sweden	0.15
87	Gotland, Smaland (S-E Sweden); Sweden	-0.57
88	Gotland; Sweden	-0.65
89	Sondermanland (S-E Sweden); Sweden	-1.21
90	Central Sweden; Sweden	-0.70
91	Norrland; Sweden	-1.88
92	Madelpad, Angermanland; Sweden	-1.73
93	S-E Sweden Cost; Sweden	-2.62
94	South Finland; Finland	-1.17
95	Karelian; Finland, Russia	-1.74
96	Hudson, Ontario; Canada	1.97

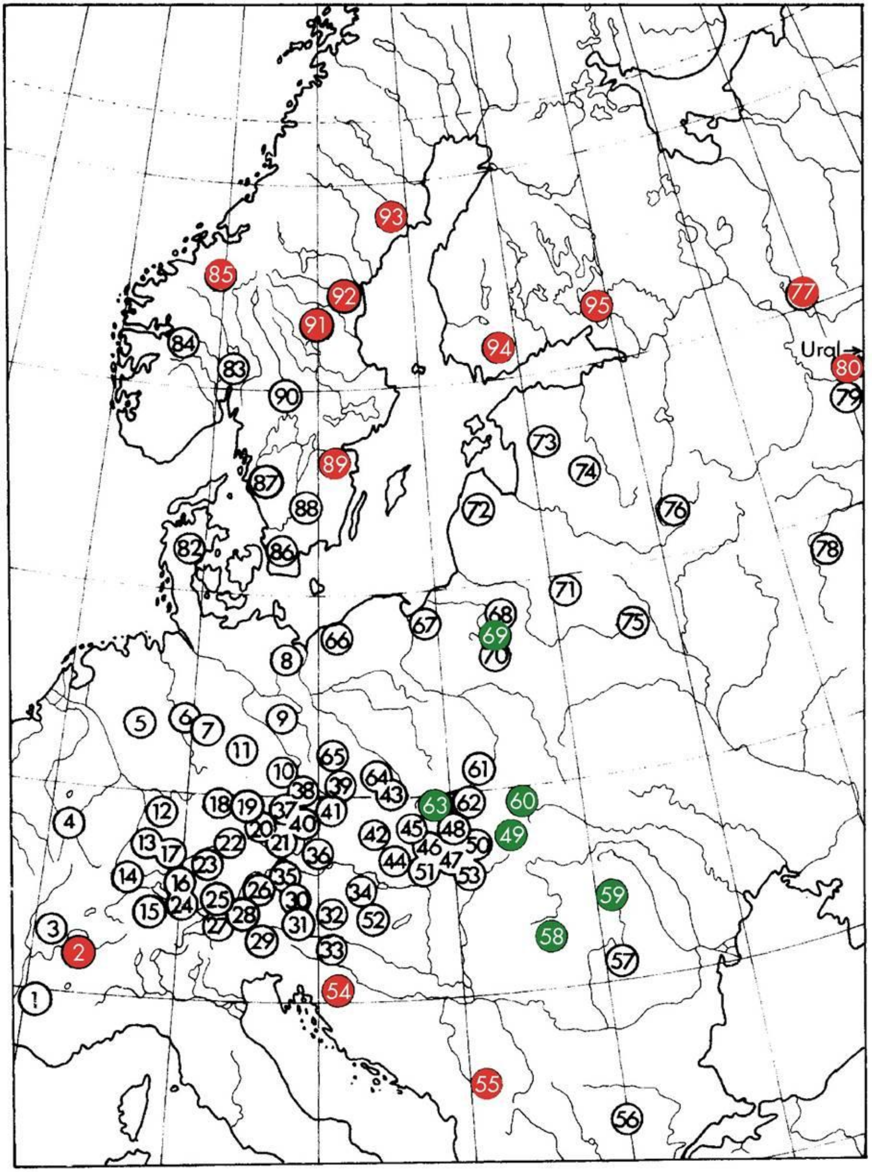
$\overline{H}_{1978} \le \bar{x} - 1S$

$\overline{H}_{1978} \ge \bar{x} + 1S$

Krutzsch regions level

Location of provenance regions of Krutzsch (1–95) after Schmidt-Vogt (1977)
Mean height of Norway spruce provenances in different years of observation.
Height is given in units of standard deviation from the block mean, IPTNS-IUFRO 1964/68, Krynica 1988

Age 25 years



● $\overline{H}_{1988} \le \bar{x} - 1S$ ● $\overline{H}_{1988} \ge \bar{x} + 1S$

No	Provenance	1988
1	Massif Central, Dauphine; France	-0.88
2	West Alps: France	-1.08
3	Jura; France	-0.81
4	Ardennes, Vosges, Eifel; Belgium, France, Germany	0.81
5	Rheinisches Schiefergebirge, Hessian, Foothills; Germany	0.27
6	Harz Mts 1; Germany	0.60
7	Harz Mts 2 (Westerhof); Germany	0.50
8	Mecklenburg Lakeland, Schwerin, Rostock; Germany	-0.12
9	Lausitz; Germany	0.06
10	Erzgebirge; Czech Republic	0.52
11	Thuringerwald; Germany	0.08
12	Odenwald; Germany	0.34
13	Schwarzwald (Baden-Wurttemberg); Germany	-0.30
14	Breisgau; Germany	-0.81
15	West (Lepontine) Alps; Switzerland	-0.88
16	Swabian Upland (Wurttemberg); Germany	-0.18
17	Swabian Jura; Germany	-0.18
18	Franconian Jury; Germany	0.40
19	Franconia, Upper Palatinate; Germany	0.63
20	Bavarian Forest; Germany	0.22
21	Bohemian Forest; Czech Republik, Germany	-0.47
22	Swabian-Bavarian Upland (Bavaria) 1; Germany	-0.15
23	Swabian-Bavarian Upland (Swabia) 2; Germany	-0.08
24	Swabian-Bavarian Upland (Swabia) 3; Germany	-0.11
25	Bavarian Alps; Germany	-0.34
26	East Alps; Germany	0.00
27	Tyrol; Austria	-0.73
28	Tyrol-Salzburg; Austria	-0.08
29	East Alps; Italy	-0.24
30	Niedrige Tauern, Styria; Austria	-0.10
31	Carinthia-Styria; Austria	-0.06
32	Styria (N-E) 1; Austria	0.04
33	Styria (S-E) 2; Austria	0.33
34	Styria (E) 3; Austria	-0.09
35	Upper Austria; Austria	-0.53
36	Bohemian Upland, Lower Austria; Czech Republic, Austria	0.45
37	West Bohemia; Czech Republic	0.62
38	Central Bohemia; Czech Republic	0.30
39	Sudetes (Krkonose, Tafelgebirge); Czech Republic	0.70
40	South Bohemia; Czech Republic	0.36
41	Bohemia; Czech Republic	0.63
42	South Bohemia, Moravia; Czech Republic	0.40
43	Moravia 1; Czech Republic	0.72
44	Moravia 2; Czech Republic	0.53
45	Moravia 3; Czech Republic	0.67
46	Velka Fatra, Mala Fatra, Slovakia	0.65
47	Nizke Tatry; Slovakia	0.96
48	Tatras; Slovakia, Poland	0.51

No	Provenance	1988
49	East Slovakia (Spis); Slovakia	1.11
50	Slovenske Rudohorie; Slovakia	0.92
51	Stiavnicke Pohorie; Slovakia	0.99
52	West Hungary; Hungary	0.75
53	North Hungary; Hungary	0.13
54	Dalmatia; Croatia	-1.01
55	Montenegro; Yugoslavia	-1.83
56	Rhodope Mts; Bulgaria	-0.79
57	Southern Carpathians, Transylvanian Upland; Romania	-0.60
58	Bihor Mts,Transylvanian; Romania	1.04
59	East Carpathians; Romania	1.34
60	East Beskids (Tarnawa); Poland	1.33
61	Little Poland Upland; Poland	0.29
62	Babia Góra, Beskid Sądecki; Poland	0.54
63	Beskid Śląski, Beskid Żywiecki;Poland	1.11
64	Kłodzko Valley; Poland	0.26
65	Silesian Lowland, Great poland Lowland; Poland	0.70
66	West-Pomeranian Lakeland; Poland	0.72
67	East-Pomeranian Lakeland, Warmia, Masuria; Poland	0.47
68	Masurian Lakeland; Poland	0.80
69	Augustów Lakeland, Podlasie; Poland	1.12
70	Białowieża Primeval Forerst; Poland	0.35
71	Vilnius Lakeland, Belarus Lakeland; Lithuania, Belarus	0.40
72	Latvia, Estonia, 1	0.19
73	Latvia, Estonia, 2	-0.26
74	Latvia, Estonia, 3	0.32
75	Belarus	0.31
76	East Russia (Valdai Hills); Russia	-0.36
77	Russia 1	-1.58
78	Russia 2 (Central Russian Upland, Smolensk-Moscow Heights)	-0.45
79	Udmurtsk (Upper Kama Upland); Russia	-1.64
80	West Siberia; Russia	-2.67
81	Knusk; Russia	0.55
82	Jutland,(Denmark)	0.74
83	Bogstad (Ostland); Norway	-0.61
84	S-E Norway; Norway	-0.81
85	Central Norway; Norway	-2.12
86	Scania; Sweden	0.34
87	Gotland, Smaland (S-E Sweden); Sweden	-0.55
88	Gotland; Sweden	-0.36
89	Sondermanland (S-E Sweden); Sweden	-1.36
90	Central Sweden; Sweden	-0.61
91	Norrland; Sweden	-2.28
92	Madelpad, Angermanland; Sweden	-2.31
93	S-E Sweden Cost; Sweden	-3.12
94	South Finland; Finland	-1.72
95	Karelian; Finland, Russia	-2.07
96	Hudson, Ontario; Canada	1.17

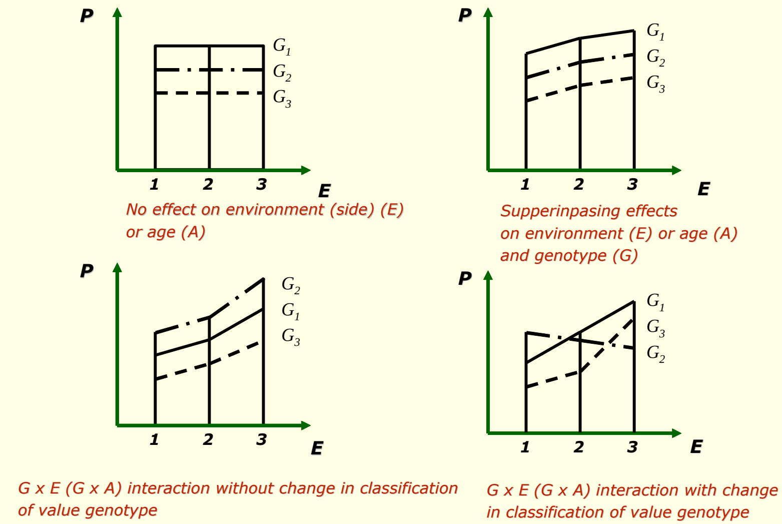
Methods

Methods of statistical analysis

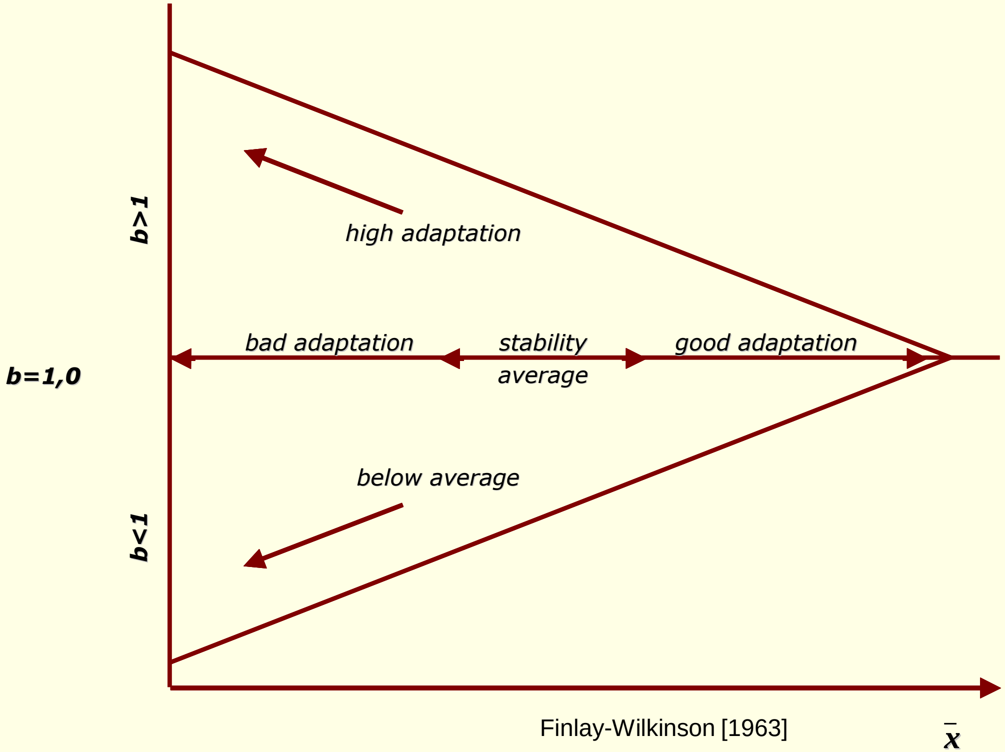
In evaluating the variability between the regions and between the years analysis of variance was applied with repetitions.

Cluster analysis with Euclidean distance was used for grouping similar provenance regions according to G x Age interaction using Finlay-Wilkinson [1963] and Mallard methods. (From Gallais [1990]).

The calculations were carried out in the STATISTICA software package.



Genotypic provenance response to environment; G_1, G_2, G_3 – genotypes; 1?3 – increasing productivity of site (E); P – value of genotype (defined by survival of trees in plantation)



Finlay-Wilkinson [1963]

Krutsch regions level

Krutsch regions level

G × Age interaction

Group 1: very good height growth, no effect of G × A interaction

Group 2: average height growth, no effect of G × A interaction

Group 3: bad height growth, no effect of G × A interaction

Group 4: very bad height growth, no G × A interaction effect

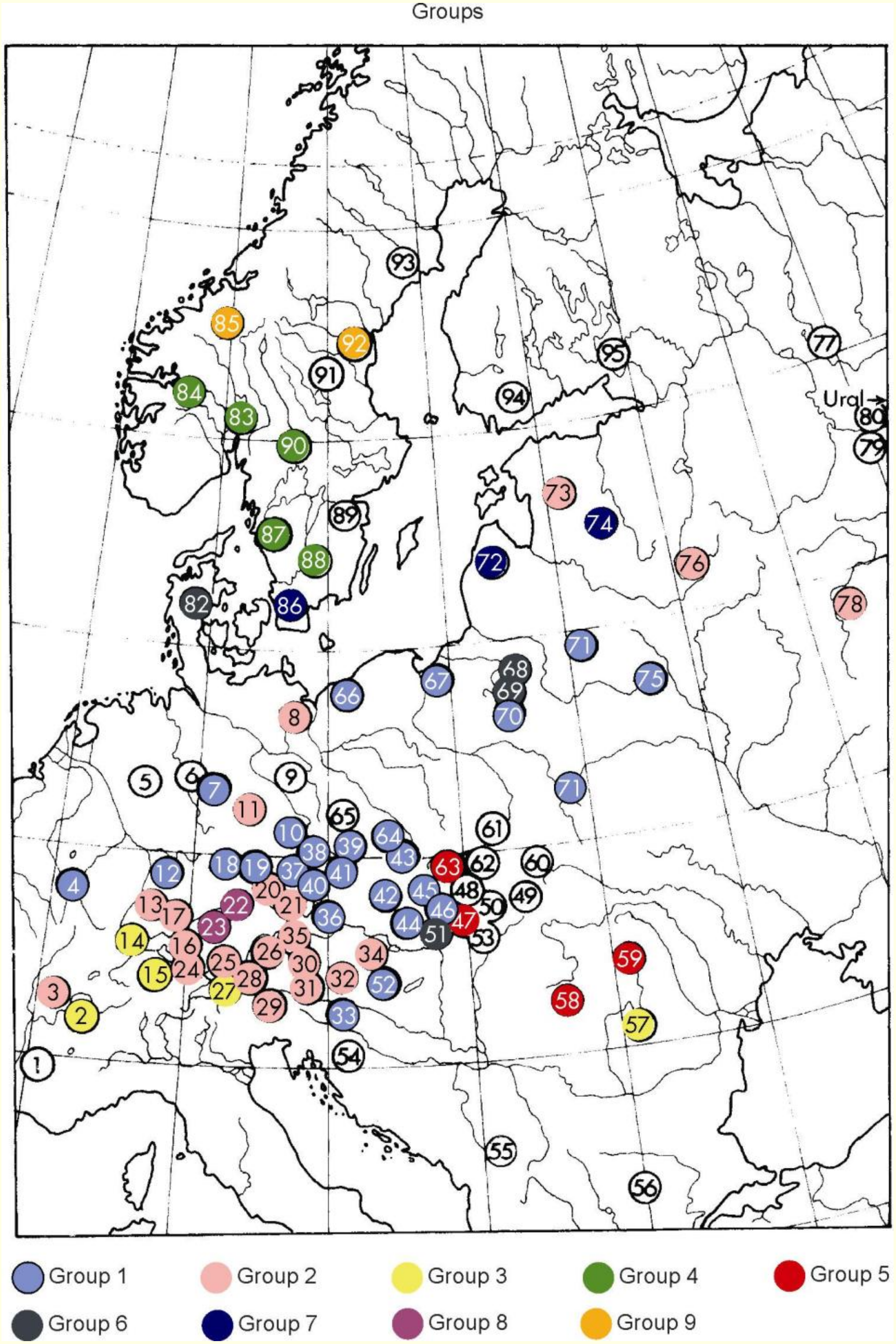
Group 5: average height growth, no G × A interaction effect

Group 6: average height growth, significant G × A interaction effect, mean height increases with age

Group 7: very bad height growth, significant G × A interaction effect, mean height increases with age

Group 8: low value of height growth, G × A interaction effect

Group 9: very low value of height growth, G × A interaction effect



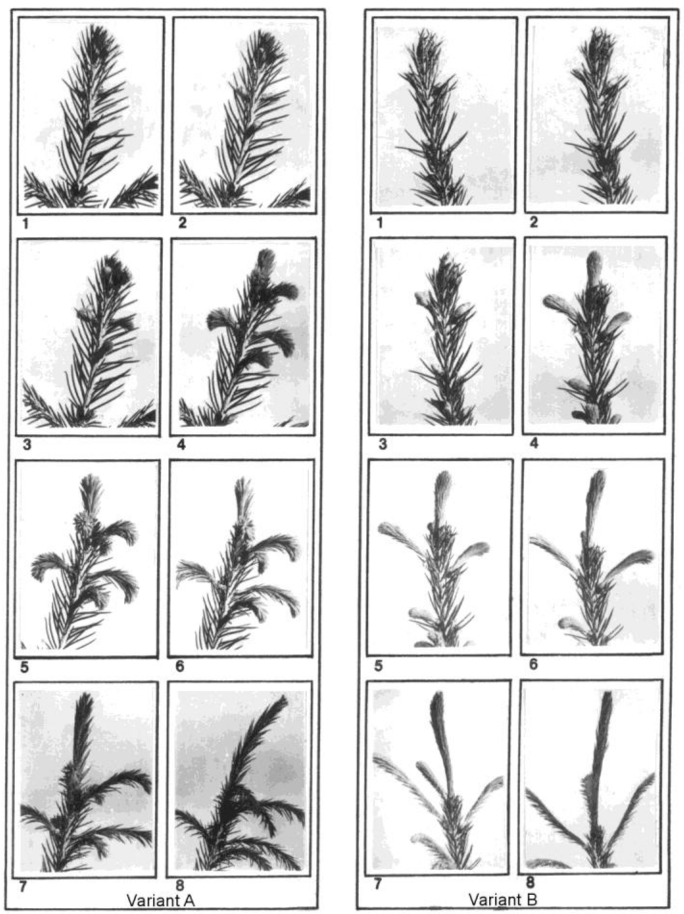
Different adaptability of Norway Spruce in IUFRO Test 1964-1968. G x A in years 1969-1988 (age 6-25)

1. West, central Europe and East Baltic Krutsch regions
2. SW Europe, Russia
3. West Alps, Southern Carpathians
4. S Scandinavian Krutsch regions
5. West Carpathians (Beskid), East Carpathians; Bihor Mts, Transylvanian, Romania
6. Poland Masurian Likeland
7. Latvia, Estonia
8. Swabian Upland, Germany
9. Central Scandinavian Krutsch regions

IUFRO 1964/68

IUFRO 1964/68 - Investigations:

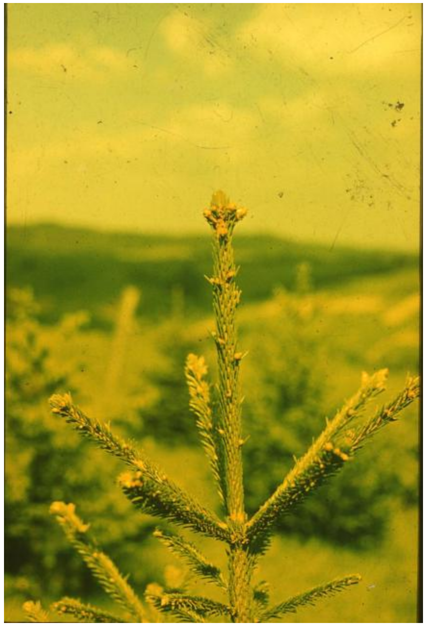
The spring flushing of Norway spruce tested at Krynica was evaluated on the basis of analyses of the degree of development of individual trees using a classification of the developmental phases of spruce worked out by Krutzsch.



Spring flushing in age 15.

Developmental phases of Norway spruce in the annual cycle of spring flushing. Variants A i B according to Krutsch.

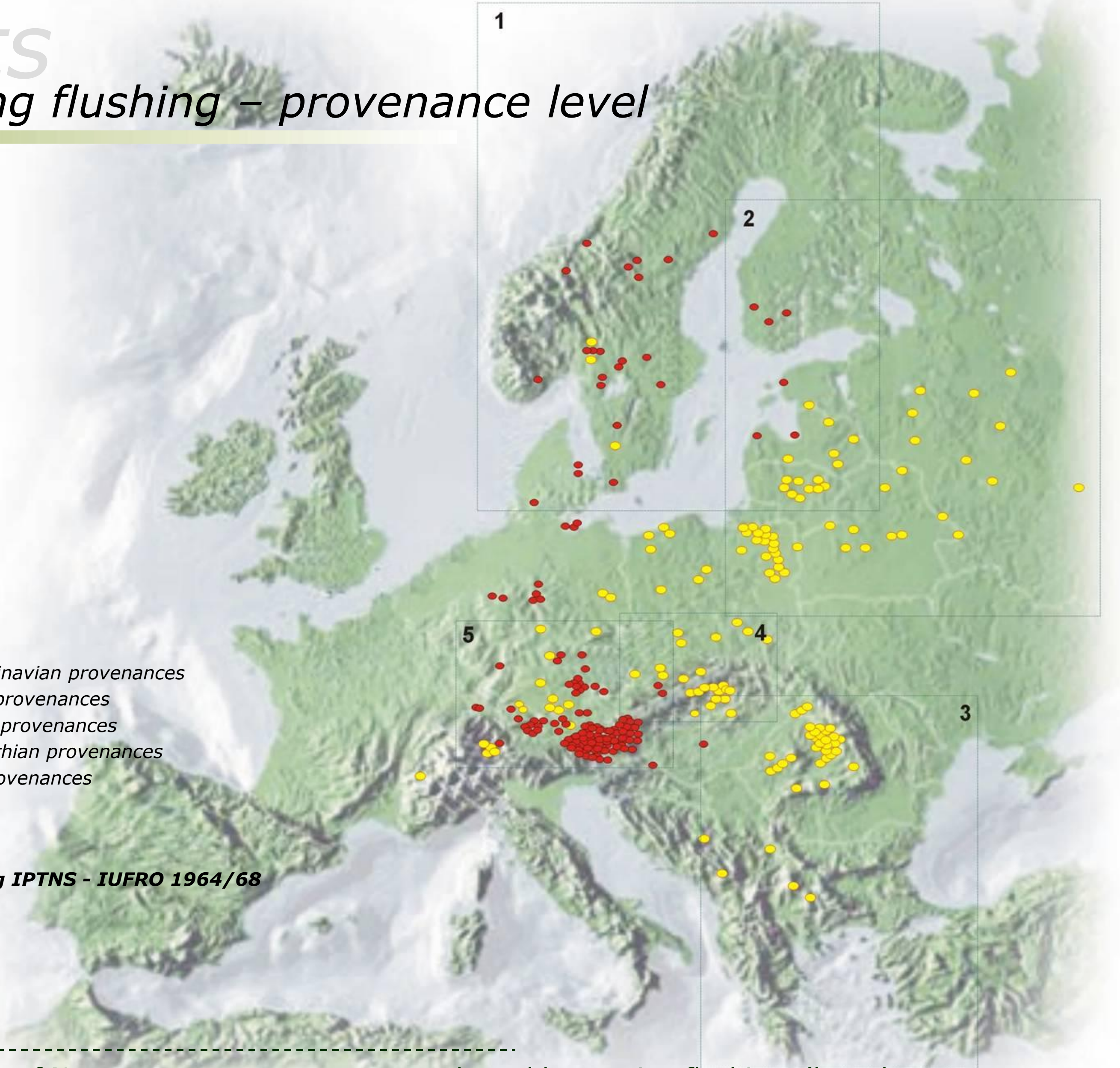
(Krutrsch P. 1973. IUFRO S. 2.02.11 Norway spruce. Development of buds. The Royal College of Forestry, Stockholm, Sweden.



Results

Results spring flushing – provenance level



REGIONS:

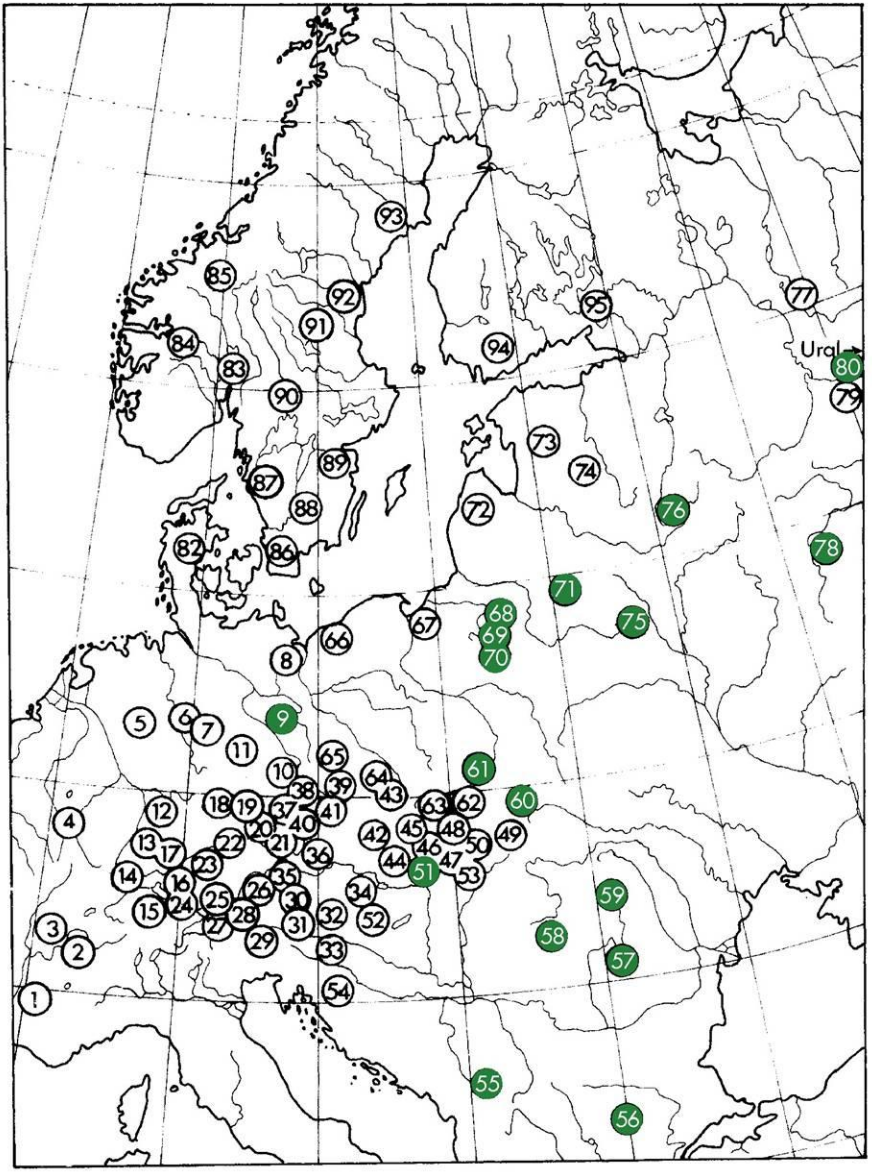
1 – Scandinavian provenances
2 – N-NE provenances
3 – South provenances
4 – Carpathian provenances
5 – Alp provenances

Numeracja pochodzeń wg IPTNS - IUFRO 1964/68

- late provenances
- early provenances

RYC.2. Distribution of Norway spruce provenances early and late spring flushing. (based on measurments of 1975). Provenance test of Norway spruce IPTNS – IUFRO 1964/68 in Krynica

Probability of occurrence of late flushing provenances in Krutzsch's regions
Fraction of provenances



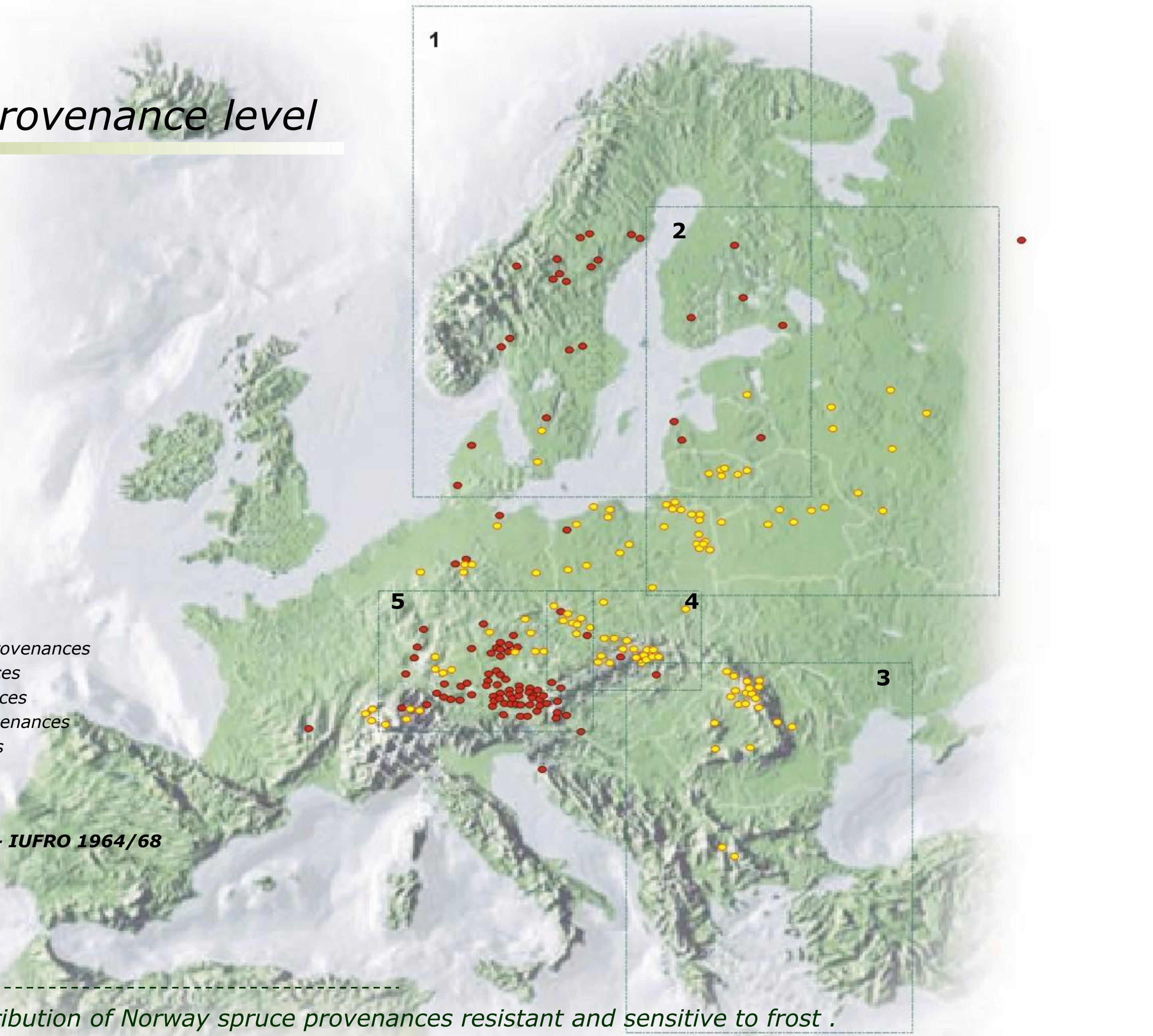
Probability ≥ 0.500

No	Provenance	late flushing
1	Massif Central, Dauphine; France	0.200
2	West Alps: France	0.077
3	Jura; France	0.000
4	Ardennes, Vosges, Eifel; Belgium, France, Germany	0.000
5	Rheinisches Schiefergebirge, Hessian, Foothills; Germany	0.000
6	Harz Mts 1; Germany	0.000
7	Harz Mts 2 (Westerhof); Germany	0.000
8	Mecklenburg Lakeland, Schwerin, Rostock; Germany	0.000
9	Lausitz; Germany	1.000
10	Erzgebirge; Czech Republic	0.091
11	Thuringerwald; Germany	0.111
12	Odenwald; Germany	0.000
13	Schwarzwald (Baden-Wurttemberg); Germany	0.000
14	Breisgau; Germany	0.000
15	West (Lepontine) Alps; Switzerland	0.235
16	Swabian Upland (Wurttemberg); Germany	0.000
17	Swabian Jura; Germany	0.000
18	Franconian Jury; Germany	0.091
19	Franconia, Upper Palatinate; Germany	0.091
20	Bavarian Forest; Germany	0.000
21	Bohemian Forest; Czech Republik, Germany	0.000
22	Swabian-Bavarian Upland (Bavaria) 1; Germany	0.194
23	Swabian-Bavarian Upland (Swabia) 2; Germany	0.059
24	Swabian-Bavarian Upland (Swabia) 3; Germany	0.000
25	Bavarian Alps; Germany	0.000
26	East Alps; Germany	0.000
27	Tyrol; Austria	0.000
28	Tyrol-Salzburg; Austria	0.000
29	East Alps; Italy	0.000
30	Niedrige Tauern, Styria; Austria	0.000
31	Carinthia-Styria; Austria	0.000
32	Styria (N-E) 1; Austria	0.000
33	Styria (S-E) 2; Austria	0.000
34	Styria (E) 3; Austria	0.000
35	Upper Austria; Austria	0.000
36	Bohemian Upland, Lower Austria; Czech Republic, Austria	0.000
37	West Bohemia; Czech Republic	0.000
38	Central Bohemia; Czech Republic	0.000
39	Sudetes (Krkonose, Tafelgebirge); Czech Republic	0.000
40	South Bohemia; Czech Republic	0.000
41	Bohemia; Czech Republic	0.000
42	South Bohemia, Moravia; Czech Republic	0.040
43	Moravia 1; Czech Republic	0.100
44	Moravia 2; Czech Republic	0.091
45	Moravia 3; Czech Republic	0.042
46	Velka Fatra, Mala Fatra, Slovakia	0.200
47	Nizke Tatry; Slovakia	0.304
48	Tatras; Slovakia, Poland	0.200

No	Provenance	late flushing
49	East Slovakia (Spis); Slovakia	0.333
50	Slovenske Rudohorie; Slovakia	0.429
51	Stiavnicke Pohorie; Slovakia	1.000
52	West Hungary; Hungary	0.000
53	North Hungary; Hungary	0.250
54	Dalmatia; Croatia	0.000
55	Montenegro; Yugoslavia	0.667
56	Rhodope Mts; Bulgaria	0.688
57	Southern Carpathians, Transylvanian Upland; Romania	0.600
58	Bihor Mts,Transylvanian; Romania	1.000
59	East Carpathians; Romania	0.880
60	East Beskids (Tarnawa); Poland	1.000
61	Little Poland Upland; Poland	0.800
62	**Babia Góra, Beskid Sądecki;** Poland	0.000
63	**Beskid Śląski, Beskid Żywiecki;**Poland	0.067
64	**Kłodzko** Valley; Poland	0.111
65	Silesian Lowland, Great poland Lowland; Poland	0.300
66	West-Pomeranian Lakeland; Poland	0.235
67	East-Pomeranian Lakeland, Warmia, Masuria; Poland	0.250
68	Masurian Lakeland; Poland	1.000
69	Augustów Lakeland, Podlasie; Poland	0.875
70	**Białowieża** Primeval Forerst; Poland	1.000
71	Vilnius Lakeland, Belarus Lakeland; Lithuania, Belarus	1.000
72	Latvia, Estonia, 1	0.000
73	Latvia, Estonia, 2	0.400
74	Latvia, Estonia, 3	0.375
75	Belarus	1.000
76	East Russia (Valdai Hills); Russia	1.000
77	Russia 1	0.400
78	Russia 2 (Central Russian Upland, Smolensk-Moscow Heights)	1.000
79	Udmurtsk (Upper Kama Upland); Russia	0.000
80	West Siberia; Russia	0.667
81	Knusk; Russia	0.667
82	Jutland,(Denmark)	0.000
83	Bogstad (Ostland); Norway	0.200
84	S-E Norway; Norway	0.000
85	Central Norway; Norway	0.000
86	Scania; Sweden	0.000
87	Gotland, Smaland (S-E Sweden); Sweden	0.000
88	Gotland; Sweden	0.125
89	Sondermanland (S-E Sweden); Sweden	0.000
90	Central Sweden; Sweden	0.000
91	Norrland; Sweden	0.000
92	Madelpad, Angermanland; Sweden	0.000
93	S-E Sweden Cost; Sweden	0.000
94	South Finland; Finland	0.000
95	Karelian; Finland, Russia	0.000
96	Hudson, Ontario; Canada	1.000

Results

Results frost – provenance level



REGIONS:

1 – Scandinavian provenances
2 – N-NE provenances
3 – South provenances
4 – Carpathian provenances
5 – Alp provenances

Numeracja pochodzeń wg IPTNS - IUFRO 1964/68

- resistant provenances
- sensitive provenances

RYC.3. Distribution of Norway spruce provenances resistant and sensitive to frost .
(based on measurments of 1977).
Provenance test of Norway spruce IPTNS – IUFRO 1964/68 in Krynica

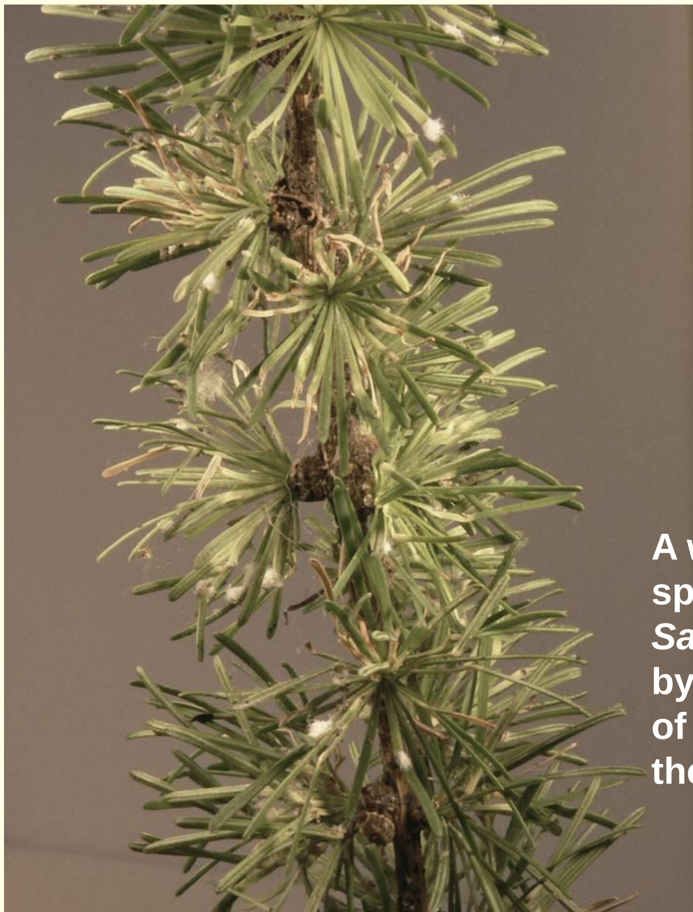
IUFRO 1964/68

IUFRO 1964/68 - Investigations:

Resistance to the infestation with Chermes viridis

Chermes viridis Ratz. (Sacchiphantes abietis L.)

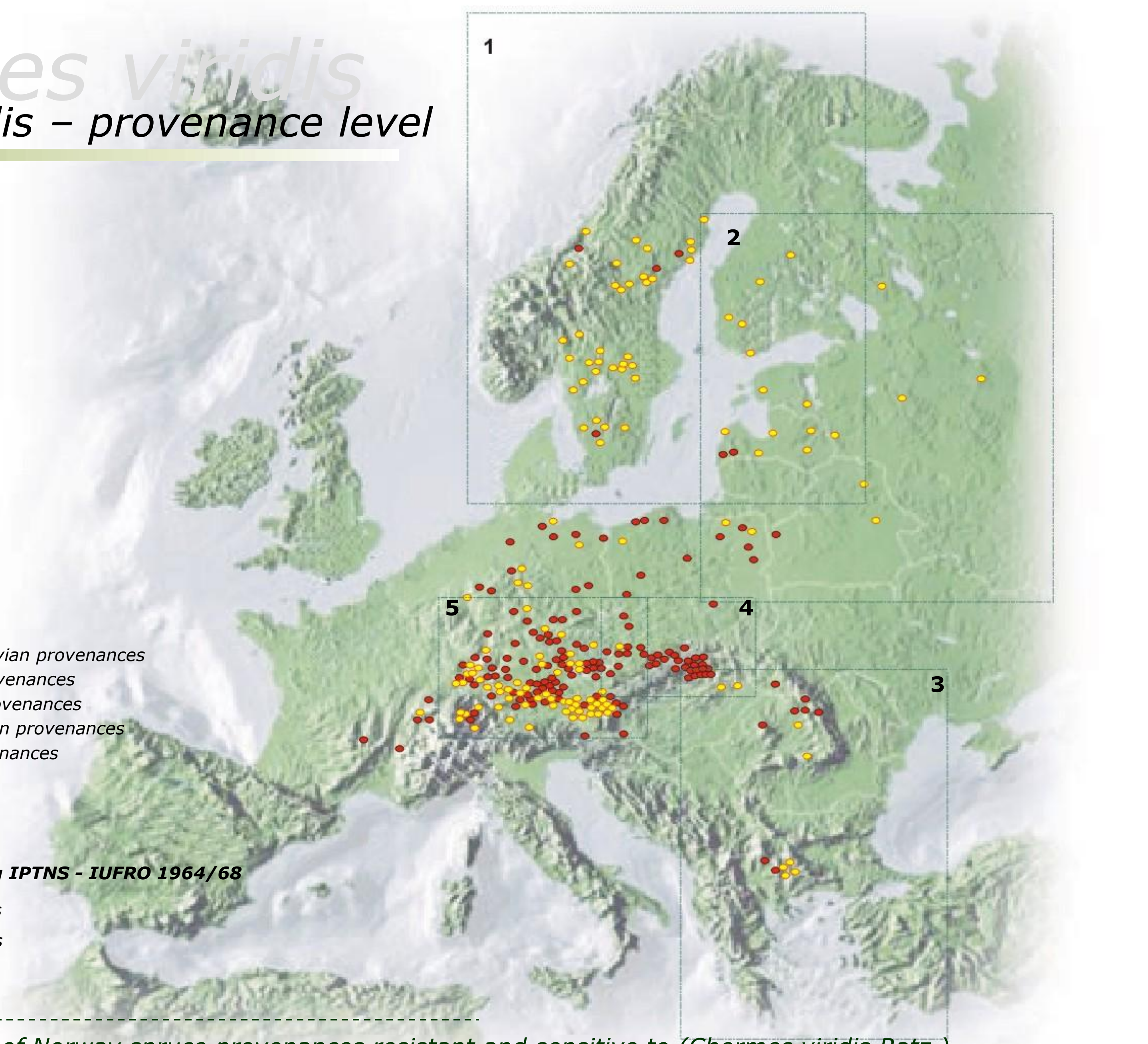
Observations were made on 11 and 12 June 1977 on all 23 843 specimens of 1095 Norway spruce provenances from the whole range of the species.



A well-known insect pest that causes much damage to Norway spruce plantations is *Chermes viridis* Ratz., called also *Sacchiphantes abietis* L. or *Adelges abietis* L. A plant infested by this aphid develops 2 – 3 cm-long excrescences at the base of young shoots, which results in their unnatural bending and the deformation of crowns in young trees.

fot. dr Robert Rosa

Chermes viridis – provenance level



REGIONS:

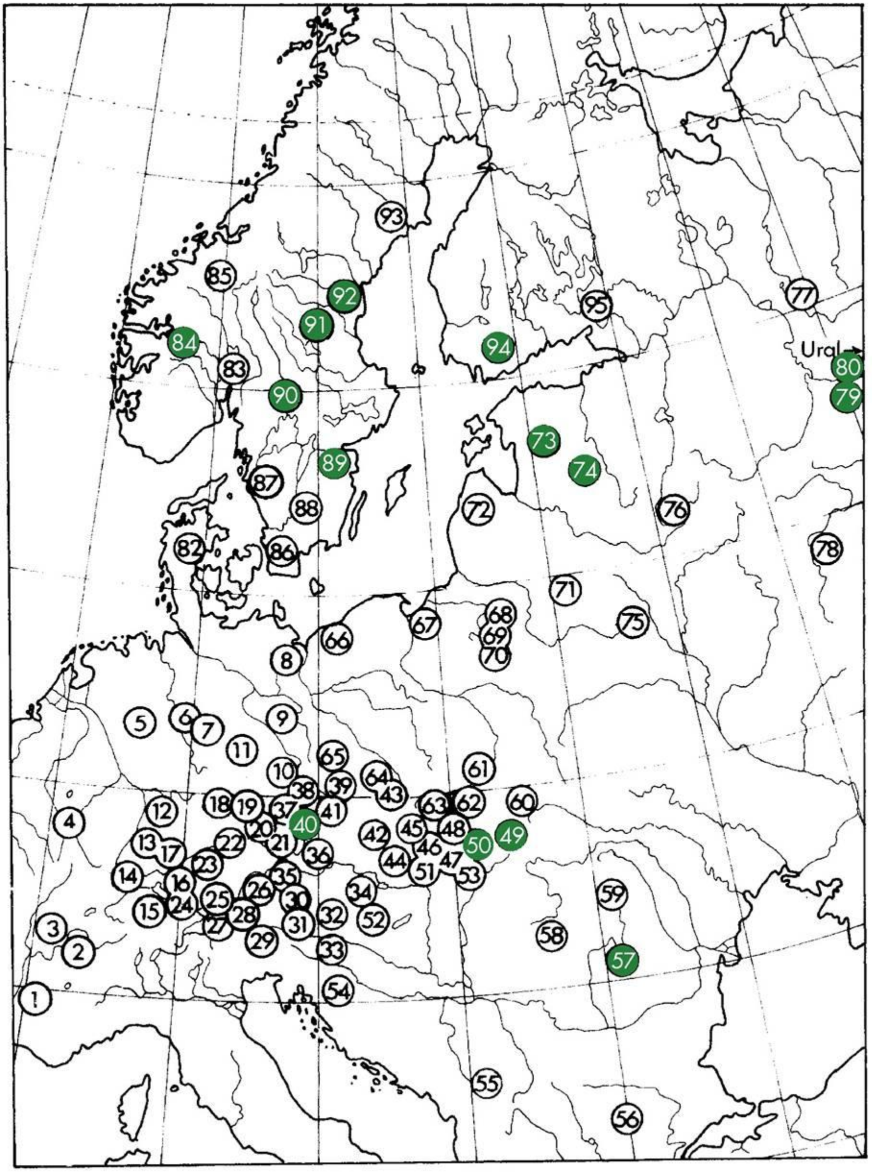
1 – Scandinavian provenances
2 – N-NE provenances
3 – South provenances
4 – Carpathian provenances
5 – Alp provenances

Numeracja pochodzeń wg IPTNS - IUFRO 1964/68

- resistant provenances
- sensitive provenances

RYC.4. Distribution of Norway spruce provenances resistant and sensitive to (Chermes viridis Ratz.). Provenance test of Norway spruce IPTNS – IUFRO 1964/68 in Krynica

Resistance of Norway spruce provenances to *Chermes viridis* Ratz. by Krutzsch region (degree of damage from the aphid, φ (°), is expressed as arc sin $\sqrt{p}$, where *p* percentage of damaged trees)IPTNS-IUFRO 1964/68, Krynica



Degree of damage φ ≤ 40.00

No	Provenance	φ
1	Massif Central, Dauphine; France	47.117
2	West Alps: France	46.516
3	Jura; France	54.368
4	Ardennes, Vosges, Eifel; Belgium, France, Germany	40.990
5	Rheinisches Schiefergebirge, Hessian, Foothills; Germany	46.767
6	Harz Mts 1; Germany	41.595
7	Harz Mts 2 (Westerhof); Germany	50.074
8	Mecklenburg Lakeland, Schwerin, Rostock; Germany	47.997
9	Lausitz; Germany	45.660
10	Erzgebirge; Czech Republic	46.184
11	Thuringerwald; Germany	46.318
12	Odenwald; Germany	48.385
13	Schwarzwald (Baden-Wurttemberg); Germany	46.216
14	Breisgau; Germany	45.953
15	West (Lepontine) Alps; Switzerland	45.844
16	Swabian Upland (Wurttemberg); Germany	44.650
17	Swabian Jura; Germany	46.596
18	Franconian Jury; Germany	51.669
19	Franconia, Upper Palatinate; Germany	47.794
20	Bavarian Forest; Germany	43.233
21	Bohemian Forest; Czech Republik, Germany	47.880
22	Swabian-Bavarian Upland (Bavaria) 1; Germany	47.086
23	Swabian-Bavarian Upland (Swabia) 2; Germany	45.850
24	Swabian-Bavarian Upland (Swabia) 3; Germany	45.890
25	Bavarian Alps; Germany	45.720
26	East Alps; Germany	48.860
27	Tyrol; Austria	40.518
28	Tyrol-Salzburg; Austria	47.024
29	East Alps; Italy	40.598
30	Niedrige Tauern, Styria; Austria	41.770
31	Carinthia-Styria; Austria	46.182
32	Styria (N-E) 1; Austria	43.918
33	Styria (S-E) 2; Austria	53.664
34	Styria (E) 3; Austria	46.385
35	Upper Austria; Austria	46.790
36	Bohemian Upland, Lower Austria; Czech Republic, Austria	50.462
37	West Bohemia; Czech Republic	48.390
38	Central Bohemia; Czech Republic	49.857
39	Sudetes (Krkonose, Tafelgebirge); Czech Republic	52.885
40	South Bohemia; Czech Republic	39.610
41	Bohemia; Czech Republic	44.838
42	South Bohemia, Moravia; Czech Republic	45.830
43	Moravia 1; Czech Republic	47.330
44	Moravia 2; Czech Republic	47.650
45	Moravia 3; Czech Republic	47.466
46	Velka Fatra, Mala Fatra, Slovakia	52.262
47	Nizke Tatry; Slovakia	51.639
48	Tatras; Slovakia, Poland	49.700

No	Provenance	φ
49	East Slovakia (Spis); Slovakia	34.753
50	Slovenske Rudohorie; Slovakia	37.255
51	Stiavnicke Pohorie; Slovakia	57.040
52	West Hungary; Hungary	47.508
53	North Hungary; Hungary	49.000
54	Dalmatia; Croatia	58.810
55	Montenegro; Yugoslavia	52.336
56	Rhodope Mts; Bulgaria	43.950
57	Southern Carpathians, Transylvanian Upland; Romania	36.644
58	Bihor Mts,Transylvanian; Romania	48.210
59	East Carpathians; Romania	47.400
60	East Beskids (Tarnawa); Poland	49.200
61	Little Poland Upland; Poland	50.580
62	Babia Góra, Beskid Sądecki; Poland	48.752
63	Beskid Śląski, Beskid Żywiecki;Poland	48.830
64	Kłodzko Valley; Poland	48.613
65	Silesian Lowland, Great poland Lowland; Poland	46.370
66	West-Pomeranian Lakeland; Poland	53.906
67	East-Pomeranian Lakeland, Warmia, Masuria; Poland	47.220
68	Masurian Lakeland; Poland	47.440
69	Augustów Lakeland, Podlasie; Poland	48.090
70	Białowieża Primeval Forerst; Poland	54.840
71	Vilnius Lakeland, Belarus Lakeland; Lithuania, Belarus	45.770
72	Latvia, Estonia, 1	53.640
73	Latvia, Estonia, 2	37.850
74	Latvia, Estonia, 3	35.790
75	Belarus	47.350
76	East Russia (Valdai Hills); Russia	48.810
77	Russia 1	41.470
78	Russia 2 (Central Russian Upland, Smolensk-Moscow Heights)	44.100
79	Udmurtsk (Upper Kama Upland); Russia	37.860
80	West Siberia; Russia	29.290
81	Knusk; Russia	40.700
82	Jutland,(Denmark)	56.490
83	Bogstad (Ostland); Norway	44.950
84	S-E Norway; Norway	33.030
85	Central Norway; Norway	44.750
86	Scania; Sweden	48.500
87	Gotland, Smaland (S-E Sweden); Sweden	40.200
88	Gotland; Sweden	41.840
89	Sondermanland (S-E Sweden); Sweden	38.425
90	Central Sweden; Sweden	36.008
91	Norrland; Sweden	38.920
92	Madelpad, Angermanland; Sweden	36.590
93	S-E Sweden Cost; Sweden	42.405
94	South Finland; Finland	28.723
95	Karelian; Finland, Russia	40.080
96	Hudson, Ontario; Canada	31.500

IUFRO 1964/68 Conclusions

1. Assessment of the height growth of Norway spruce, carried out on trees in the juvenile period (5 to 25 years) on the IUFRO trial plot in Krynica (Beskid Sądecki, Carpathian Mts), revealed that trees from the provenances representing the Krutzsch's regions in which the number of spruce provenances exceeds 10 show a significant variation both at provenance and regional level. Based on a dendrogram, six distinct provenance groups were identified differing in genetic height reactivity. The groups are as follows:

Group 1: region 48 - Tatras, Slovakia, Poland; good height growth, strong G × A interaction effect.

Group 2: regions 47 - Nízkie Tatry, Slovakia; 59- East Carpathians; Romania; 63 - Beskid Śląski, Beskid Żywiecki; very good height growth, significant G × A interaction effect, mean height increases with age.

Group 3: regions 22, 23, 24 – Swabian - Bavarian Upland (1 - Bavaria, 2, 3 - Swabia) Germany; 13 - Schwarzwald (Baden-Wurttemberg)Germany; 34 - Styria (E) 3 Austria; 25 - Bavarian Alps, Germany; 21 - Bohemian Forest, Czech Republik; 17 - Swabian Jura, Germany; 28 - Tyrol – Salzburg, Austria; 30 - Niedrige Tauren, Styria; 32 - Styria (N-E) 1 Austria; 31 – Carinthia - Styria Austria; 26 - East Alps, Germany; 16 - Swabian Upland (Wurttemberg) Germany; 8 - Meclenburg Lakeland, Schwerin, Rostock; Germany; average height growth, no G × A interaction effect.

Group 4: regions 36 - Bohemian Upland, Lower Austria; Czech Republic; Austria, 66 – West -Pomeranian Lakeland, Poland; 41 - Bohemia; Czech Republic; 19 - Franconia, Upper Palatinate; Germany; 18 - Franconian Jury, Germany; 45 - Moravia 3, Czech Republic; 10 -Erzgebirge; Czech Republic; 37 - West Bohemia, Czech Republic; 44 - Moravia 2, Czech Republic; 42 - South Bohemia, Moravia, Czech Republic; 7 - Harz Mts 2 (Westerhof), Germany; good height growth, no G × A interaction effect.

Group 5: regions 56 - Rhodope Mts; Bulgaria; 27 - Tyrol; Austria; 14 - Breisgau, Germany; 15 - West (Lepontine) Alps; Switzerland; 2 - West Alps; France; 5; poor height growth, weak G × A interaction effect.

Group 6: region 90 - Central Sweden; poor height growth, no G × A interaction effect.

As shown by an analysis of variance, the effect of study year (seedling age) and of the interaction study year (seedling age) × provenance region was significant for groups 3, 4 and 5. The provenances from the western and southern Carpathians, belonging to group 4 (fast height growth, favourable G × A interaction), and those from Bohemia, Austria and the Hartz Mts, belonging to group 4 (good height growth, no change in incremental dynamics due to interaction), can be considered the most suitable for juvenile selection.

IUFRO 1964/68 Conclusions

2. Late flushing provenances of a high spring frost resistance are those from regions **55 -61, 68-71, 75-78 and 80, i.e. the mountain regions of southern Carpathians, Bihor Mts and Rhodope Mts and the northeastern regions lying within the lowland range of spruce - from Masuria, Białowieża and central Russia**. The studies conducted so far foud a high heritability of this trait.

3. Spruces from the Bohemian provenances and a part of southern Carpathian ones are resistant to *Chermes viridis* Ratz. Those extremely late or early flushing from regions **40 South Bohemia, Czech Republic, 49 East Slovakia, 50 Slovenskie Rudohorje and 57 Southern Carpathians, Transylvanian Applend, Romania** exhibit a high resistance to the infestation by this insect species.

4. As suggested by the height of trees aged 25 years and the frost resistance (late flushing) of spruces, the provenances from regions **67 East Pomeranian Lakeland, Masuria Poland, 69 Augostów, Lakeland Poland, 50 Slovenskie Rudohorje , 75 Belarus, 96 Canada (Hudson, Ontario) and 58 Bihor Mts., Transylwania, Romania** have the greatest genetic and breeding value.

5. The current results on the variability of height and resistance traits indicate a high marketing potential of the seeds and seedlings of Norway spruce originating from the **western and southern Carpathian regions as well as from the lowland regions of Poland and Russia** lying within the northeastern range of the species.

6. Analysis of dependence between the altitudinal location of the experimental plot in Krynica, the altitudinal location of parent populations and the total height of their progeny at age of 25 which determines **the breeding success of the vertical transfer of the spruce reproduction material, was carried out distinctly showing the necessity of a strict regime in the selection of seed basis in mountainous conditions**. At age of 25 years the best growth characterized the progeny representing spruce stands of the altitudinal location similar to that of the comparative plantation. In the progeny of spruce populations from sites both lower or higher than the experimental plot decreases in height were found significant in the range of -0.95 for stands from the altitudes exceeding 1700 m above sea level to -0.26 for stands from 100 to 0 m above sea level, being proportional to differences in the altitude of the location of plantations and parent stands of the provenances tested.

Norway Spruce Symposium IUFRO WP S. 2.02.11

Stara Lesna, Wisła, Krynica

September 1 – 7, 8, 9 1997

IUFRO W.P S2 02. 11

Conference „Norway Spruce in the Conservation of Forest Ecosystems in Europe”
Warszawa – Malinówka – Białystok – Warszawa,
September 3-5, 2007

A review of the Irish Birch and Alder Improvement Projects

Teagasc and UCC collaboration

Ellen O' Connor[1], Niamh O' Dowd[2], Martin Steer[3], Michael Bulfin[4], Nuala Ni Fhlatharta[4], and Barbara Doyle[1].

1) University College Cork, 2) Dublin City University, 3) University College Dublin, 4) Teagasc.

Funded by:

Ireland: Forestry land cover

1999 = 9 %

2004 = 10 % (680,000 ha.)

National forestry strategy 2035 = 17 %

- Of which 20% will be broadleaves Financial incentives to promote planting and the range of species planted
- A 10 % minimum commercial broadleaf requirement advised for each planting - role for birch

EU average = 35%.

‘In Northern Europe birch is commercially the most important broadleafed species’

J. Hynynen et al. Forestry 2010 83: 103-119

Unable to put birch on the recommended species list as had not seen any evidence of good form in Ireland -

Dr Niall OCarroll Chief Inspector of the Forest Service

- Potential 10% min. broadleaf requirement on poor quality soil;
- *B. pendula* and *B. pubescens* are native species;
- Increased diversity of Irish forestry species;
- Can produce high quality timber;
- Shorter rotation than most other broadleaved trees (Barrett 2000).
- It can be used as a nurse tree for other timber species.
- Other European *Betula* improvement programmes have shown this genus to be amenable to form and vigour improvement.

Summary of performance of two trials of foreign birch in Ireland assessed in 1998. (O' Dowd, 2004)

Site	Species	Age (years)	Origin	Tallest individual (m)	DBH (cm)	Survival (%)
Comeragh Forest	*B. pendula*	32	Sweden A	12.5	8.1 ± 0.9*	53
	B. pendula	32	Sweden B	17.0	9.2 ± 1.4	53
Kilmacurragh **	*B. pubescens*	14	Ireland	10.5	10.3	100
	B. pubescens	14	Finland	10.3	10.2	69
	B. pendula	14	Finland3	12.0	10.0	22
	B. pendula	14	Finland6	8.0	7.9	6

* standard error ** data supplied by Coillte, standard error not available

The development of a sustainable supply of improved, adapted and healthy seed within the framework of the EU Forest Reproductive Material (FRM) regulations.

- Locating the best examples of mature trees (plus-trees) of these species on which to base the improvement programme;
- Collecting scion wood from plus-trees i.e clones;
- Establishing clone banks to preserve the clones;
- Establishing seed orchards;
- Establishing progeny trials to assess the value of the trees as parents.

Birch:

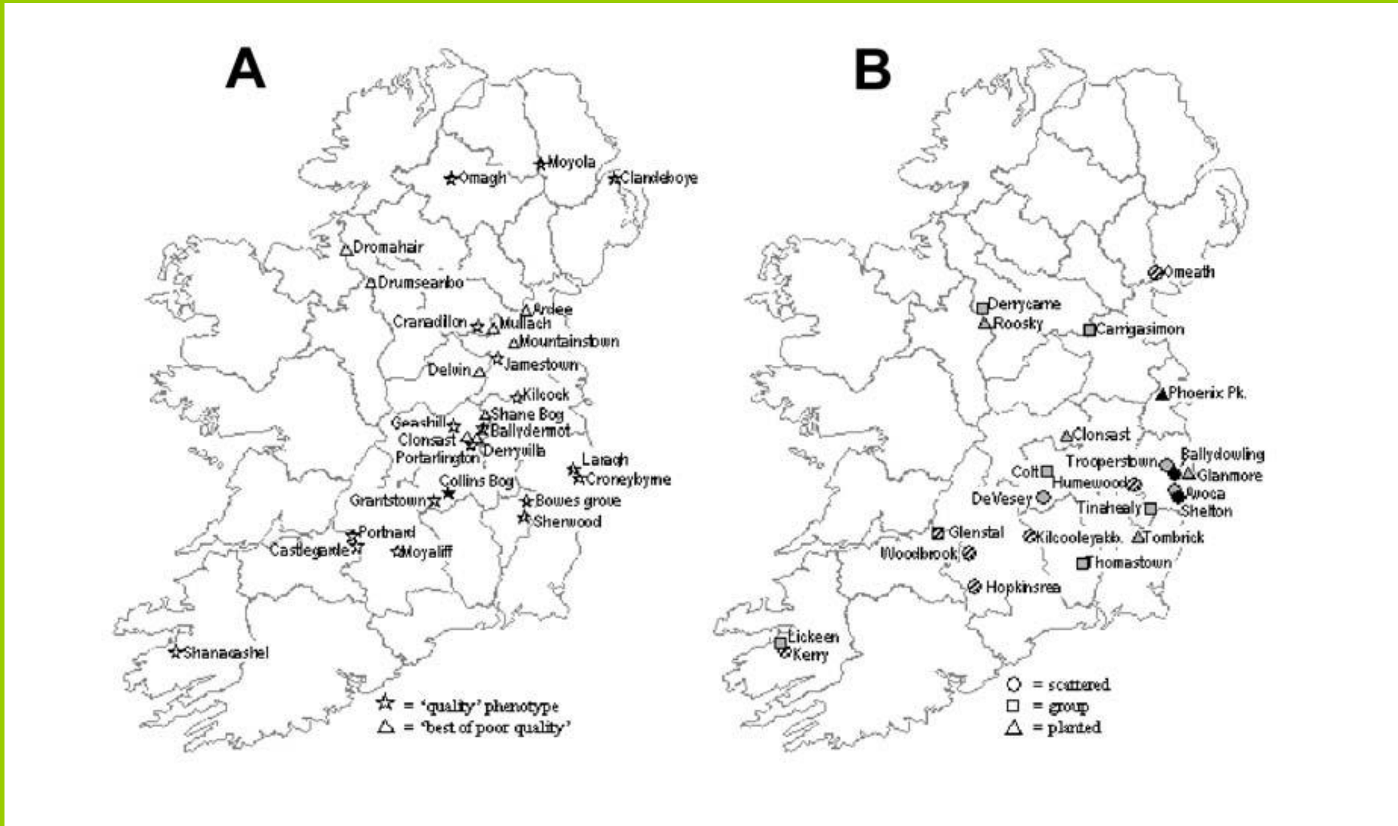
- ‘Pilot project for the genetic improvement of Irish Birch’ (1998 – 2000).
- ‘Irish Birch Improvement Project’ (2001– 2004).

Plus-tree locations

A = birch woods

B = scattered or individual trees

(O’ Dowd, 2004)



Birch to date

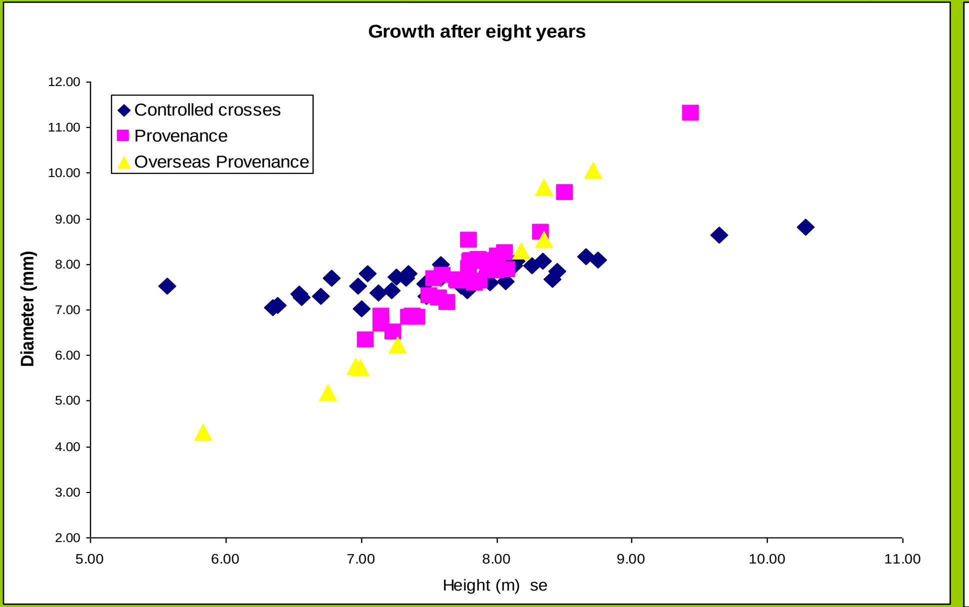
- **Establishment of provenance/progeny trials**

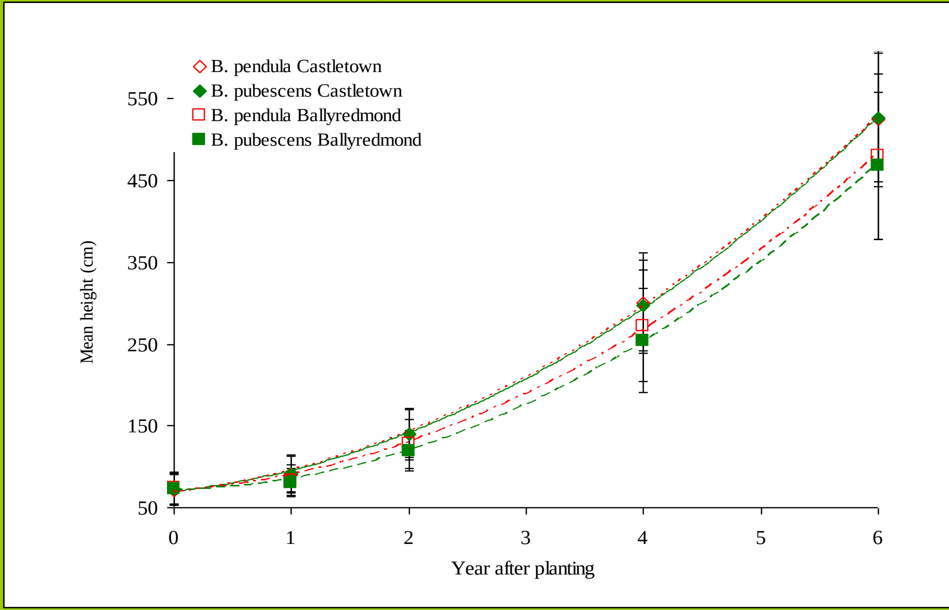
- Three sites, 9 ha.
- 27 *B. pubescens*
  - 94 *B. pubescens* families
- 16 *B. pendula* provenances
  - 27 *B. pendula* families,
- 37 controlled crosses of plus-trees (*B. pubescens*)
- Overseas *B. pendula*
  - 7 Scottish provenances,
  - 2 German breeding populations
  - 1 French family.
- Now 10 years-old

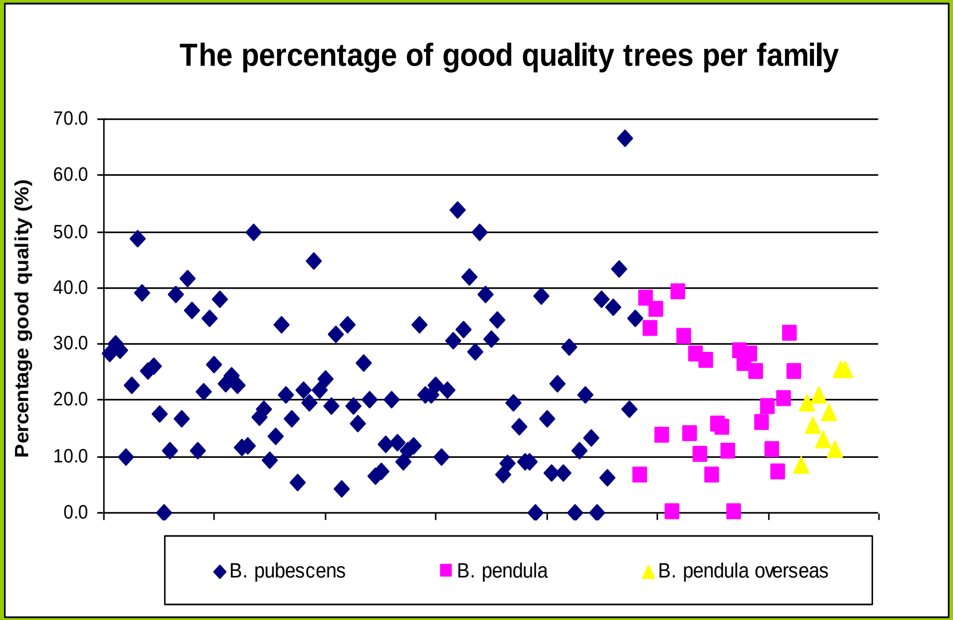
- **Clone banks established**
- **Untested seed orchard**

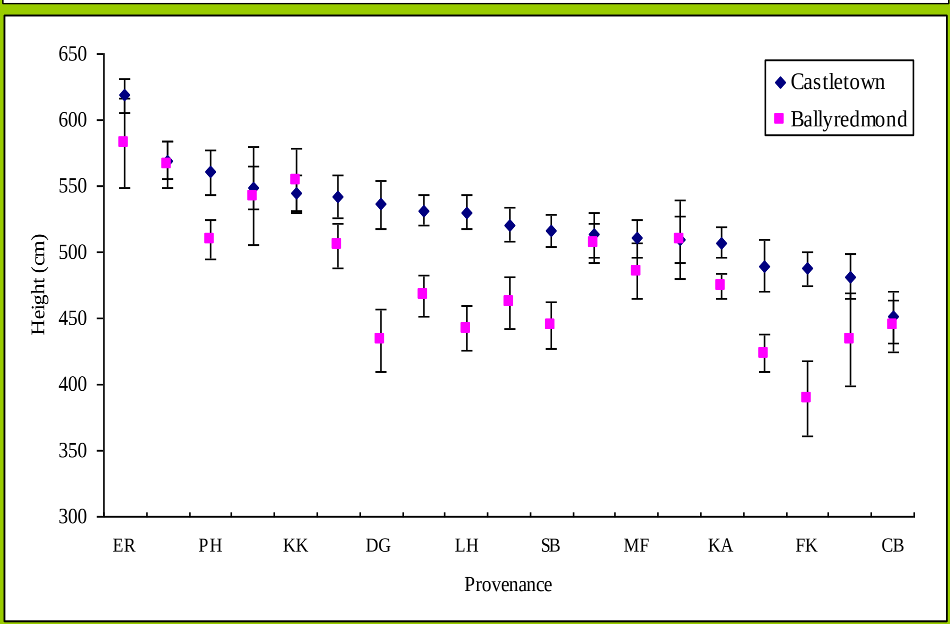
Results from birch progeny trials;

Survival and growth Quality trees Stability on two sites

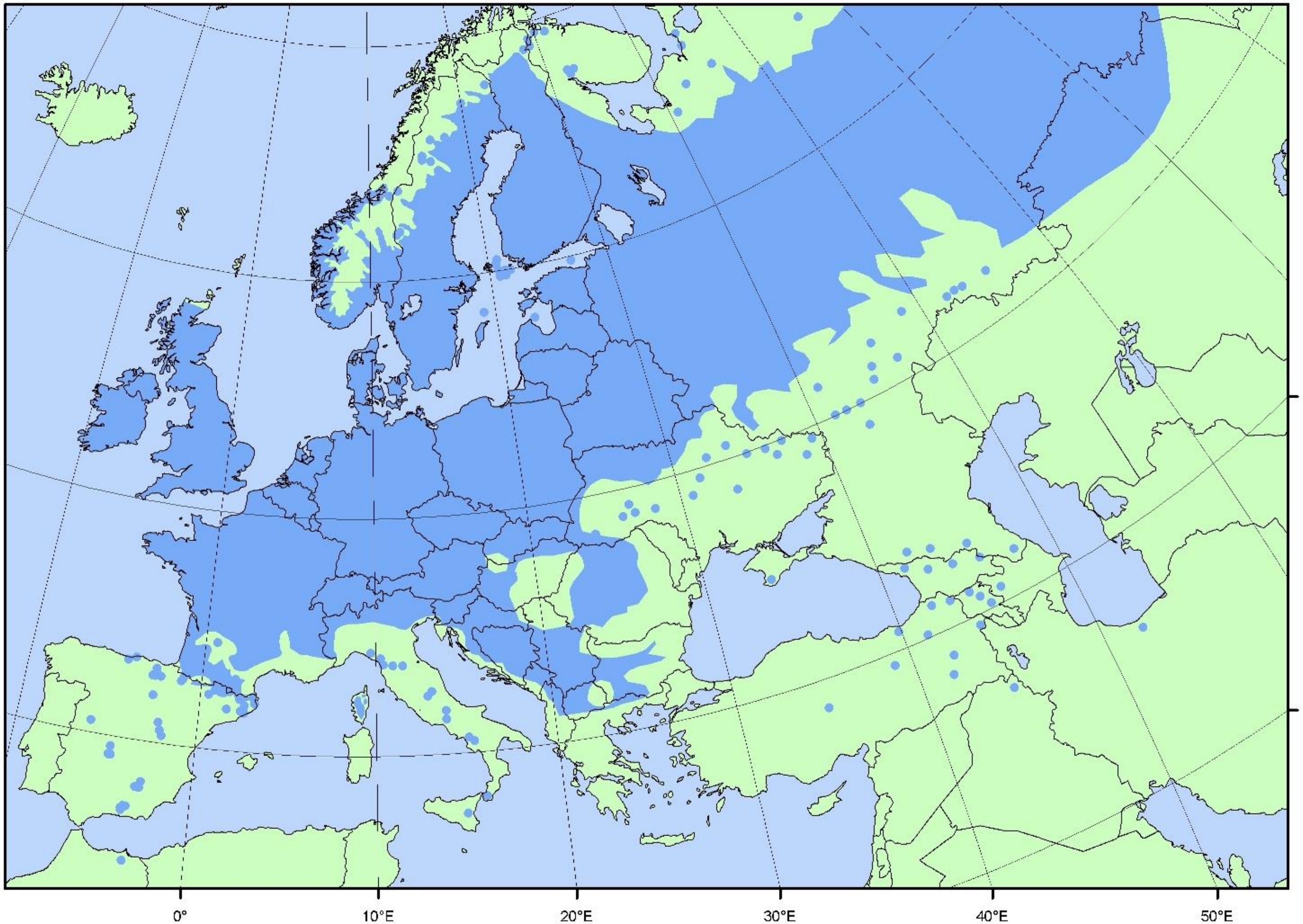








Betula pendula



EUFORGEN

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More information, updates
and other maps at:
www.euforgen.org

This distribution map, showing the natural distribution area of *Betula pendula*, was compiled by members of the EUFORGEN Networks

Citation: Distribution map of silver birch (*Betula pendula*) EUFORGEN 2009, www.euforgen.org

First published online on 10 December 2009

Km
0 375 750 1,500

Alder:

- Initiated in 2005
- On recommended list
- Inadequate supply for demand
- Imported material used extensively
- Two collections (2007 and 2009)
- Untested seed orchard
- Clone banks established at two locations
- Three progeny trials established (2008 and 2009)

The future

- Adoption by the Forest Service of birch as a recommended species and a sustainable supply of improved, adapted and healthy seed is the ultimate aim.

New phase of research;

To measure and trace genetic diversity in the collections

Assess that the heritability variation

To test the relatedness of clones

Reduce field testing

Maintain genetic diversity in breeding populations and collections

Authenticate pedigree

Physiological studies

Response to climate change

Challenges;

Pests e.g. hares, deer and squirrel

Diseases e.g phytophthora

Long-term security of research sites

Funding

Outputs:

- Bi-annual reports for COFORD
- Project reviews for COFORD Annual report
- O'Dowd, N. 2004. *The improvement of Irish birch. Phase 1: Selection of individuals and populations*. Project Reports COFORD, Dublin.
- O' Connor, E. 2007. *Progress in the selection and improvement of Irish birch*. COFORD Connects, COFORD, Dublin.
- Skovsgaard, J.P., O'connor, E., Graversgaard, H.C., Hochbichler, E., Mohni, C., Nicolescu, N., Niemistö, P., Pelleri, F., Spiecker, H., Stefancik, I., Övergaard, R. (2006) *Procedures for forest experiments and demonstration plots.* http://www.valbro.uni-freiburg.de/
- Hemery, G., Clark, J., Aldinger, E., Claessens, H, Malvolti, M., O'Connor, E., Raftoynnis, Y., Savill, P. and Brus, R. (2010) Growing scattered broadleaved tree species in a changing climate – risks and opportunities. *Forestry* 83: 65-81

Transfer of research into commercial sector:

- Initially, small amounts of seed will be produced by the project.
- Demonstration trials to confirm improvement are in the next phase.
- Long-term, parent material for commercial nurseries to produce their own sources of seed will be available.
- Protocols to manage these indoor seed orchards are being developed.

Project team

- Dr Ellen O' Connor, University College Cork*
- Mr. Oliver Sheridan, Teagasc
- Dr Nuala Ni Fhlatharta, Teagasc
- Dr Barbara Doyle-Prestwich, UCC
- Other staff such as Christy Roberts and Jenny O' Callaghan
- Students

Early birch work

- Dr. Niamh O' Dowd
- Dr. Linda Williams
- Michael Bulfin
- Prof. Martin Steer, UCD

* Correspondence email: e.o'connor@ucc.ie

Partner 12

Treebreedex Seminar
"What
do large genetic field experimental networks across Europe bring
to the scientific community?"
June 22-24, 2010
Sękocin Stary, Warsaw, POLAND

International trials concerning forest species in Italy

Anna De Rogatis, Fulvio Ducci & Lorenzo Vietto (CRA PLF)

CRA

CRA SEL

Italy and specially CRA SEL always had shared efforts for establishing international experiments on forest species.

- Only large experiments can allow the understanding of **productive potential** and **adaptation traits** of species.
- This concept was clear and shared through all Europe since the early last century.
- Most of international tests were initially focused on conifers, mostly exotics but also hardwood species...

Pseudotsuga menziesii

introduced in Italy since1882, in Tuscany (Chianti area), while the first introduction tests were established in 1887, in Tuscany (in Vallombrosa, near Florence).
annual yeld ranging between 13.5 and 16.4 m3/ha/year. In Tuscan Apennines standing volumes range between 500 and 820 m3/ha at age 50.

Aerial view of Faltona field trials.
The photo shows the differences in adaptation to environmental conditions of site of the IUFRO provenances used in this test.

- Iufro 1953 – 11 provenances (Or, Wa)
- IUFRO 1957 – 4 provenances (Wa)
- Iufro 1969/1970 – 85 provenances, 21 of them from interior + 10 Italian
- Eudirec Burnt Wood prov. progenies + 10 Italian

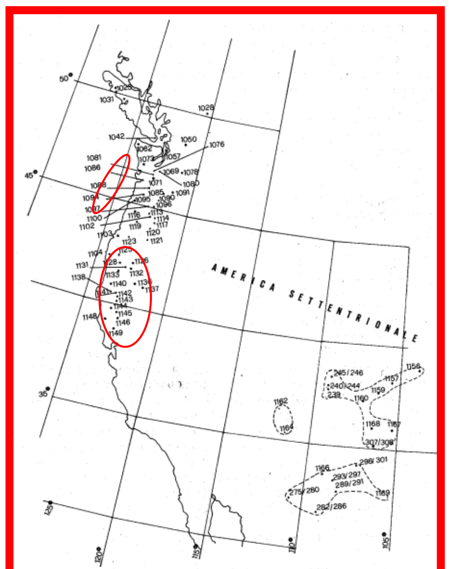
Main Results:

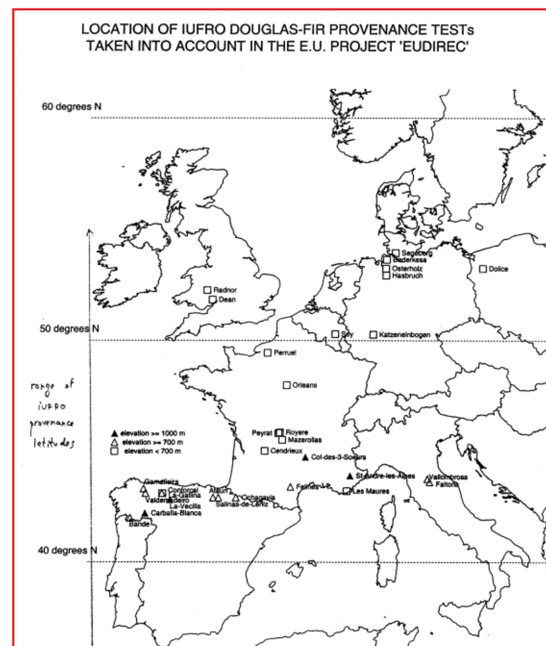
-- Best origins and best artificial seed stands;

-- Phenotypic traits

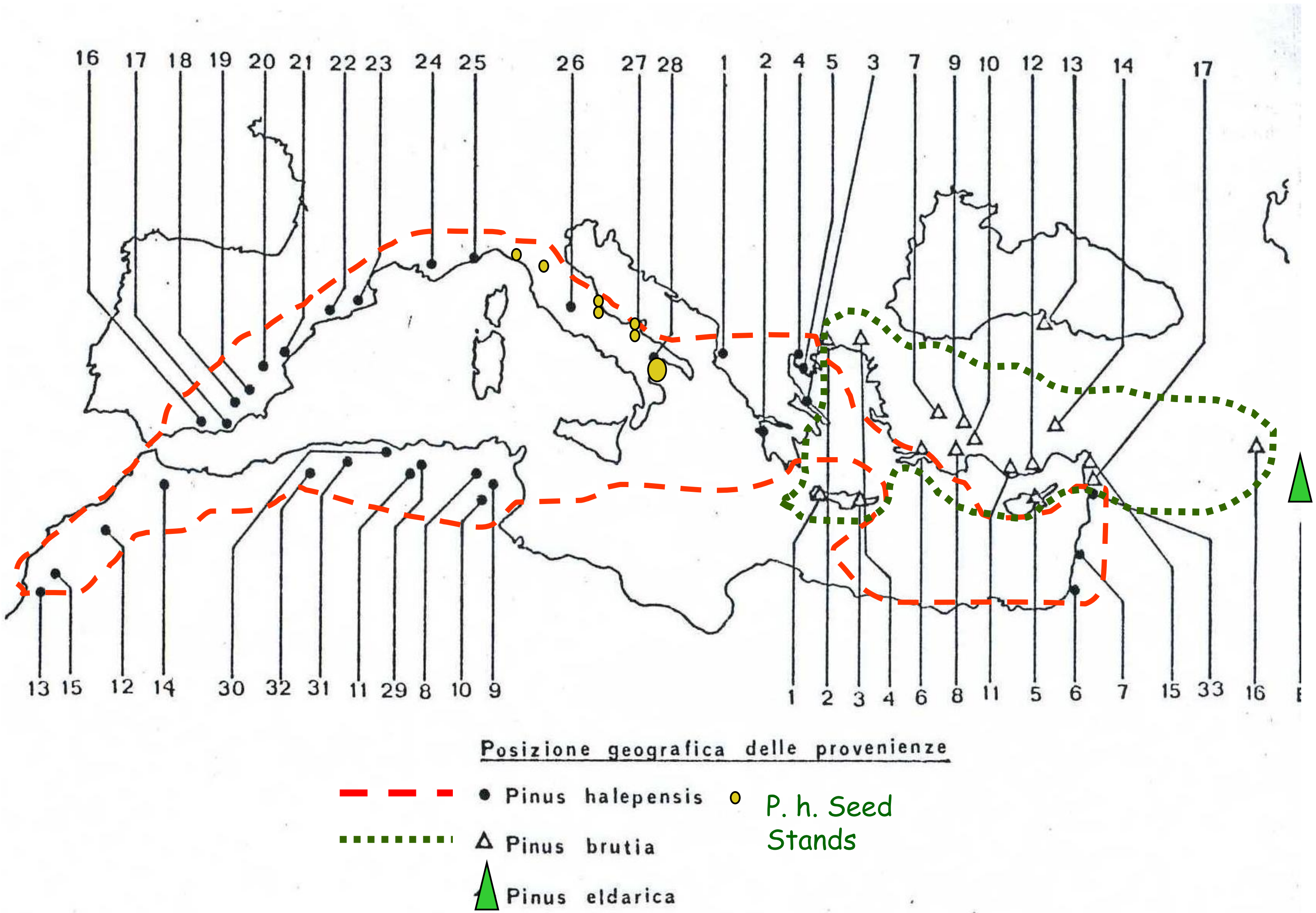
-- phenology;

-- adaptation (survival)

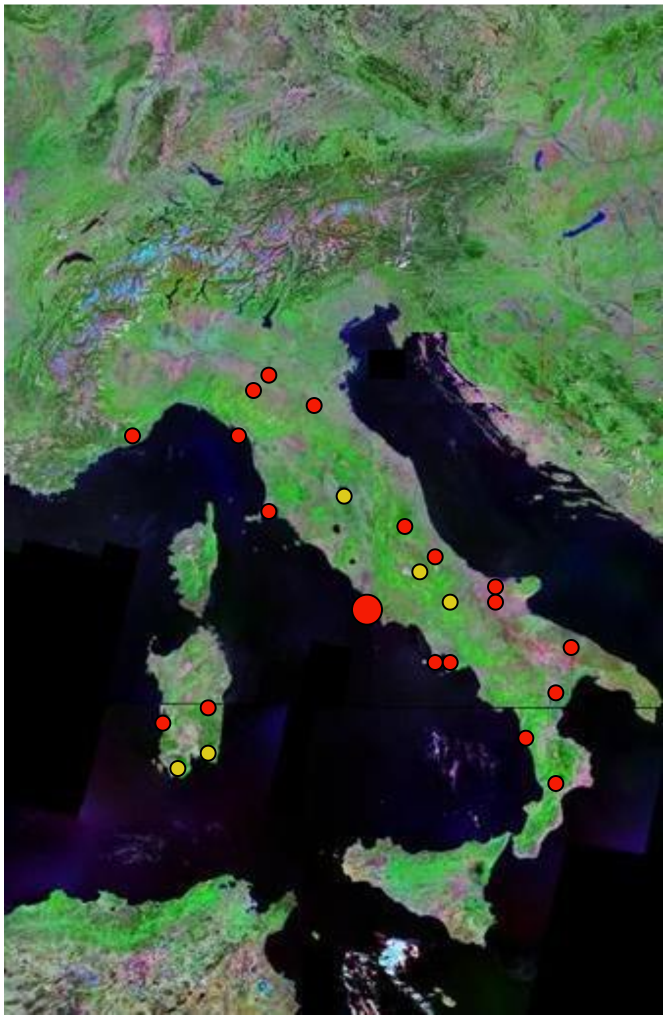




The international network of FAO/4bis (Coord. Ex ISSEL)
on ***Pinus helepensis Section*** Species/Provenances shared by 8 Medit. partners



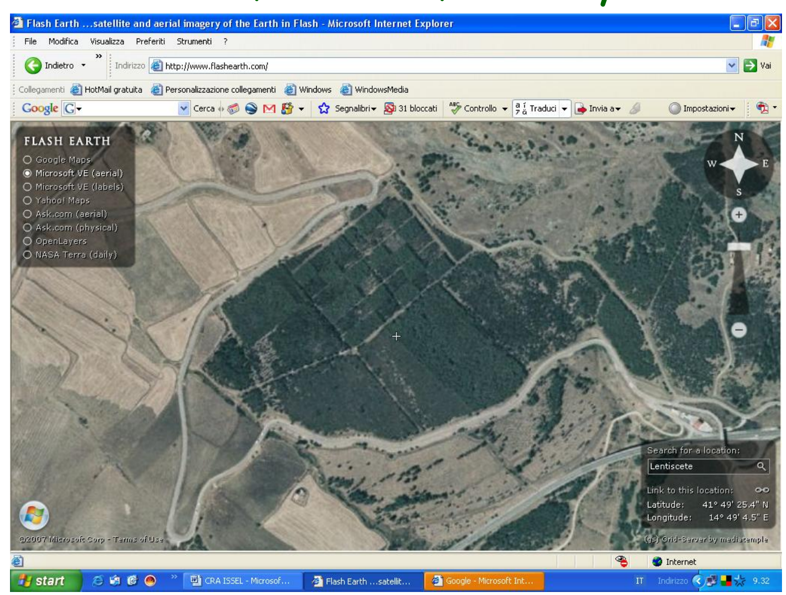
Mediterranean Pines (Haleppo pines section - International trilas in Italy



- Network CRA - PLF
- Network CRA - SEL

36 test still exist on 70 initially planted since 1975 in Italy, among about 300 tests were established in the framework of **FAO Silva mediterranea**.

Algeria, France, Greece, Israel, Italy, Morocco, Tunisia, Turkey

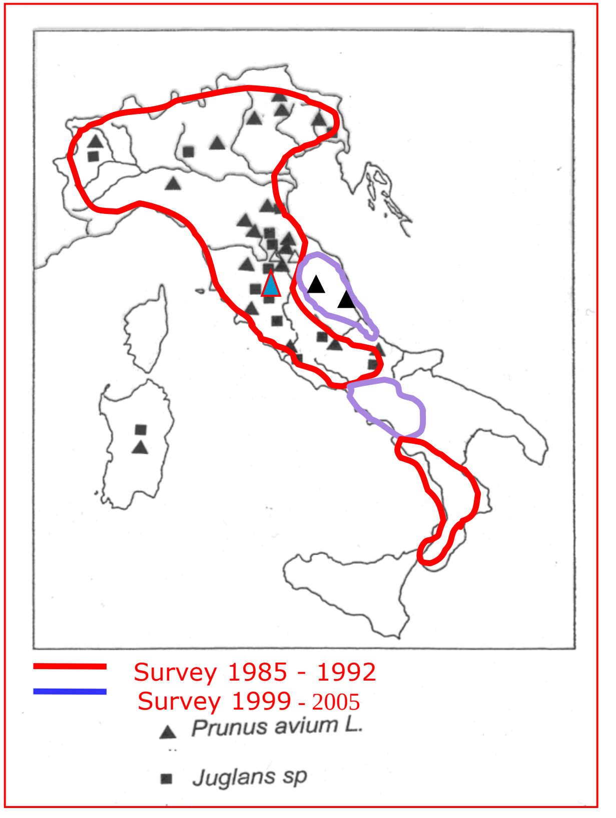


Lentiscete test site

southern Apennines CRA SEL

Prunus avium

- **1993, 29 Provenance/progenies from Caucasus** shared with INRA P1 (bilateral coll.) in 3 Italian sites (1 lost in 2008);
- **1993, 14 Italian clones + 11 French clones** (AIR Always) in 3 Italian sites;
- **2003, 11 full sib families FR x IT** shared with INRA P1 (bilateral coll.); only 1 Italian site.
- **2009, Seeds/seedlings exchanges** among EU countries (B. De Cuyper) for establishing trials.



Prunus avium

- The genetic variation of wild cherry trails was examined with severals tools, in order to have a multivariate approach:

- Molecular markers SSRs (10 loci) on trees from 30 populations

- Biochemical markers (9 isoenzyme) on the same populations

- Leaf shape on a set from the same populations

- Flower phenology recorded for 3 years in 3 clonal archives, where the above 250 clones are hosted

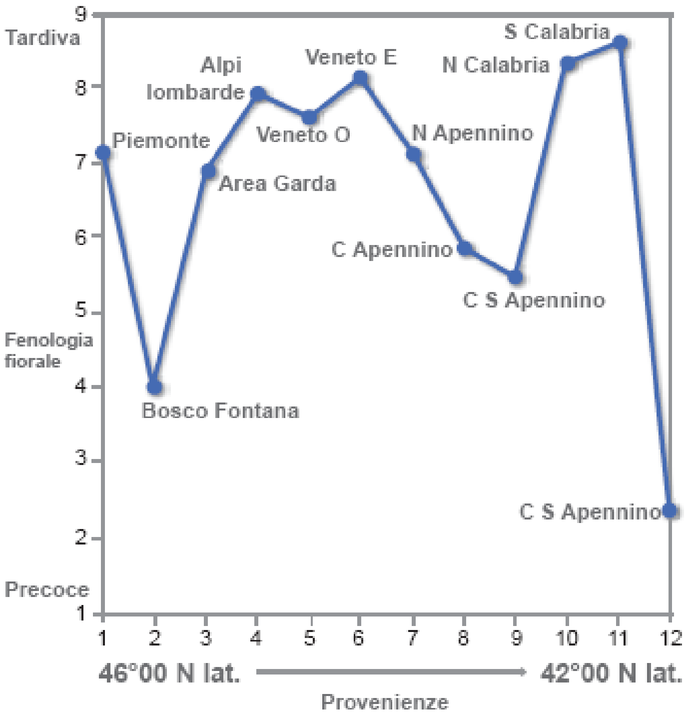
- Selection of *Prunus avium* L. clones for resistance to *Phytophthora* sp. : early screening on micropropagated cherry clones, tested *in vitro* to avoid the *Phytophthora* spread in the environment, 2 wild cherry tissues, callus from leaf shoots and micropropagated plantlets were tested *in vitro*

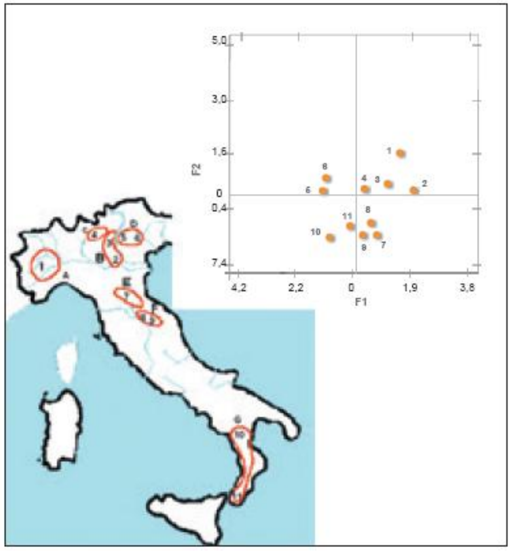
  Characterization of correlated proteins to pathogenous resistance by N*ative Page* electrophoresis

Prunus avium

Leaf shape
PCA
Provenance group

Early clones - 42°-45° latit.: BF, VG, VM, VTN, VTS, CT,AP, VLN
Late clones – 44°-46° latit.: AS, ML, PVS, TO, VC, VF
Factors: altitude and latitude





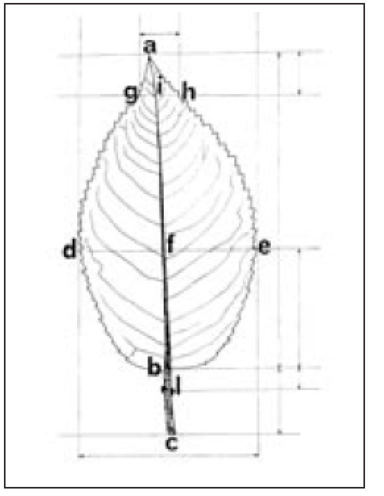
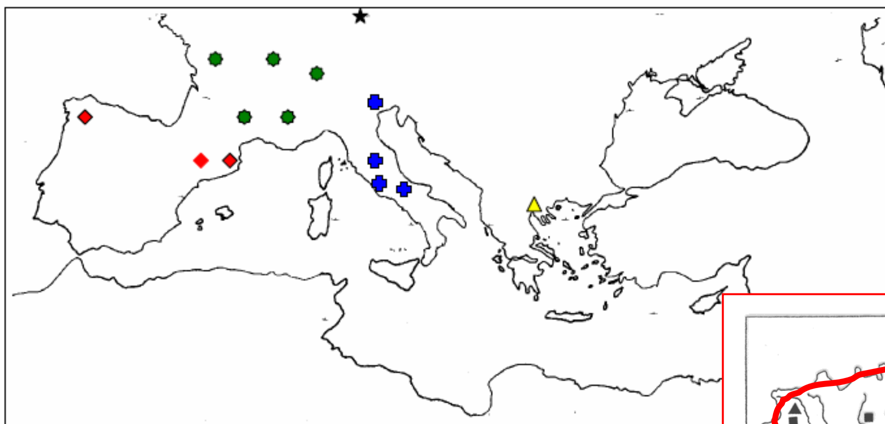


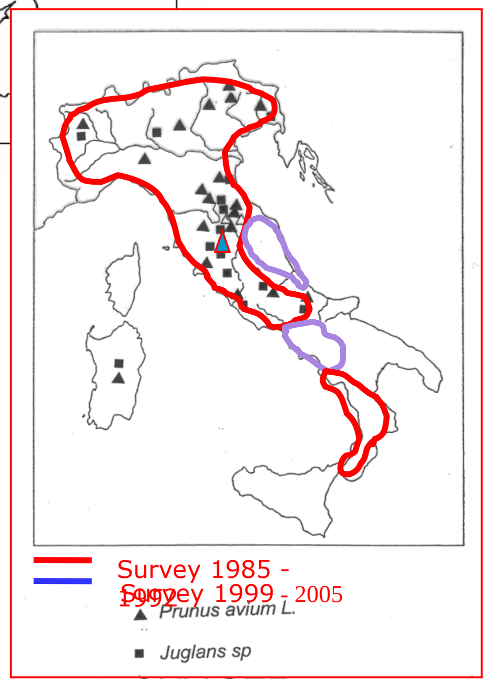
Figura 5 b - Parametri impiegati per la forma delle foglie (Ducci *et al.* 1996).

Juglans sp.

Walnuts and *Brains* EU PRJs-International trails on EU walnuts materials.

Figure 1 - The field test network established between 1995 and 1996 in the frame of Walnut Air Programme and continued during the Brains programme.

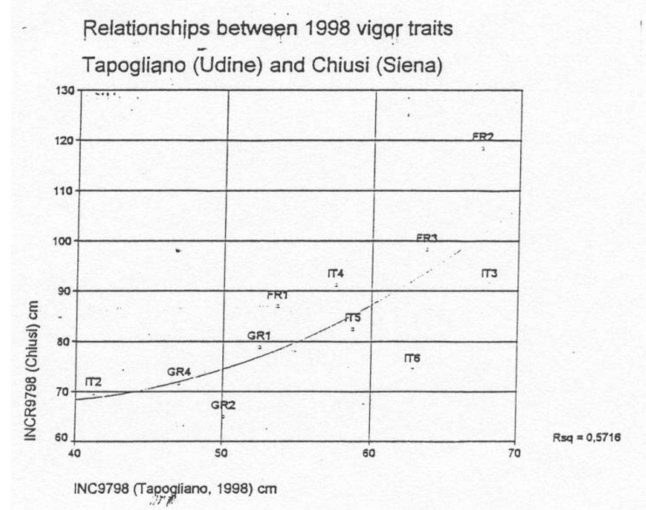


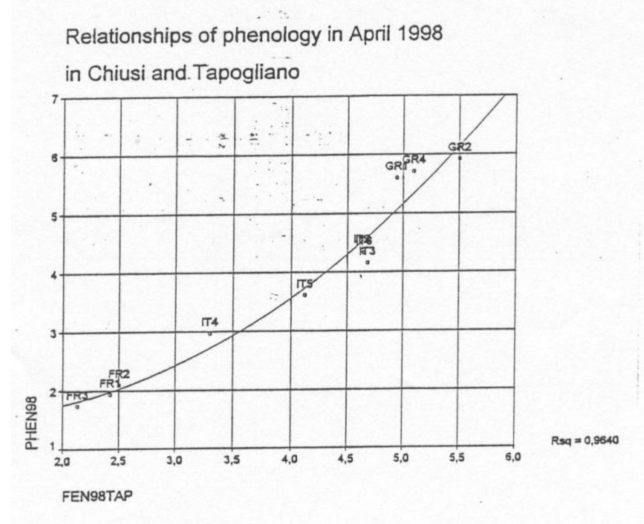


- Phenotypic traits;
- growth;
- tolerance/resistance to frosts;
- physiology of resistence to frosts.

Very good information for adaptation (phenology) and stem quality and architecture variability.

Database of tests does exist.

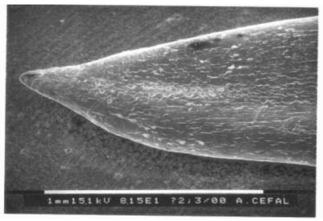




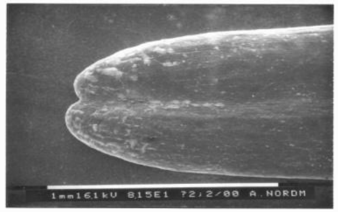
Stability of provenance phenology in two very different sites: northern Italy and South.

The Italian Greek fir and other Mediterranean firs

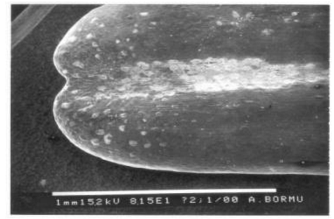
International field networks IUFRO



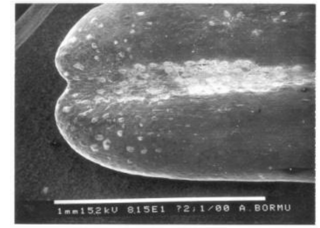
A. cephalonica



A. nordmanniana



A.bornmuelleriana



A. equi-trojani

Species	Provenances
A. bormulleriana	Cangal
	Uludag
	Kokez
	Arag
A. nordmanniana	Karalindere
	Ardanug
A. Equi-troiani	Kazdag
A. alba	Camaldoli,

<u>Best provenances for growth:</u>

Cangal and Arag for *A. bormuelleriana*

Kazdag – *A. equi-trojani*

Good growth performance of *A. bormuelleriana* for dry regions

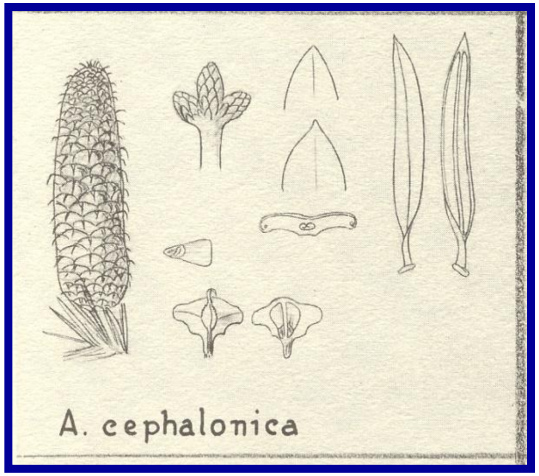
A. alba good perrformance for hight

A. nordmanniana: bad results

Abies cephalonica

1970 - 3 Comparative provenances field tests :

- Londa (Florence – Tuscany)
- Monte Capraro (Isernia – Molise)
- Colle Soda (Pescara – Abruzzo)



Shared with France INRA and Greece AUTH

sigla	popolazioni	massiccio montuoso	lat.	long.	altitud.	prec.med. annua	temp.med. annua	substrato geologico	specie
Vlah	Vlaika	Mainalon	37°35′	22°11′	1200	1200	---	calc. dol.	A. cephalonica
Kapo	Kapota	Mainalon	37°35′	22°11′	1300	1200	---	calc. dol.	A. cephalonica
Pnas	Parnassos	Parnaso	38°35′	22°30′	1050-1250	1200	10.4	flysch	A. cephalonica
Kolo	Kolokithovrissi	Parnaso	38°33′	22°29′	1250	1200	---	flysch	A. cephalonica
Mevr	Megali Vrisi	Parnaso	38°33′	22°29′	1220	1200	---	flysch	A. cephalonica
Brom	Bromopigado	Parnaso	38°33′	22°34′	1800	1200	---	calcare	A. cephalonica
Koro	Koromilies	Parnaso	38°35′	22°31′	1500	1200	---	calcare	A. cephalonica
Pril	Profitis Ilia	Taigeto	37°05′	22°16′	1450	1300	---	calcare	A. cephalonica
Pesc	Pescopennataro	/Alto \Molise	41°50′	14°13′	850-1450	838	7.4	flysch	A. alba

- Total height:: 1977,1982, 1990.........
- DBH in 1990;
- Annual increments: 1973 to 1978;

- Bud phenology in May/June 1978 (Debazac,1965-1967, method):

0 – dormant bud → 4 – young shoot

Populus sp.

Several international international trials were carried out in the past in the framework of the following.....

- **Bacterial and fungal pathogenesis** in relation to EC poplar breeding programmes (FOREST, MA1B 006C).
- Risk evaluation and prevention through **durable resistance** (MA2B CT91 0012)
- Inter disciplinary research for **poplar improvement** (AIR1 CT92 0349)
- **Poplars for farmers** (AIR3 CT94 1753)
- Strengthening of research capacity for **poplar and willow** multipurpose plantation growing in Serbia (STREPOW – FP7 REGPOT 2007-3)

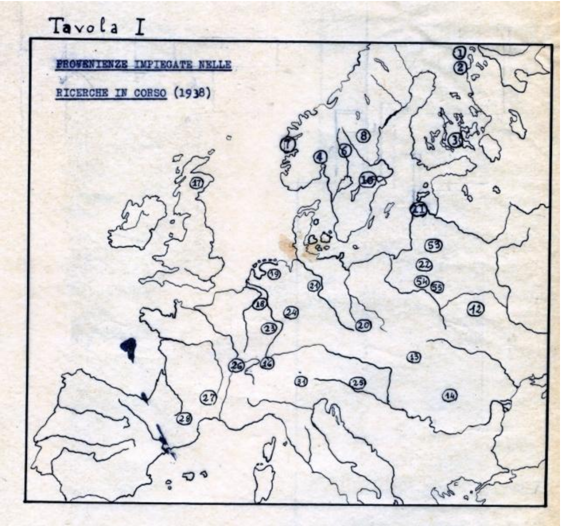
Old trials still existing and maintained

Pinus sylvestris

International IUFRO TRIALS

- 1938 IUFRO Field test located in Brenna (Como-Lombardy) Lat 45° 40' N Long. 9°10' E
- 1958 National field test 1958 – 1962 located in Caldaro (Bozen) Lat.46°25' 17" Long. 11°13' 00"
- 1958 National field test 1958 – 1962 located in Pievepelago (Bologna) Lat.44°12'Long. 10° 37'

–**IUFRO 1938:** Provenances from **central Europe (Germany, Hungary, Tchekia and Belgium)** and from **central oriental groups (Poland, and Germany)** showed the best performances for adaptation (*survival*) as well as for *growth*. Concerning *stem form* the best material was the Italian from Olgelsca (stand n. 63 and Val di Fiemme (n. 131).



Larix decidua

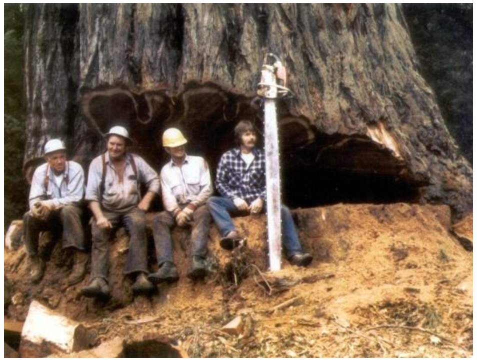
In Italy first field trials of *L. decidua* were planted by CRA SEL in 1944 in the frame work of IUFRO programmes. 22 provenances of European larch were used.

No breedng programmes are at present ongoing, beaing suitable areas for larch restricted to the natural range, requested only selected materials for afforestation in the frame work of traditional mountain silviculture.

Anyway, plots stil exist and can be used for monitoring adaptation etc..

Conclusion

- International trials allow the evaluation of materials based on large environmental range, either for interaction *genotype x environment* for multiple productive and adaptive traits.
- Nowadays, in view of the global change effects, they are **open air laboratories** for studying deeply **adaptation** and **genetics of adaptation** and supply information on FGR reactions strategic for mitigation activities and preserving resources ***in situ*** and ***ex situ*.**
- Many problems for long term managing, for maintainance, conserving continuity in the time, problems due to changes in people, but now also to the increased ferquence of **extreme events**.



Managing trials, problems of oversized materials!!!...

Pme in Tuscany...☺

Forest fires after the hard drought in 2007,

Pha FAO collection in S Italy.

Caucasus collection lost after extreme rainfalls in spring 2008. **Pav** in N Italy.

Thank you very much!

Provenance trial networks as a tool for biochemical and molecular genetics of forest trees

Berthold Heinze

BFW – TBX P02 – Vienna, Austria

TBX Seminar on Large field trial networks, Sekocin, PL, June 2010

I - Field trials as a "quick and easy" way to collect material

- collect diverse material for genetic marker studies in one place

pros:

- many diverse sources at one place
- replicated (other labs can use the same material) - standardisation & comparison
- relevant for practical purposes – hope to distinguish better and worse provenances with markers

Lagercrantz and Ryman 1988, 1990

- first to assess range-wide variation in a forest tree with isoenzyme (allozyme) markers
  - Norway spruce IUFRO 1964/68 trial in Sweden
- key innovation: using diploid material from buds for analysis
- multivariate trends in accordance with geography

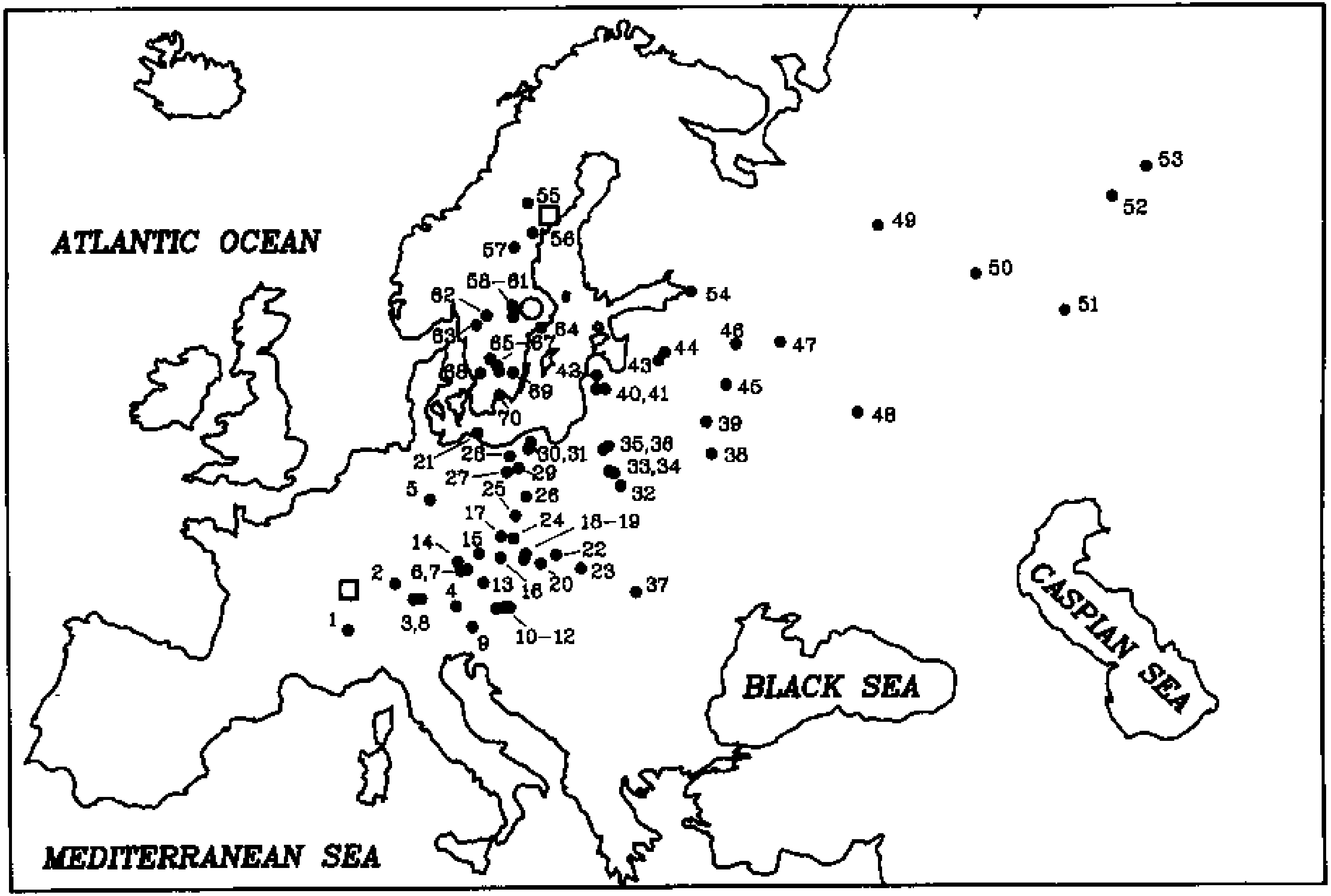


FIG. 1. Geographic locations of the original seed collections of Norway spruce (see Table 1). The open squares indicate experimental sites for morphological data from the field trials of the IUFRO 1964/68 program; the open circle indicates the experimental site for the nursery experiment in central Sweden.

Further examples

- Prus-Glowacki and Bernard 1984,
- Oleksyn et al. 1994 *(Pinus sylvestris):*
  - correlation of genetic data with pollution of the field trial site
- Kannenberg and Gross 1999 *(Picea abies):*
  - geograpic patterns at some loci
  - higher variation in the North and in the Balkans
- Mihai and Teodosiu 2009 (*Larix decidua*):
  - high diversity at the edge of the range

Kannenberg and Gross 1998

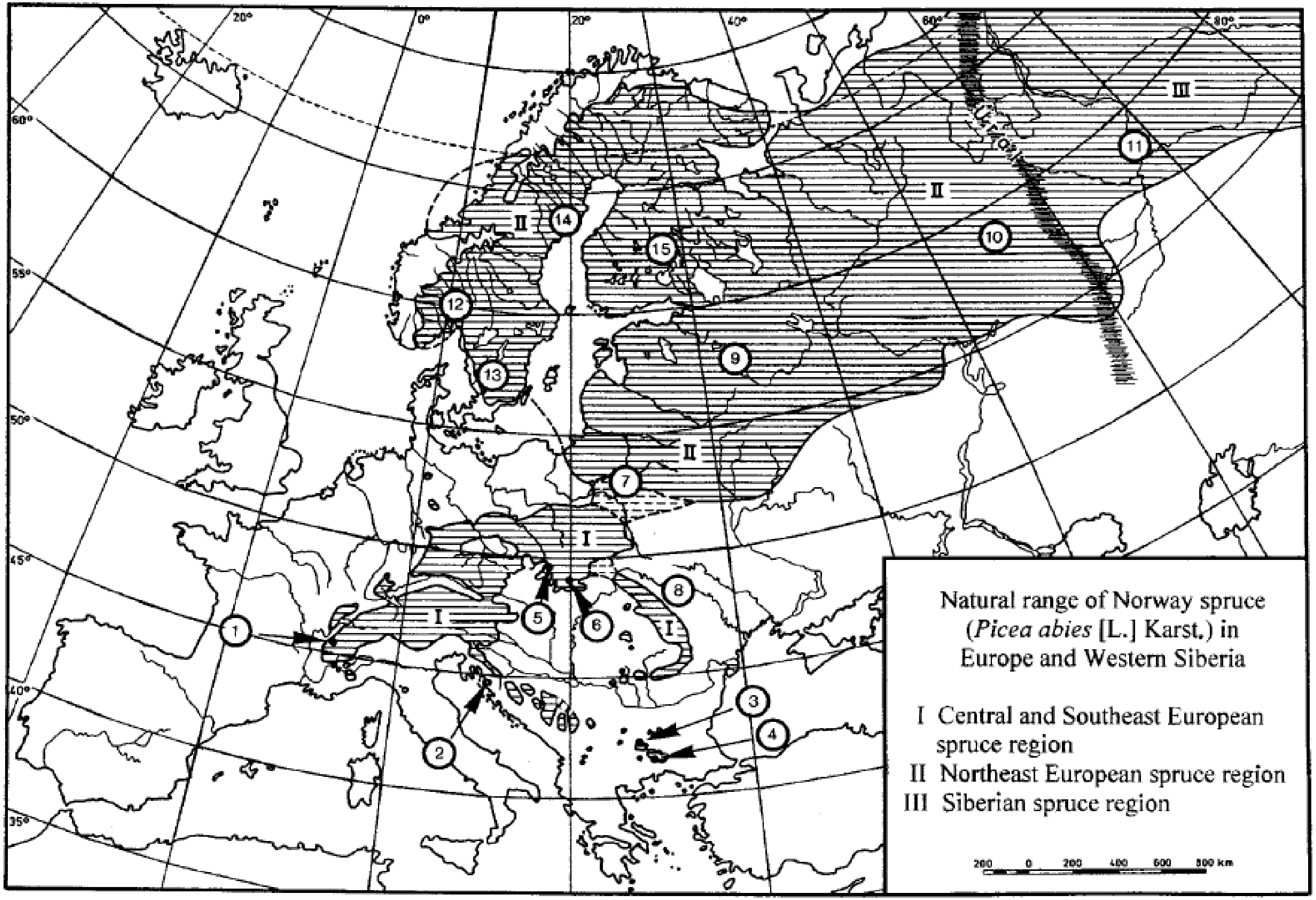


Figure 1. – The European natural range of Norway spruce [from SCHMIDT-VOGT (1977), slightly modified] and the places of origin of the 15 spruce provenances investigated.

Nice example from Poland

- Chalupka et al. 2008 (*Picea abies*):
- reconstitution of Kolonowskie seed source
- original stand of IUFRO seed collection disappeared
- source was very good at many test sites
- seed orchard constructed from offspring genotypes in tests
- confirmed with genetic markers

Other types of markers in traditional studies

- marker type is largely irrelevant from the point of view of trial management
- other nuclear DNA markers:
  - Perry et al. 1999, *Picea abies*
  - sequence-tagged sites (PCR [RFLP])
- chloroplast microsatellites:
  - Vendramin et al. 2000, *Picea abies*
  - geographic variation in congruence with only two glacial refugia
- mitochondrial minisatellites:
  - Sperisen et al 2001, *Picea abies*
  - confirmed two glacial refugial populations colonizing Europe

Further example

- chloroplast and mitochondrial markers combined:
  - Gugger et al. 2010, *Pseudotsuga menziesii*
  - differentiation of Rocky Mountain populations, but not those at the coast
  - zone of introgression / hybridization
  - use this information to trace origins of early introductions in Europe?

Department of Genetics

Disadvantages

- exact identification of source
  - especially in older trials
  - area/region vs. stand
- exact descent of material
  - how many mothers - which is which?
- source material may have disappeared
  - seed stands cut for timber
- possible natural genetic selection in the nursery /at the trial site
- comprehensiveness (range-wide?)

Disadvantages - examples

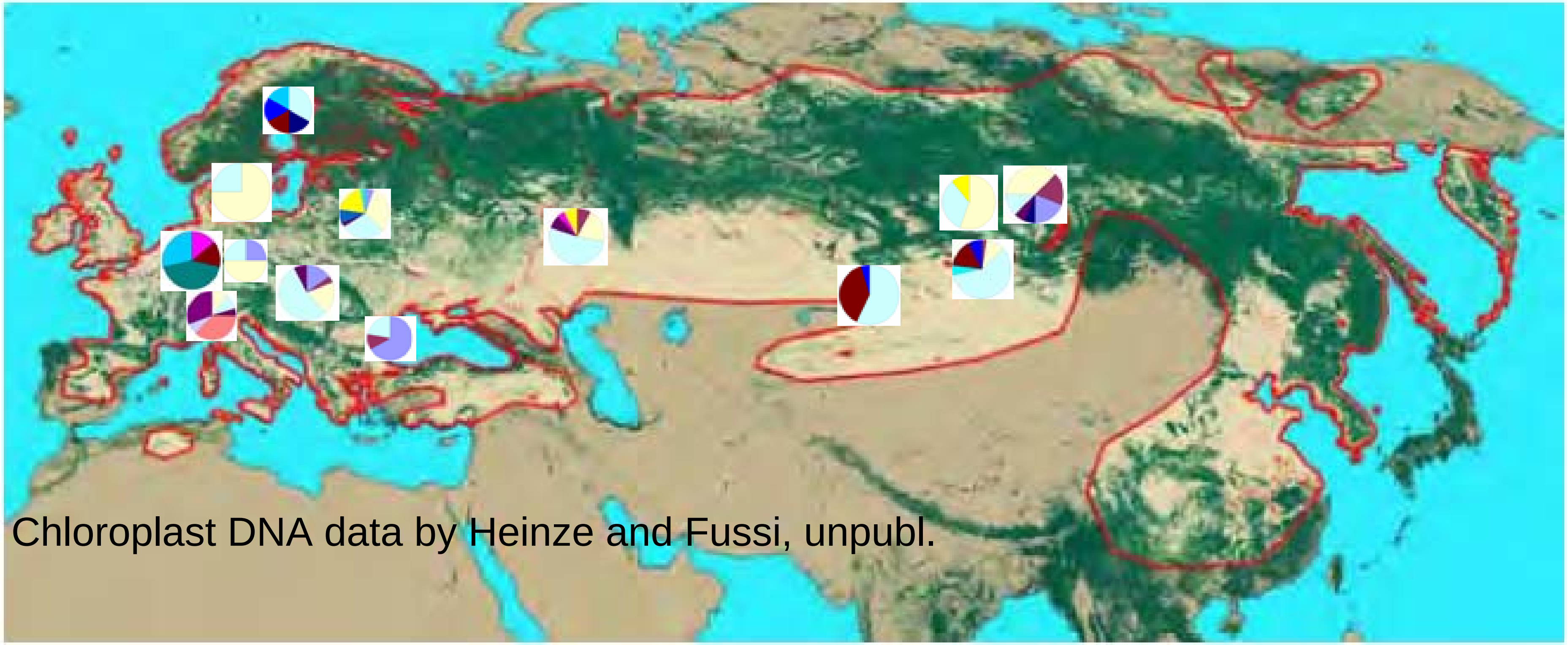
- Cieslar 1905 *Quercus robur*
  - (Cieslar 1923)
  - 1 or 2 mother trees only
  - no repetitions
- pre-IUFRO trials in general
  - often inferior statistical design
  - sources not traceable any more?
- IUFRO trial series restricted to few species
  - spruce, larch, Doug fir
- RAP Fraxinus – not range-wide

Alternatives for obtaining diverse material

- request seeds (or collect yourself)
  - preferred for conifers
  - haploid megagametophytes
- visit stands
  - preferred for controlling relatedness of material
  - e.g. 30/50 m between sampled trees
- correspondents
  - dried leaf material in a letter
  - leaves in silica gel

Example: *Populus tremula* range

- would be impossible to visit multiple sites
- nor to send seeds easily



Map 18. Natural range of *Populus tremula* in Eurasia and Africa. Redrawn from Fenaroli and Gambi (1976).

„Added value“ of large trial network?

- not really present yet
- multiple-site studies are rare
- multiple-lab studies are rare
- has the value not yet been realised?
  - selection effects at different sites?
  - pedigree reconstruction?
  - genetic diversity and plasticity?

Selection, adaptation and epigenetic effects

- seedlings planted in various climates may undergo selection
- difficult to disentangle selection and local adaptation effects
  - first vs. further generations?
- epigeneitc effects described in *Picea abies*
  - T. Skroppa, O. Johnson et al.
  - seedlings behave different if harvested in different climate, but from identical trees
  - Hungarian example – Ujvari Jarmay and Ujvari 2006:
  - *Picea abies* seeds harvested in IUFRO trial
  - selected mother trees often exceeded growth of local material
  - well-known „maternal effect“ (seed nutrition after-effects)
  - evident in high altitude *Picea abies* in the Alps

Little "marking" capacity for really interesting growth traits

- incongruence between observable growth and marker patterns (in some examples)
- often low Fst vs. high Qst
  - little genetic differentiation,
  - high quantitative variation
- reasons?
  - too few markers
  - selectively neutral markers
  - too simple models of inheritance
    - polygenic traits
    - more complex genetic interactions

II - The dawn of the age of genomics

http://www.mansfield.ohio-state.edu/~sabedon/2001_dawn05.jpg

II - The dawn of the age of genomics

- genetic mapping
  - required family pedigrees, not provenances
- maps of markers only, initially
- then QTLs:
  - quantitative trait loci
  - chromosome regions with statistical correlation to quantitatively measured traits
- progeny trials more interesting

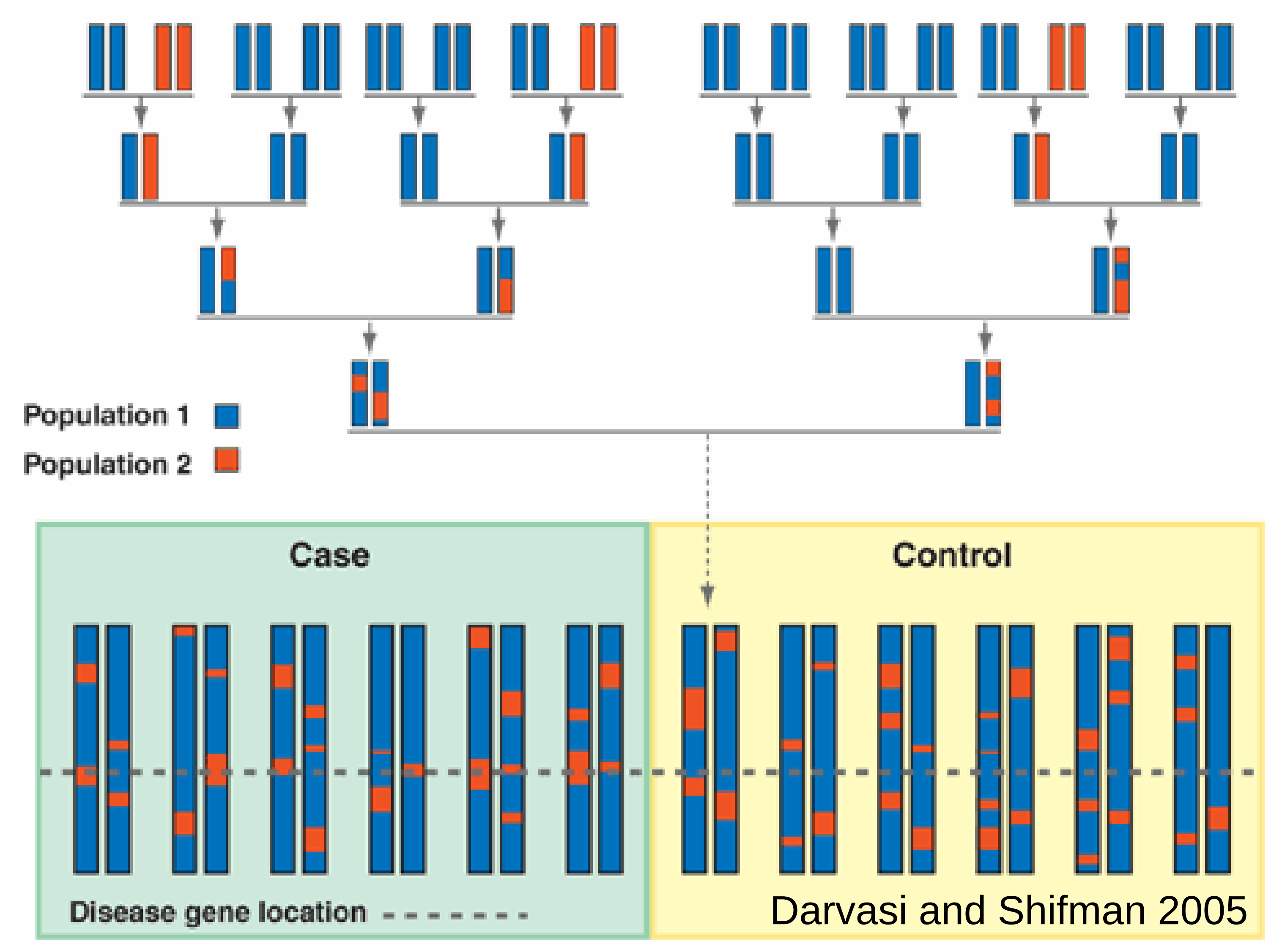
Problems with QTL mapping

- transferability:
  - markers or traits or QTLs (or all of those) not always transferable from one family to the next
  - from one experiment to the next one
  - effect of deleterious alleles in some families
    - vs. real superior alleles
  - interactions (genetic epistasis) are broken in a new genetic background)

Alternatives from human genetics

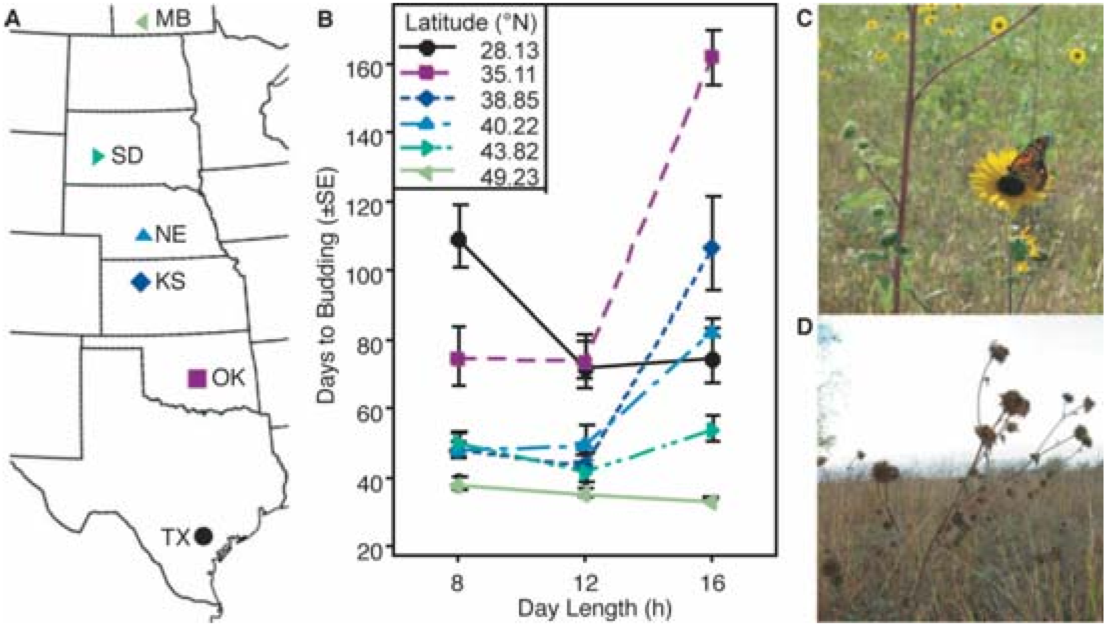
- building large pedigrees is also not feasible
- admixture mapping:
- linkage disequilibrium building up through natural hybridization and backcrossing

Alternatives from human genetics



Examples in plants –
Loren Rieseberg's lab

- work in hybrid sunflower
- backcrosses loose most genes from other species
- but retain the ones that give them an advantage



http://www3.botany.ubc.ca/riesebergla b/research.html

III - Another alternative: association studies

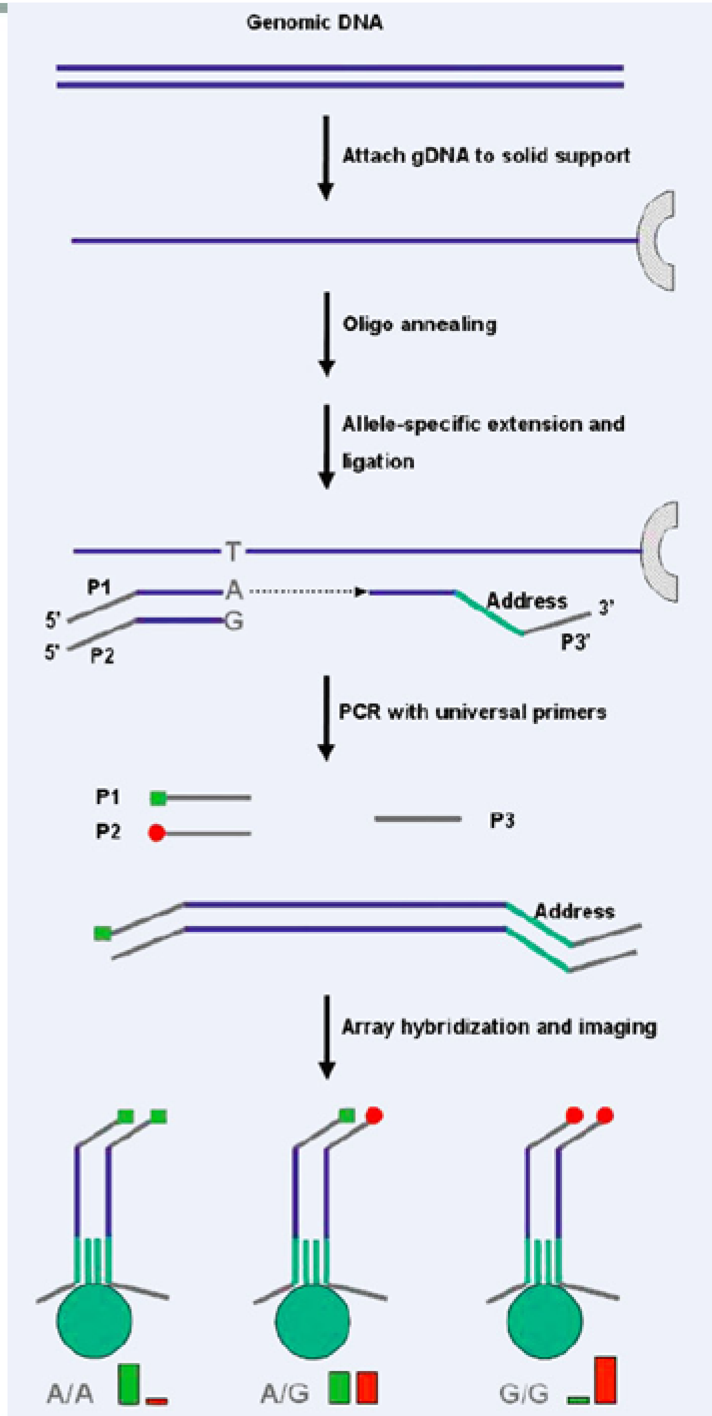
- simple correlations between markers and traits
- going back to the original idea of genetic markers
- at candidate genes
- across the whole genome
  - *Arabidopsis* and other models
- simple, but what are the problems?

Digression - technical advances

- next generation sequencing
  - new sequencing methods for very high throughput
- massively parallel SNP assays
  - assess hundreds of single nucleotide polymorphisms in hundreds of samples
- methods often available from larger centres or specialised companies

Illumina Golden Gate assay

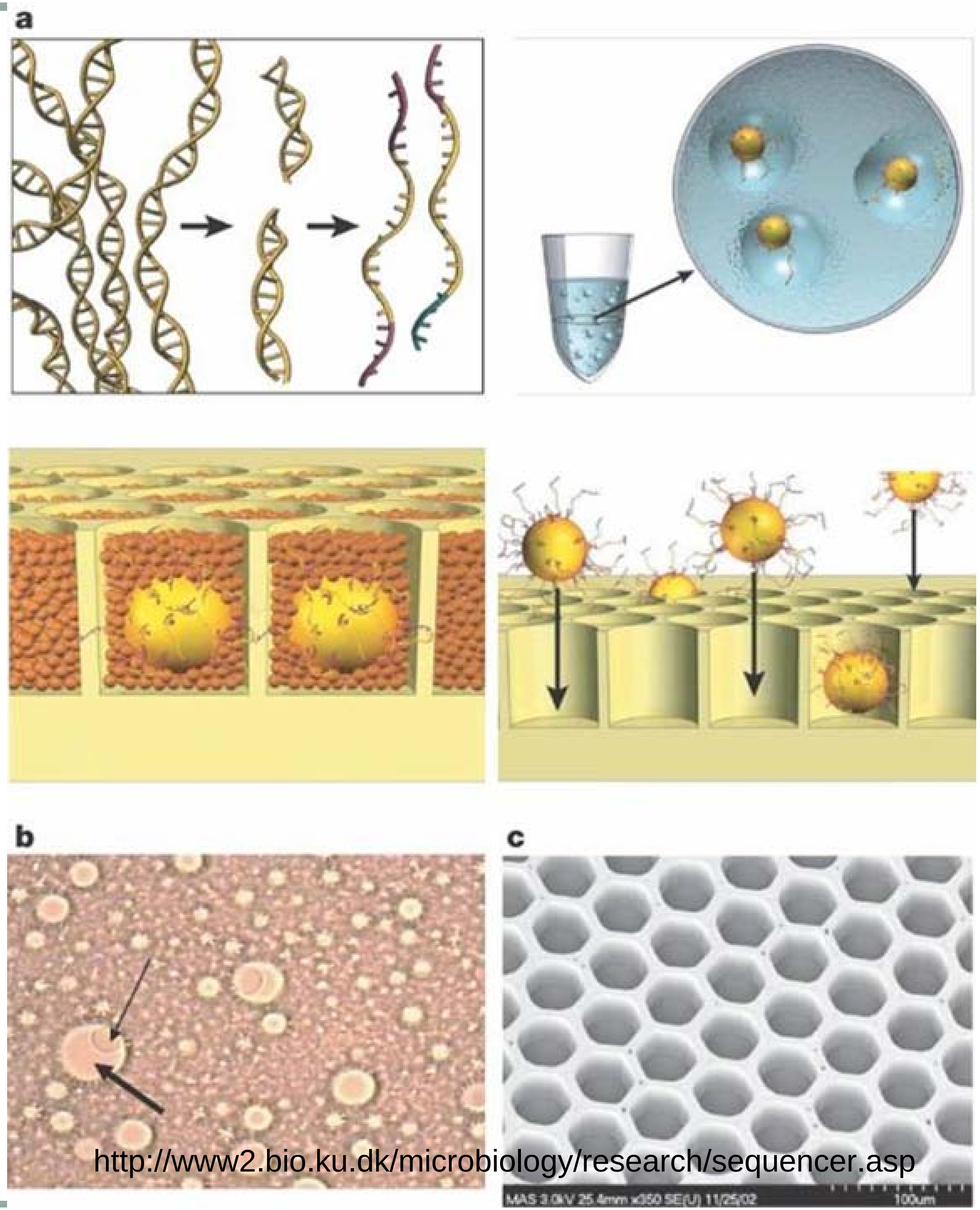
- 1536 pre-defined SNPs in one run
- hundreds (thousands) of individuals



http://www.genomecenter.ucdavis.edu/dna_technologies/illumina.html

Next generation sequencing technology example

- Roche/454 pyro-sequencing



http://www2.bio.ku.dk/microbiology/research/sequencer.asp

Table 1 | **Comparison of next-generation sequencing platforms**

Platform	Library/ template preparation	NGS chemistry	Read length (bases)	Run time (days)	Gb per run	Machine cost (US$)	Pros	Cons	Biological applications	Refs
Roche/454's GS FLX Titanium	Frag, MP/ emPCR	PS	330*	0.35	0.45	500,000	Longer reads improve mapping in repetitive regions; fast run times	High reagent cost; high error rates in homo-polymer repeats	Bacterial and insect genome *de novo* assemblies; medium scale (<3 Mb) exome capture; 16S in metagenomics	D. Muzny, pers. comm.
Illumina/ Solexa's GA_{II}	Frag, MP/ solid-phase	RTs	75 or 100	4‡, 9§	18‡, 35§	540,000	Currently the most widely used platform in the field	Low multiplexing capability of samples	Variant discovery by whole-genome resequencing or whole-exome capture; gene discovery in metagenomics	D. Muzny, pers. comm.
Life/APG's SOLiD 3	Frag, MP/ emPCR	Cleavable probe SBL	50	7‡, 14§	30‡, 50§	595,000	Two-base encoding provides inherent error correction	Long run times	Variant discovery by whole-genome resequencing or whole-exome capture; gene discovery in metagenomics	D. Muzny, pers. comm.
Polonator G.007	MP only/ emPCR	Non-cleavable probe SBL	26	5§	12§	170,000	Least expensive platform; open source to adapt alternative NGS chemistries	Users are required to maintain and quality control reagents; shortest NGS read lengths	Bacterial genome resequencing for variant discovery	J. Edwards, pers. comm.
Helicos BioSciences HeliScope	Frag, MP/ single molecule	RTs	32*	8‡	37‡	999,000	Non-bias representation of templates for genome and seq-based applications	High error rates compared with other reversible terminator chemistries	Seq-based methods	91
Pacific Biosciences (target release: 2010)	Frag only/ single molecule	Real-time	964*	N/A	N/A	N/A	Has the greatest potential for reads exceeding 1 kb	Highest error rates compared with other NGS chemistries	Full-length transcriptome sequencing; complements other resequencing efforts in discovering large structural variants and haplotype blocks	S. Turner, pers. comm.

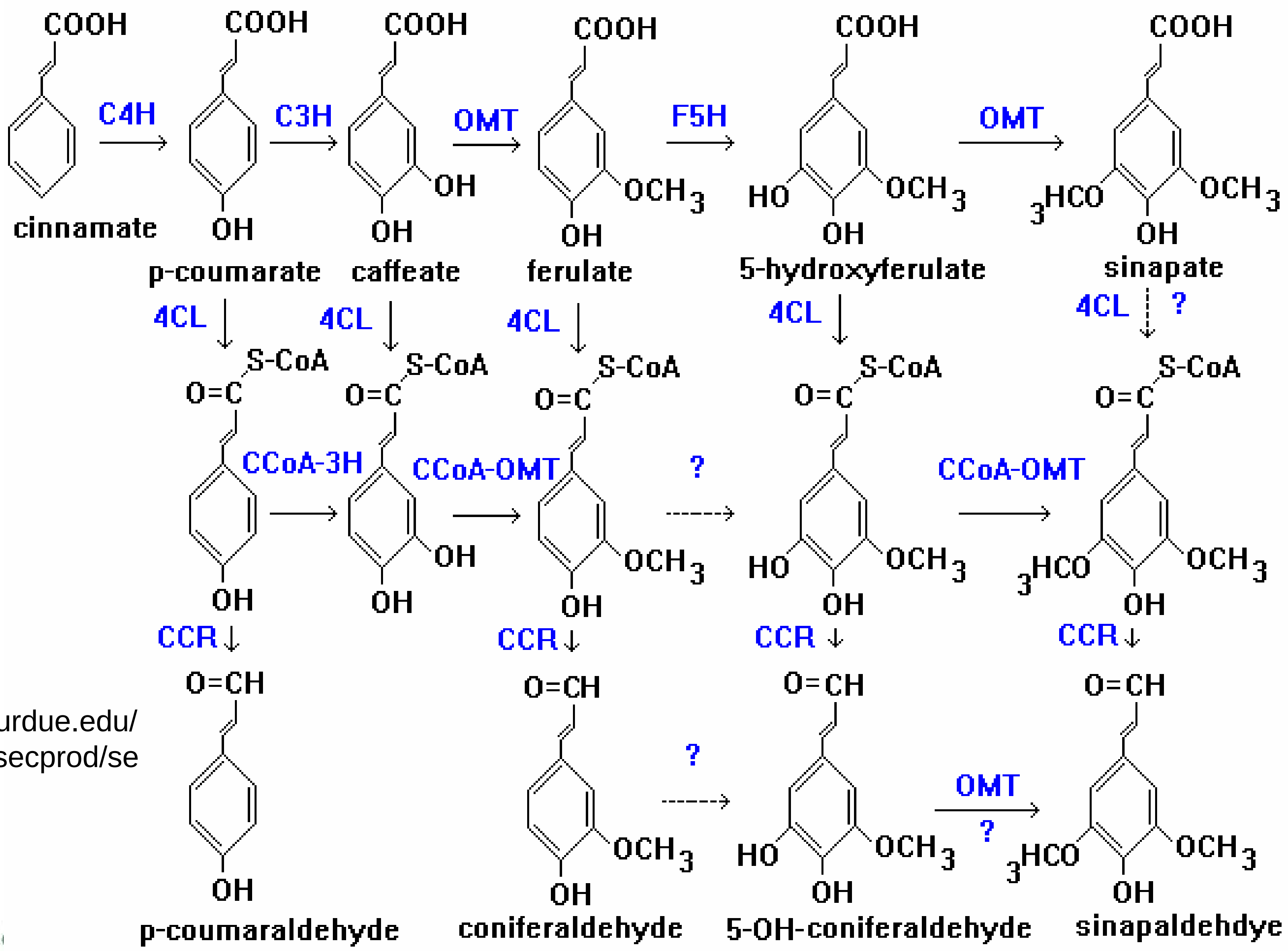
*Average read-lengths. ‡Fragment run. §Mate-pair run. Frag, fragment; GA, Genome Analyzer; GS, Genome Sequencer; MP, mate-pair; N/A, not available; NGS, next-generation sequencing; PS, pyrosequencing; RT, reversible terminator; SBL, sequencing by ligation; SOLiD, support oligonucleotide ligation detection.

Metzker 2010

How to do an association study

- collect material
- measure phenotypes
  - height, diameter, diseases, ...
- analyse as many markers as possible:
- candidate genes
  - for biological function
  - gene expression
  - from model organisms
  - from QTL regions
  - ...
- alternatively – whole genome sequencing
  - individual genomes in *Arabidopsis*
  - pools for other organisms (Futschik and Schlötterer 2010 in press)

Example - lignin pathway genes



http://www.hort.purdue.edu/rhodcv/hort640c/secprod/se00016.htm

B F W Department of

Genetic analysis in association studies

- mostly done by sequencing genes
  - PCR & sequencing
- or analysis of SNPs
  - sometimes a selection only
- next generation sequencing for sequence / SNP discovery
  - but not yet for re-sequencing = analysing the individual samples

How to do an association study (II)

- assess structure in the sample
- need to control for population substructure / family structure
  - e.g. STRUCTURE, pedigree reconstruction
- calculate statistical associations
  - dedicated software
  - special tests if structure is present
- verify in independent sample
  - e.g, 2/3 of sample in association
  - and 1/3 of sample for verification

Advantages of association studies

- ease of the approach for sampling
- inherently simple approach
- no building of pedigrees necessary
  - but family pedigrees can enhance the study

IV - Examples of association studies in trees (overview)

Demography

Heuertz et al. 2006
Picea abies
22 loci
excess of rare and high-freq. mutations; bottleneck

Pyhäjärvi et al. 2007, Palmé et al. 2008
Pinus sylvestris
16 candidate genes / EST databases
demography / selective sweeps

Eveno et al. 2007
Pinus pinaster
11 candidate genes
„outlier“ loci

Keller et al. 2010
Populus balsamifera
412 SNPs in 474 individuals + 11 sequenced genes in 94 individuals
3 geographical clusters; massive expansion inferred (after Ice Age)

Local adaptation

Ingvarsson et al. 2008, Luquez et al. 2008, ...
Populus tremula
77 gene fragments
excess of low-frequency mutations; bottleneck; association of flowering pathway genes with bud set (PHYB)

Namroud et al. 2008
Picea glauca
534 SNPs in 345 expressed genes
genes involved in local adaptation of some populations (e.g. drought, heat)

Holliday 2009 (dissertation)
Picea sitchensis
candidate genes from microarray studies; 768 SNPs
widespread purifying selection; some positive / diversifying selection; 28 associations for cold hardiness and budset (explained ~ 30% of phenotypic variation in mapping population from 12 geographical locations)

Gonzalez-Martinez et al. 2007, 2008; Eckert et al. 2010 in press

Pinus taeda

SNPs in up to 3059 genes

wood properties; carbon isotype discrimination; abiotic stress response; expansion from Mexico and Florida

Eckert et al. 2009a, b

Pseudotsuga menziesii

384 SNPs in 117 candidate genes / 121 candidate genes

cold-hardiness traits – 30 associations in 12 genes; 7 markers differentiated coast / interior; small effects of genes; selective sweeps at 3-8 loci; bottleneck

Wood traits

Dillon et al. 2010 in press

Pinus radiata

149 SNPs in cell wall candidate genes

10 significant associations with wood property traits

Characteristics of first generation of studies

- using traditional Sanger sequencing of some candidate genes and / or
- SNP detection panel
  - only a handful of samples
- followed by SNP assay on many individuals
- testing for deviation from neutrality
  - genes or alleles that show reduced or enhanced diversity
  - „footprints of selection“
  - „selective sweeps“
- testing for association with „geography“, wood traits

Issues with association studies

- sequences/primers not available for all species
- when testing many markers in many individuals, how to distinguish false positives from true association?
- association (statistical correlation) does not mean causal explanation
- often only a low percentage of variation explained by the markers/alleles/ SNPs
  - few percent, even if added
- would make marker-based selection inefficient

Recent exception - Pär Ingvarsson - *P. tremula*

- when considering also LD between markers, they explain up to 50% of phenotypic variation !
- approach suggested by Lewontin and Krakauer, 1970ies
  - P. Ingvarsson, @ EVOLTREE conference El Escorial, Spain, June 2010

HK Wildermieming/T (400-900 m), 22-jährig

Plantage Hamet (P3) - Lammerau (400-700 m), 22-jährig

Conclusions

- genome-wide („genomic“) studies will hopefully reveal genetic control of traits in many species soon
- technology advances make it possible to study many genes / whole genomes
- experimental networks are an ideal basis for such studies
- both provenance and progeny trials can be used
  - mix of unrelated material and crosses for plants
  - Myles et al. 2009
- basic research into gene function is necessary before gene markers can be used for selection

Phenotyping (measuring, observing, assessing, testing, counting ...) = „phenomics“ will become more and more important for genetic studies as genotyping becomes easier

Some of the studies are based on pedigrees, but ...

... does this mark the return of the provenance trials?

The return of the son of the provenance trial: genetic association studies in trees


Acknowledgement

- Wladislaw and Jan for the invitation ...
- ... and inspiration!
- Michael Mengl for literature hints
- Lambert Weißenbacher for provenance trial pictures
- Christian Lexer and Barbara Fussi for collaboration in *P. tremula / P. alba*

- thank you for your kind and lasting attention

Forest Research Institute

80 lat IBL

„Characteristics of genetic diversity and differentiation of progeny and mother stands of European Beech in Poland"

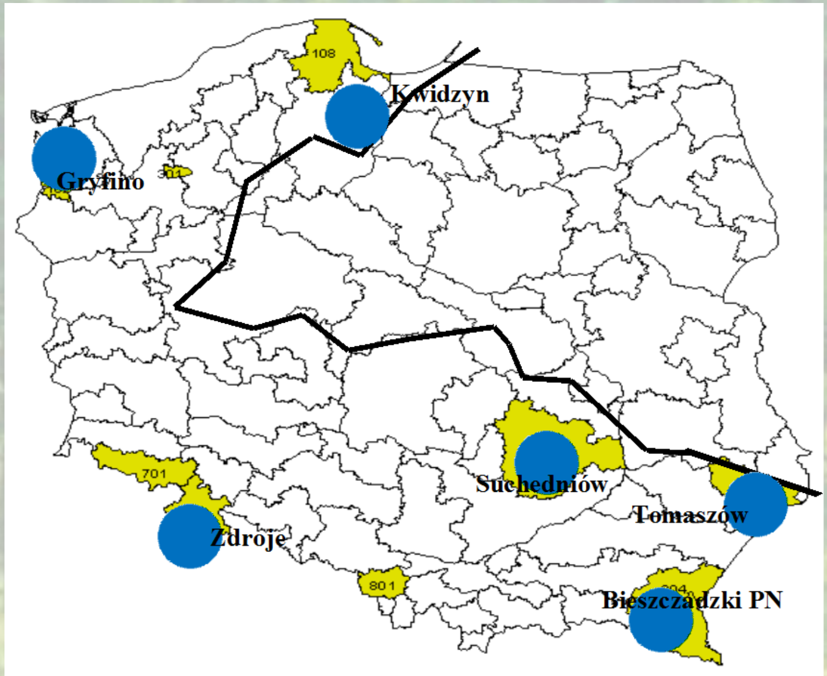
Małgorzata Sulkowska, Justyna Nowakowska

Sekocin   2010

Present genetic structure of European beech (*Fagus sylvatica* L.) populations was formed within last few thousand years influenced many different factors not only environmental (glacial epoch) and genetic (selection) but also anthropogenic. Beech is very important forest tree species in Poland and it ocupies 5,1% of forest area in Poland.

In Poland, beech attains its north-eastern limit of natural range, which is limited by: continental climate, soil conditions, winter temperatures and air humidity.

Methods



The investigated beech populations represent Beech Trial in Bystrzyca Klodzka. The were classified according to phytosociogical characteristics as the following plant associations: *Galio-odorati-Fagetum* (Gryfino and Kwidzyn), *Dentario glandulosae-Fagetum* (Bieszczadzki National Park), *Luzulo-luzuloides-Fagetum* (Suchedniów, Tomaszów), *Dentario enneaphyllidis-Fagetum* (Zdroje). The genetic structure of these populations was analyzed. Thirty individuals per one generation (mother, progeny stands) in every provenance were investigated.

Methods

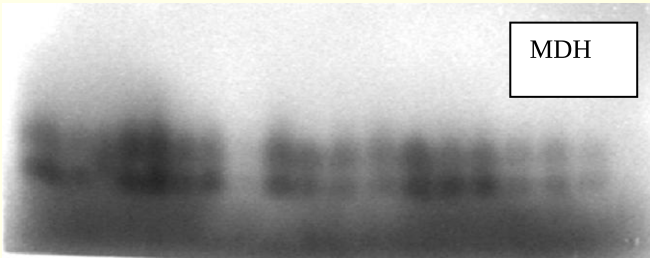
The genetic variation and differentiation of mother stands and their open-pollinated progeny were characterized on the basis of isoenzyme and DNA microsatellite chloroplast markers.

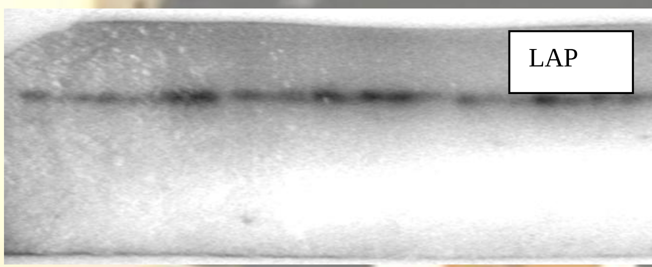
There were calculated following genetic parameters for both markers: average number of alleles per locus, percentage of polymorphic loci and heterozygosity observed and expected (on the of isoenzyme markers).

Parameters of genetic diversity (Hs and Ht) and differentiation (Gst and Gcs) were counted and compared between mother and progeny generation.

Dendrogrammes based on Nei (1972) genetic distances were constructed.

Methods



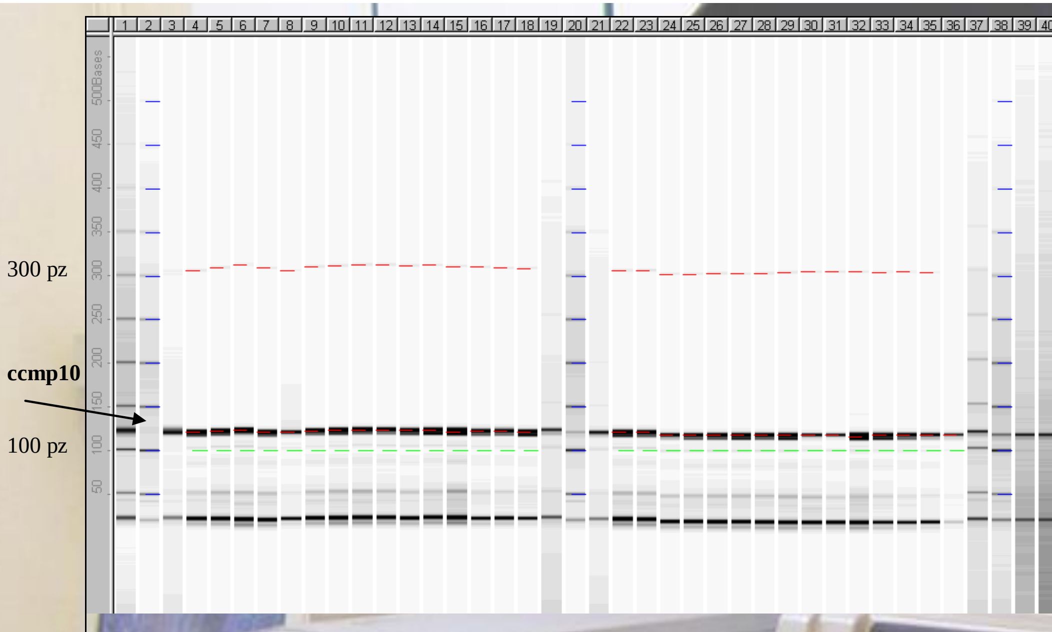


Following enzyme systems were analysed: glutamate-oxaloacetate transaminase (GOT – EC 2.6.1.1 – *Got-2*), leucine aminopeptidase (LAP – EC 3.4.11.1 – *Lap-1*), malate dehydrogenase (MDH – EC 1.1.1.37 – *Mdh-1*, *Mdh-2*, *Mdh-3*), menadione reductase (MNR – EC 1.6.99.2), phosphoglucomutase (PGM – EC 2.7.5.1), phosphoglucose isomerase (PGI – EC 5.3.1.9 – *Pgi-2*), shikimate dehydrogenase (SKDH – EC 1.1.1.25).

80 lat IBL

Sekocin 2010

B.



DNA microsatellite chloroplast markers: ccmp4, ccmp7 and ccmp10 were analysed in 8 % acrylamide gel using automatic sequencer ALFexpress II (Amersham Pharmacia Biotech). The obtained results were elaborated with ALFwin Fragment Analyser™ 1.0 software.

80 lat IBL

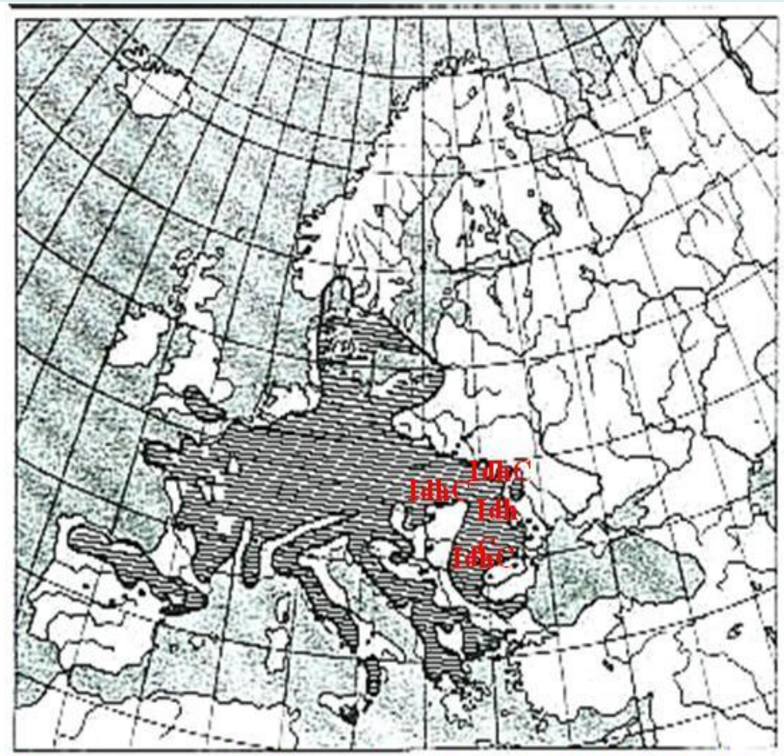
Sekocin 2010

Estimation of genetic differentiation of beech in Poland on the basis of isoenzyme analysis

•There is slight decrease of genetic variation of beech populations towards the north of Poland, which can be explain the migration paths and selection after glacial period.

•The genetic differentiation of beech in Poland do not allowed to distinguish provenance regions

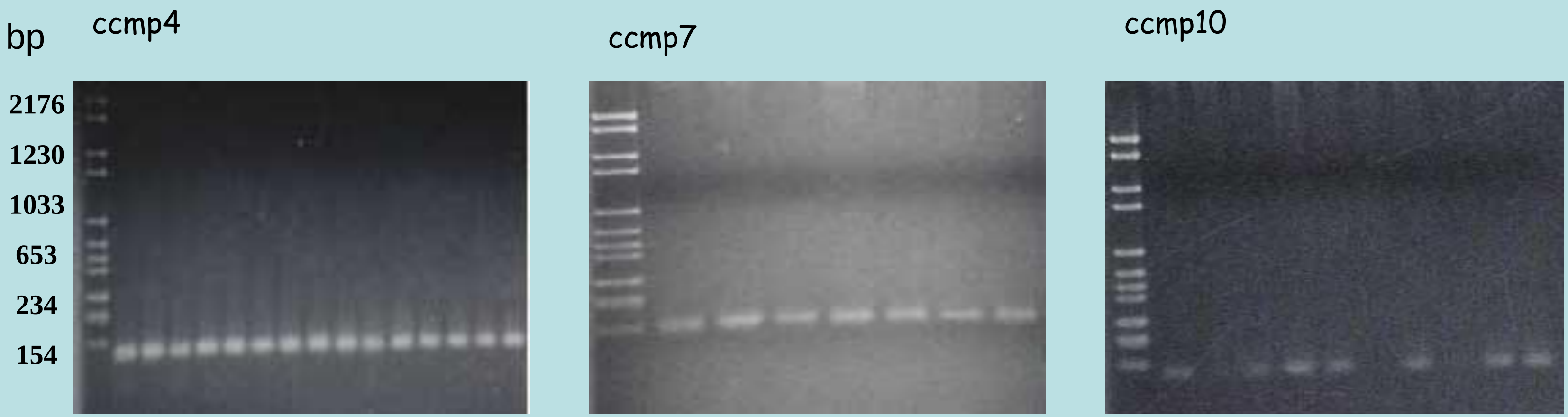
•The data showed mosaic character of species differentiation and its ecotype variation.



Migration path of beech on basis of Idh C allel.

Sułkowska, M. 2002: Analiza izoenzymatyczna wybranych proweniencji buka zwyczajnego (*Fagus sylvatica* L.) na powierzchni doświadczalnej w Bystrzycy Kłodzkiej. Sylwan 146 (2): 129-137.

Gömöry, D., Paule, L., Schvadchak, M., Popescu, F., Sułkowska, M., Hynek, V. & Longauer, R. 2003: Spatial patterns of the genetic differentiaton in European beech (*Fagus sylvatica* L.) at allozyme loci in the Carpathians and adjacent regions. *Silvae Genetica* 52(2): 78–83.

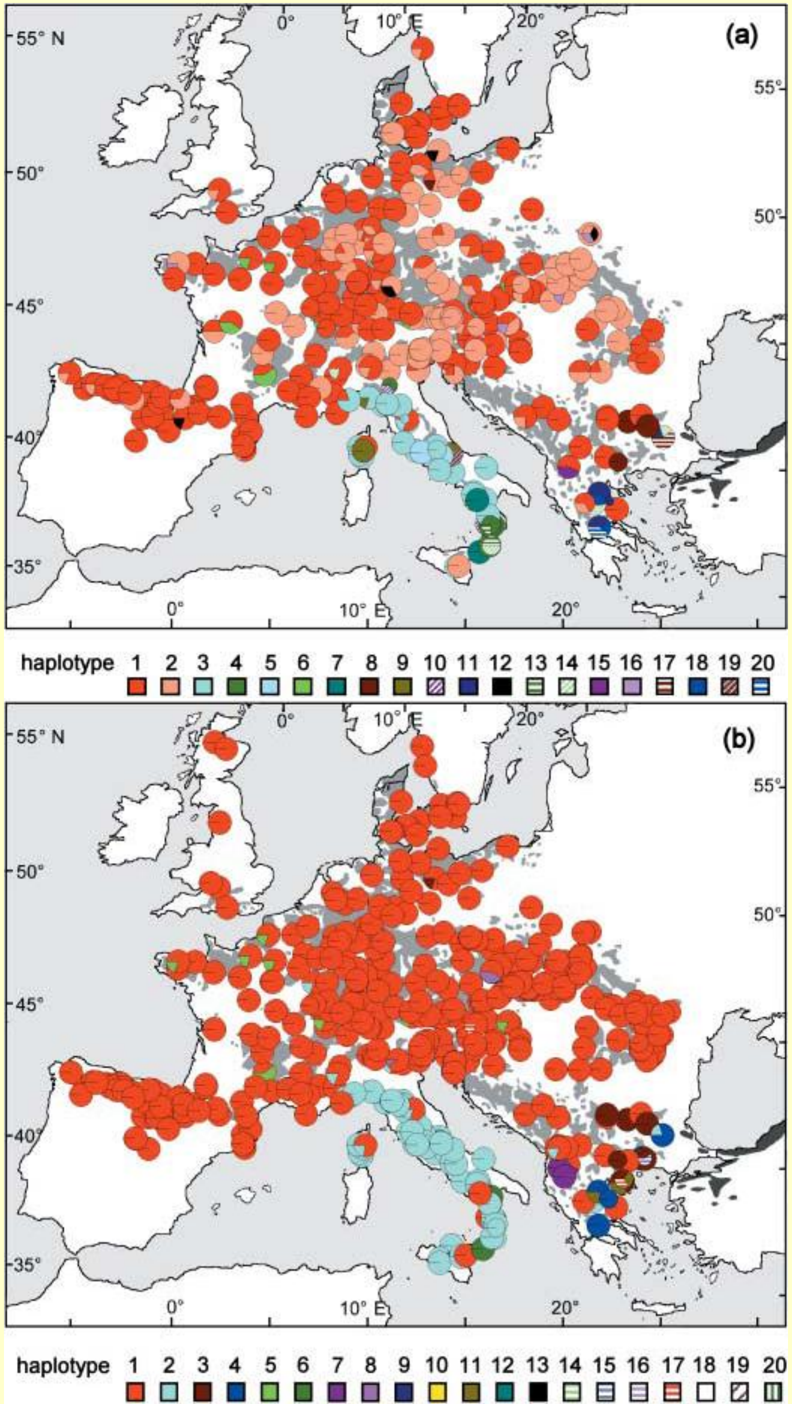


Familienstrukturen in Buchenbeständen (*Fagus sylvatica*)

Dissertation zur Erlangung des Doktorgrades, der Fakultät für Forstwissenschaften und Waldökologie

der Georg-August-Universität Göttingen

vorgelegt von, **Aikaterini Dounavi**, geboren in Athen (Griechenland), Göttingen 2000



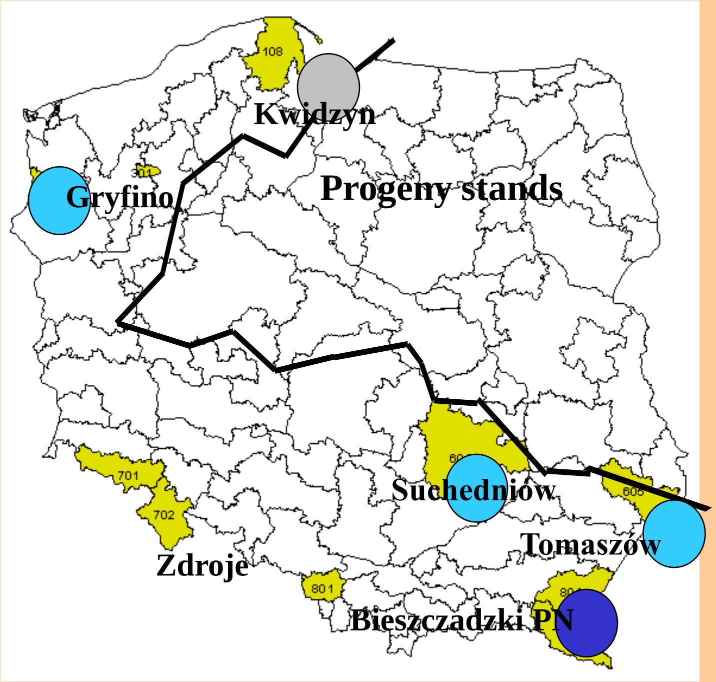
Geographical distribution of

(a) chloroplast haplotypes detected using polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP),

(b) microsatellites (data for the Italian Peninsula were taken from Vettori *et al.*, 2004)

In: MAGRI, D., VENDRAMIN, G.G., COMPS, B., DUPANLOUP, I., GEBUREK, TH., GÖMÖRY, D., LATAŁOWA, M., THOMAS LITT, PAULE, L., ROURE, J.M., TANTAU, I., VAN DER KNAAP, W. O., PETIT, R.J., DE BEAULIEU, J-L 2006: A new scenario for the Quaternary history of European beech populations: palaeobotanical evidence and genetic consequences . New Phytologist 171 (1): 199-221

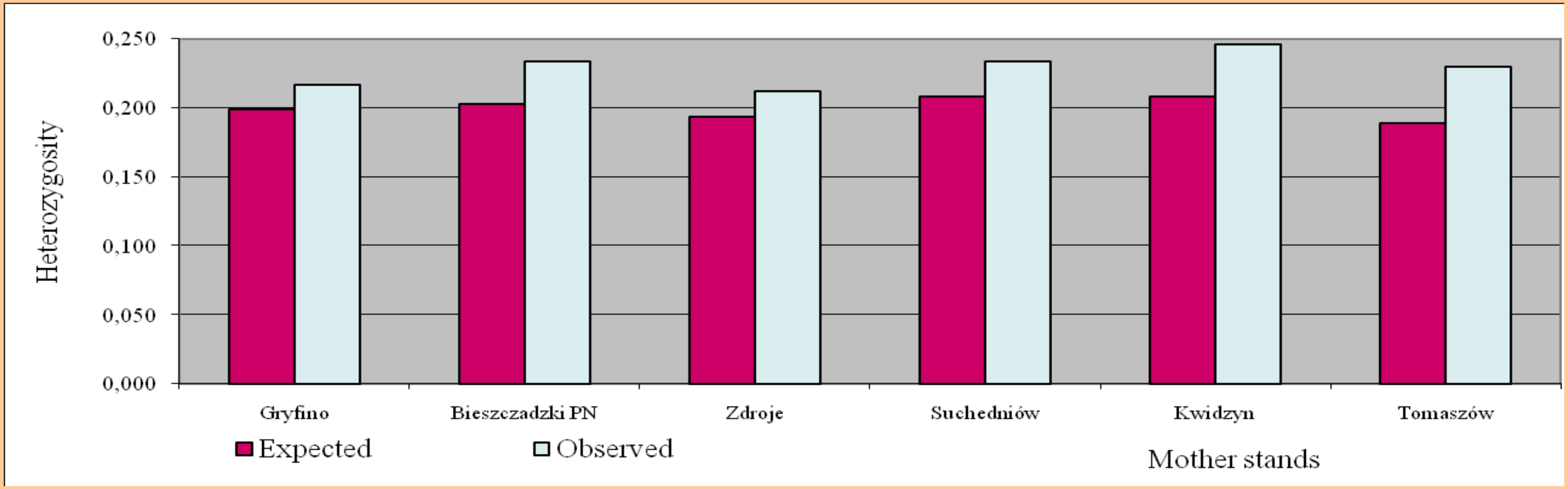
Isoenzyme markers – Average number of alleles per locus

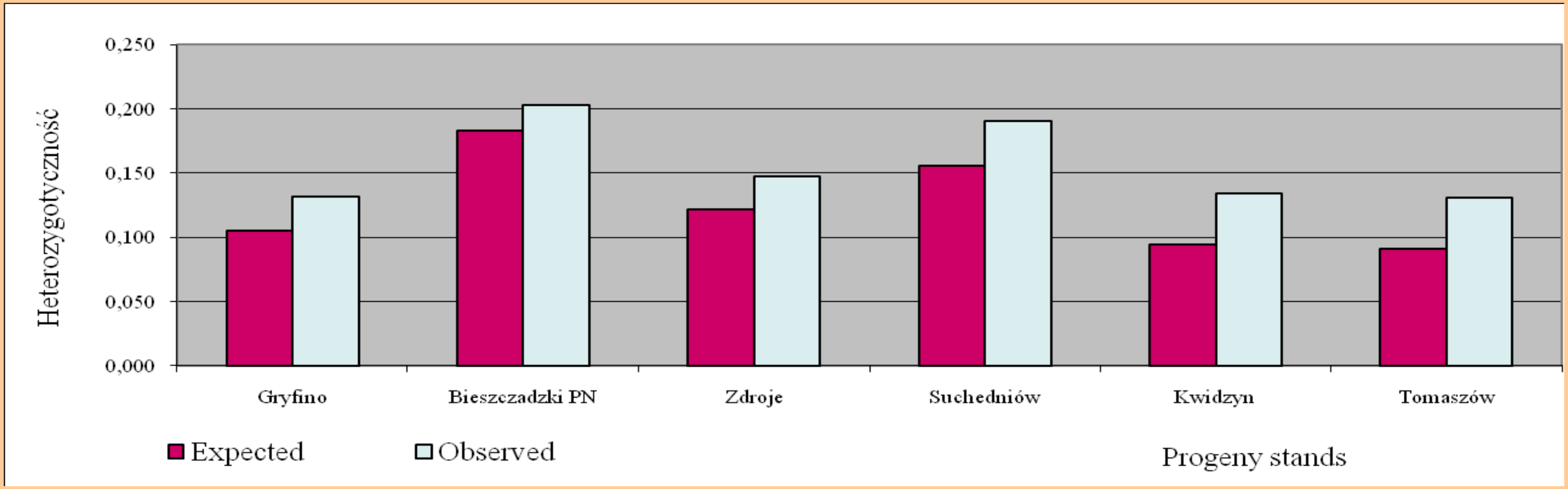


Average number of alleles per locus ● 1,7 ● 1,8 ● 1,9 ● 2,0 ● 2,1 ● 2,3

Sekocin 2010

Isoenzyme markers – heterozygosity





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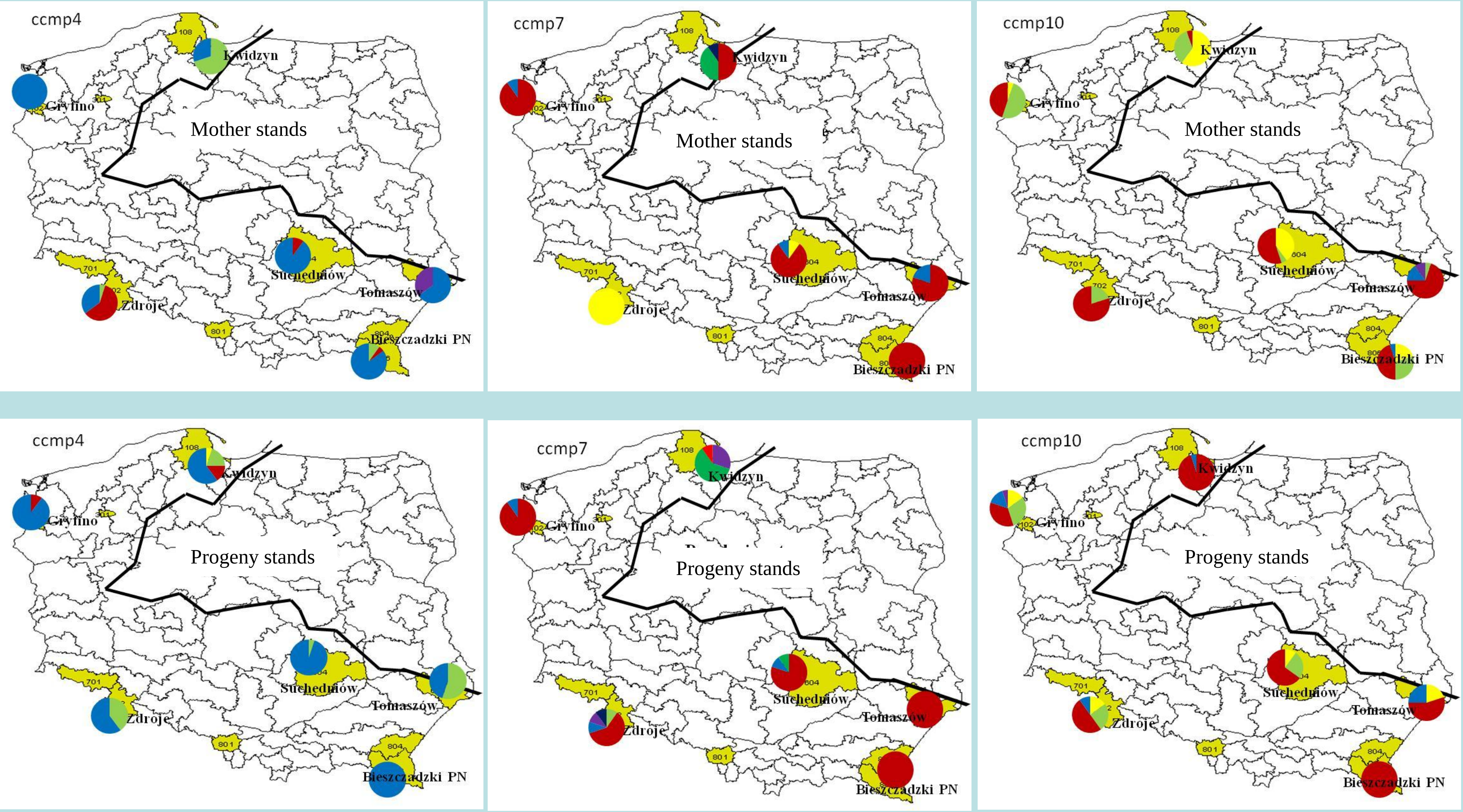
Chloroplast DNA Markers – Gene percentage of alleles



ccmp4

116	117	118	119	120
1	2	3	4	5

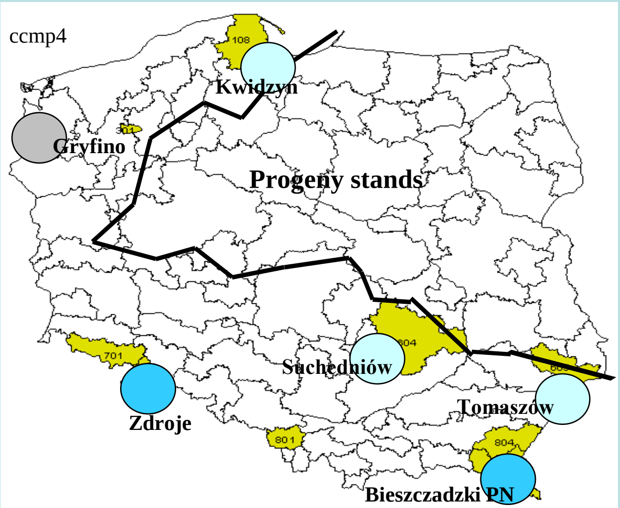
ccmp7

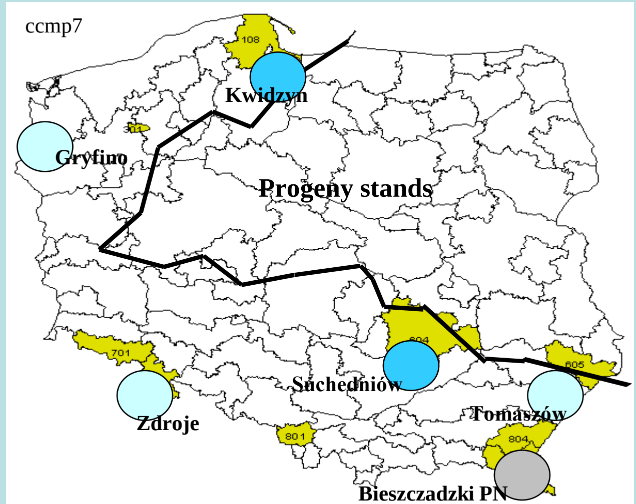
144	145	147	148	149	150	151	152
1	2	3	4	5	6	7	8

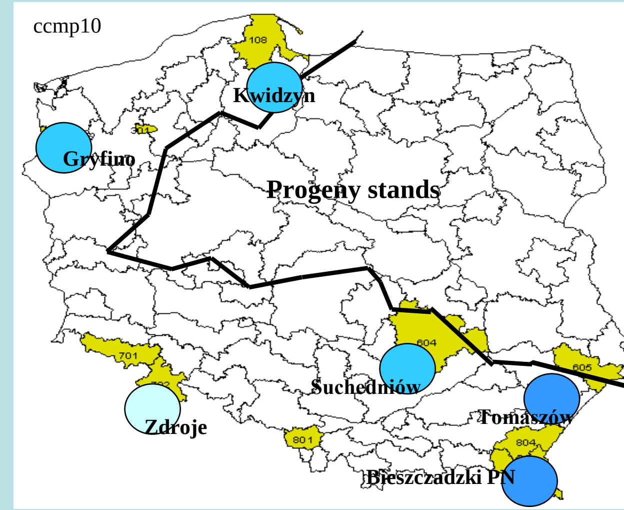
ccmp10

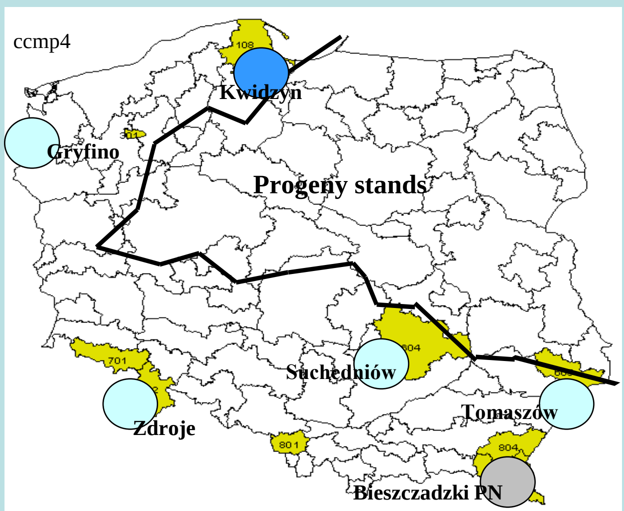
116	117	118	119	120
1	2	3	4	5

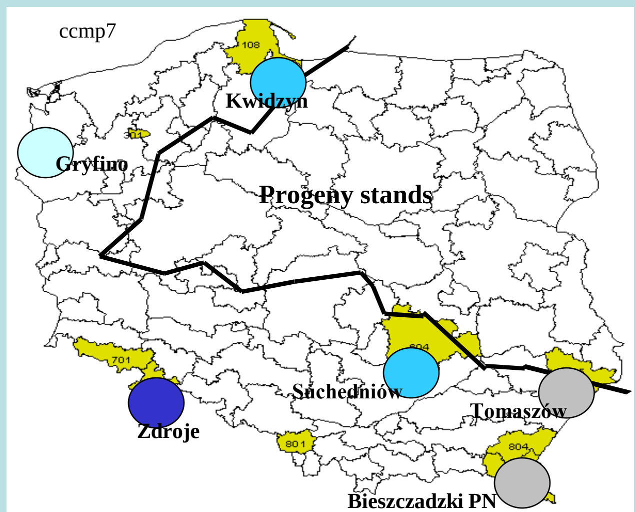
Chloroplast DNA Markers – Average number of alleles per locus

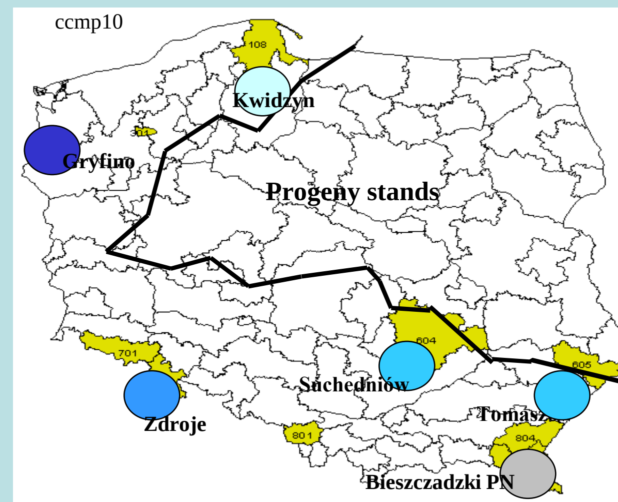












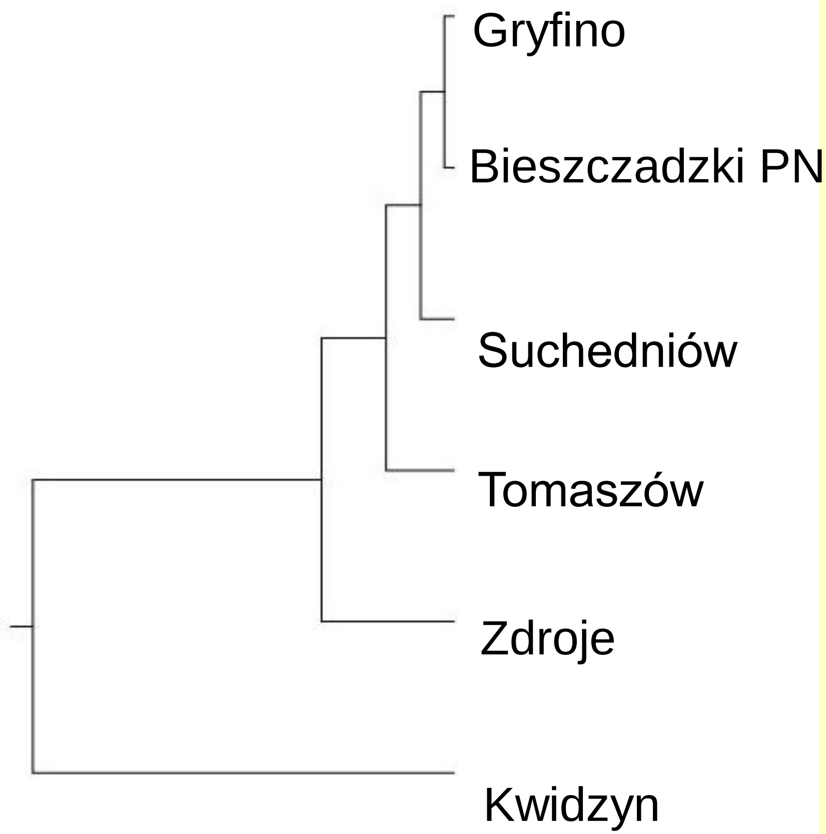
Average of alleles per locus ● 1 ● 2 ● 3 ● 4 ● 5

80 lat IBL

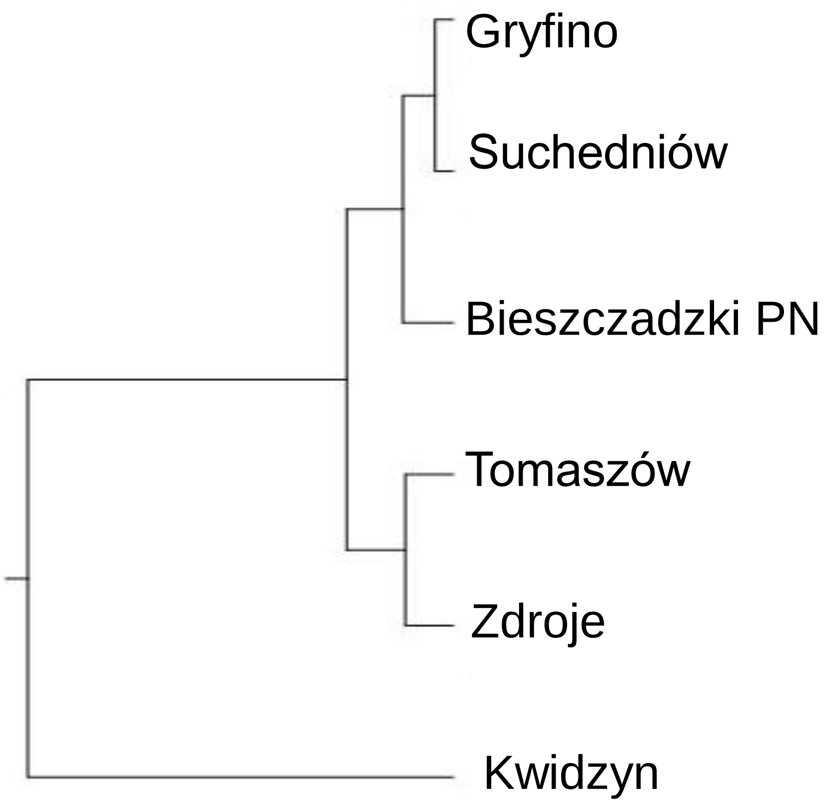
Sekocin 2010

DNA markers

Mother stands



Progeny stands



80 lat IBL

Sekocin 2010

Nei's Analysis of Gene Diversity

Mother stands

Locus	Ht	Hs	Gst
ccmp4	0.5053	0.3058	0.3947
ccmp7	0.3228	0.2667	0.1738
ccmp10	0.6468	0.5092	0.2128
Mean	0.4916	0.3606	0.2666
St. Dev	0.0264	0.0169	

Progeny stands

Locus	Ht	Hs	Gst
ccmp4	0.3957	0.3042	0.2313
ccmp7	0.4650	0.2767	0.4050
ccmp10	0.5193	0.4317	0.1688
Mean	0.4600	0.3375	0.2663
St. Dev	0.0038	0.0068	

Summary statistics

Locus	Hc	Gcs
ccmp4	0.3050	0.3230
ccmp7	0.2717	0.3103
ccmp10	0.4704	0.1932
Mean	0.3490	0.2665
St. Dev	0.0113	

Ht – total heterozygosity within population
Hc – total heterozygosity within group
Hs – total heterozygosity among populations
Gst – total genetic differentiation among populations
Gcs – total genetic differentiation in groups of populations

Sekocin 2010

Conclusions

- The very high inter-population diversity was shown.
- The investigations reviled the importance of using local European beech ecotypes, taking into account its plasticity, which is the best advice to obtain success in forest management and for protection of genetic resources of the species.

Thank You very much for Your attention!

And also to our colleague:

Jolanta Bieniek for her technical assistance

80 lat IBL

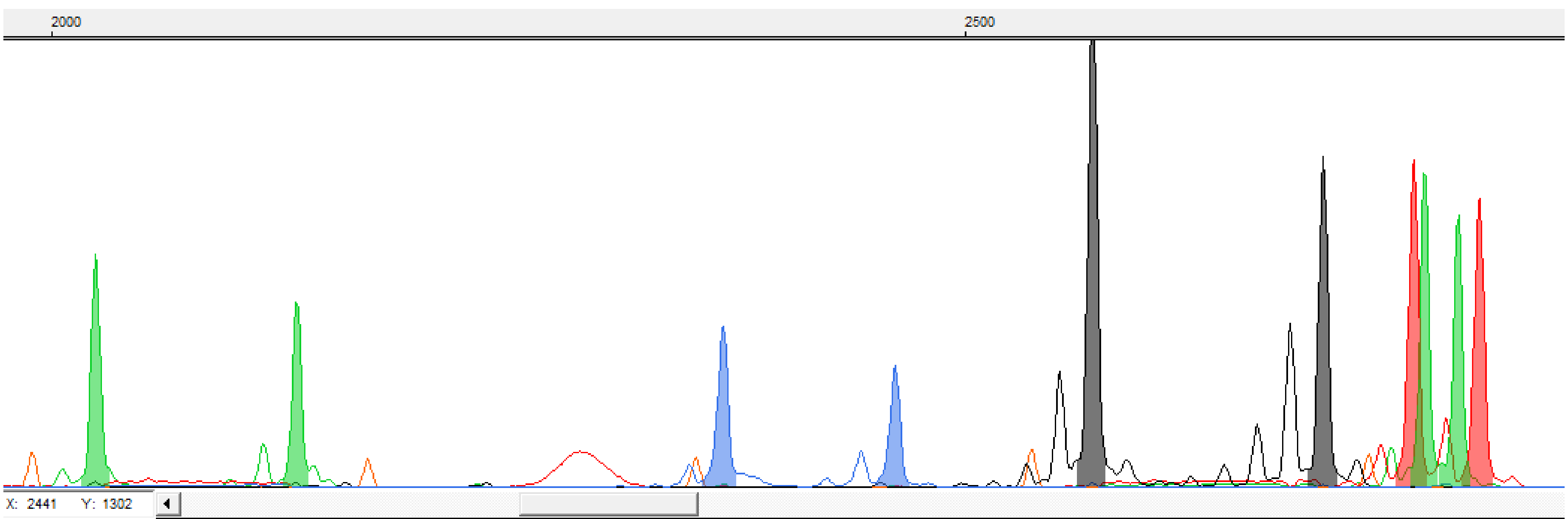
Sekocin 2010

UNIWERSYTET KAZIMIERZA WIELKIEGO W BYDGOSZCZY

Microsatellites and genetic diversity in seed orchard and provenance test

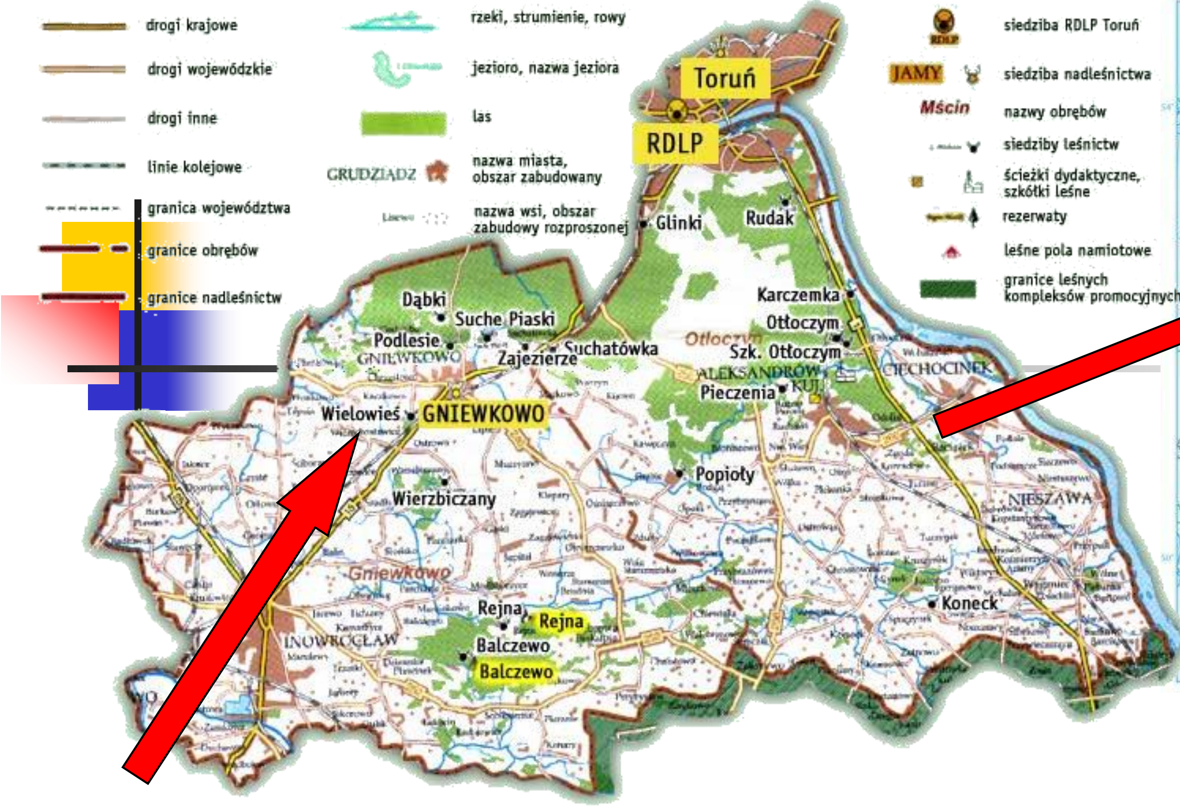
Magdalena Trojankiewicz

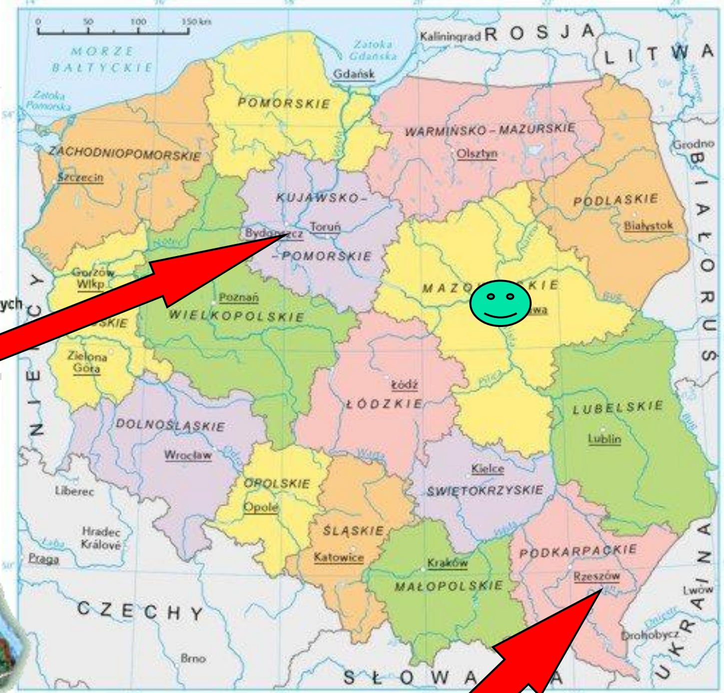
Microsatellites



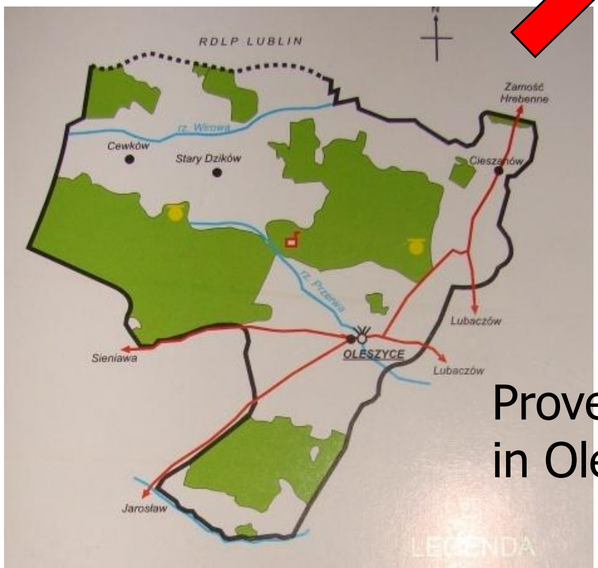
Seed orchard *Pinus silvestris*

Provenance test *Quercus robur*





Seed orchard in Gniewkowo Forestry



Provenance test
in Oleszyce Forestry

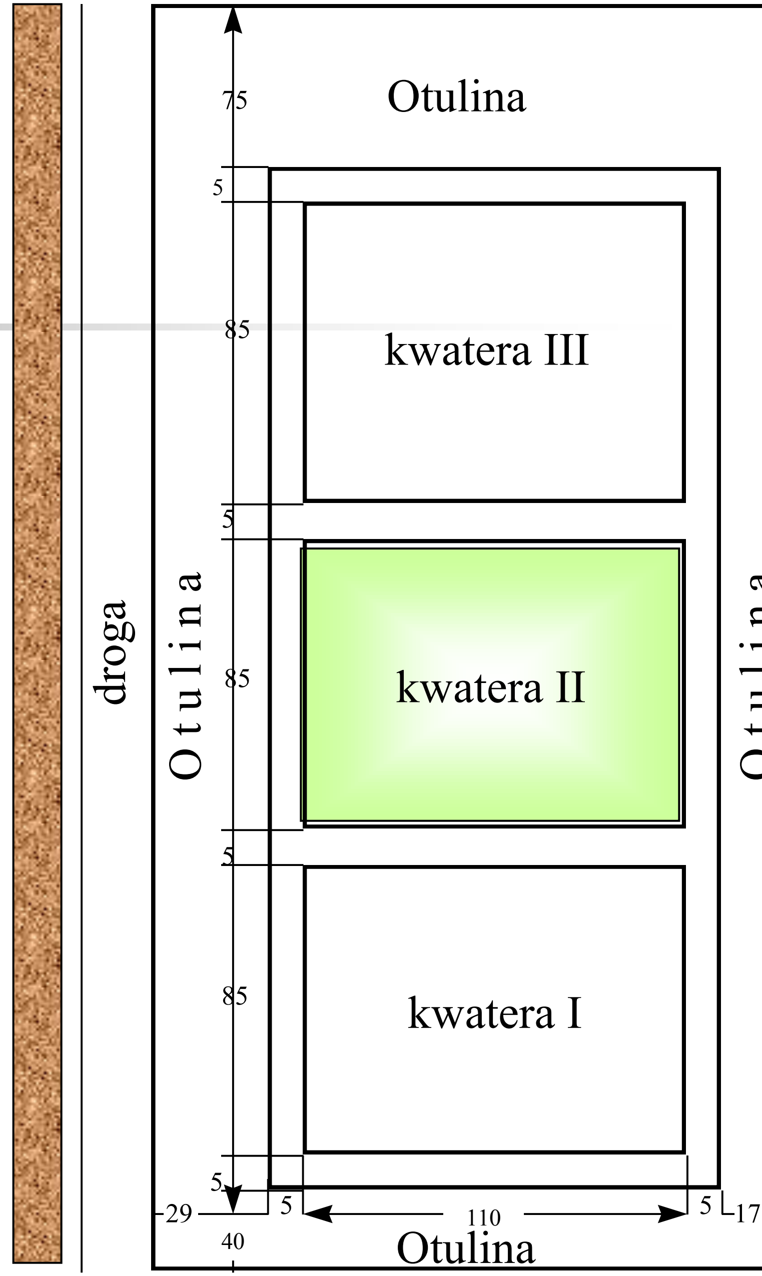
Seed orchard in Gniewkowo forestry

The aim of this study was to investigate reproductive processes in seed orchard

- Genetic diversity of parental and progeny population
- Mating system and pollen dispersal
- Effective population size of male paterns

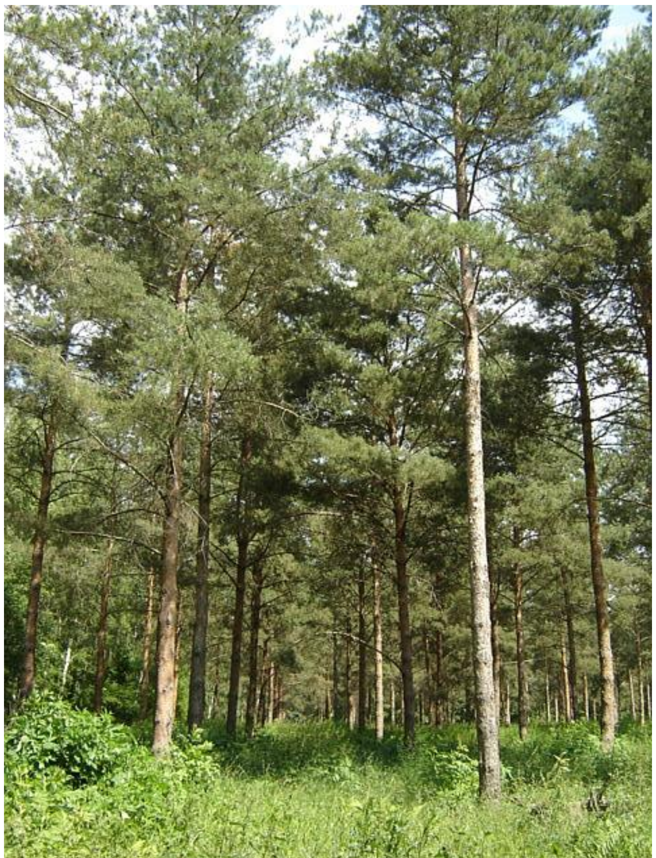
32 clones **1122** ramets

29 clones **187** ramets



1972-73 **3.3** ha

Location of clones in seed orchard

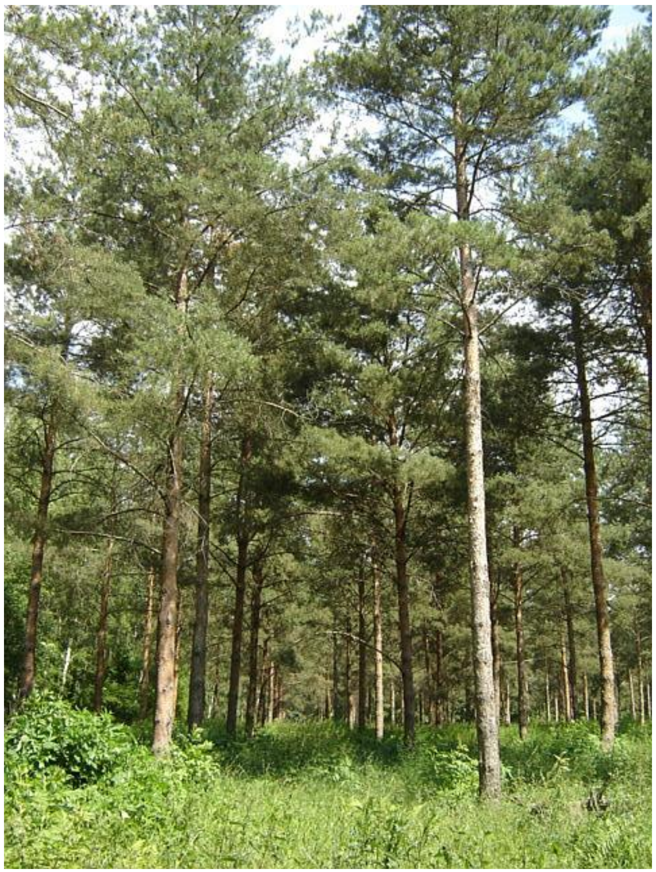


	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1		211	221	216			233		221		234	220	233		221		234
2	229				223	220		214		214	228		229	225		231	223
3					228		213		225		235		211				228
4					235	217	232		231	212			240	230		237	235
5	227										223				236		238
6	233	219			230		233		221	218	**230**		233		221		
7	229	214		218		220					223		229		225		
8			224	217			**239**			220		236			225	215	
9	220				235		240		212		234		232				232
10			236	225		232		236	**219**	223			218		236		
11	233		221				233		239		230		233		221		230
12	229		233		223		219	236	213	213	228	231		217	238		223
13					228		231		**225**		235		234			220	
14	212	220			235	216	236		231		225		240		212		219
15	233		236		234		215		240		**232**	220			234		
16	233	225			230		233	230	235	230	230		233			239	230
17	229		233				229		229		223				238		228
18	234	232	224		219		234	231		217	228		234			223	235
19	220						240		212		237		232		212		
20	218		236		237	220		224	235	239	240		220	224		240	214
21	233		226		229		233		226				233		226		233
22		219	238	216	217			230			217	223		225	238		217

Characteristics of nuclear microsatellites
(*Pinus sylvestris*, seed orchard)

Locus		Sequence 5' – 3'
PtTx3025	**(CAA)$_{10}$**	**F: TTC TAT ATT CGC TTT TAG TTT C** **R: CTA TTT GAG TTA AGA AGG GAG TC**
PtTx3107	**(CAT)$_{14}$**	**F: AAA CAA GCC CAC ATC GTC AAT C** **R: TCC CCT GGA TCT GAG GA**
PtTx 3116	**(TTG)$_7$(TTG)$_5$**	**F: CCT CCC AAA GCC TAA AGA AT** **R: CAT ACA AGG CCT TAT CTT ACA GAA**
PtTx4001	**(GT)$_{15}$**	F: CTA TTT GAG TTA AGA AGG GAG TC R: CTG TGG GTA GCA TCA TC
Spag7.14	**(AT)$_5$(GT)$_{19}$**	**F: TCA CAA AAC ACG TGA TTC ACA** **R: GAA AAT AGC CCT GTG TGA GAC A**
Spac12.5	**(GT)$_{20}$(GA)$_{10}$**	F: CTT CCT CAC TAG TTT CCT TTG G R: TTG GTT ATA GGC ATA GAT TGC

Localtion of clones in seed orchard after corrections



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1		211	221	*214*			*233*		221		234	220	233		221		234
2	*236*				223	220		214		214	228		*310*	225		231	223
3					228		213		*221*		235		211				*228*
4					235	*220*	*213*		*301*	212			240	230		237	235
5	227										223				236		*213*
6	233	219			230		*232*		*302*	218	230		233		221		
7	*309*	214		218		220					223		229		225		
8			224	217			*221*			*307*		236			225	215	
9	*229*				235		240		212		234		232				232
10			236	225		*220*		*315*	219	223			218		236		
11	233		221				*240*		*221*		230		233		221		230
12	*235*		233		223		*306*	236	*233*	213	228	231		*305*	238		223
13					228		*238*		225		235		234			220	
14	*219*	220			235	216	236		*301*		225		240		212		219
15	*219*		236		234		*303*		240		232	220			234		
16	*313*	225			230		*312*	230	235	*236*	230		233			*216*	230
17	*304*		233				229		229		*230*				238		228
18	234	232	224		219		*233*	*232*		217	228		234			*308*	235
19	*302*						*234*		212		237		*231*		212		
20	218		236		237	220		224	235	*314*	240		220	224		*216*	*211*
21	233		226		*219*		*240*		226				233		226		233
22		*212*	*236*	216	*229*			*224*			217	223		225	238		*234*

Genetic diversity

Genetic diversity of parental population

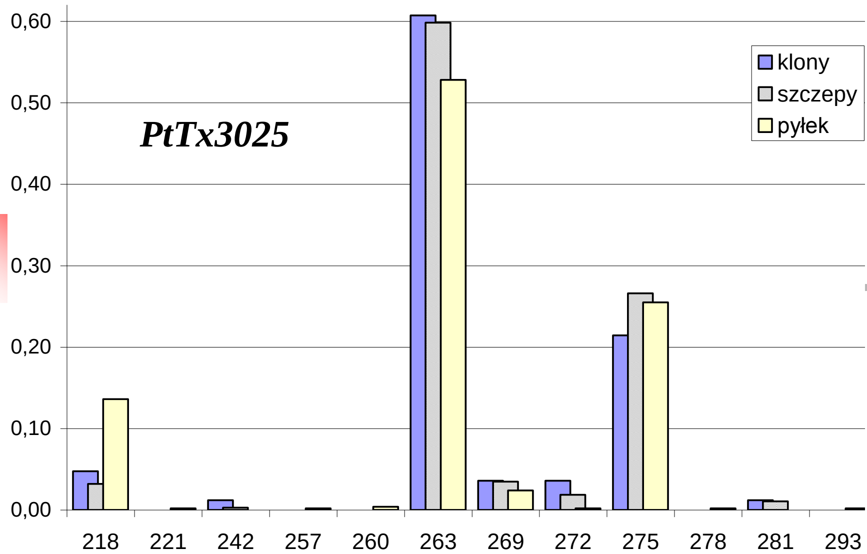
Locus	A	A_e	H_e	H_o	*PE(1)*	*HW*	*Null*	*F*
PtTx3025	8	2.38	0.581	0.619	0.187	NS	-0.07	-0.07
PtTx3107	10	6.41	0.844	0.667	0.501	NS	0.12	0.21
PtTx3116	9	4.18	0.761	0.810	0.350	NS	-0.05	-0.06
PtTx4001	9	3.67	0.728	0.762	0.318	NS	-0.04	-0.05
Spag7.14	26	23.8	0.958	0.905	0.805	NS	0.02	0.06
Spac12.5	24	19.23	0.948	0.952	0.772	NS	-0.01	0.00
average	14.33	9.94	0.803	0.785	0.992		0.005	0.015

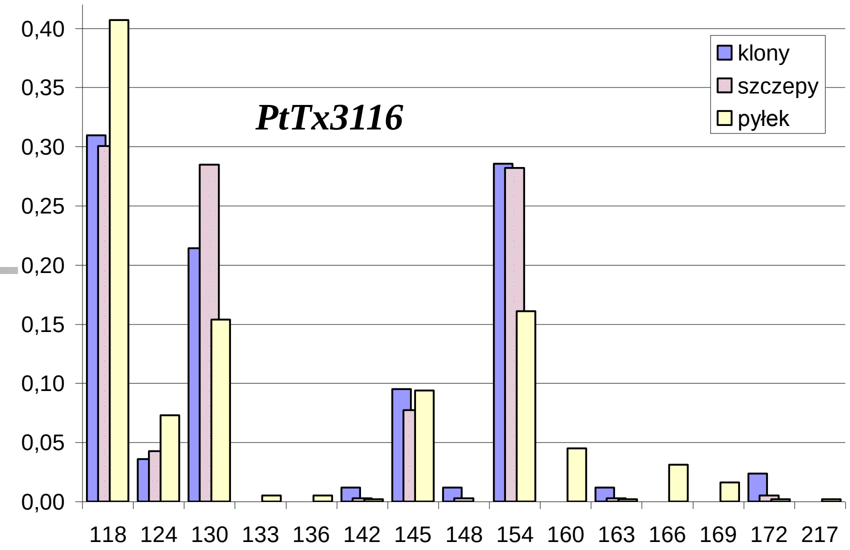
A – number of allels. A_e – effectiv number of allels. H_o H_e – observed and expected heterozygosity. *PE(1)* - exclusion probability. F = 1 – (Ho/He)

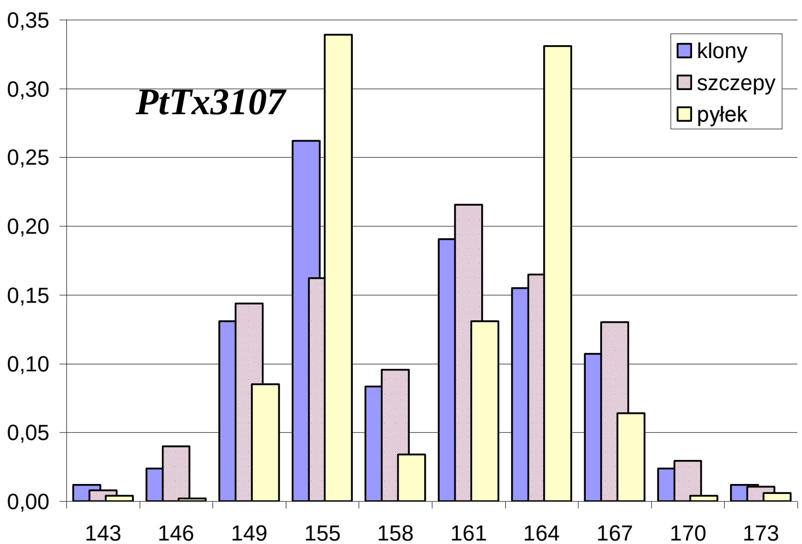
Genetic diversity of offspring population

Locus	*A*	A_e	H_e	H_o	*PE(1)*	*HW*	*Null*	*F*
PtTx3025	11	2.56	0.609	0.736	0.204	**	-0.109	-0.21
PtTx3107	10	3.23	0.690	0.829	0.284	**	-0.111	-0.20
PtTx3116	14	4.18	0.761	0.915	0.366	**	-0.099	-0.20
PtTx4001	11	3.26	0.693	0.797	0.291	**	-0.081	-0.15
Spag7.14	32	8.85	0.887	0.855	0.633	NS	0.0169	0.04
Spac12.5	33	11.49	0.913	0.952	0.703	NS	-0.022	-0.04
average	19.33	5.9	0.759	0.847	0.972		-0.068	-0.127

A – number of allels. A_e – effectiv number of allels. H_o H_e – observed and expected heterozygosity. *PE(1)* - exclusion probability. F = 1 – (Ho/He)


PtTx3025
klony
szczepy
pyłek
0,60
0,50
0,40
0,30
0,20
0,10
0,00
218 221 242 257 260 263 269 272 275 278 281 293


PtTx3116
klony
szczepy
pyłek
0,40
0,35
0,30
0,25
0,20
0,15
0,10
0,05
0,00
118 124 130 133 136 142 145 148 154 160 163 166 169 172 217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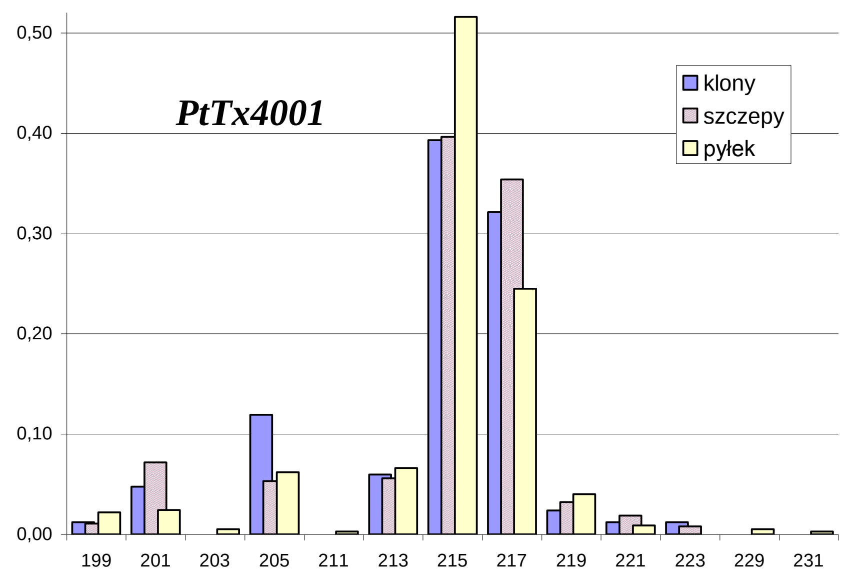
PtTx4001
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pyłek
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0,20
0,10
0,00
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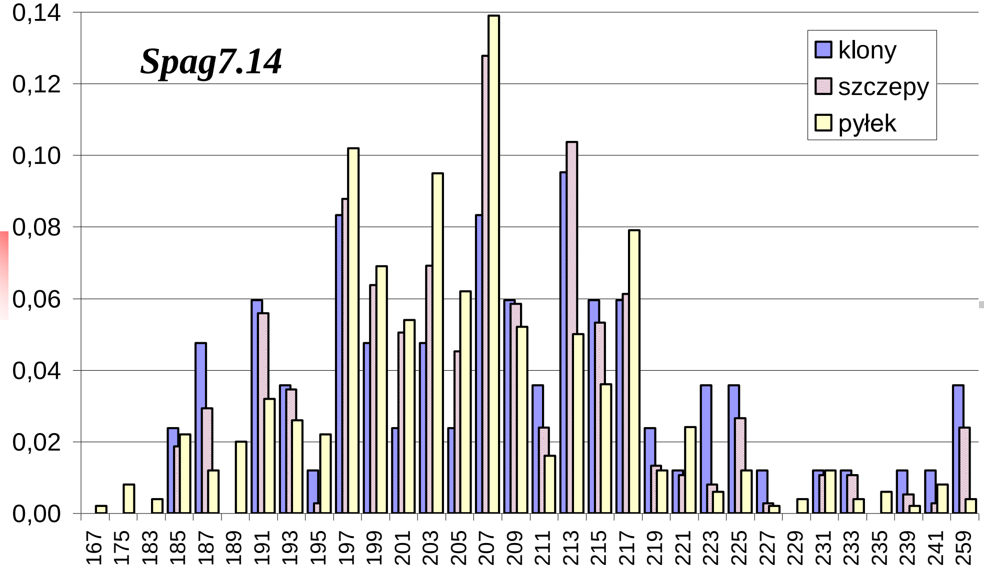
Spag7.14
klony
szczepy
pyłek
0,14
0,12
0,10
0,08
0,06
0,04
0,02
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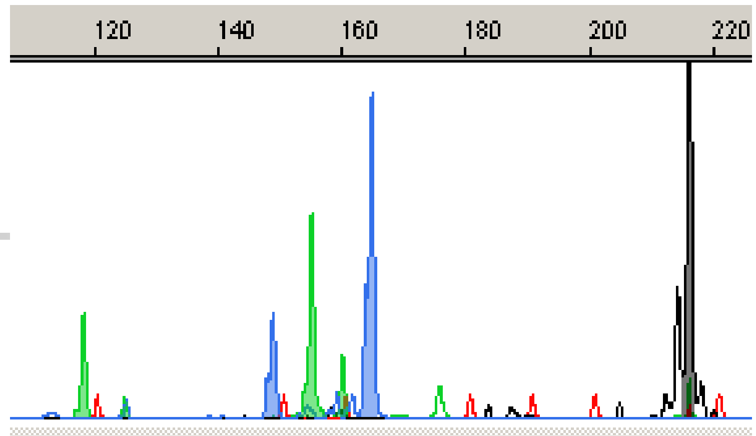
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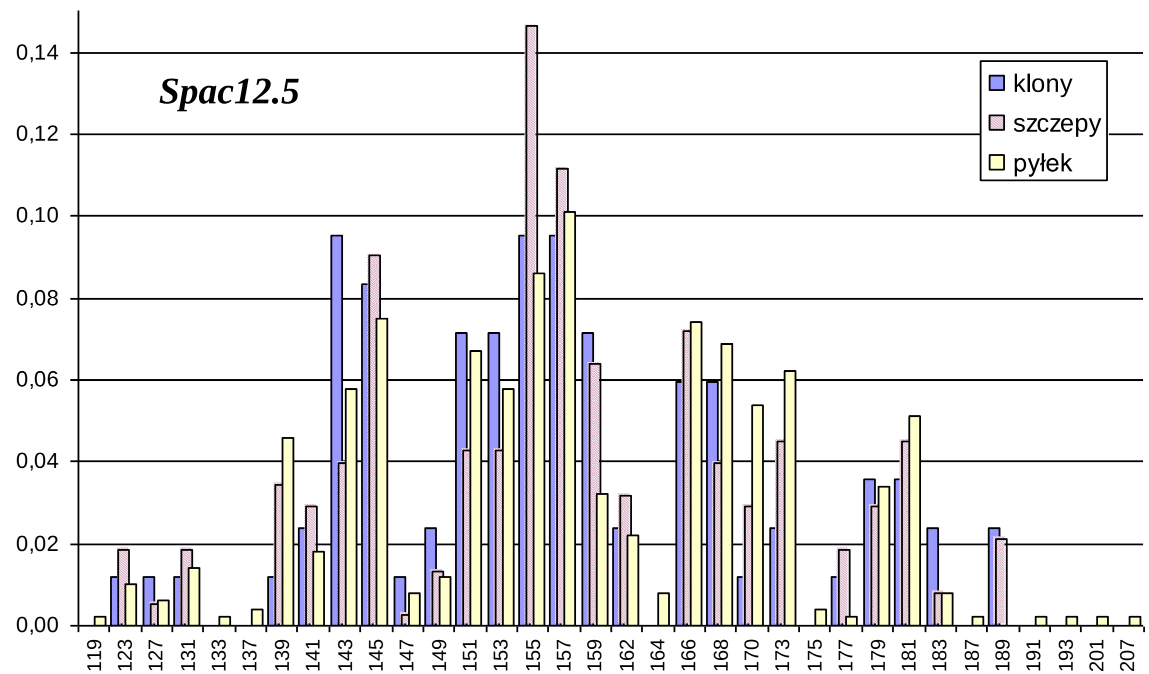
Spac12.5
klony
szczepy
pyłek
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0,08
0,06
0,04
0,02
0,00
119 123 127 131 133 137 139 141 143 145 147 149 151 153 155 157 159 162 164 166 168 170 173 175 177 179 181 183 187 189 191 193 201 207

Effective population size

Effective population size of male parents calculated based on different methods

Methods used to calculate effective population size	***Ne***
Variance of allele frequencies – $N_{e(v)}$ Wariancja częstości alleli	24.80
Correlation of paternity analysis – $N_{e(r)}$ Analiza korelacji ojcostwa	21.74
Genetic structure of pollen pool TWOGENER - $N_{e(p)}$	52.57
Paternity analysis – reproductive success $N_{e(f)}$ Analiza ojcostwa – sukces kojarzenia -	17.14

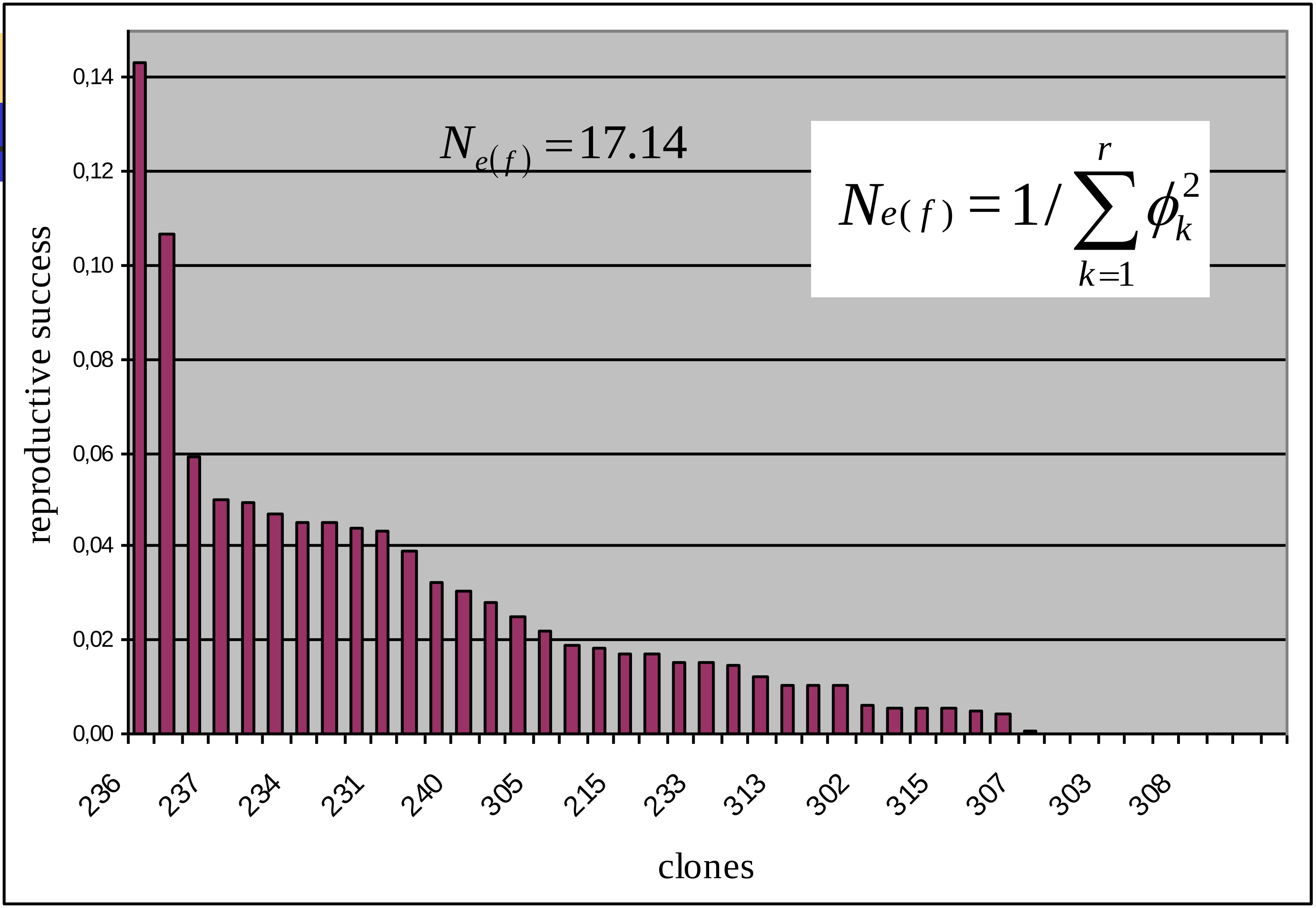
Variance effective population size

Locus	$N_{e(v)}$
PtTx3025	10.96
PtTx3107	8.02
PtTx3116	20.07
PtTx4001	28.25
Spag7.14	54.58
Spac12.5	77.00
	24.80

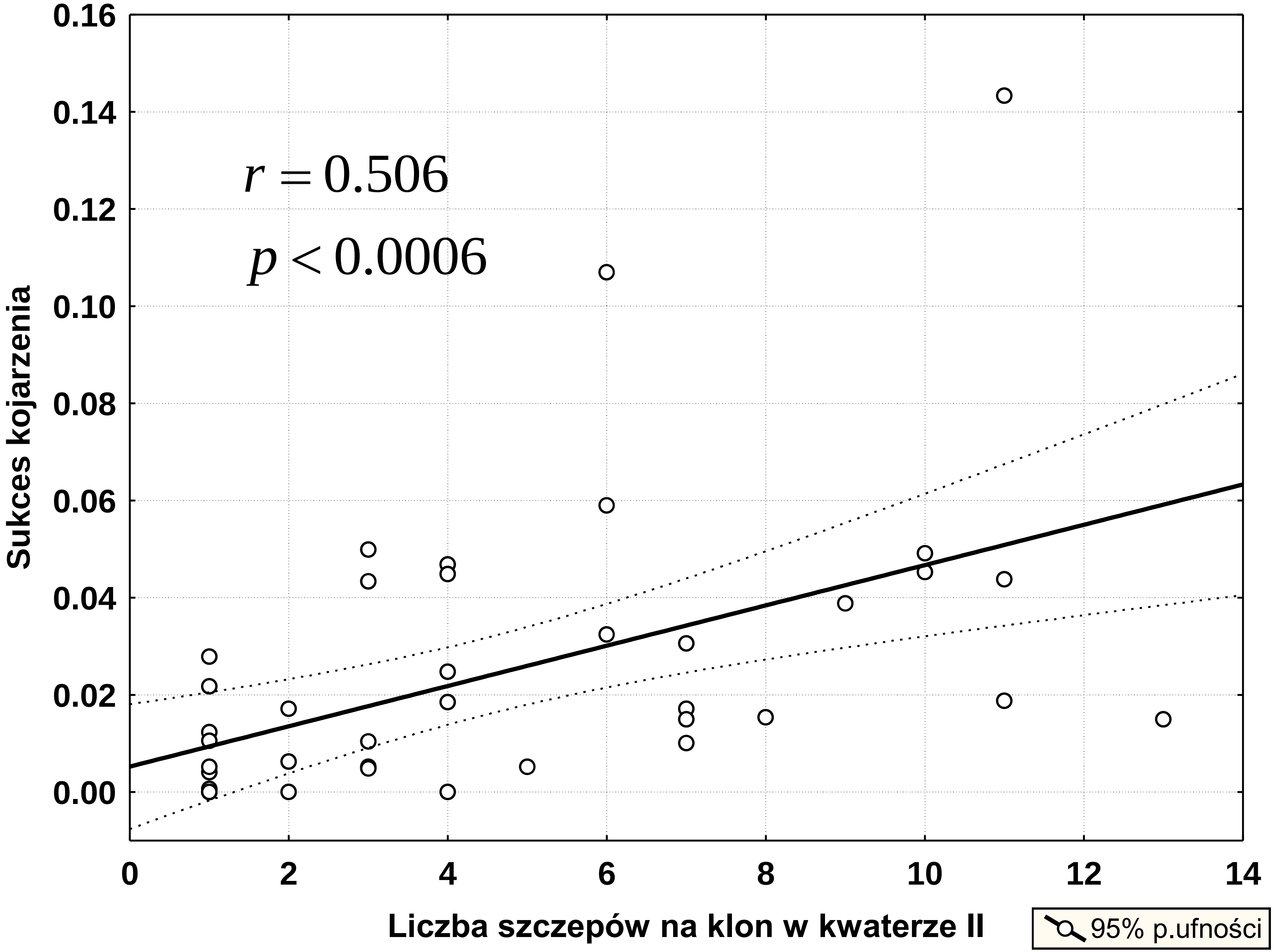
$$N_{e(v)} = \frac{(n-1)}{2(f_{(p)}n-1)}$$

Roberds et al. 1991, Burczyk 1996,

Effective population size - paternity analysis

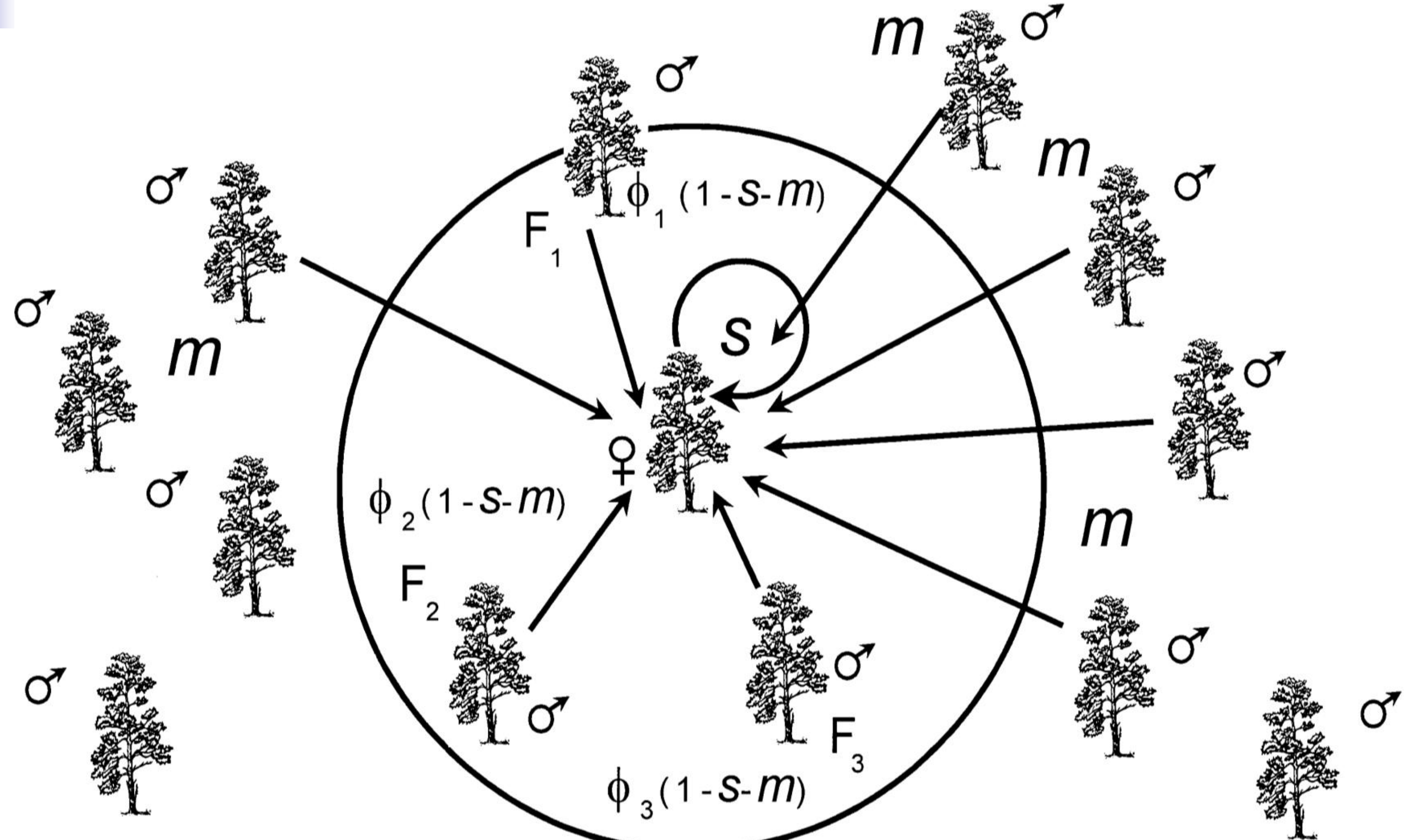


Highly variable contribution of individual clones in production of progeny population



Relationship between reproductive success of clons and the number of ramets per clone

Determinants of male reproductive success

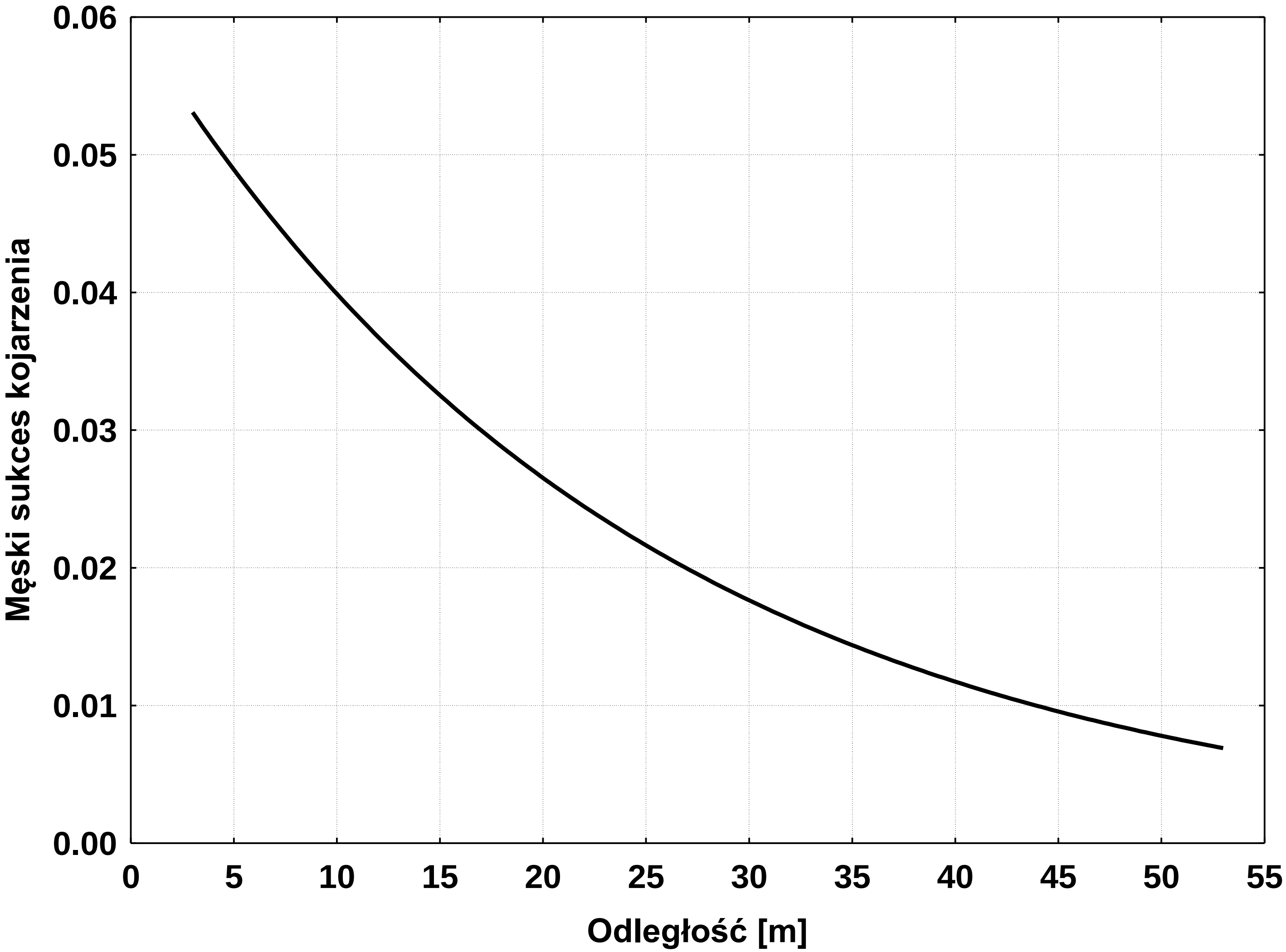


Determinants of male reproductive success

Model	Imigration (m)	Determinants of miting success			$N_{e(s)}$ (% $N_{e(s)}/N$)
		Distance (β)	Fecundity (γ)	Diameter (δ)	
$m\ \beta$	**0.6034 (0.0326)**	**-0.0408 (0.0137)**	-	-	124.2 (66.4%)
$m\ \gamma$	**0.6118 (0.0329)**	-	**0.2885 (0.0960)**	-	139.9 (74.7%)
$m\ \delta$	**0.5966 (0.0326)**	-	-	**0.1868 (0.0564)**	150.9 (80.7%)
$m\ \beta\ \gamma\ \delta$	**0.5899 (0.0323)**	**-0.0302 (0.0114)**	**0.2785 (0.0762)**	**0.1643 (0.0594)**	92.7 (49.6%)

$N_{e(s)}$ – effective number of ramets.

$\%N_{e(s)}/N$ – percet effevtive number of ramets to number of ramets



Relationship between mating success and distance from maternal trees.

Results

1. **Genetic diversity and genetic structure :**

- Genetic diversity of offspring population is similar to genetic diversity paternal population.

- Inbreding level is similar in both ppulation.

2. Mating system and level of pollen imigration:

- Level of self-fertilization is low (close to 0)

- Level of pollen immigration is large (60%)

3. Effective number of male paterns:

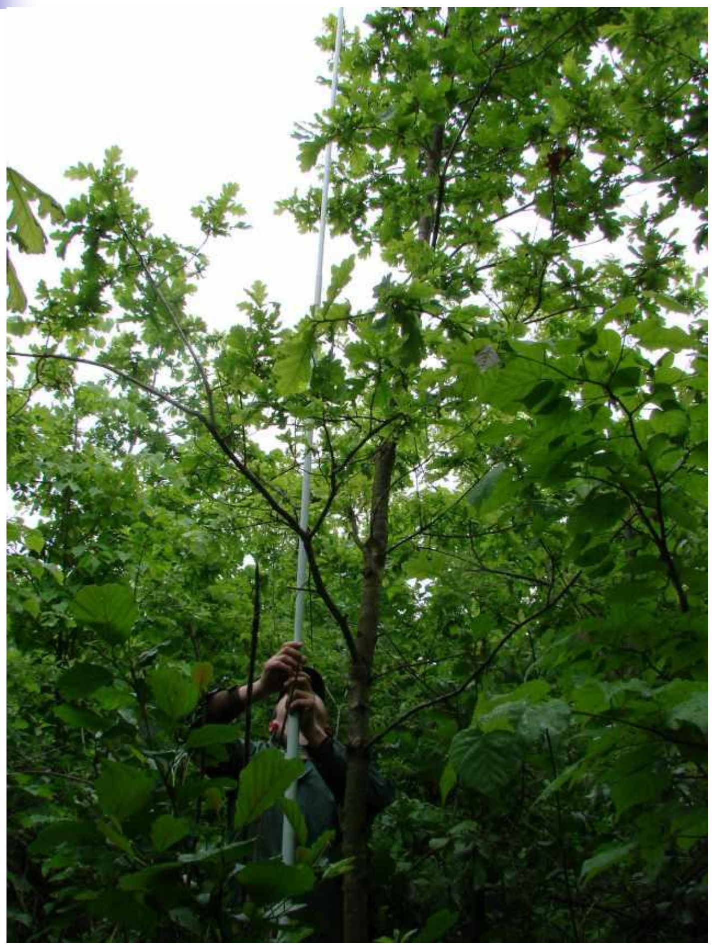
- Effective population size of male patrens is extensive (17 – 52, pollen pool imigration 22-79)

  and comparable among different methods

4. Male mating success of individual ramets depends on:

- Distance to sampled mothers
- Flowering intensity and tree diameter

Provenance test in Oleszyce Forestry



	Kolumna																														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
64	53	11	5	58	54	26	70	55	94	24	76	16	25	86	52	7	67	71	78	75	81	63	57	96	36	31	47	9	14	90	
63	61	21	45	84	6	10	66	91	72	40	35	13	37	19	60	56	33	59	83	88	64	95	77	44	89	92	18	65	23	51	
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58	37	40	18	13	83	65	64	10	60	95	89	19	23	56	45	59	35	21	61	44	33	88	72	91	66	51	77	92	6	84	
57	31	14	75	57	71	53	7	67	90	5	96	70	55	54	26	47	9	36	16	25	58	76	86	52	24	81	11	94	63	78	
56	19	83	56	13	36	96	84	33	23	40	86	14	21	89	31	78	70	26	7	5	53	77	94	63	91	88	51	76	47	9	
55	45	18	52	25	90	67	54	58	24	72	61	35	55	60	75	57	11	66	81	10	71	92	16	64	6	59	44	95	37	65	
54	14	91	77	31	33	21	89	36	63	47	88	19	96	84	13	53	26	7	76	51	78	56	9	23	83	86	5	70	40	94	
53	95	71	59	54	57	16	25	37	60	11	10	75	92	24	35	90	72	6	65	61	18	55	67	44	66	52	64	45	58	81	
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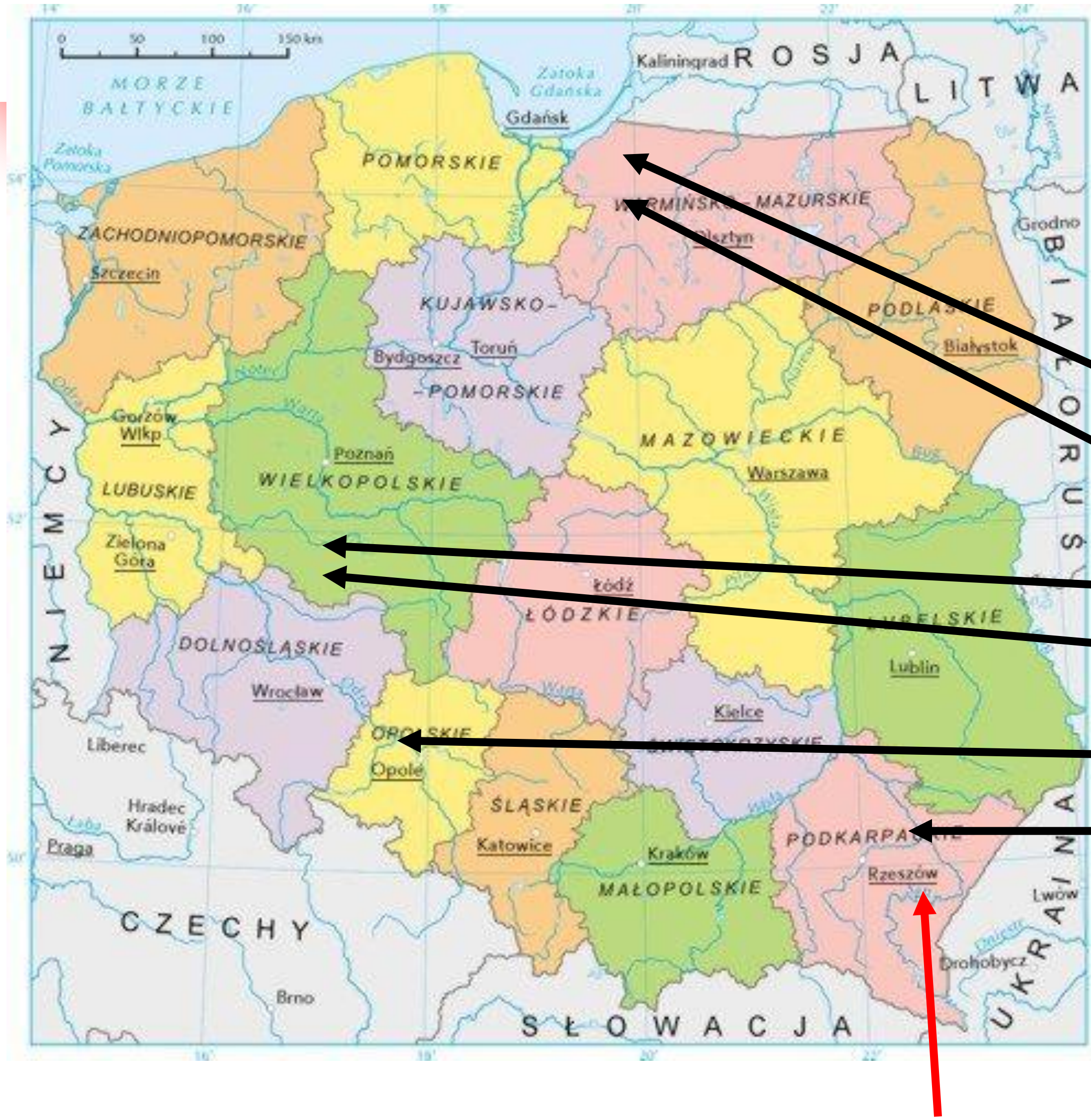

Provienience	Number of half-sibs
Młynary II	8
Młynary I	19
Milicz	9
Krotoszyn	8
Opole	8
Sieniawa	8
total	60

Provenence test in Oleszyce forestry

Microsatellites

Locus		Average size (Bp)	Sequence
ssrQrZAG 7	$(TC)_n$	150	5’-gca att aca ggc tag gct gg -3’ 5’-gtc tgg acc tag ccc tca tg -3’
ssrQrZAG 20	$(TC)_n$	178	5’-cca tta aaa gaa gca gta ttt tgt -3’ 5’-gca aca ctc agc cta tat cta gaa -3’
ssrQpZAG 9	$(AG)_n$	196	5’-gca att aca ggc tag gct gg -3’ 5’-gtc tgg acc tag ccc tca tg -3’
ssrQpZAG 110	$(AG)_n$	234	5’-gga ggc ttc ctt caa cct act -3’ 5’-gat ctc ttg tgt gct gta ttt -3’
MSQ 4	$(GA)_n$	219	5’-tct cct ctc ccc ata aac agg -3’ 5’-gtt cct cta tcc aat cag tag tga g -3’

Aims of the study

1. To verify the composition of individual half-sibs (identify individuals that do not belong to particular half-sibs due to contamination at the time of trial establishment).

   Such contamination may inflate the variance of quantitative traits within 'half-sibs'

2. To investigate effective number of males contributing to each half-sib.

   Low effective number of males may narrow the variance of quantitative traits within 'half-sibs'

Aims of the study

1. Quantitative genetic analyses will be done based on initial (original) and corrected data to see the differences.

2. We will test if genetic markers can be efficiently used for verification of family trials.

Work done so far…

- Phenotypic traits are measured (tree diameter and height)
- All individuals are sampled and DNA is being isolated
- SSR analyses started…

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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2010

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) 2. No (short 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. Are you aiming at high intensity breeding to obtain high benefit at the cost of large investments?	1. Yes (high input breeding) 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).	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.
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	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

	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.

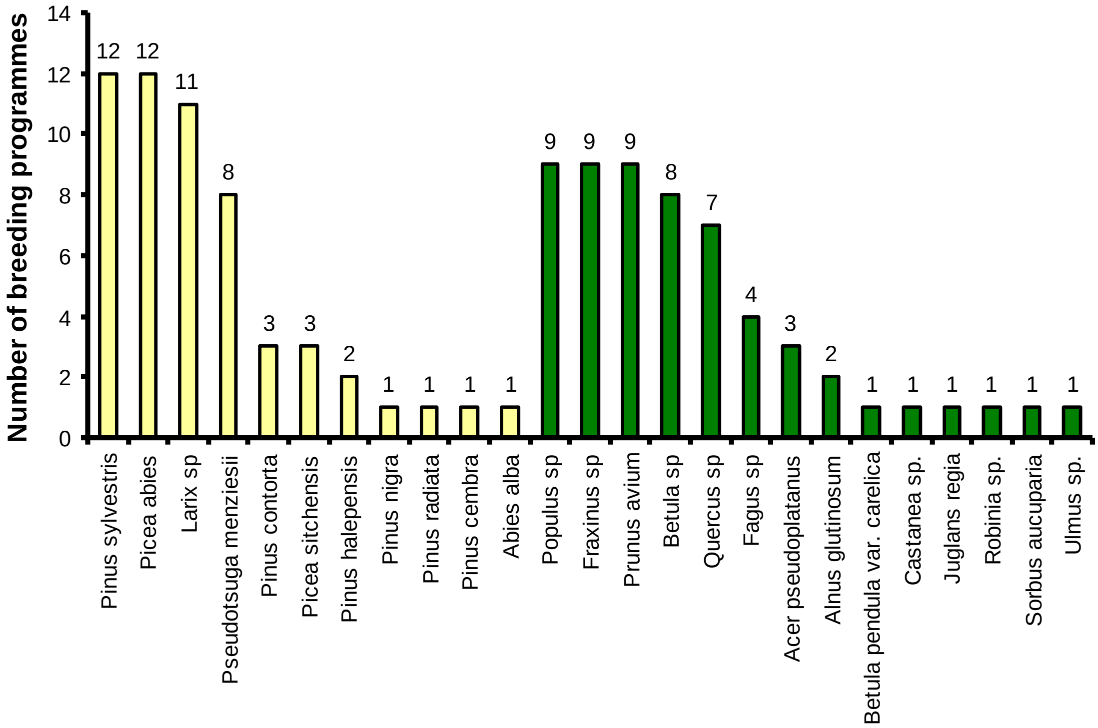


Fig. 3.1.1. Number of breeding programmes for each tree species sorted by coniferous (left) and broadleved (right).

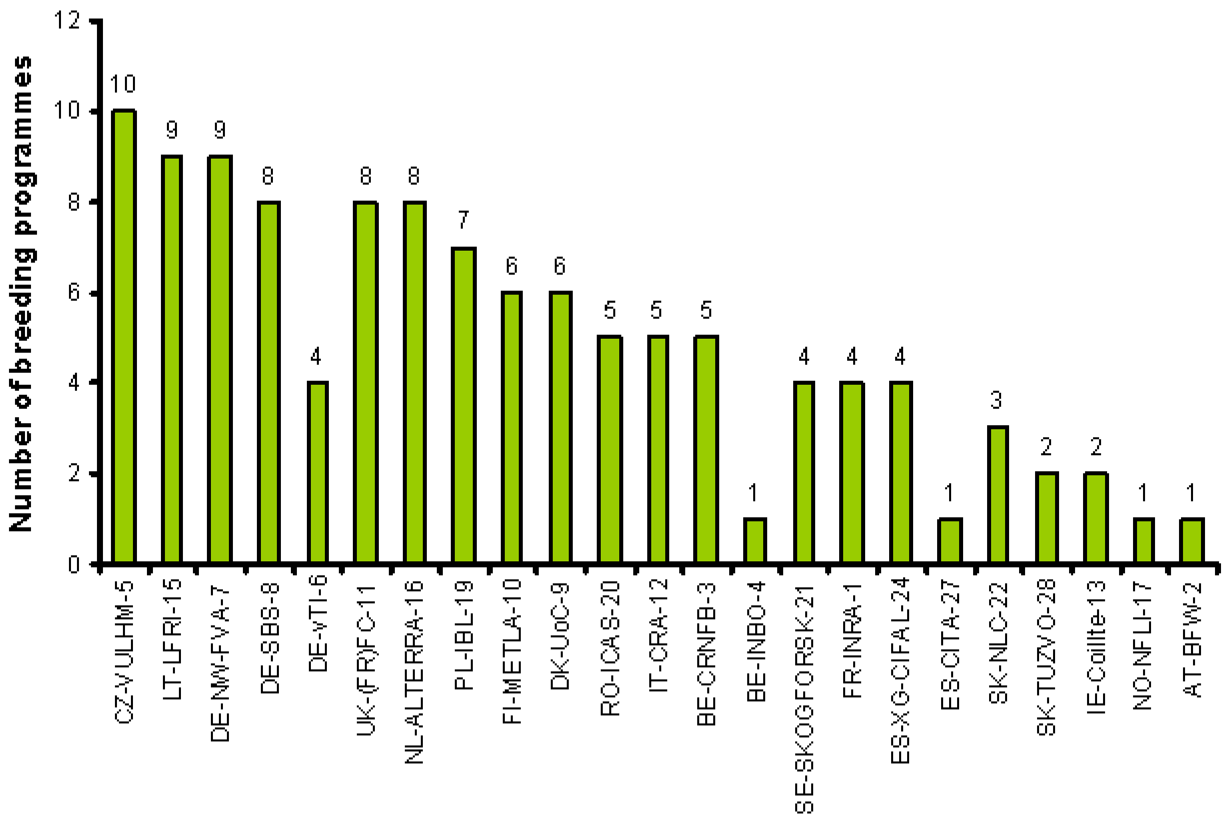


Fig. 3.1.2. Number of breeding programmes per Treebreedex institution. Abbreviation explained "LT-LFRI-15" means "country code - institution's abbreviation – Treebreedex number".

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 attentio n
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.)*

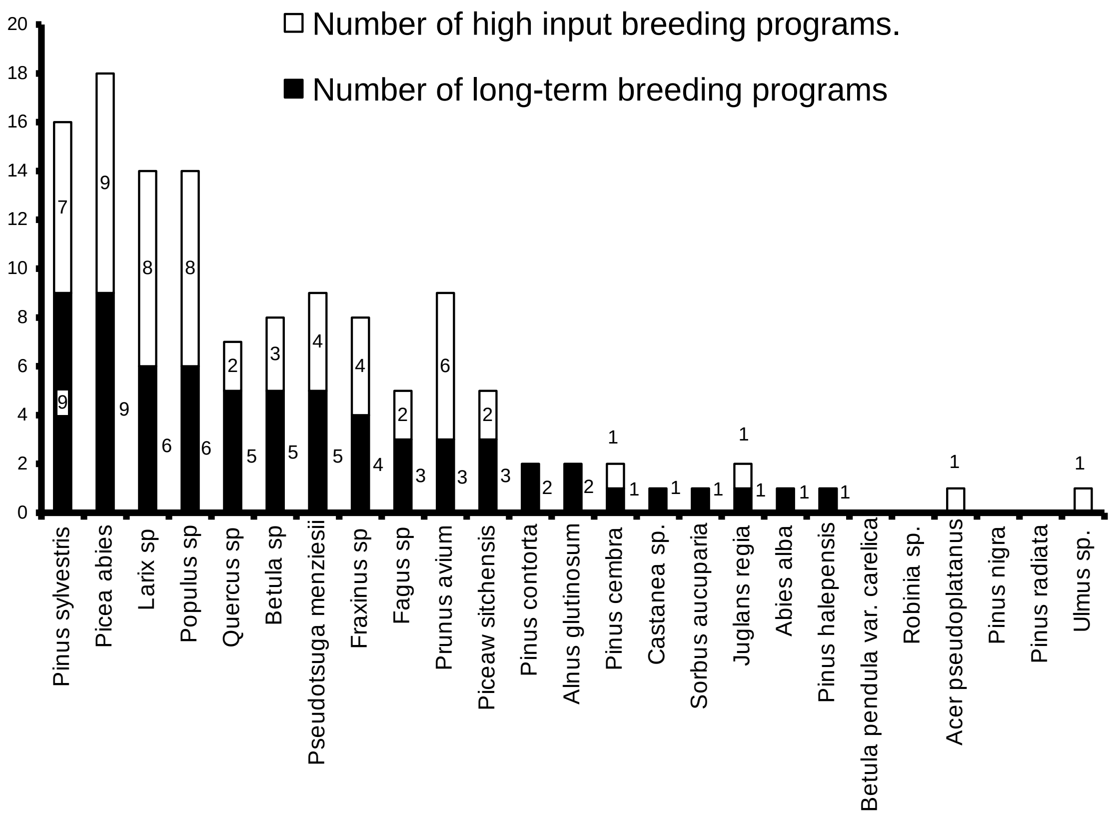


Fig. 3.2.1. Number of long-term and high-input breeding programmes for each. Numbers at the bars show the total number of breeding programmes for each species.

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.

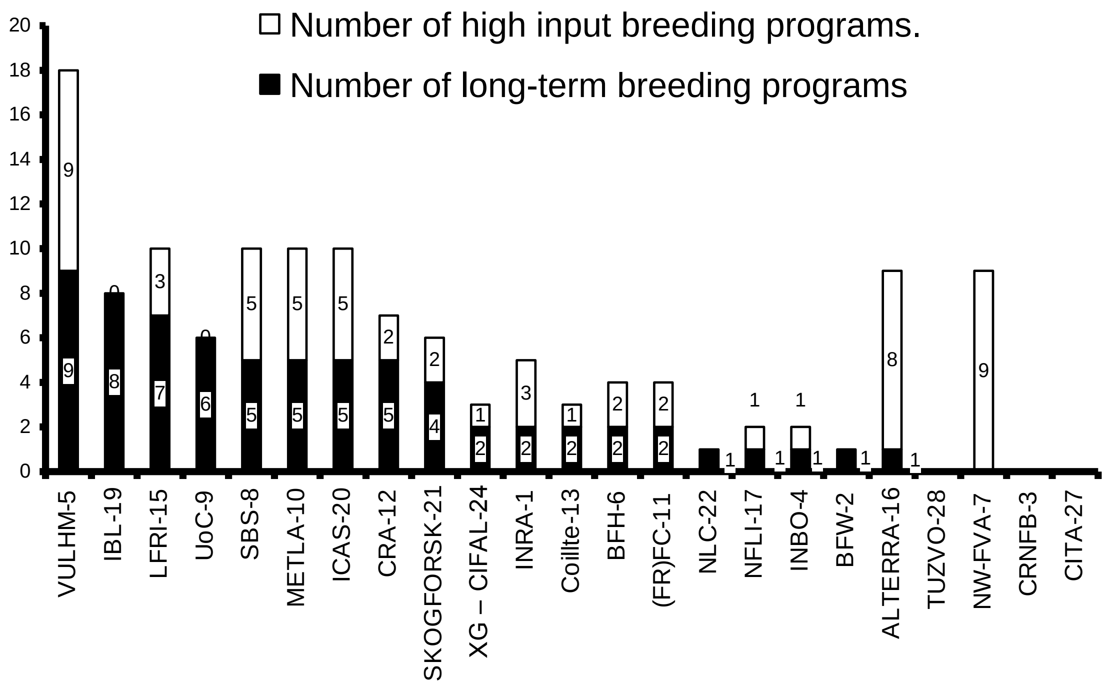


Fig. 2.2.2. Number of long-term and high-input breeding programmes for each participant of Treebreedex. The plot is summarising the answers to the questions 1 and 2. Numbers at the top of the bars show that total number of breeding programmes for each species.

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..

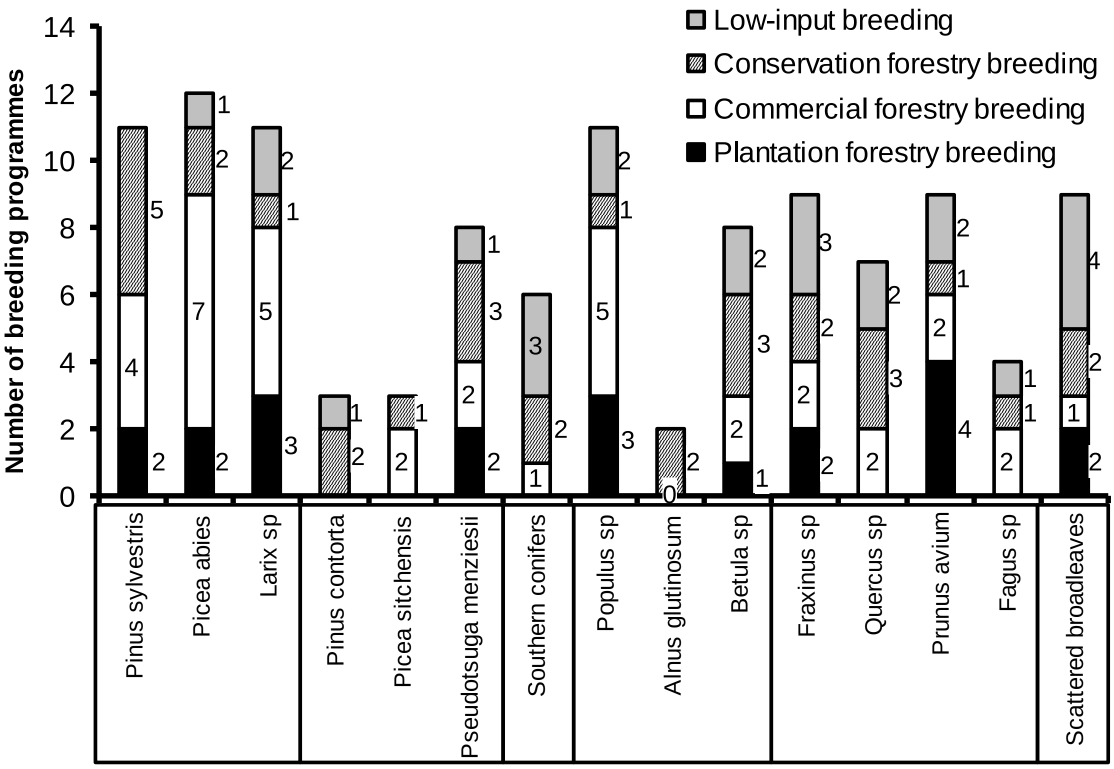


Fig. 2.2.3. Species comparison based on the 4 strategies regarding the balance of economic versus conservation goals. “Low input breeding” means low cost and short term programs; “Conservation forestry breeding” means long-term and low-input programs; “Commercial forestry breeding” means long-term and 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.

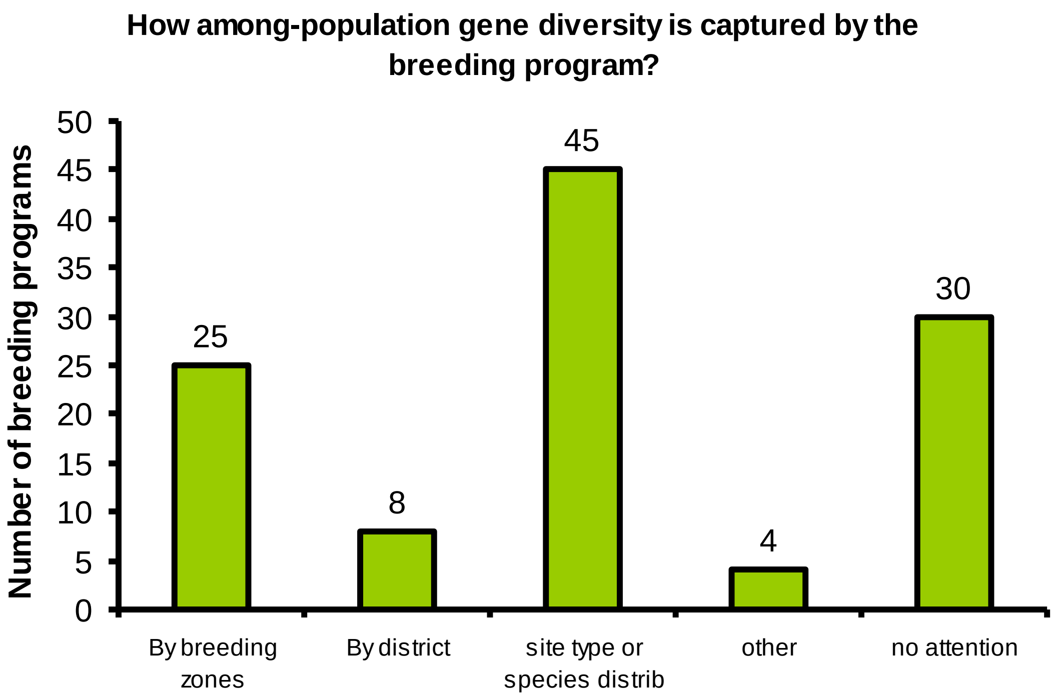


Fig. 3.3.1. Summary on how species gene diversity is captured by a breeding program overall all breeding programs in this survey.

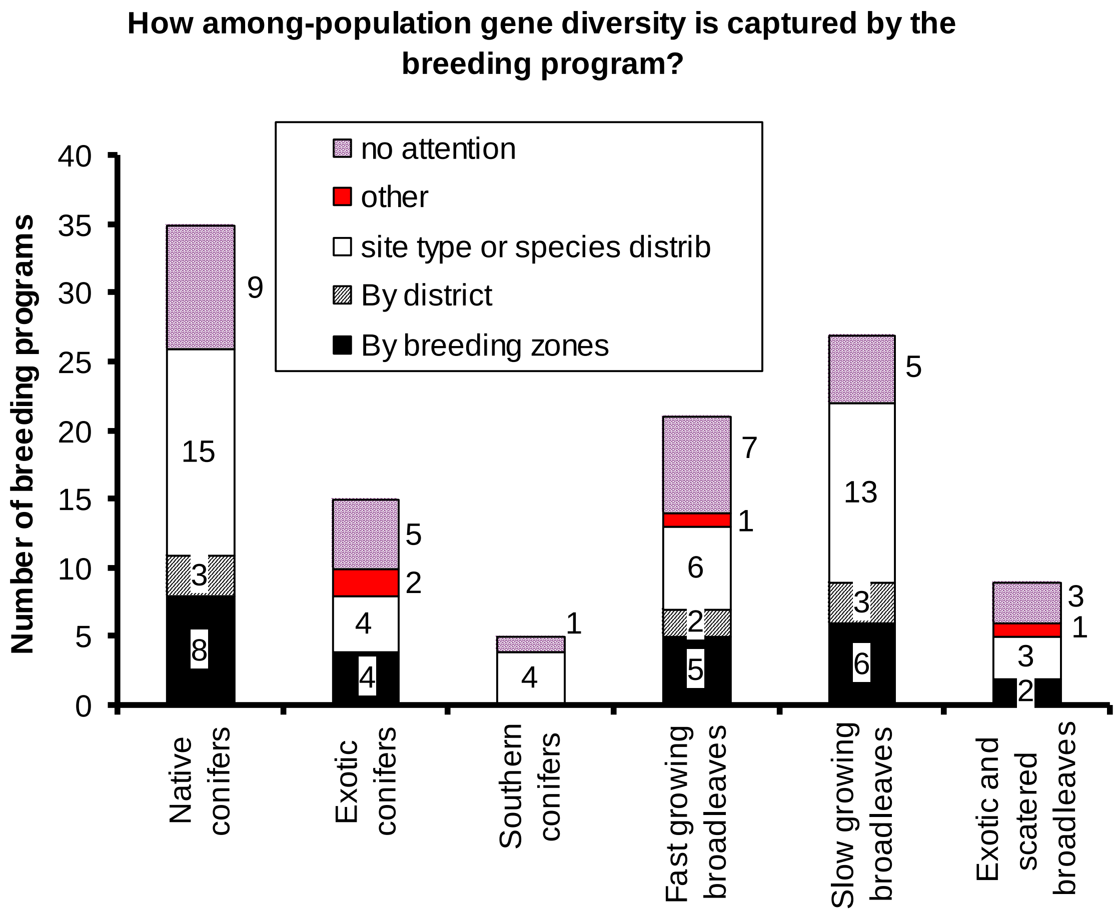


Fig. 3.3.3. Summary of answers to the question "How species gene diversity is captured by a breeding program?" by species groups.

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.

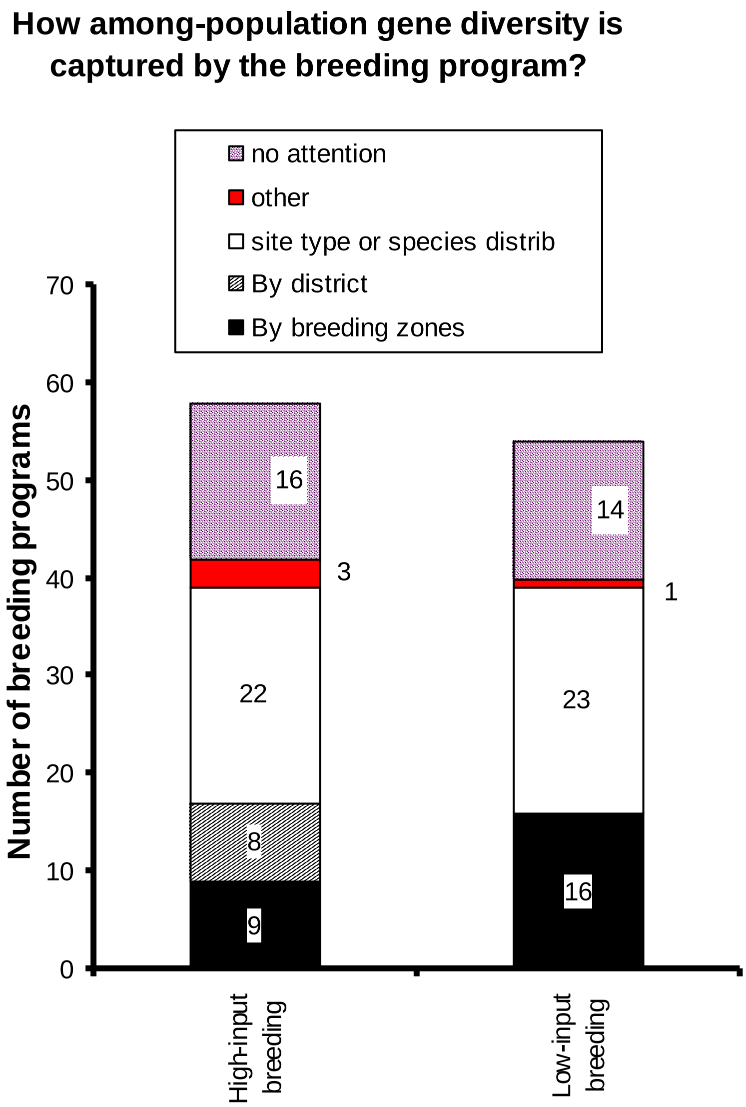


Fig. 3.3.4. Summary of answers to the question "How species gene diversity is captured by a breeding program?" by type of input into breeding program.

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.

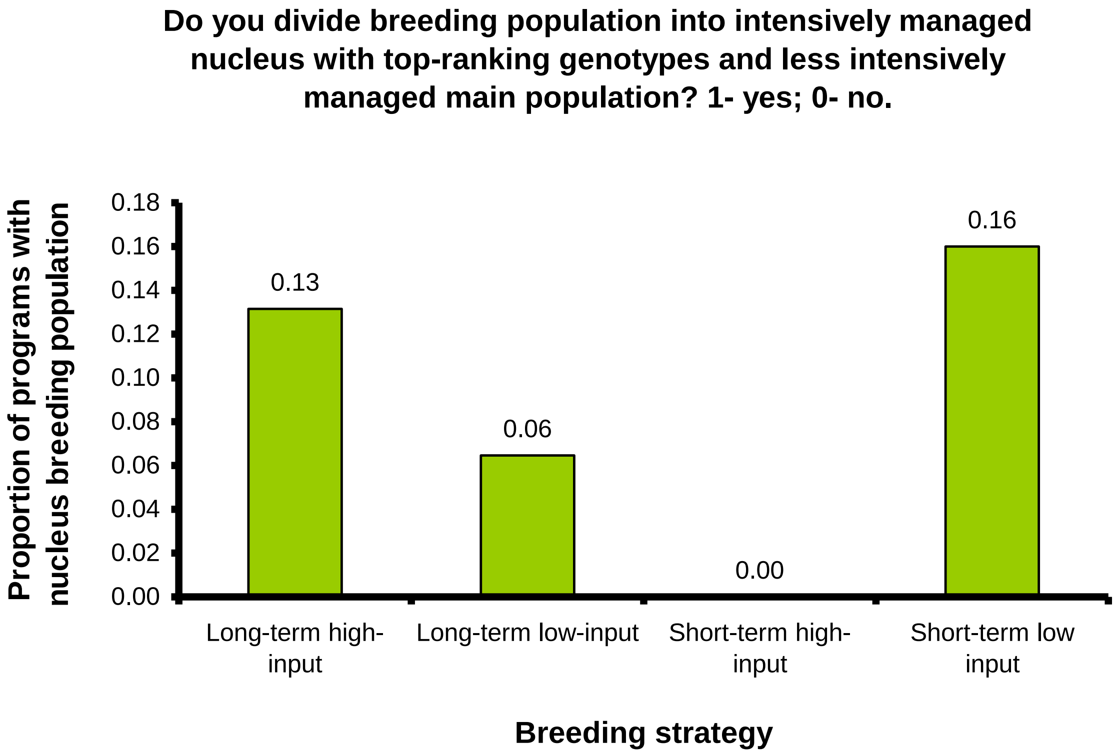


Fig. 3.4.1. The answers grouped by the breeding strategies as regards their terms and input.

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.

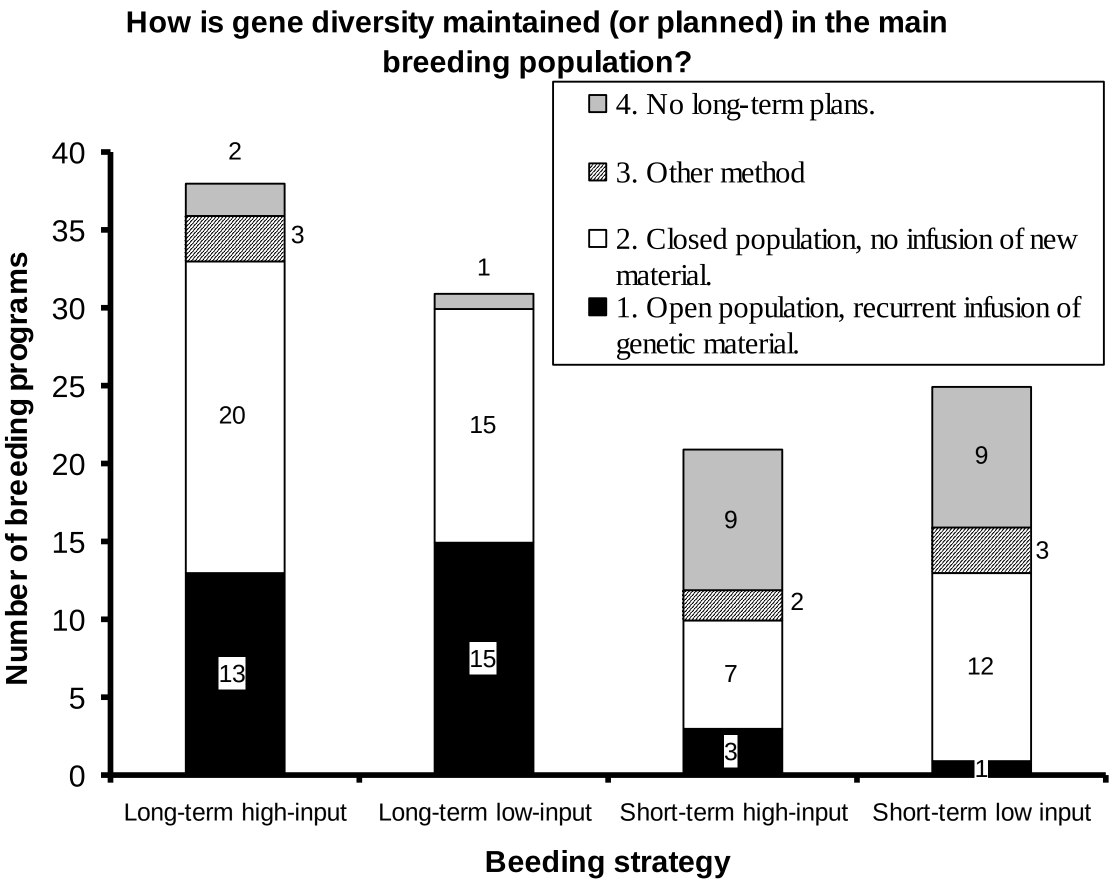


Fig. 3.5.1. How gene diversity is maintained within breeding populations for each breeding strategy.

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.

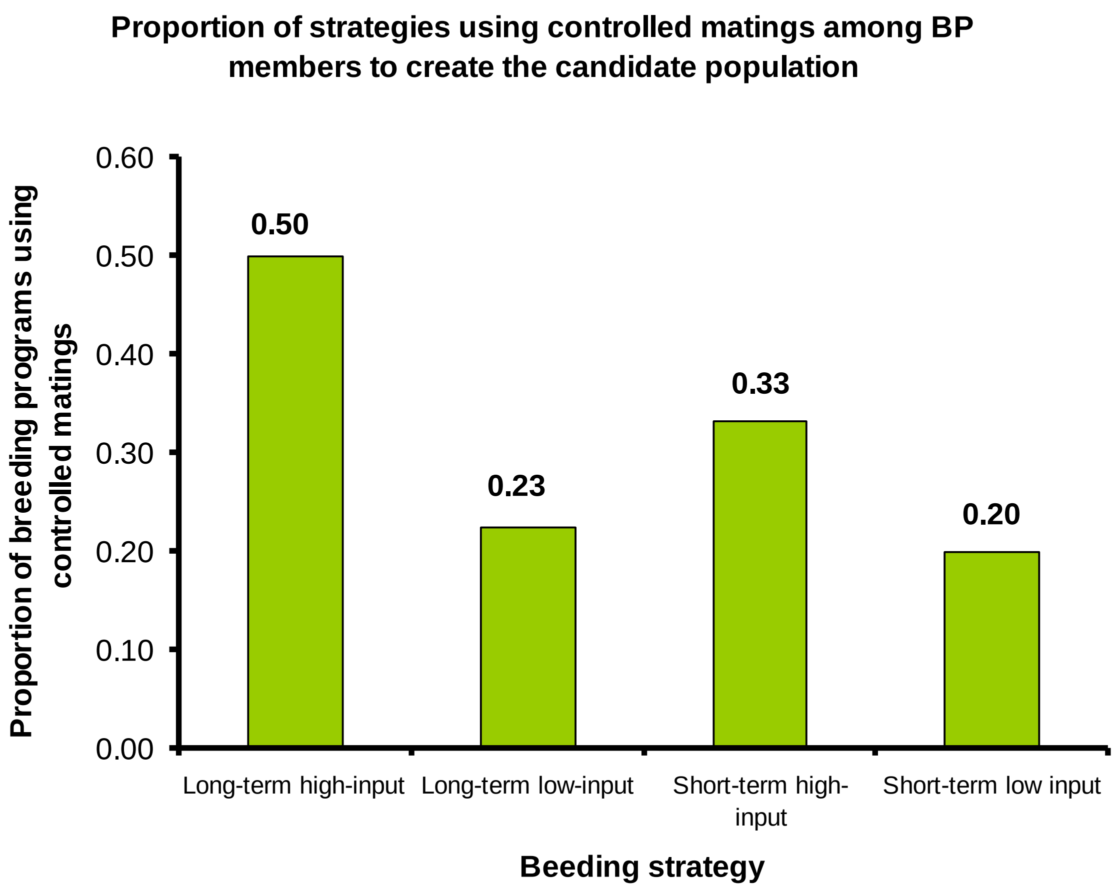


Fig. 3.6.1. Proportion of breeding programs using controlled pollination to create the candidate population given by breeding strategies.

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.

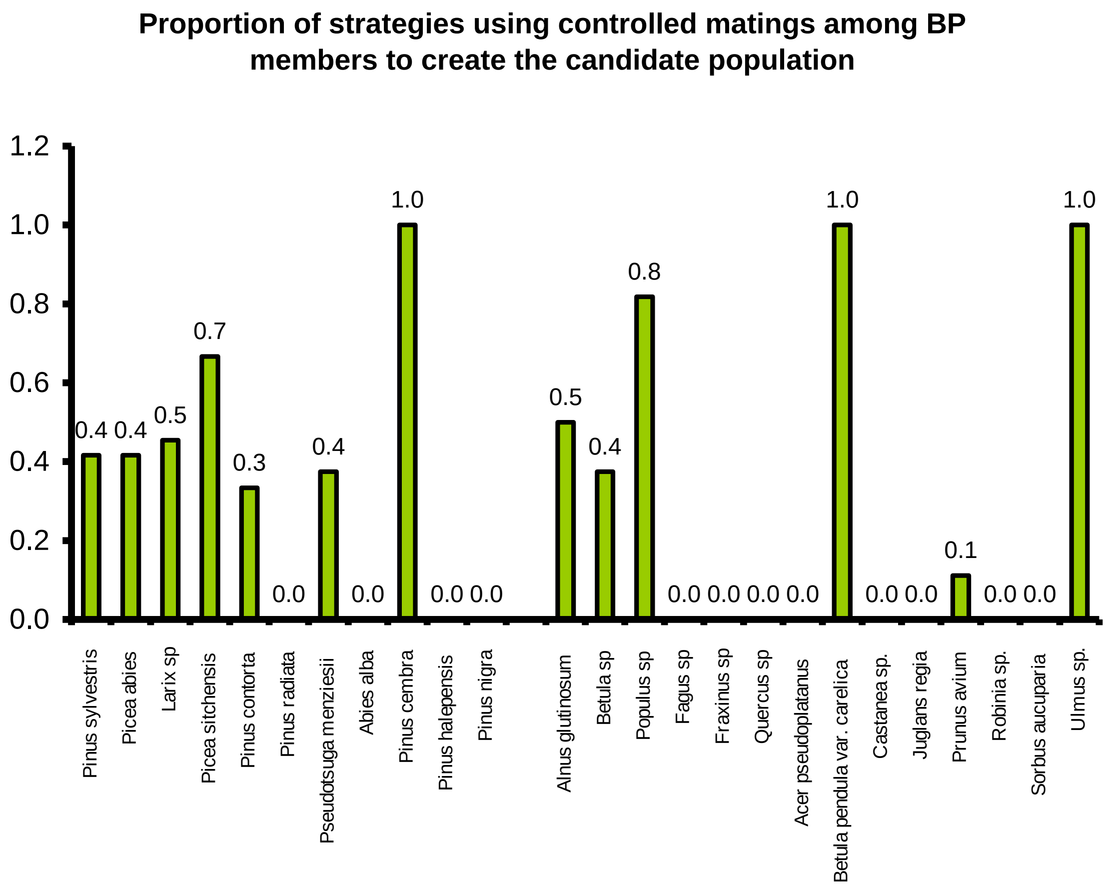


Fig. 3.6.2. Proportion of breeding programs using controlled pollination to create the candidate population given by species.

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.

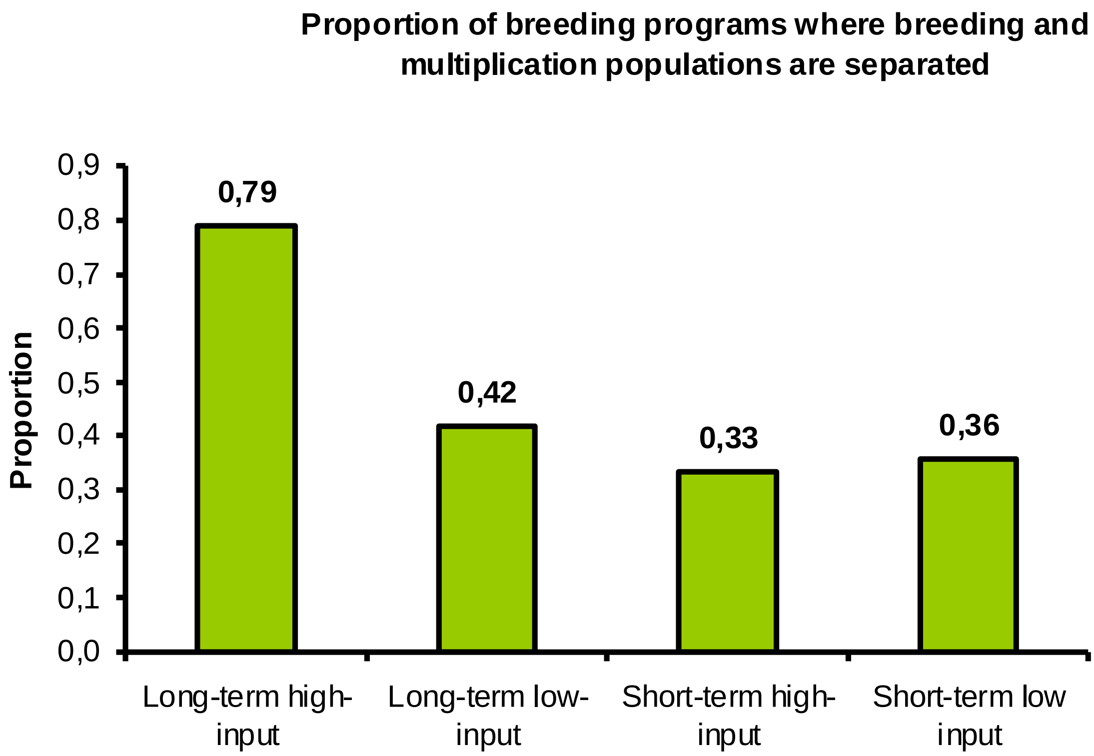
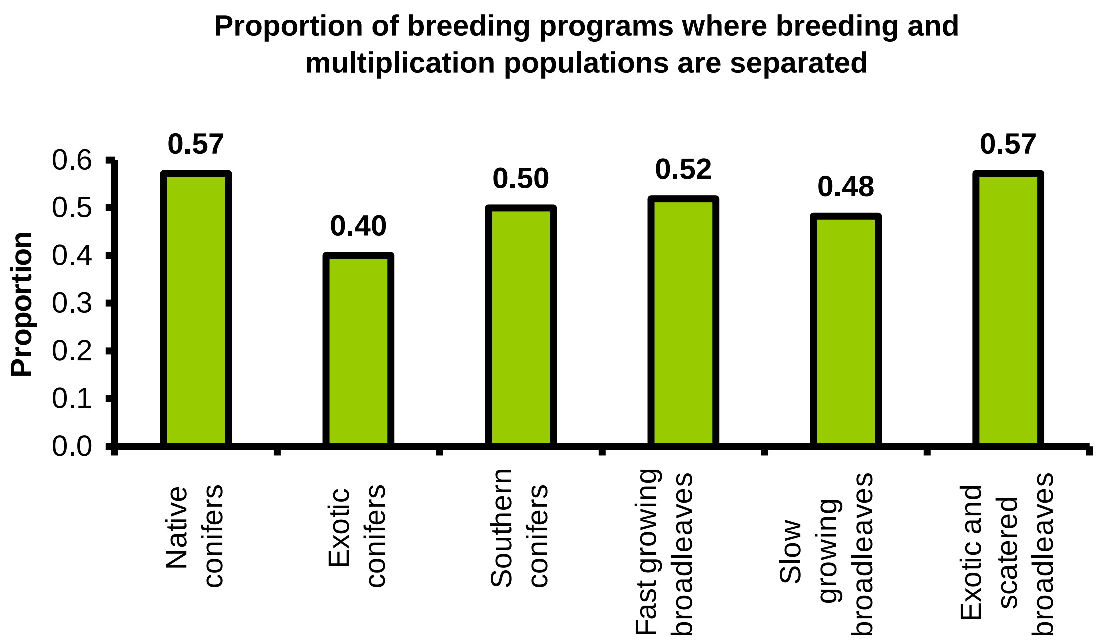


Fig. 3.8.1. Proportion of breeding programs with separate breeding and multiplication populations by the type of breeding.

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).



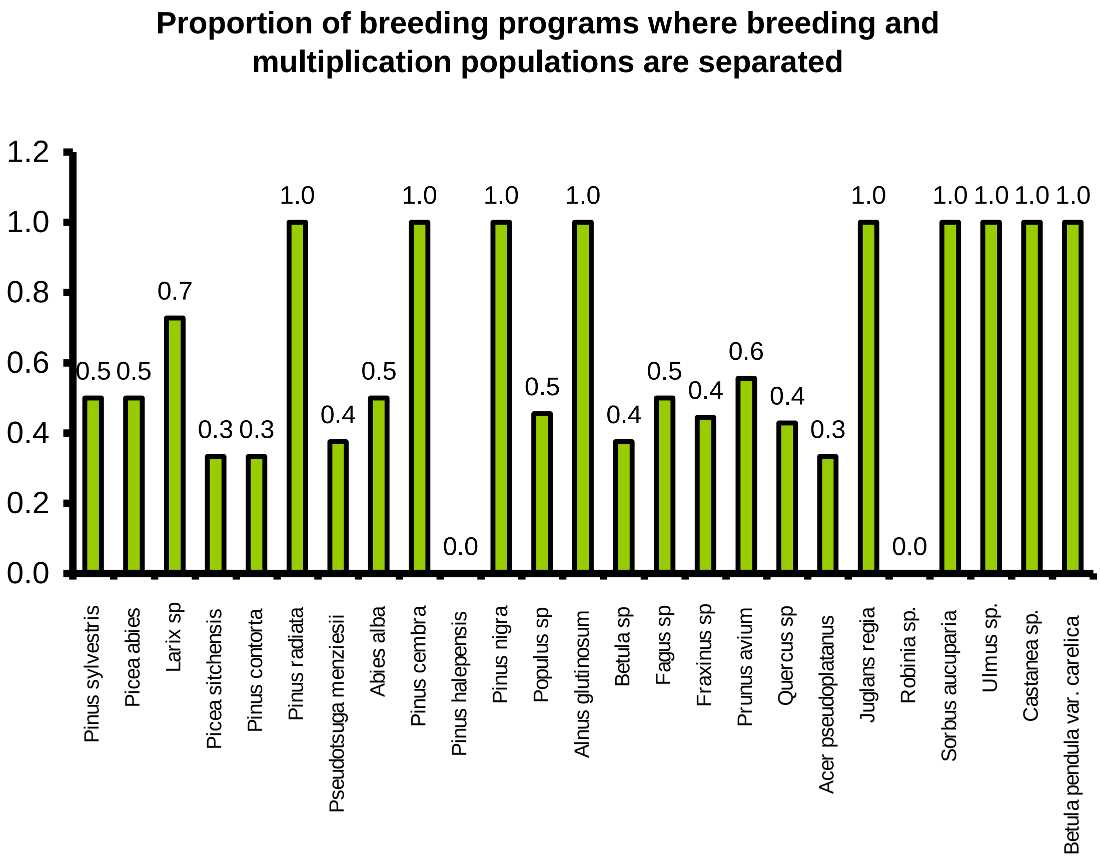


Fig. 3.8.2. Proportion of breeding programs with separate breeding and multiplication populations given by species groups (top) and species (bottom).

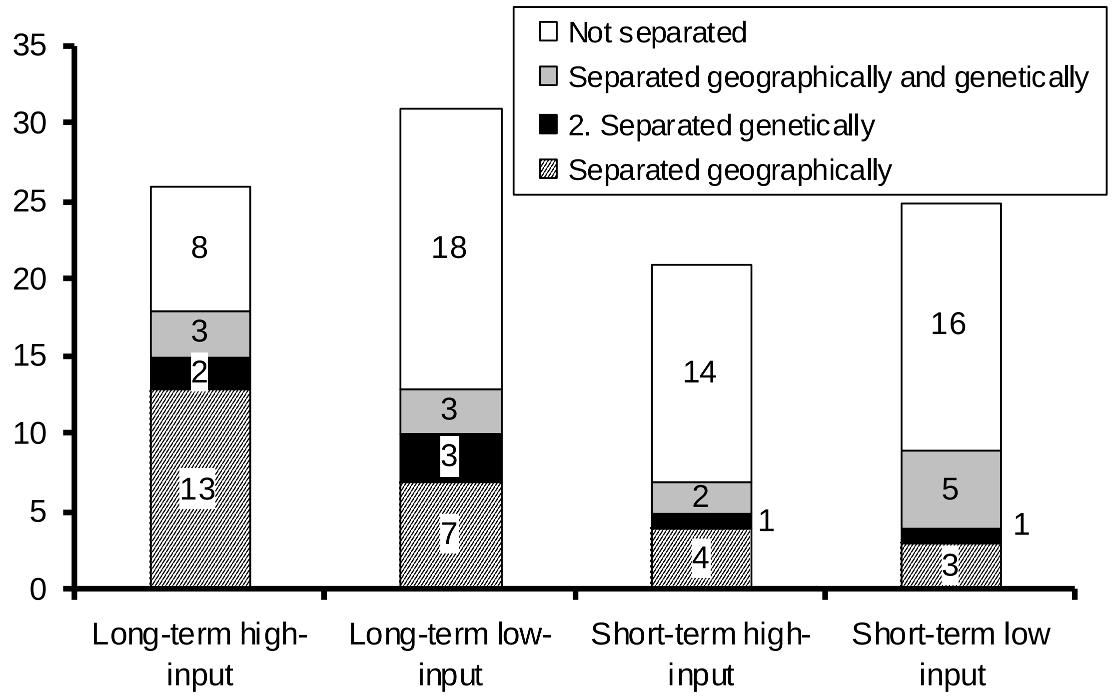


Fig. 3.8.3. Answers to the question are breeding and multiplication populations kept separated with specifying the type of separation.

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).

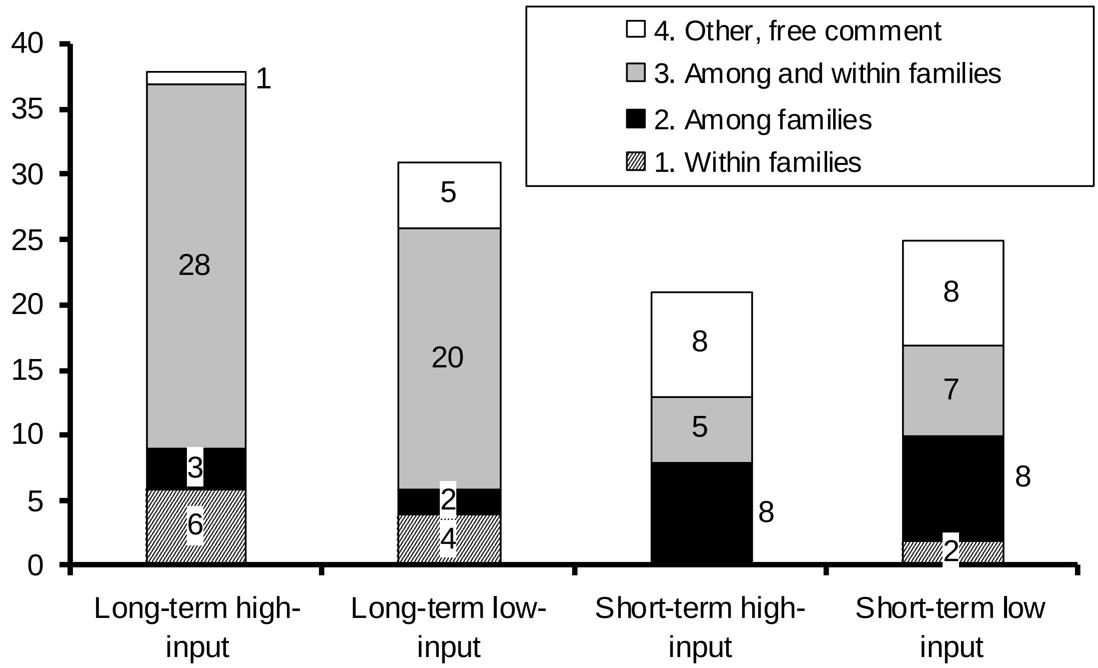


Fig. 3.9.1. The genetic level of the selection of the new breeding population members is made in each breeding cycle, given by the type of the breeding programmes.

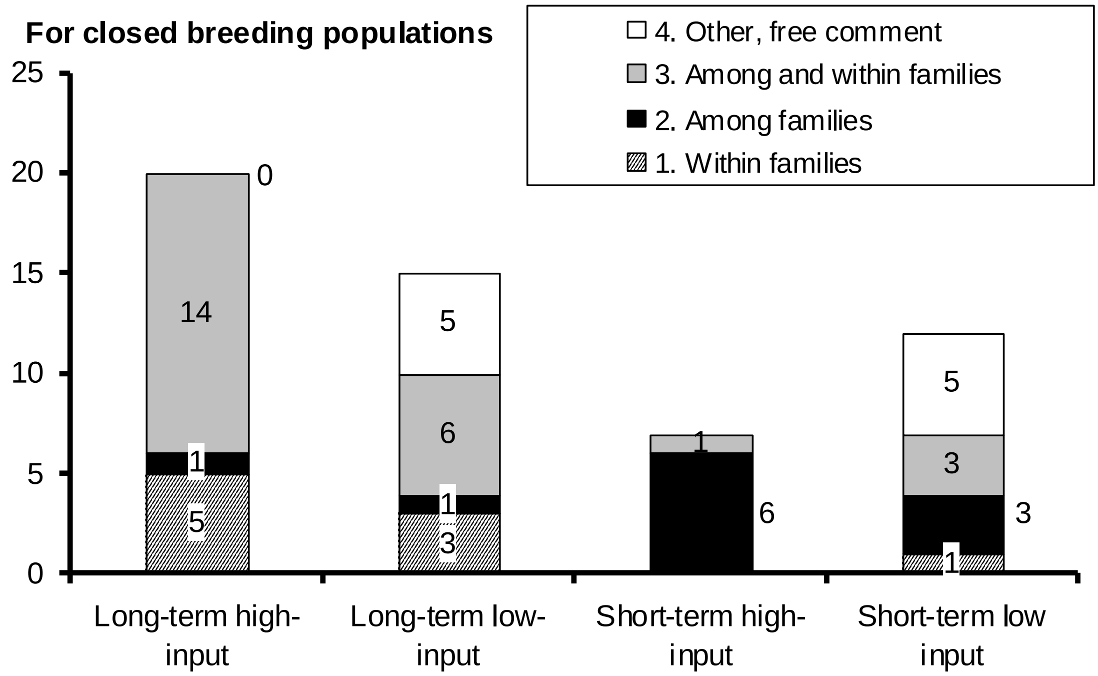


Fig. 3.9.2. The genetic level at which the selection of the new breeding population members is made in each breeding cycle, given only for these programmes where breeding populations are kept closed (see question 3).

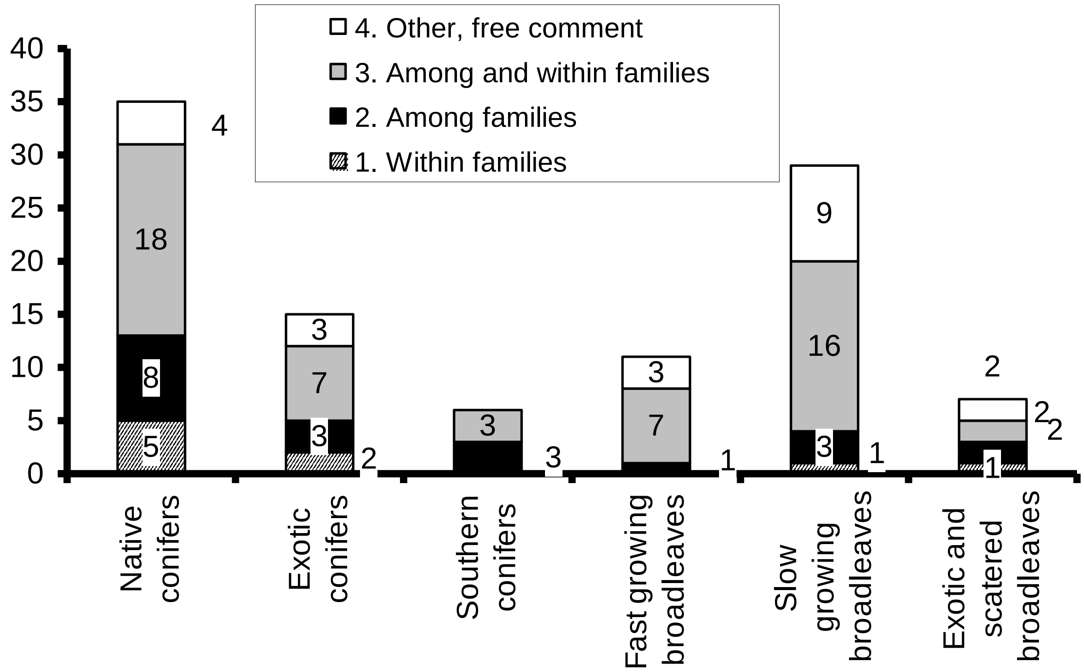


Fig. 3.9.3. The genetic level at which the selection of the new breeding population members is made in each breeding cycle, given by species groups.

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.

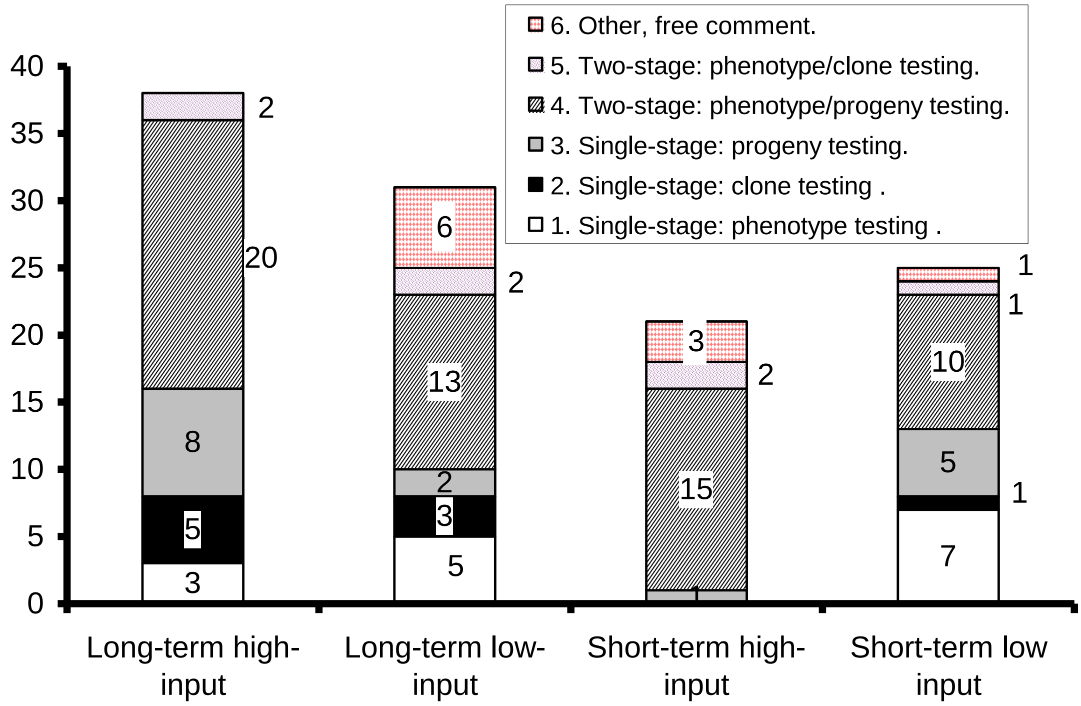


Fig. 3.10.1. Number of testing strategies used in each type of breeding.

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).

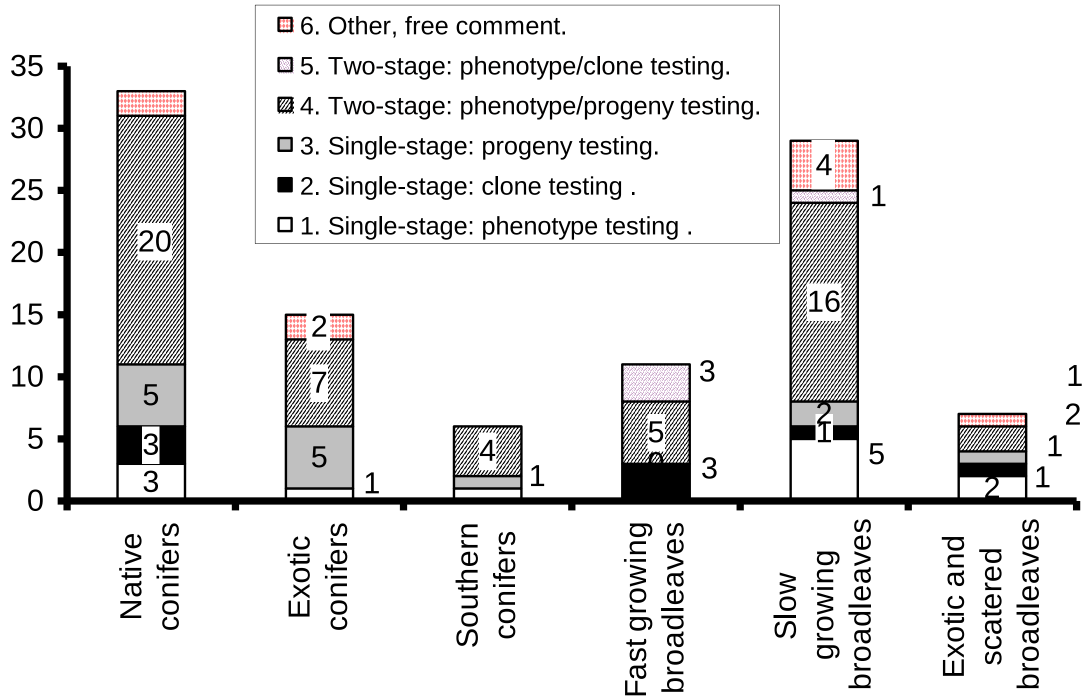


Fig. 3.10.2. Number of testing strategies used in each species group.

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.

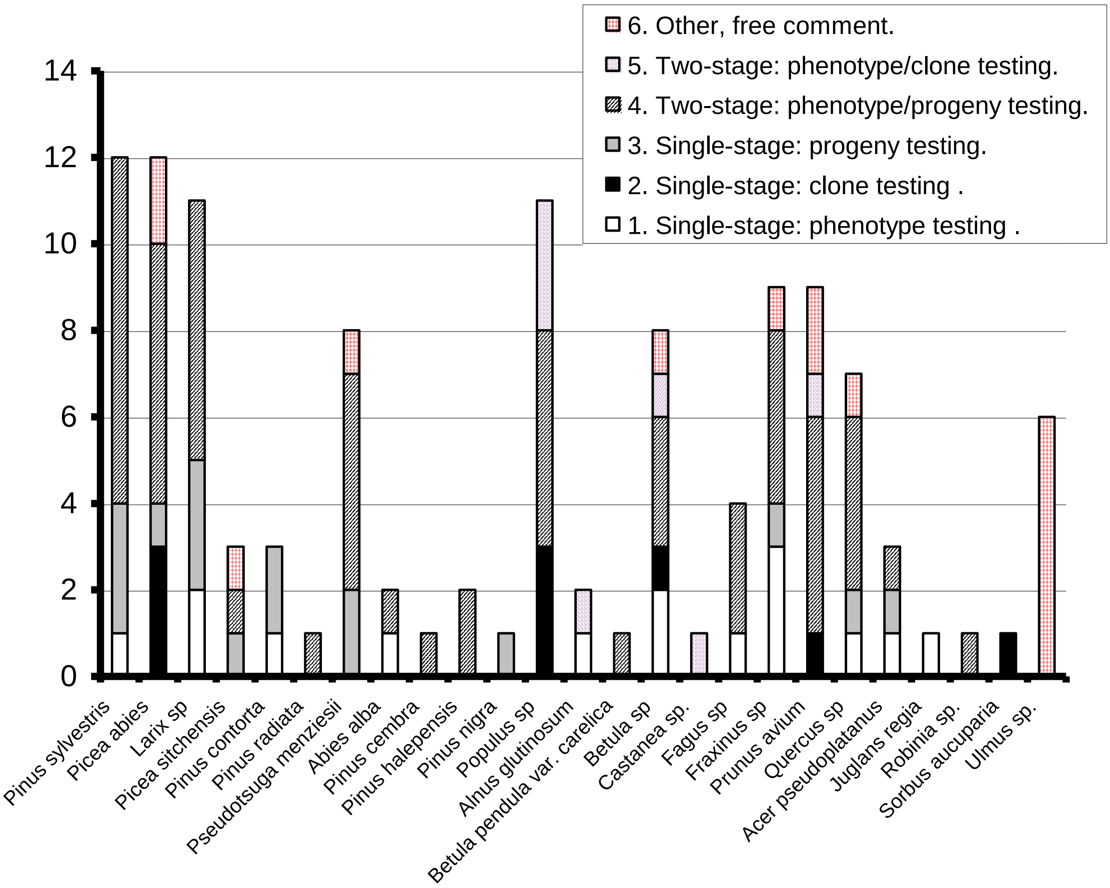


Fig. 3.10.3. Number of testing strategies used in each species group.

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

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	k/ 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

Impact of the results of large genetic field experimental networks to practical forestry supporting industry.

Dag Lindgren

Presentation 100622 at

TREEBREEDEX Activity 5 seminar

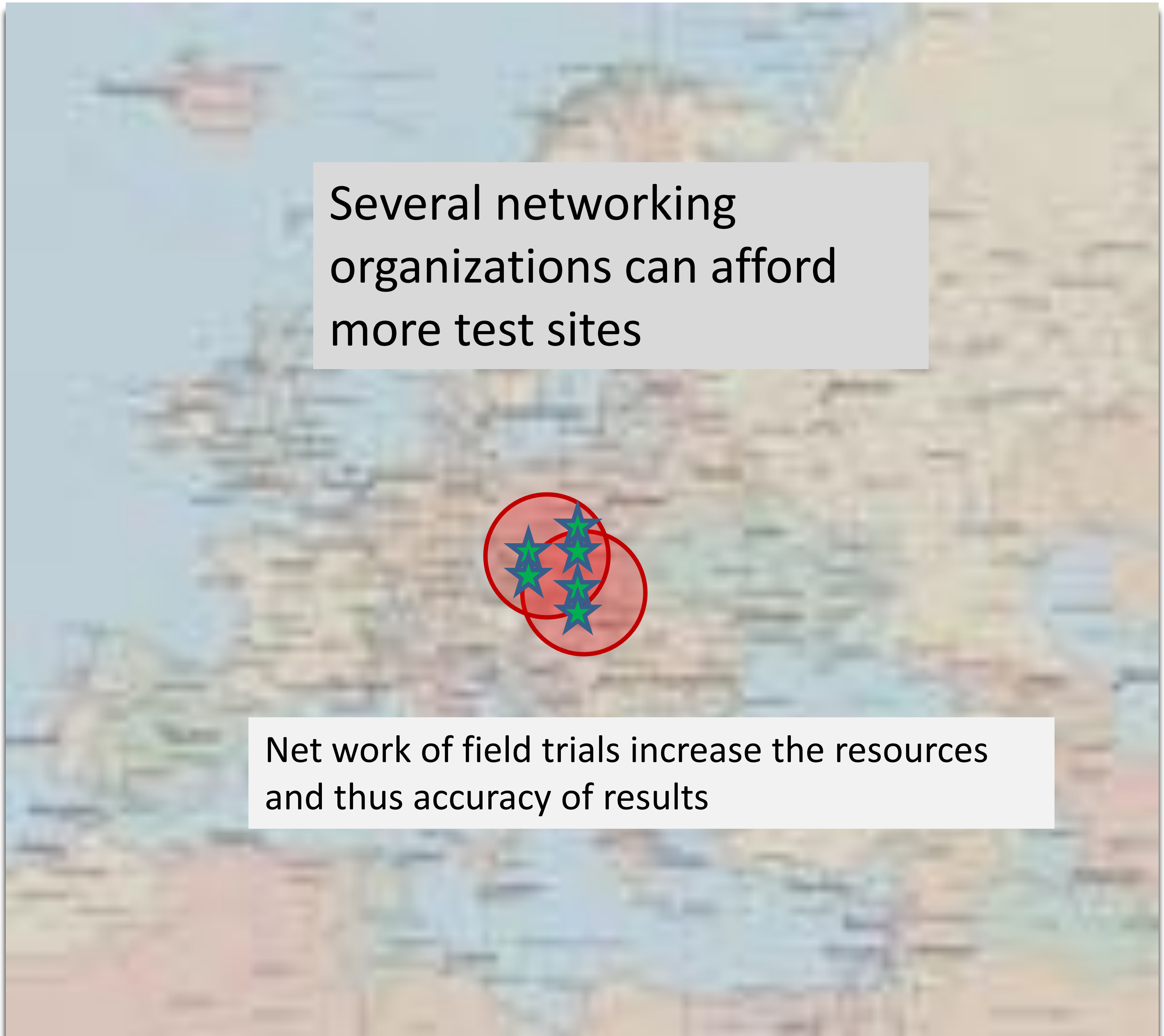
What do large genetic field experimental networks across Europe bring to the scientific community?

June 22 – 24, 2010, Sękocin Stary (Poland)

Some expected impacts for Industry

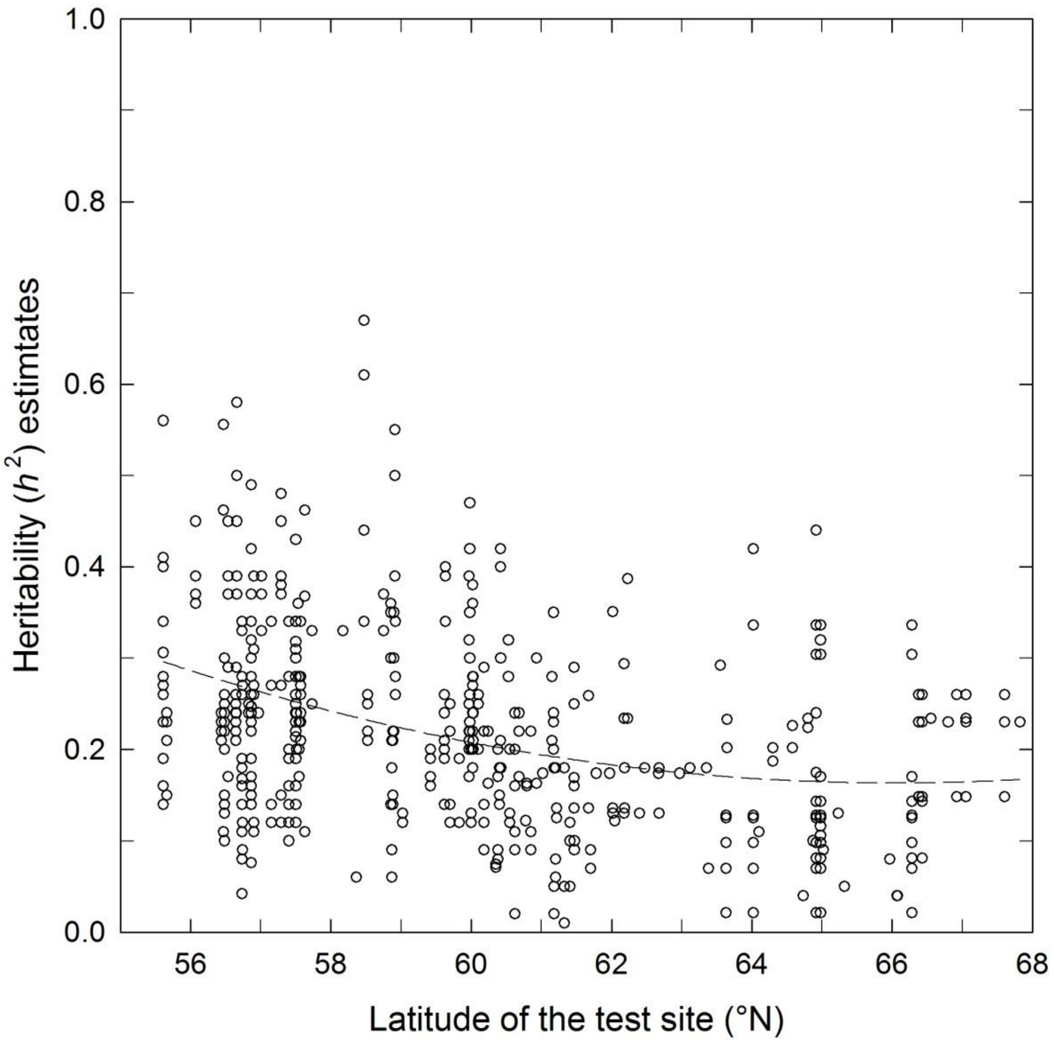
- More reliable and applicable breeding values
- Better forest regeneration materials now and in the future
- Better known and documented forest regeneration materials
- Reduced risk of failures with FRM
- Better forecasts of forest growth
- More discussion and attention focusing on the forest in the field
- Better contacts among those dealing with similar forests in different organizations (countries)
- More focus of scientists (like forest geneticists), education and administrators of what happens with industrial plantations
- Easier to claim that Industry knows something about what they are doing and tries to get it better known (e.g. diversity)!


One organization
One organization can afford a few test sites


Several networking organizations can afford more test sites
Net work of field trials increase the resources and thus accuracy of results

- Performances estimated are not as general as desirable. Many sites and replication in time and experimental technique will improve generality. Networks may help with that.

P. sylvestris – h^2 for tree height at age 10-20 yrs, >200 trials, 6.000 families, 1.000.000 trees

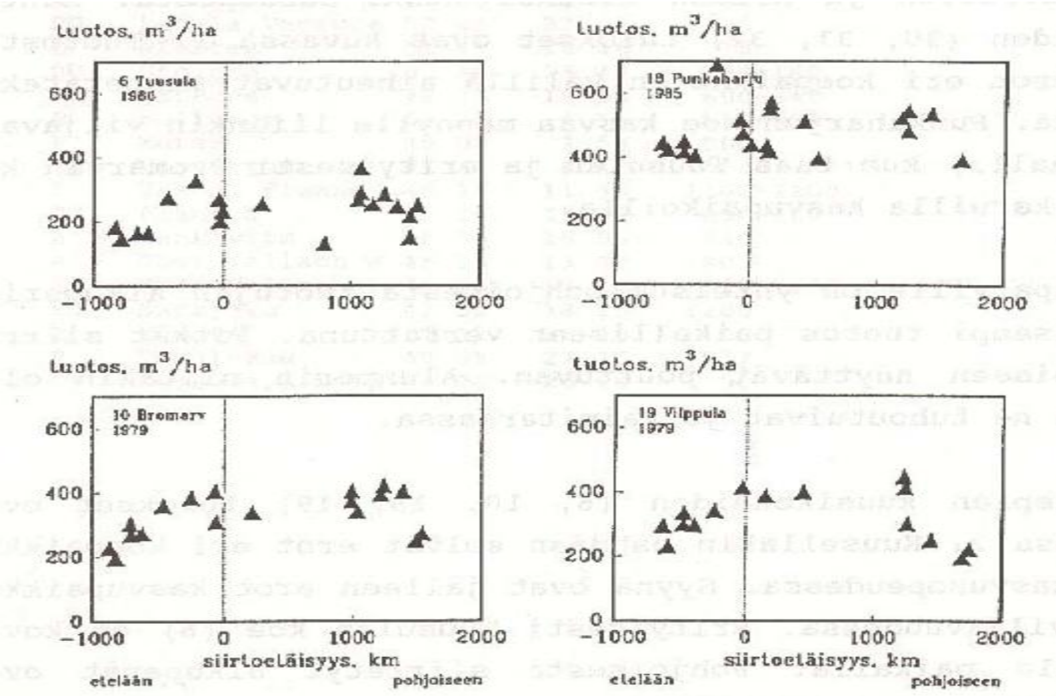


Sites are very different genetically!
Many sites desirable for reasonable general and reliable BVs!
Still more to describe the variation among sites!

Modified from Andersson 2009, TREEBREEDEX presentation Orleans

Norway spruce provenance performance at four Finnish trial sites

Norway spruce *Volume production (m3/ha) 40 to 50 yrs age*

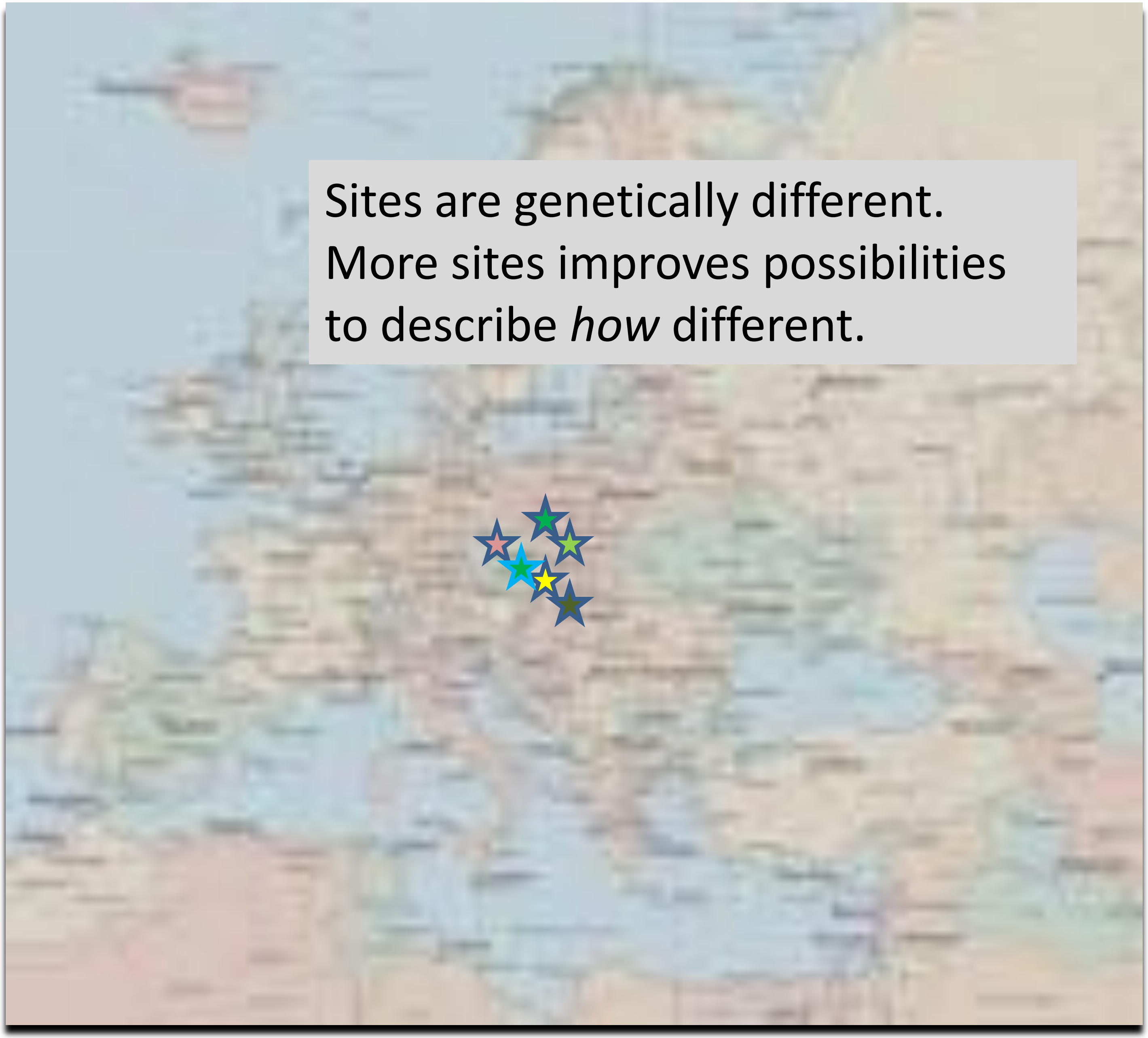


Stands seeds vary among what is typical for the "provenance origin" in an usually unpredictable way.

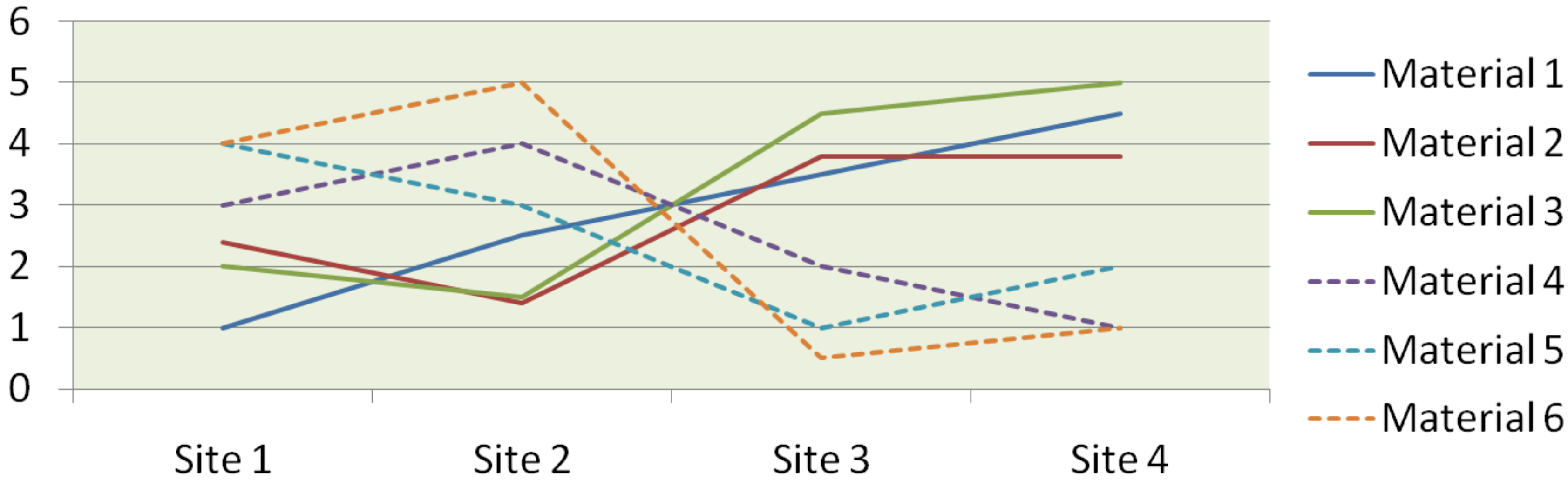
Large trials required to know these residuals better

At the X-axis is transfer distance, 0 is local and the higher values is transfers from a location with higher heat sum

from Koski 1989 extracted from Ruotsalainen 2008 TREEBREEDEX presentation Pirna


Sites are genetically different.
More sites improves possibilities to describe *how* different.

Genotype-Environment Interaction

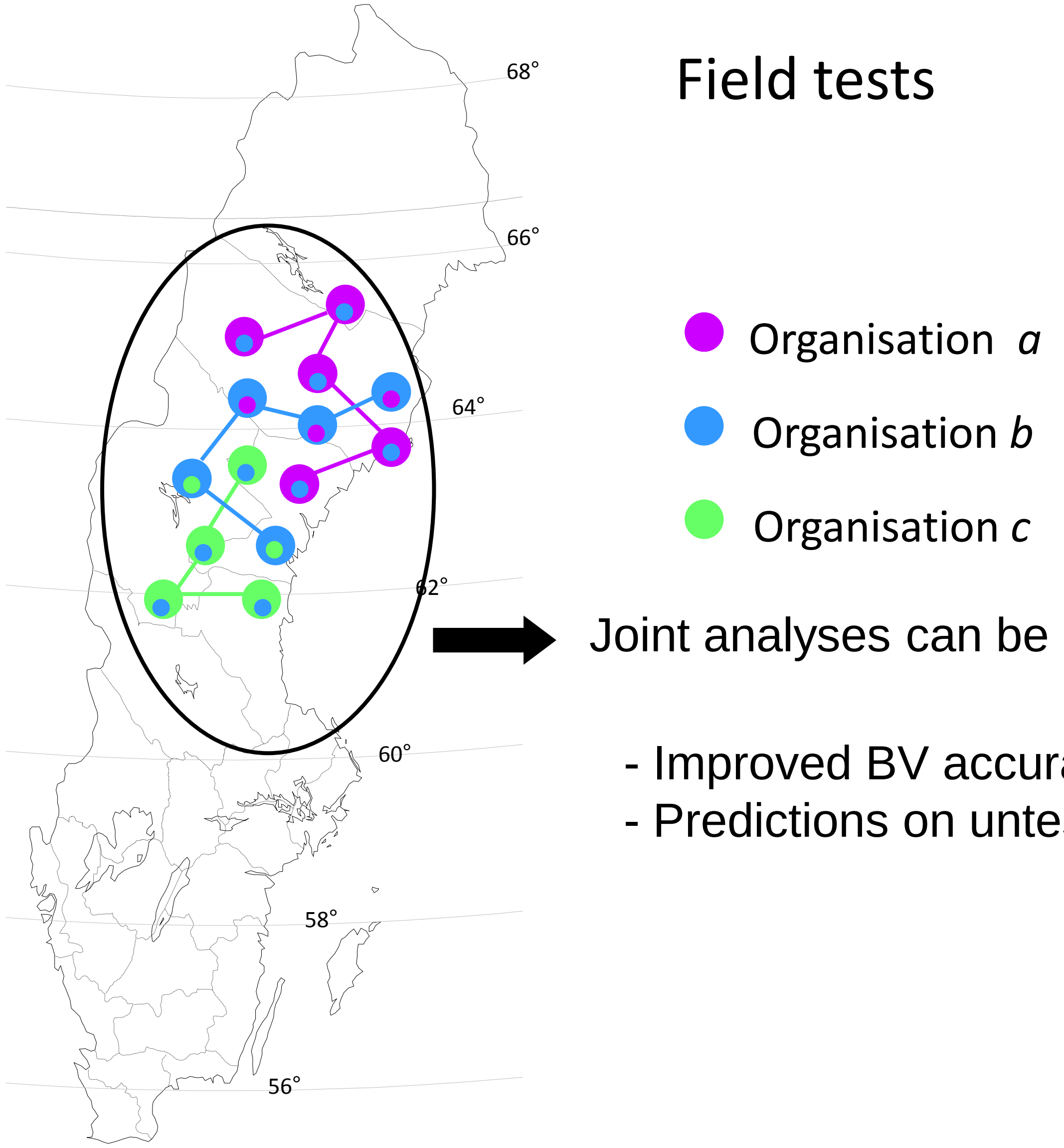


If there is a pattern so some material types are relatively better on some site types, this can be utilized to improve gain!

Useful such grouping requires generally many sites!
Networking improves possibilities!


Seeds produced by one organization may be used by another if materials are relevantly tested.

Field tests



Joint analyses can be made if materials overlap:

- Improved BV accuracy
- Predictions on untested sites

Modified from Andersson 2009 TREEBREEDEX presentation Orleans

Calculated inoptimality loss for Scots pine as a function of zone size and origin range at the same altitude

Zone size (Latitudes)	Range of origins (Latitudes)	Loss (%)
4	0	5.3
2	0	1.3
2	2	2.0
2	4	4.0

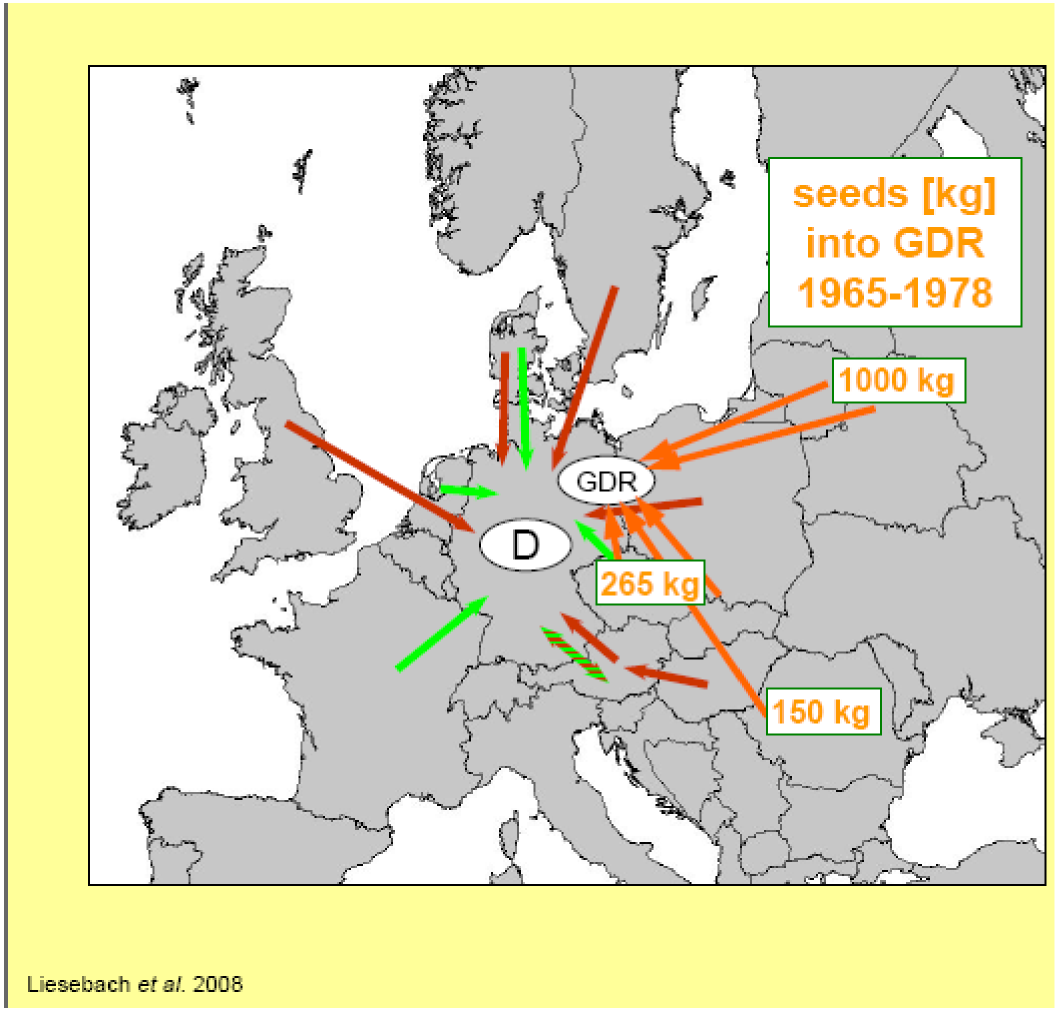
Conclusions:

- **Zone size ranging over 2-3 latitudes for a seed orchard is OK**
- **Avoid larger range of origin for clones than 3 latitudes in seed orchards**

Modified from Lindgren 2009 TREEBREEDEX presentation Hann Münden

The message is that areas served by genetic materials extends over organizational (national) borders.
For Swedish Scots pine it is somewhat less than two latitudes, thus almost two latitudes south or north of Sweden.
The example is an underestimate as Scots pine is sensitive to latitudinal transfer and sensitivity to latitude transfer is less south of Sweden.

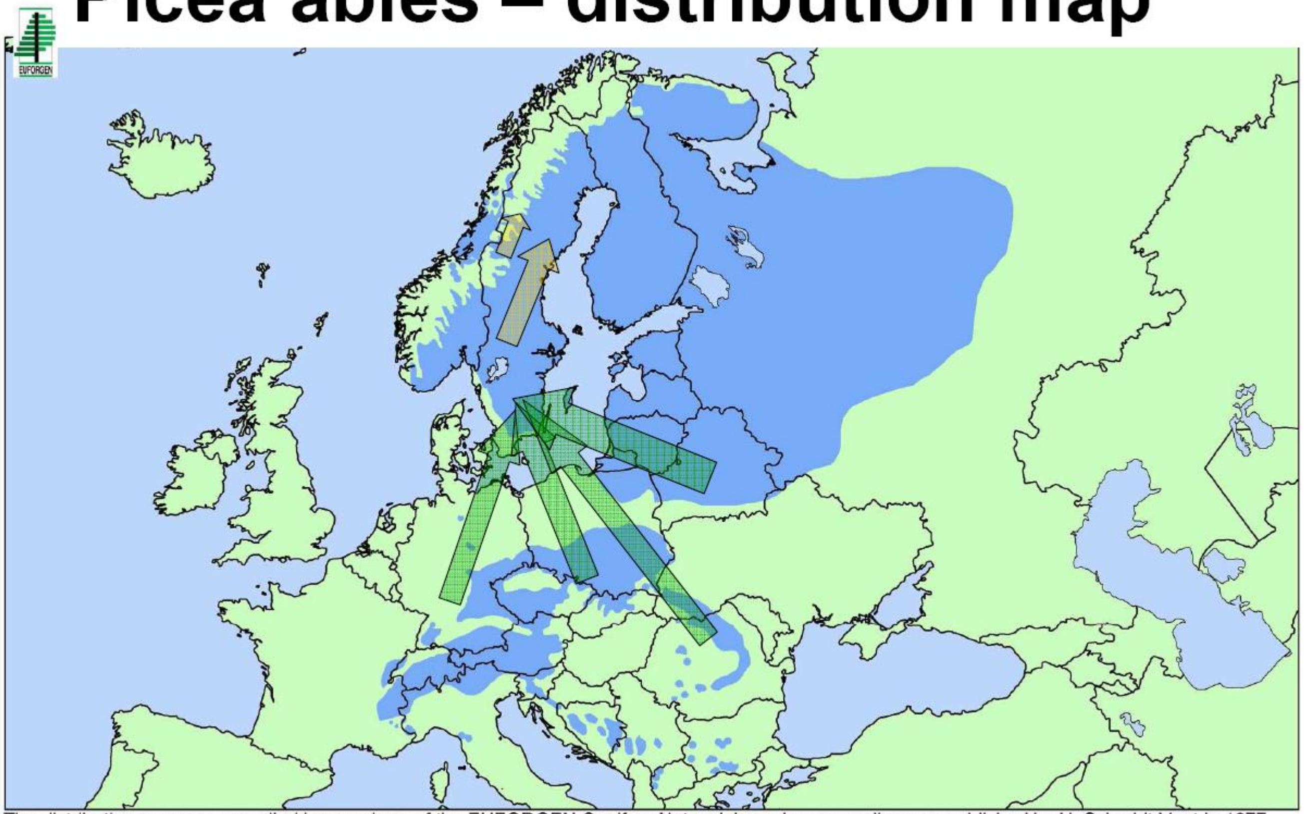
Imports of Scots pine FRM into Germany



Extracted from Liesebach et al 2008 TREEBREEDEX presentation Pirna

Norway spruce transfers in Sweden
Extends national borders!

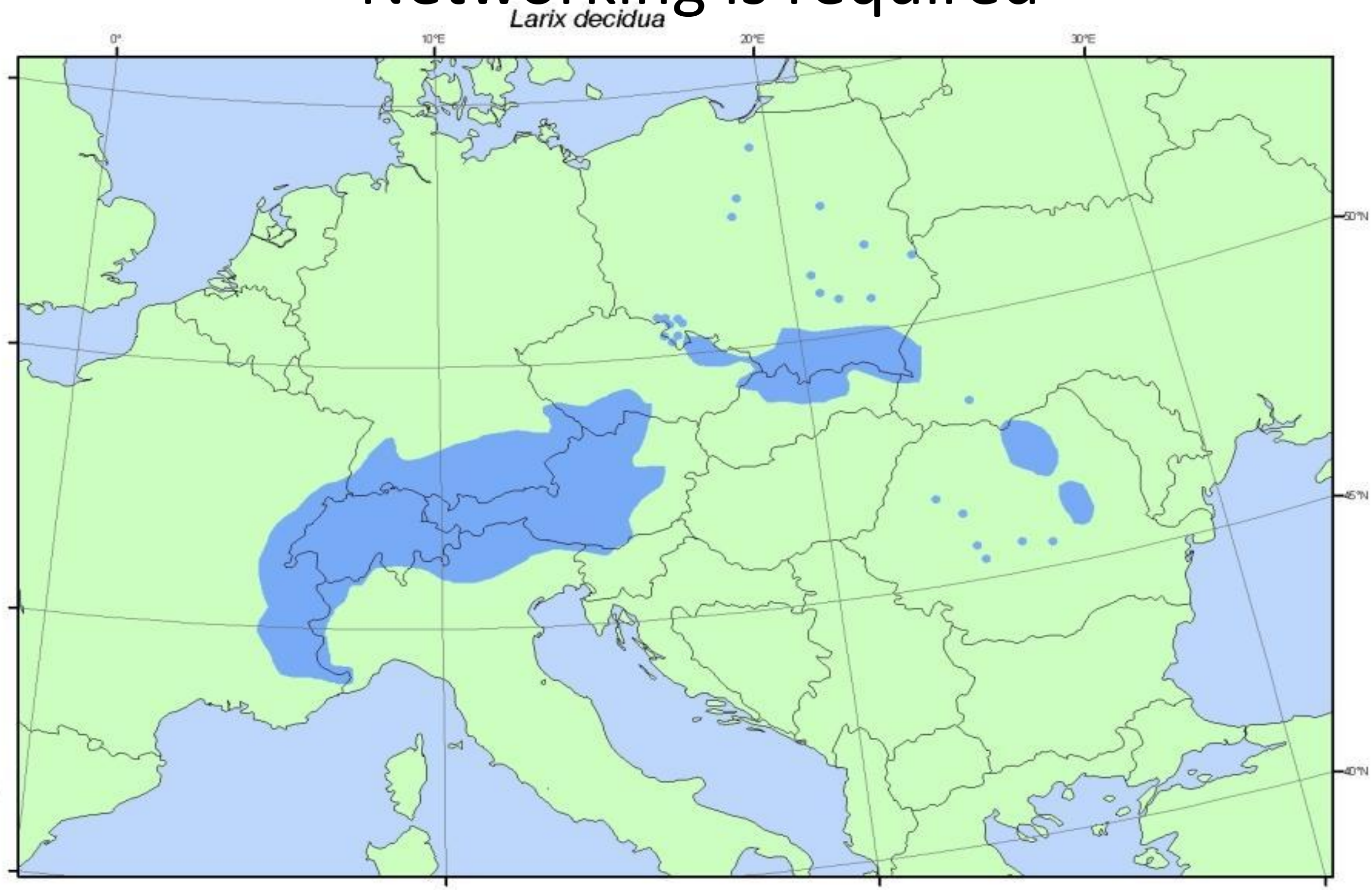
Picea abies – distribution map



The distribution map was compiled by members of the EUFORGEN Conifers Network based on an earlier map published by H. Schmidt-Vogt in 1977 (Die Fichte, Verlag Paul Parey, Hamburg and Berlin, p.647).
and was published in:
Skrøppa, T.. 2003. EUFORGEN Technical Guidelines for genetic conservation and use for Norway spruce (Picea abies). International Plant Genetic Resources Institute, Rome, Italy. 6 pages

Modified from Westin 2008 TREEBREEDEX presentation Pirna

Exploitation of the genetic resources of a species requires samples from its range tested over its potential use. Networking is required



EUFORGEN Secretariat
c/o Bioversity International
Via dei Tre Denari, 472/a
00057 Maccarese (Fiumicino)
Rome, Italy
Tel. (+39)066118251
Fax: (+39)0661979661
euf_secretariat@cgiar.org
More information
and other maps at:
www.euforgen.org

This distribution map, showing the present natural distribution range of *Larix decidua*, was compiled by members of the EUFORGEN Conifers Network and will be published in: Matras J. and L. Paques EUFORGEN Technical Guidelines for genetic conservation and use for European larch (*Larix decidua*). Bioversity International , Rome, Italy.

First published online on October 2007-

Km
0 125 250 500

From Pâques 2009 TREEBREEDEX presentation *Hann-Münden, 2009*

Countries or organization are just not large enough to handle the relevant range of sites or origins

When environments changes, the test sites established by one organization may not be the relevant ones.

Networks is a preparation and part of the solution to environmental change (Global warming)

Environment or demands of organization may change!

The most suitable test environments for use of test results may be found outside the organization

- **since the environments have changed**
- **or the predictions of genetic materials performance has changed**
- **or requirements of production have changed!**

This is easier to handle if organizations are networking

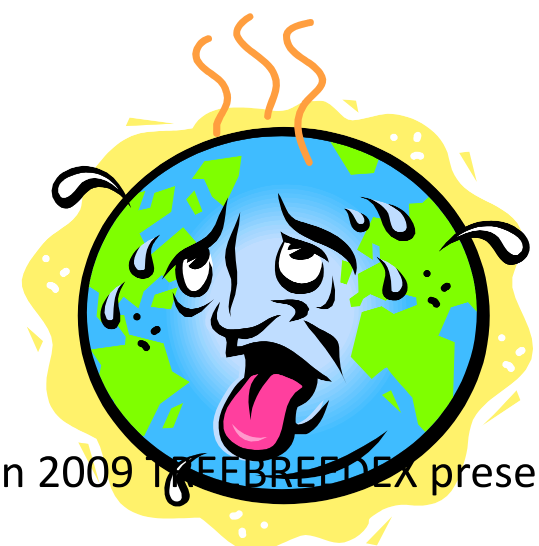
Message:
test some common materials together with neighbors and over time,

preferable well-defined reproducible “standard materials”,

to connect test sites and to improve the value of the network for industry.

Global warming is here!!!
Networks help to quantify!

- **Immediately: implement temperature raise half a degree compared to history, but no other climate change, when interpreting test results for choosing FRM!**
- **Immediate action with little risk of overreaction (be a bit conservative)**



Recommendation Lindgren 2009 TREEBREEDEX presentation *Hann-Münden, 2009*

Thus, there are reasons to assume networking should be good…but

Networking over organizational borders is desired, but does networking requires ready networks? Are not the benefits rather independent of pre-organized networks? There are lots of interfaces today, is that not enough?

E.g. certainly Sweden has benefitted greatly on European spruce provenances over centuries, (recently mainly from Belarus), but was it really networking of mutual benefit? Does Sweden have a network with Belarus? What was the benefit for Belarus?

Now Swedish companies market FRMs in Finland, but is it really thanks to organized networks?

Better FRM-directed networks are for the same or similar materials so is it a benefit in networking with countries with different climates and species? E.g. Sweden may need near Russia contacts more than interaction with Spain and Italy.

Can not networks complicate matters if they are rigid, timeconsuming and incomplete?

At IUFRO World congress 1995 (Finland) I reviewed "provenance trials revisited" and made the following table

Table . Some international provenance trials with conifers.

Species	Establishment Year (may vary within series)	Reference (example)
Scotch pine	1907-1908	Giertych and Oleksyn (1992)
	1938	- " -
Norway spruce	1938	Giertych (1976), Krutzsch (1992)
	1964/68	Dietrichson et al (1976). Skröppa et al (1993), Persson and Persson (1992), Krutzsch (1992)
Larch	1944	Weisgerber and Sindelar (1992)
	1958/59	Schober (1985)
Pinus contorta	1971	Fletcher and Barner (1978): Lindgren (1993b).
Douglas fir	1971	Brunet and Roman-Amat (1987)
Sitka spruce	1975	Ying and McKnight (1993)

Since 1995 rather little (but something) appeared based on these trial series.
Where something appeared the networking character is seldom evident.
When something appeared it is seldom focused on the use for practical forestry.
Provenance research should still be very relevant for industry. I guess that about half FRM of practical forestry today are more or less stand seeds. In spite of its importance little of the research efforts is on provenance research and still less linked to the IUFRO networks.

I looked into the IUFRO structure, which is expected to be the basic instrument for international networking. Once the species working parties were mainly for the international IUFRO trials

- 2.00.00 – Physiology and Genetics - a single proceedings with very little genetics
- 2.02.00 – Conifer breeding and genetic resources - nothing
- 2.02.11 – Norway spruce breeding and genetic resources – one conference (in Poland!! Prof Szabor) three years ago with about six papers referring to IUFRO trials with limited international coverage.
- 2.02.18 – Scots pine breeding and genetic resources - nothing

My impression is that IUFRO does not fill the role of networking around large networks of genetic field trials well or enough any more. It is a pity as I think IUFRO is the only organization, which can do this networking in a general sense.

- Networking connected to field tests should be open (more like IUFRO) and flexible and not closed and fixed (like TREEBREEDEX). In the later case important elements will usually be missing.
- Often it is easier to network with people from other organizations than the own organization!!! (a reason for networks!)
- Long term field trials have not been winners in University pecking orders or ways to get Scientific Fame.

There are other things networks could be good for, I mentioned some in the first slide.

- More discussion and attention focusing on the forest in the field. Wider discussions and more experiences.
- Better contacts among those dealing with similar forests in different organizations (countries)
- Discussions Industry-Science.
- More focus of scientists (like forest geneticists), education and administrators of what happens with industrial plantations
- Easier to claim that Industry knows something about what they are doing and tries to get it better known

So much attention on Industrial plantations would not occur if networks do not have large genetic field experiments in focus.

Networks or not!

Large genetic field experiments are one of the keys to survival of the human race and civilization!

- Without them we do not know what we should do or have done when managing forest land.
- Gives a sustainable support for an increasing world population with a reasonable standard of living!
- Emphasize on sustainability and basic environment friendliness. The forest creates raw material from air, water and sun-shine.
- Demonstration that we care for the future and plan long term.
- Basis for predicting the impact of the present and future forest.

Thank you - end

Photo Ola Rosvall 2009

Climate-growth-relations of *Fagus sylvatica* provenances of the International Beech Provenance Experiment of 1993/95 growing in Central Europe

Mirko Liesebach (P6)

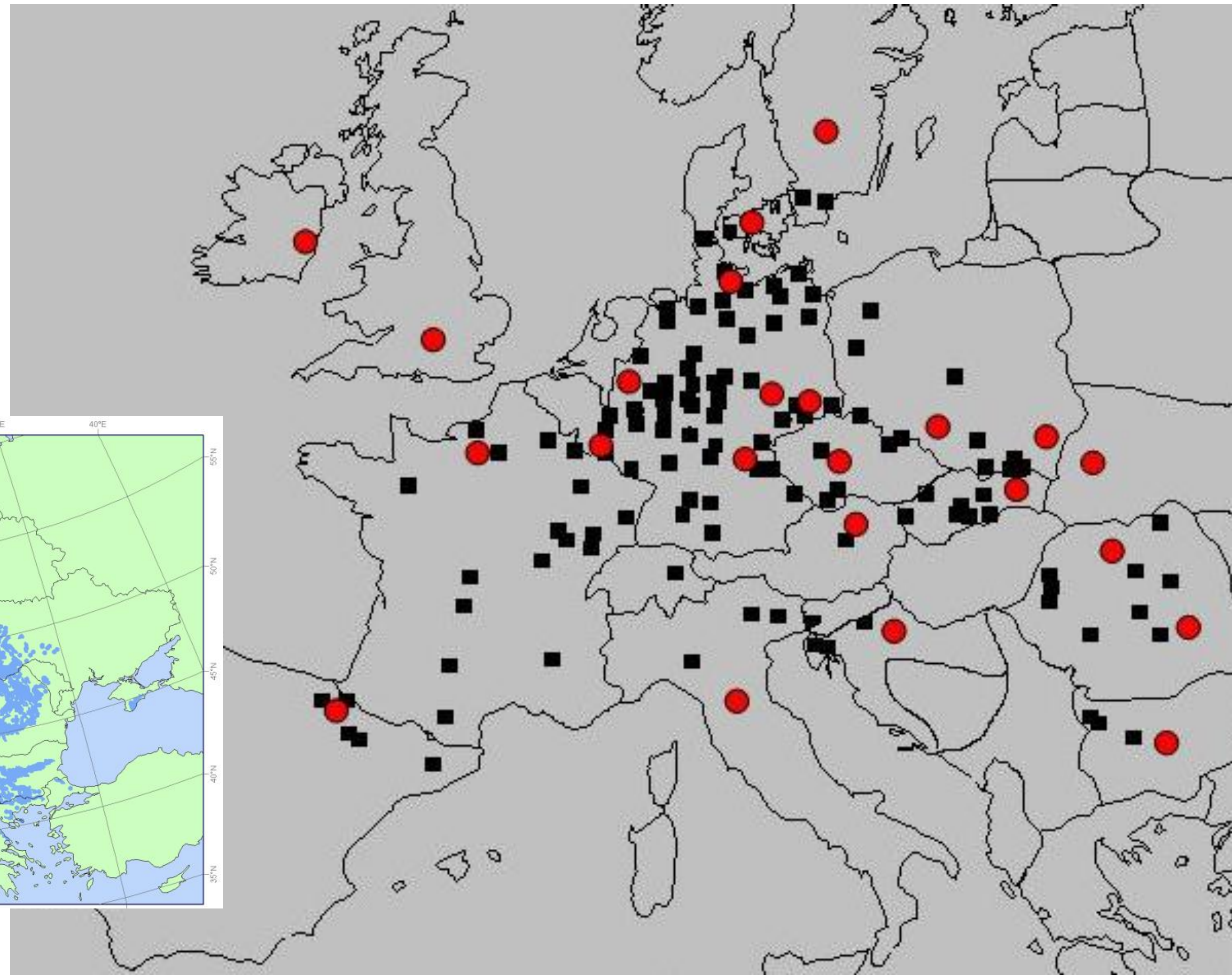
Silvio Schüler (P2)

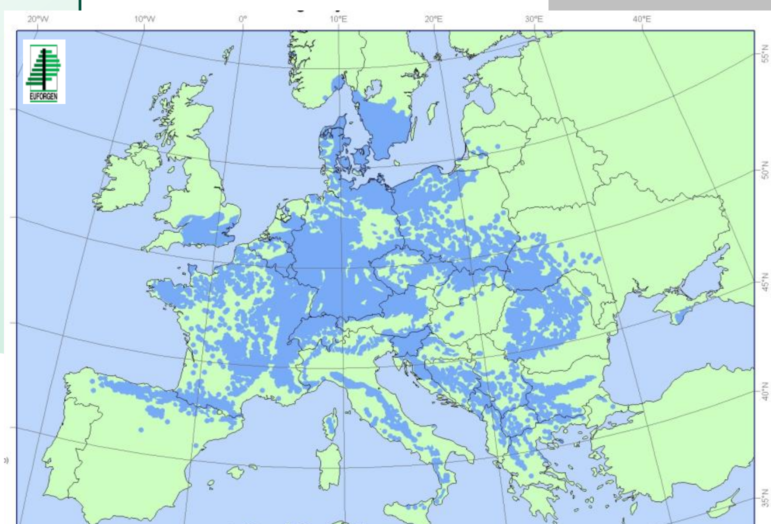
Heino Wolf (P8)

International Beech Provenance Experiment 1993/95

23 trial sites

126 provenances





International Beech Provenance Experiment 1993/95

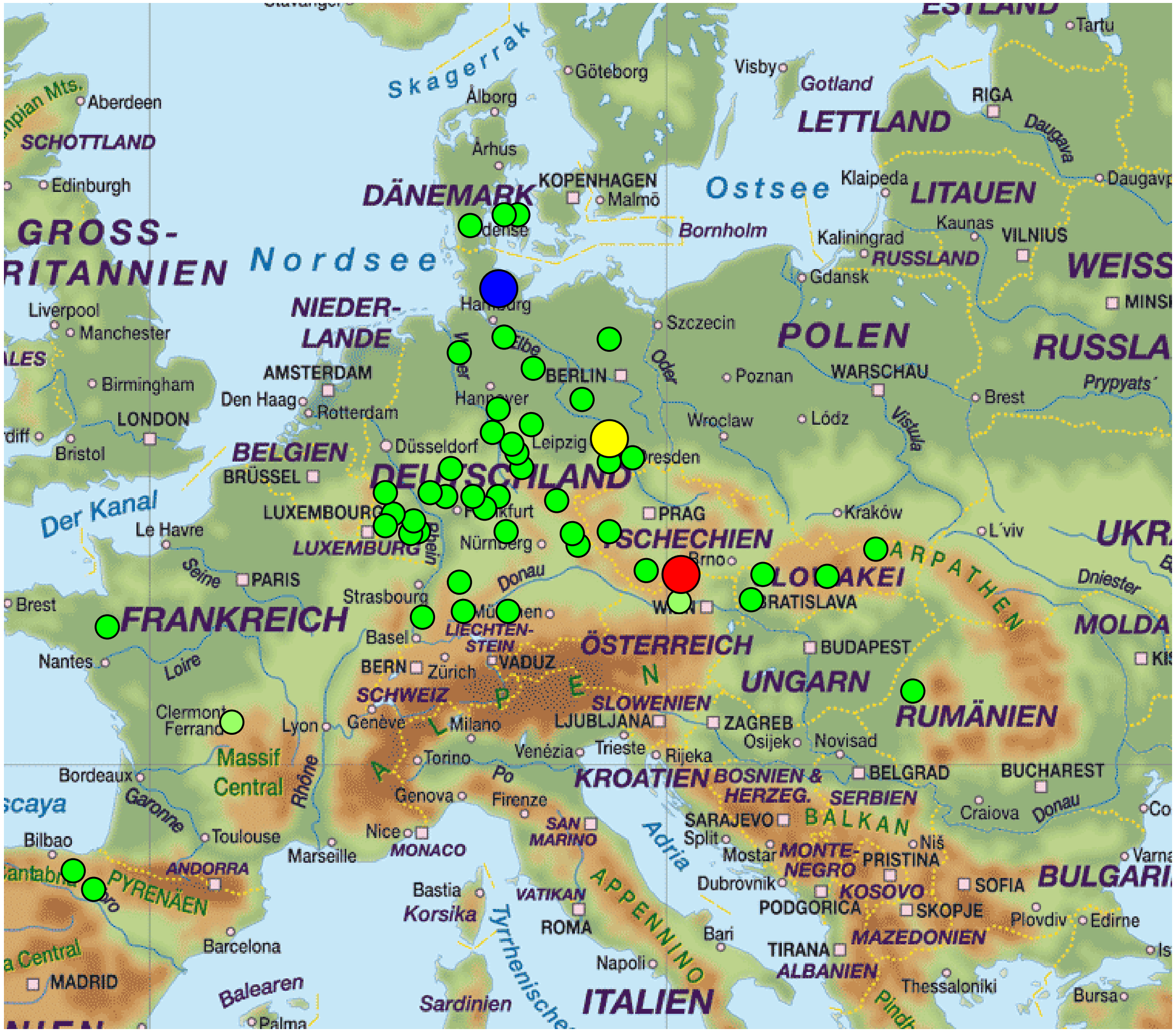
Schädtbek (Schleswig-Holstein)
40 m asl
100 (49) provenances
before acre

Malter (Saxony)
360 m asl
100 (47) provenances
before acre

Gablitz (Lower Austria)
350 m asl
49 provenances
before spruce forest

47 common provenances

2 ES
1 (+1) FR
3 DK
33 DE: 6 NI
2 BB
1 NW
5 HE
3 TH
2 SN
6 RP
3 BW
5 BY
(1 AT)
2 CZ
5 SK
1 RO



Climatic characteristics of the trial sites (1)

	Schädtbek	Malter	Gablitz
annual temperature	8,3 °C	7,8 °C	8,9 °C
temperature (V-IX)	14,6 °C	14,7 °C	16,6 °C
temperature (Jan.)	0,1 °C	-1,4 °C	-2,2 °C
temperature (July)	16,8 °C	16,8 °C	19,0 °C
temperature-range	16,7 °C	18,2 °C	21,2 °C
annual precipitation	729 mm	787 mm	729 mm
precipitation (V-IX)	354 mm	397 mm	395 mm

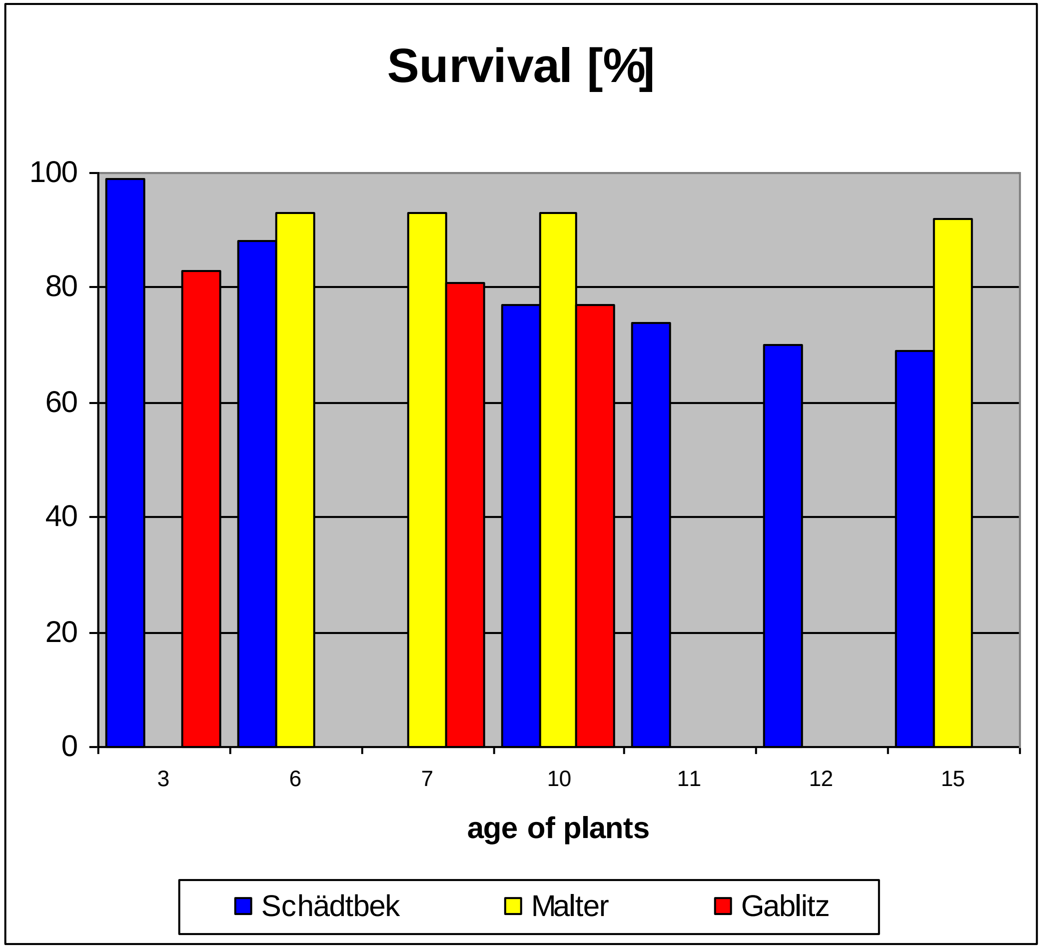
Climatic characteristics of the trial sites (2)

	Schädtbek	Malter	Gablitz
Aridity-index	Aridity-index annual precipitation / [annual temperature + 10]		
Continental I.	Continental index altitude / annual precipitation		
Climate-factor	Climate-factor by Amann annual precipitation * annual temperature / temp.-range		
Ellenberg-q.	Ellenberg-quotient temperature(July) *1000 / annual precipitation		

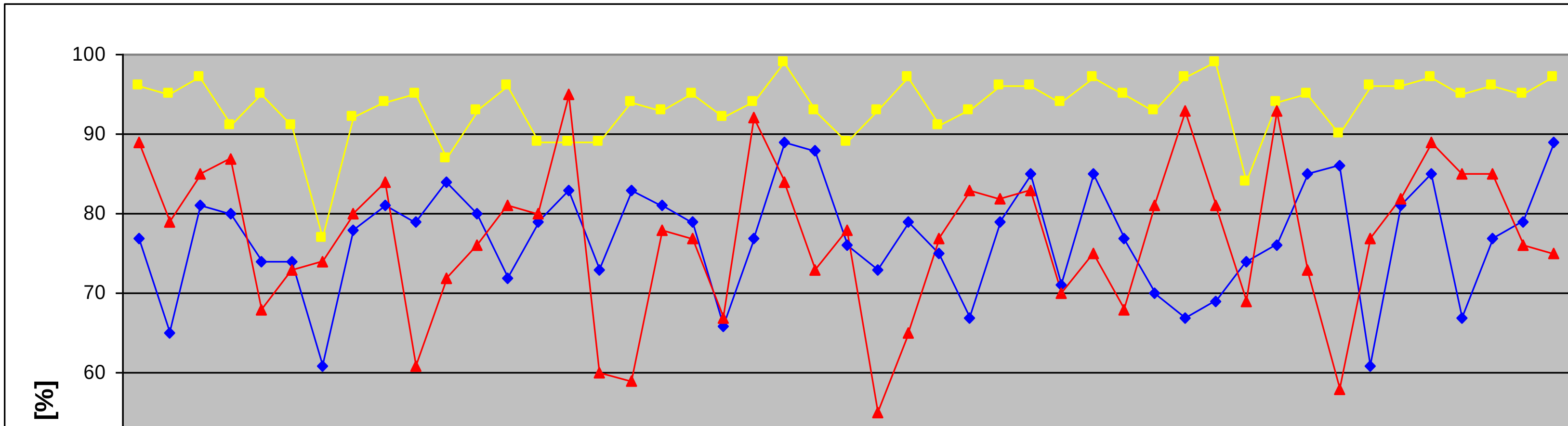
Survival

Schädbek (SH) and Gablitz (AT) decreasing

Malter (SN) constant

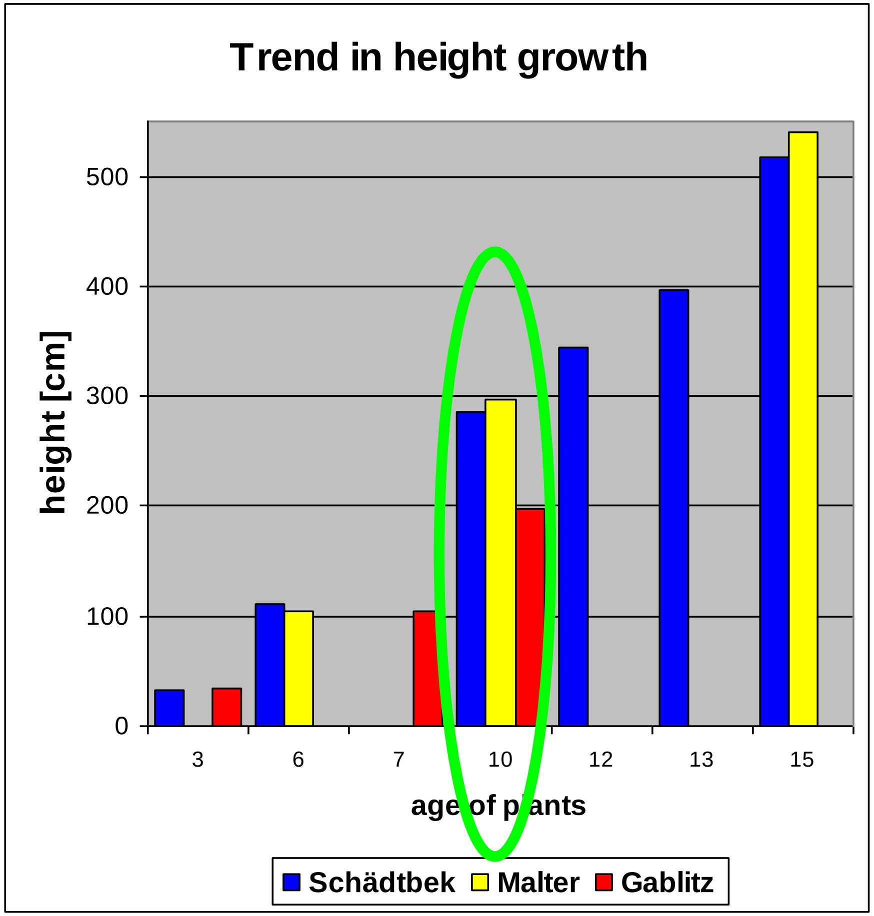


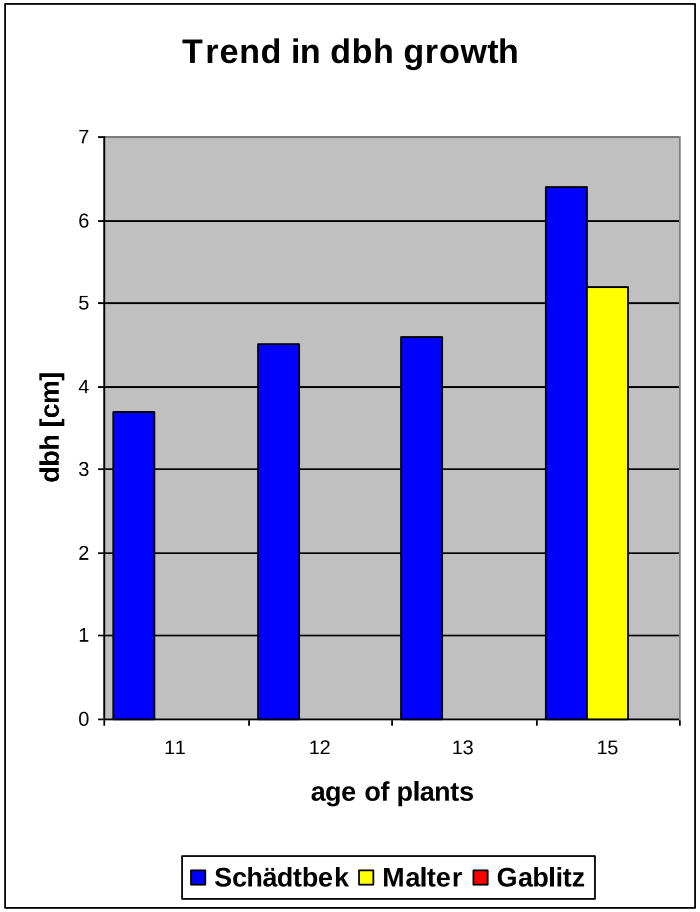
Survival, age 10 (47 provenances)



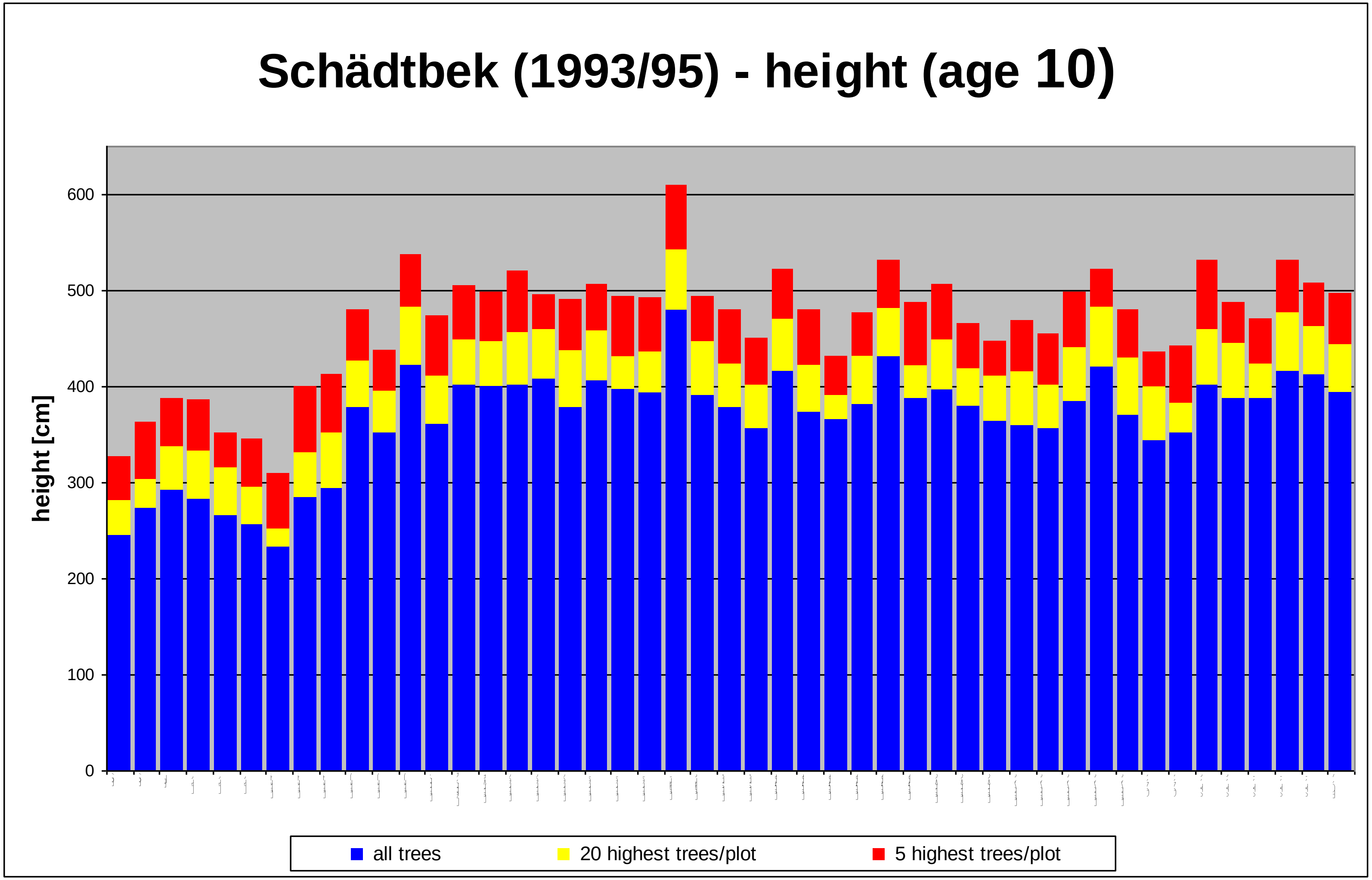
	Schädtbek	Malter	Gablitz
range	61% - 89% (28)	77% - 99% (22)	55% - 95% (40)
highest surv.	77 TH; 146 RO	77 TH; 101 BY	58 NW
lowest surv.	111 CZ	36 NI	25 DK
„local“ prov.	*Farchau (91 %)*	83 Heinzebank (89%) 42.; 84 Tharandt (93%) 31.	*109 Neuberg-M. (86%)*

Height and dbh growth

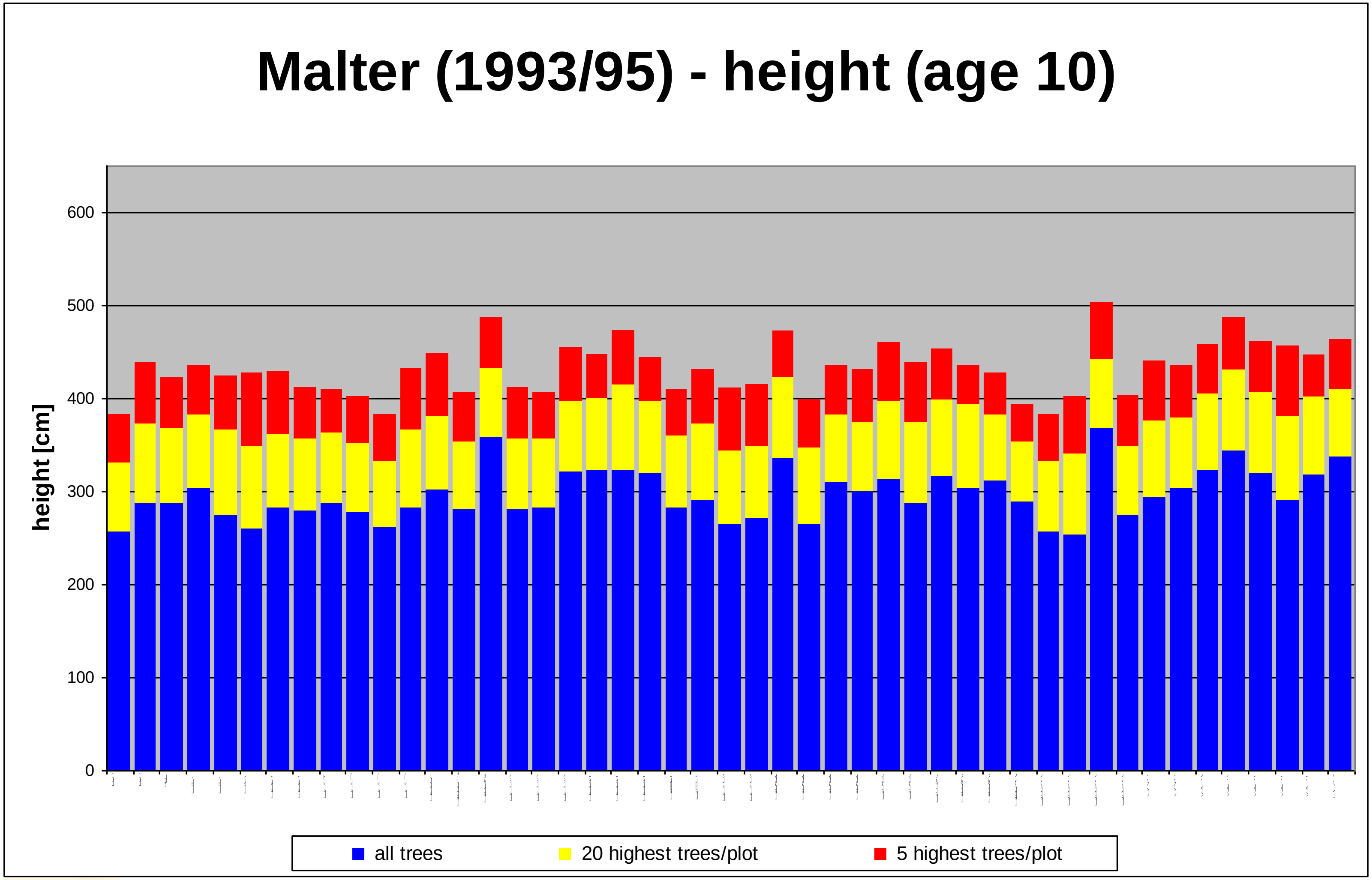




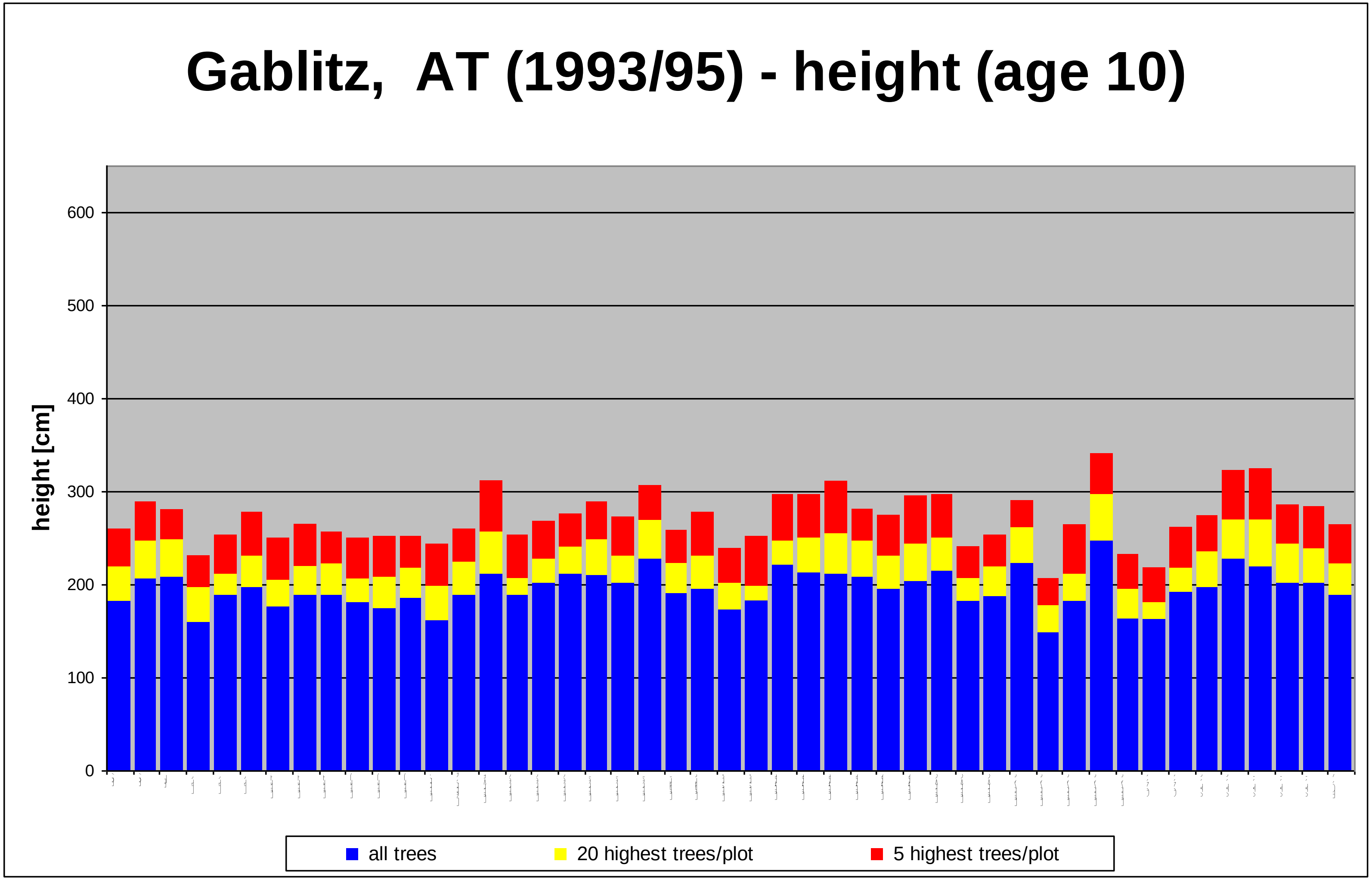
Height growth (1)



Height growth (2)



Height growth (3)



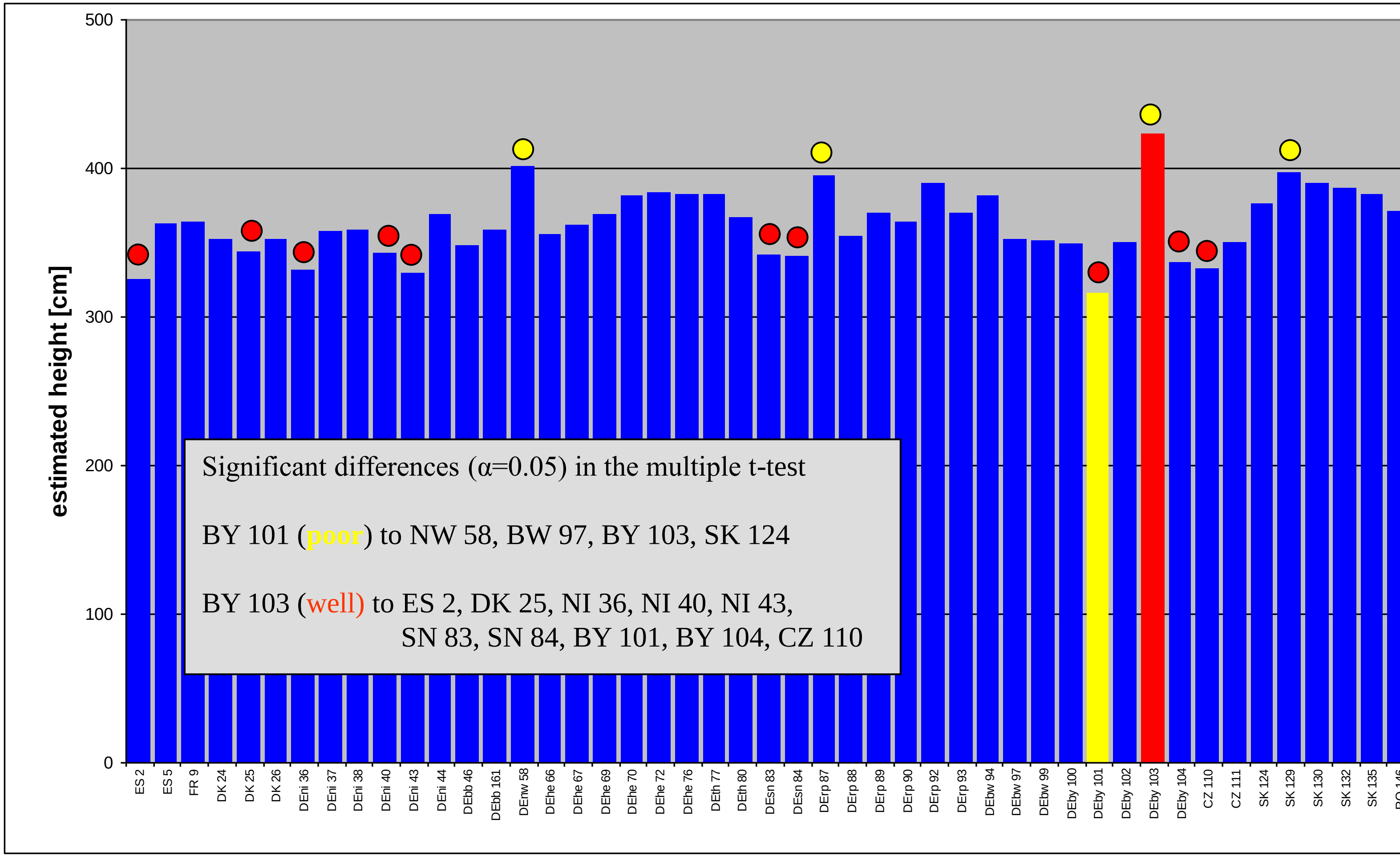
Height growth (4) – analysis of variance

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	140	2266176.344	16186.974	9.53	<.0001
HK	46	202680.793	4406.104	2.59	<.0001
vers	2	1932502.765	966251.383	568.83	<.0001
HK*vers	92	130992.786	1423.835	0.84	0.8397
Error	282	479025.517	1698.672		
Corrected Total	422	2745201.861			

Significant differences (α =0.05) between
provenances (HK) and
sites (vers)

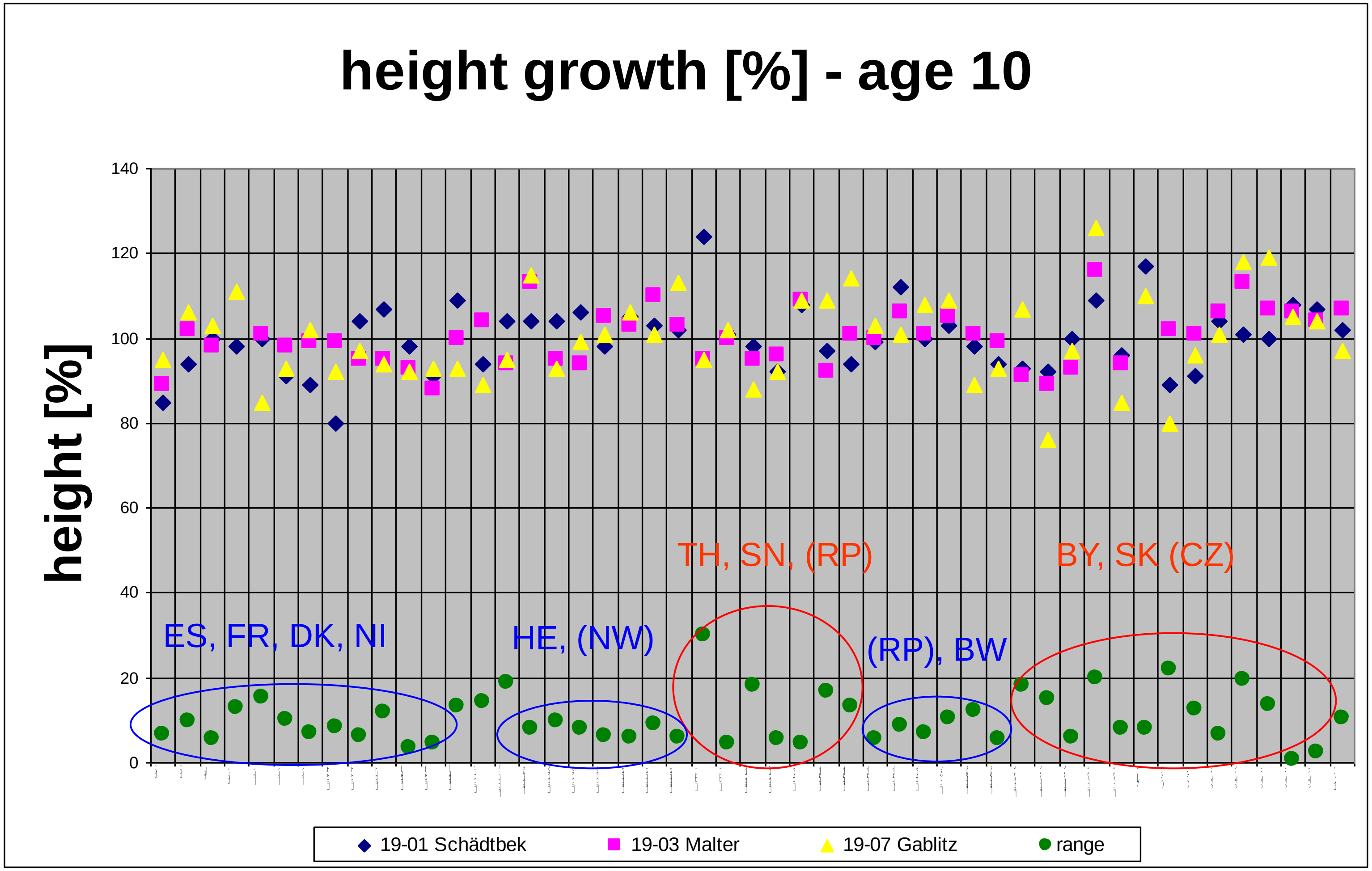
Treebreedex

Height growth (4)



vTI BFW Sachsenforst Wald braucht Zukunft

unresponsive – sensitive provenances



Results (height, age 10, Schädtbek) – stepwise selection

1) all trees
   4 variables: temp. (July), temp. (May-Sept.), Climate-factor, altitude
   R^2= 0,1461

2) 20 highest trees / plot
   5 variables: temp. (July), temp. (May-Sept.), Climate-factor, Aridity-index, precipitation (May-Sept.)
   R^2= 0,1875

3) 5 highest trees / plot
   5 variables: temp. (July), temp. (May-Sept.), Climate-factor, Aridity-index, precipitation (May-Sept.)
   R^2= 0,2188

Summary of Stepwise Selection

Step	Variable Entered	Variable Removed	Number Vars In	Partial R-Square	Model R-Square	C(p)	F Value	Pr > F
1	Temp. (Juli)		1	0.0560	0.0560	8.4843	5.22	0.0247
2	Temp. (Veg.)		2	0.0327	0.0888	7.2073	3.13	0.0806
3	Klimafaktor		3	0.0686	0.1573	2.3446	7.00	0.0097
4	Ariditätsindex		4	0.0328	0.1902	1.0572	3.45	0.0668
5	Nieders. (Veg.)		5	0.0286	**0.2188**	0.1911	3.08	0.0830

Results (height, age 10 + 15, Malter) – stepwise selection

Age 10:

1) all trees
2) 20 highest trees / plot
3) 5 highest trees / plot

} no variable

Age 15:

1) all trees
   3 variables: temp. (July), temp. (May-Sept.), temp. (January)
   R^2= 0,1336
2) 20 highest trees / plot
   3 variables: temp. (July), temp. (May-Sept.), temp. (January)
   R^2= 0,1412
3) 5 highest trees / plot
   3 variables: temp. (July), temp. (May-Sept.), longitude
   R^2= 0,1470

Results (height, age 10, Gablitz) – stepwise selection

1) all trees
   1 variable: Climate-factor
   R^2= 0,0722

2) 20 highest trees / plot
   1 variable: Climate-factor
   R^2= 0,0602

3) 5 highest trees / plot
   1 variable: Climate-factor
   R^2= 0,0612

Conclusions

- Differences between sites with different environmental conditions
- Variation between provenances
- In height growth (age 10) a tendency indicates between geographical regions of
  (1) only unresponsive provenances, and
  (2) unresponsive and sensitive provenances, respectively.
- On the site Schädbek height growth is explained by up to 5 climate variables (22 %).
  This result could not be confirmed on other sites, and when changing the number of provenances.
- There might be significant difference in an higher age, because growth of beech is culminating later than in other tree species.

General conclusions

- Even knowledge on common species is incomplete
- Knowledge on rare species is missing or under-represented
- New problems (increasing demand on wood, “climate change”)
- Therefore, large and long-term experiments are necessary

Treebreedex

Thank you!

to my co-authors,

technical assistance,

nursery

vTI B F W Sachsenforst Wald braucht Zukunft

Euro-Asiatic transcontinental provenance experiment on Scots pine

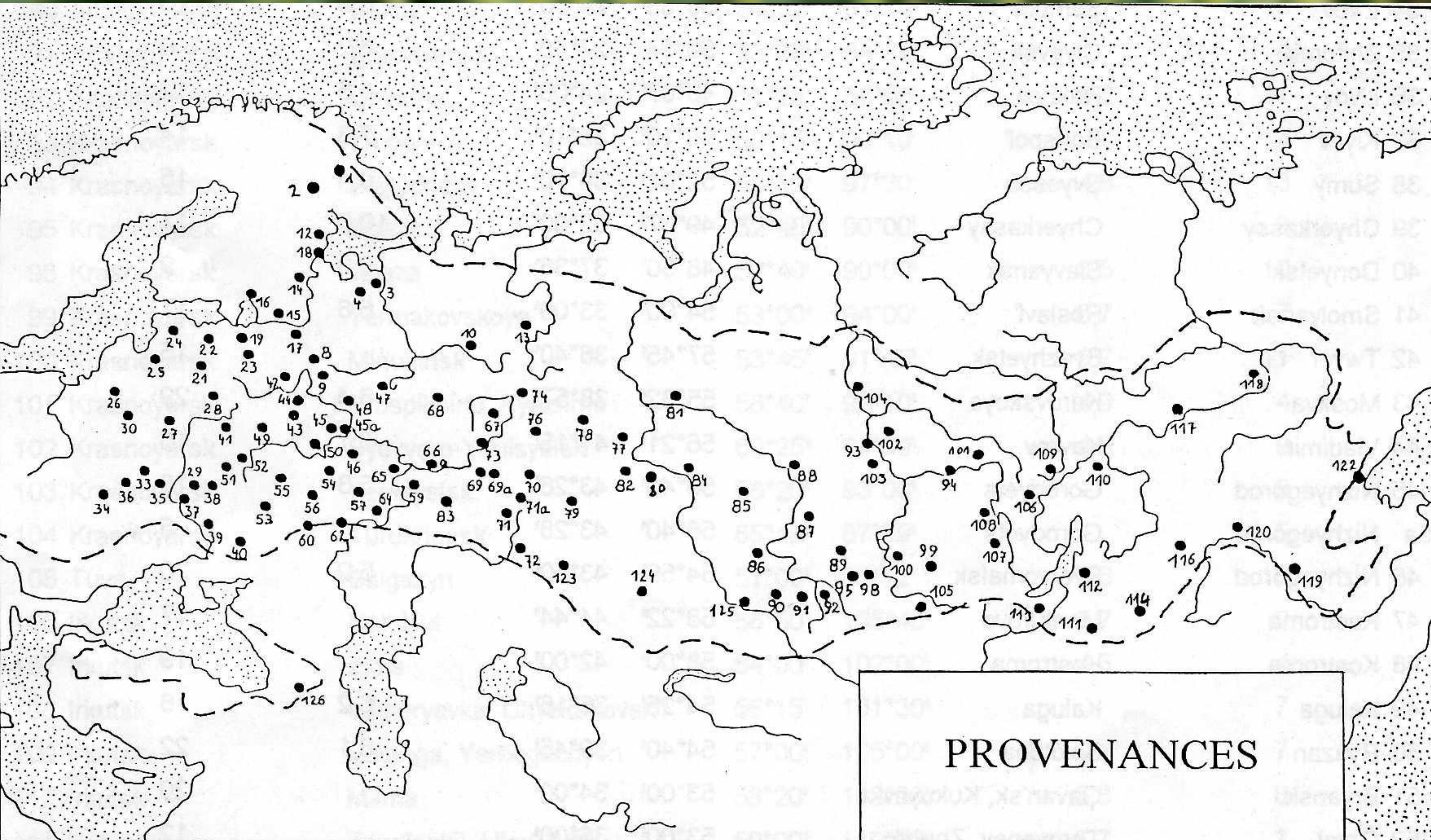
(*Pinus sylvestris* L.)

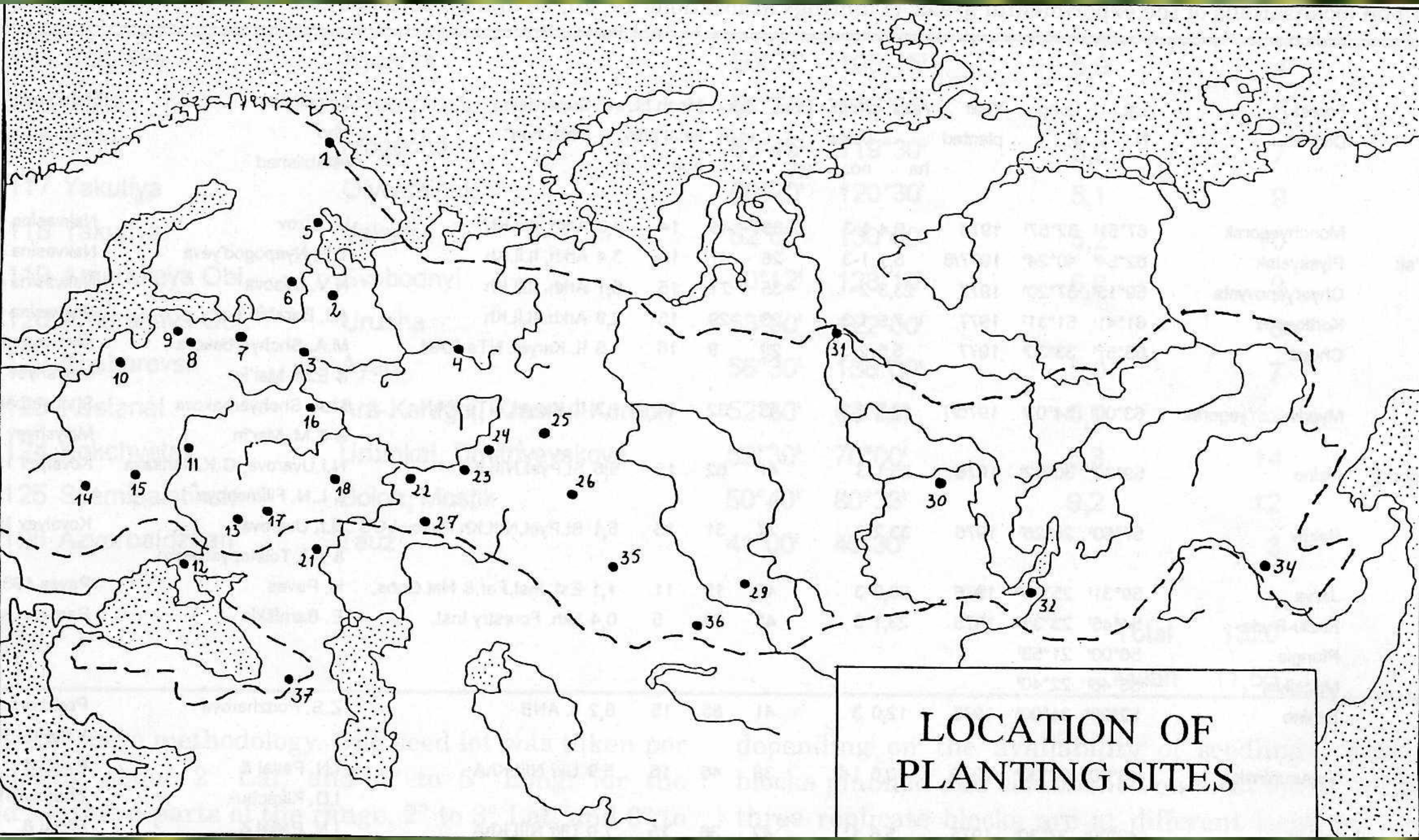
Władysław Chałupka

Polish Academy of Sciences,
Institute of Dendrology, Kórnik
Partner 18

BASIC INFORMATION ON THE EXPERIMENT

Initiative:	All-Union Forest Research Institute at Pushkino near Moscow
Author of program:	Ye. P. Prokazin
Establishment of experiment:	1976
Number of provenances:	113
Number of planting sites:	33


PROVENANCES



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LOCATION OF
PLANTING SITES

CURRENT STATUS OF THE EXPERIMENT

Countries with the experimental sites on their territories:

Azerbaijan	1
Belarus	1
Estonia	1
Kazakhstan	2
Lithuania	1
Russian Federation	23
Ukraine	4

Height Growth Variation in a Comprehensive Eurasian Provenance Experiment of (*Pinus sylvestris* L.)

By A. M. SHUTYAEV[1]) and M. GIERTYCH[2])

[1]) Research Institute of Forest Genetics and Breeding, Lomonosova 105, 394043 Voronyezh, Russia
[2]) Institute of Dendrology, 62-035 Kórnik, Poland

(Received 26th May 1997)

Summary

In the years 1974 to 1976, on the initiative of the Forest Research Institute in Pushkino, near Moscow, a major Scots pine experiment was established with 113 provenances over 33 planting sites, well scattered over the whole former USSR. Basing on reports from co-operating institutions information is compiled on the provenances used, on the planting sites and on the mean tree height at latest measurement. Interaction parameters are calculated and the data on tree heights, converted to units of standard deviation from location means, is plotted onto maps of the locations demonstrating the extent of genotype environment interaction. The range of the species in the former USSR can be divided into regions (North-western, Baltic, Western Continental, Northern Russia, Central European Russia, Middle Volga, Central Trans-Urals, Southern fringe, Eastern Siberia), that have characteristic for them responses to seed transfer in terms of height growth performance at various locations. Western populations (Baltic

Genetic Subdivisions of the Range of Scots Pine (*Pinus sylvestris* L.) Based on a Transcontinental Provenance Experiment

By A. M. SHUTYAEV[1]) and M. GIERTYCH[2])[3])

(Received 16th February 2000)

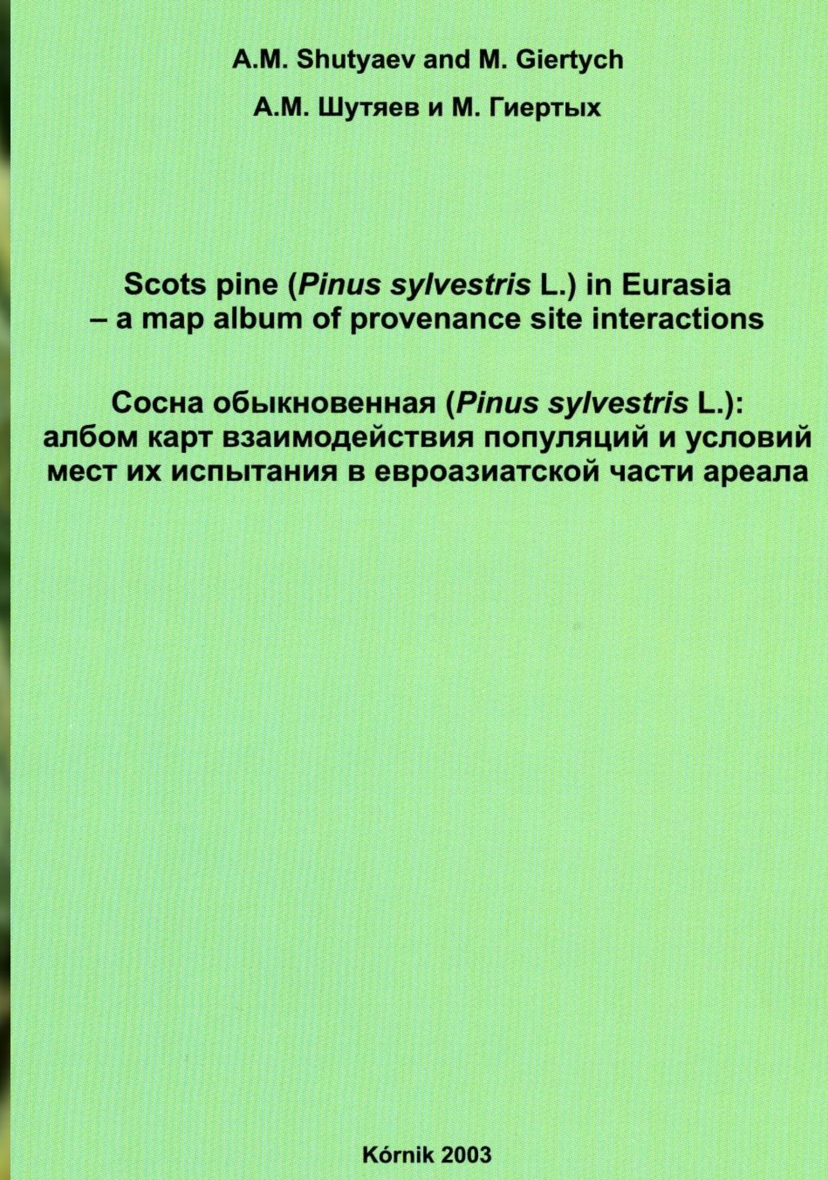
Summary

Studies were continued on the variability of 113 Scots pine provenances based on an experiment established at 33 locations in the former USSR in 1974 to 1976. Following on the analysis presented earlier for height measurements (SHUTYAEV and GIERTYCH, 1997) now an analysis is made of data on survival, stem diameter and stem straightness. A synthetic volume estimate (based on height, diameter and survival) was evaluated for phenotypic stability. On the basis of growth performance in various environments the range of Scots pine in the former USSR is divided into 10 regions (A- to J) and these divisions are compared with earlier attempts at subdividing this vast area. There is agreement in the opinions about

[1]) Research Institute of Forest Genetics and Breeding, Lomonosova 105, 394043 Voronezh, Russia

[2]) Institute of Dendrology, PL-62-035 Kórnik, Poland

[3]) M. GIERTYCH is the corresponding author



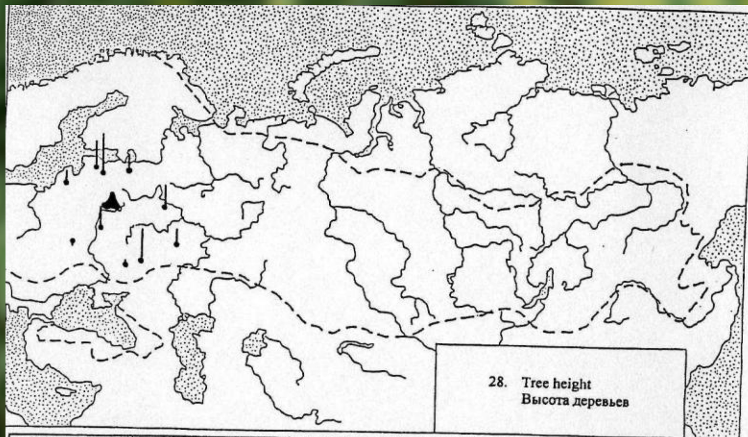
A.M. Shutyaev and M. Giertych

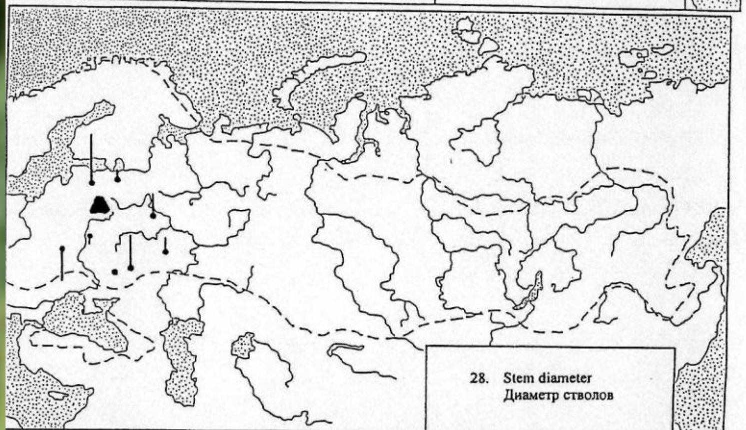
А.М. Шутяев и М. Гиертых

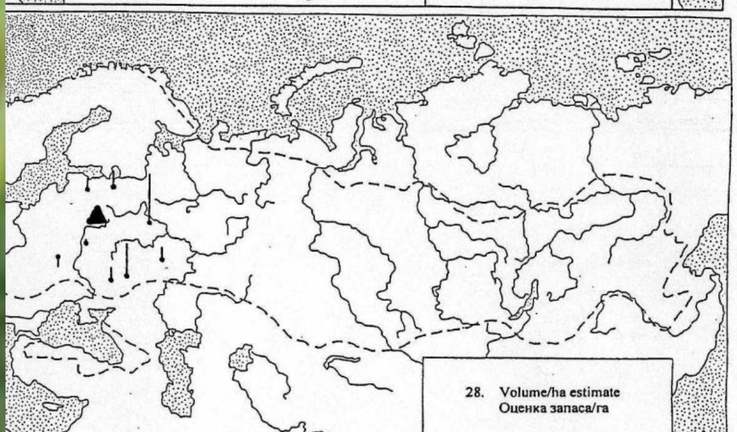
Scots pine (*Pinus sylvestris* L.) in Eurasia – a map album of provenance site interactions

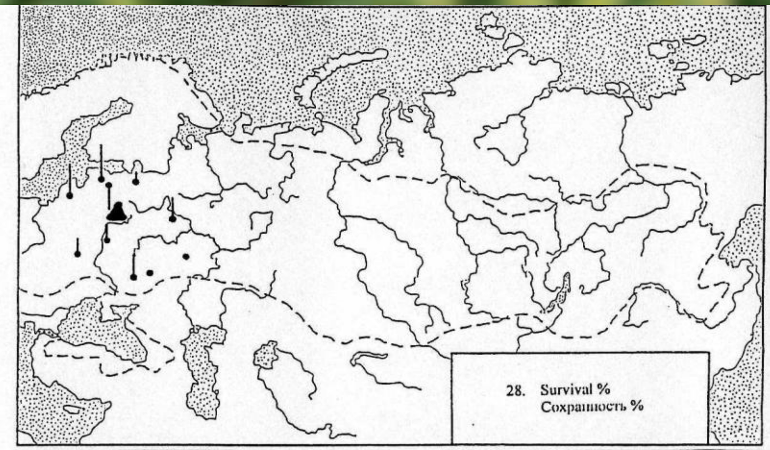
Сосна обыкновенная (*Pinus sylvestris* L.): албом карт взаимодействия популяций и условий мест их испытания в евроазиатской части ареала

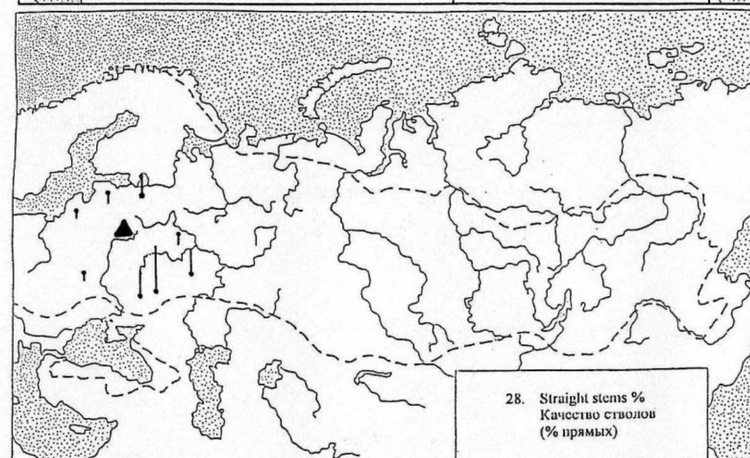
Kórnik 2003









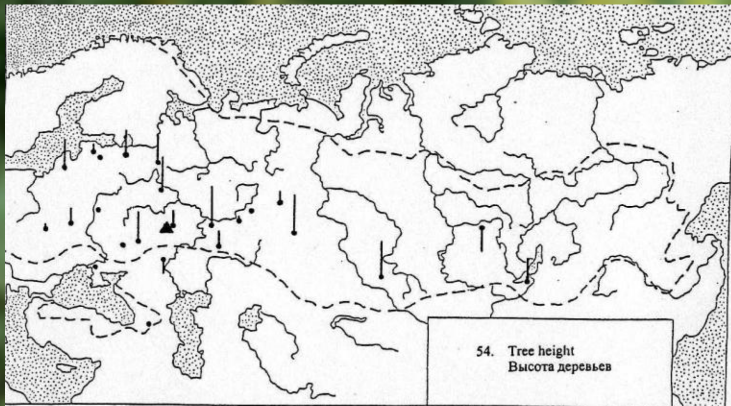


№ 28. 56°00'N, 29°20'E zone C III
Vitebsk Prov., Rossony For. Distr., Belarus

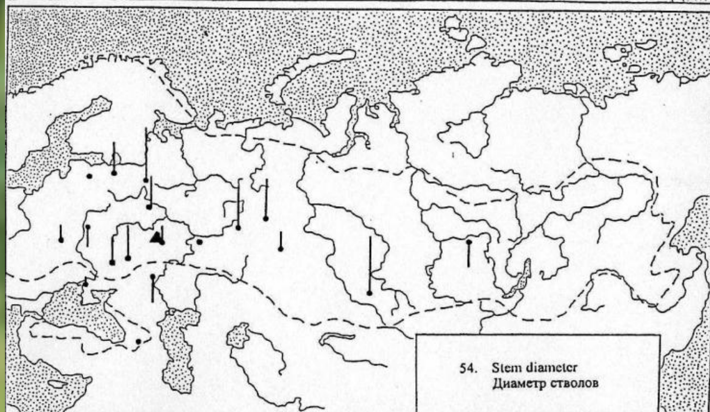
Growth almost everywhere very good, with good and medium survival. Stems straight but their quality declines on western sites.

№ 28. 56° 00' N, 29° 20' E регион C III
Витебская обл., Россонский лесхоз, Беларусь

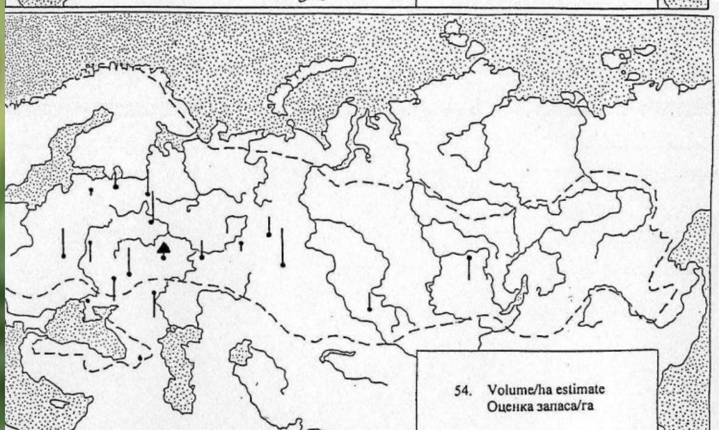
Интенсивность роста почти везде хорошая, при хорошей и средней сохранности. Стволы прямые, в западныхе пунктах качество ухудшается.



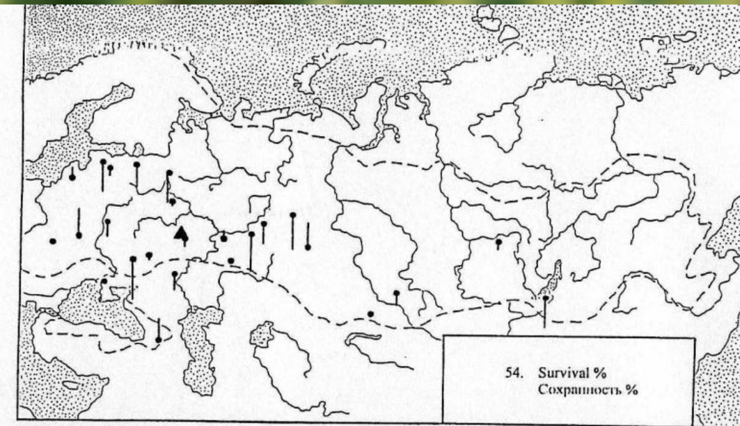
54. Tree height
Высота деревьев



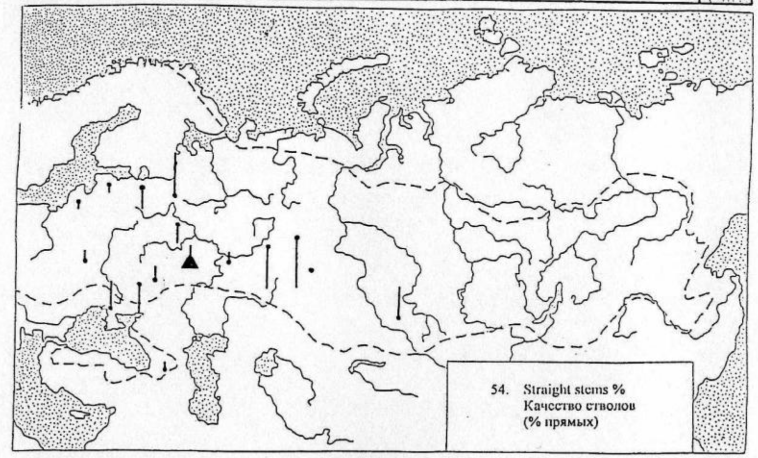
54. Stem diameter
Диаметр стволов



54. Volume/ha estimate
Оценка запаса/га



54. Survival %
Сохранность %



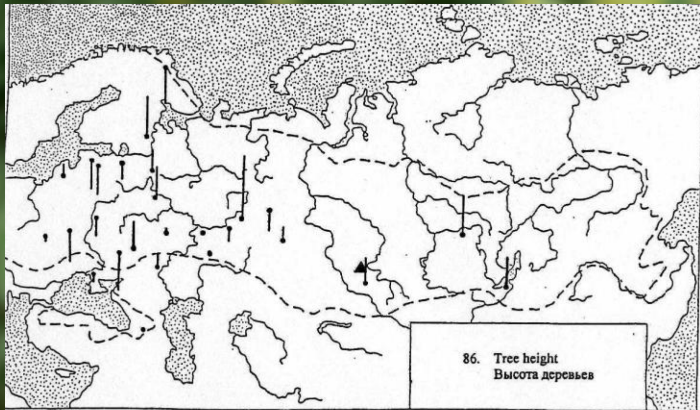
54. Straight stems %
Качество стволов
(% прямых)

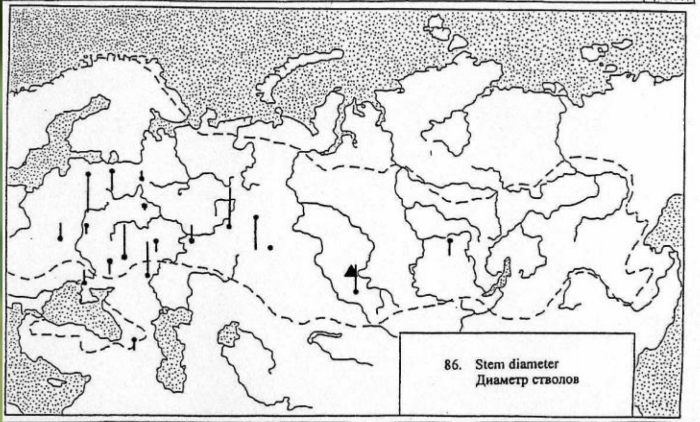
№ 54. 53°12'N, 41°20'E zone F III
Tambov Prov., Chelnovaya, Sosnovka For. Distr., Russia

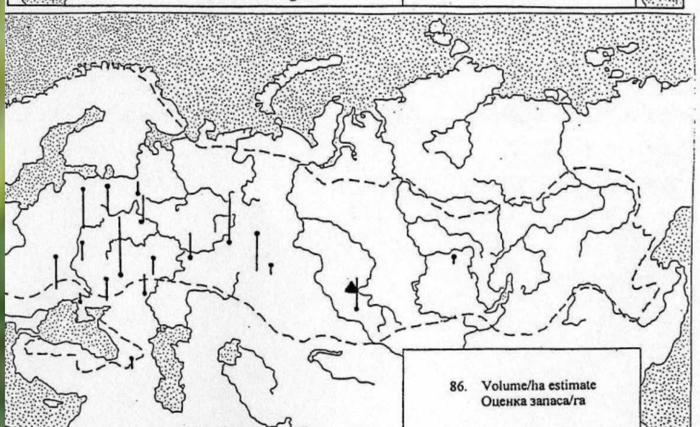
Survival generally poor, in places medium. Growth parameters in most places very good except in central Siberia and on the Caucasus. Stems straightness variable.

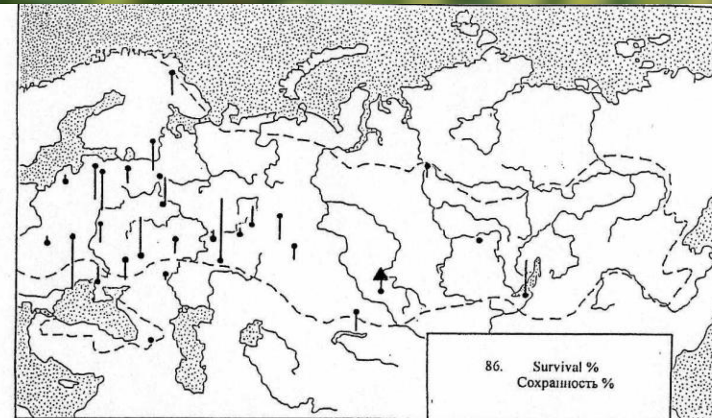
№ 54. 53° 12' N, 41° 20' E регион F III
Тамбовская обл., Челновский лесхоз, Россия

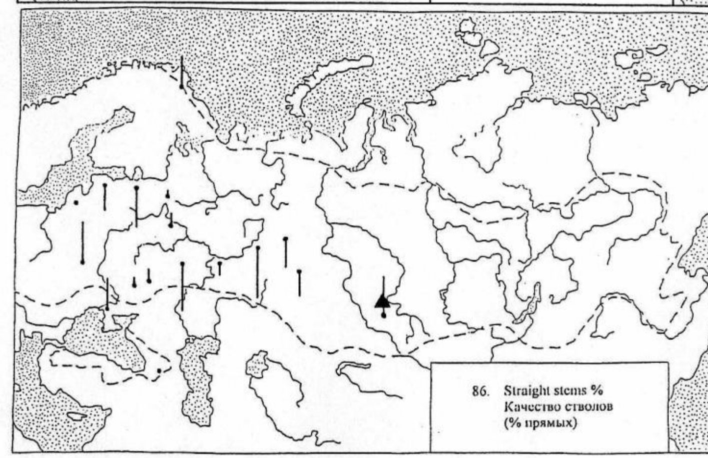
Сохранность пониженная, местами средняя. Показатели роста в основном очень хорошие за исключением центральной Сибири и Кавказа. Прямизна стволов изменчива.









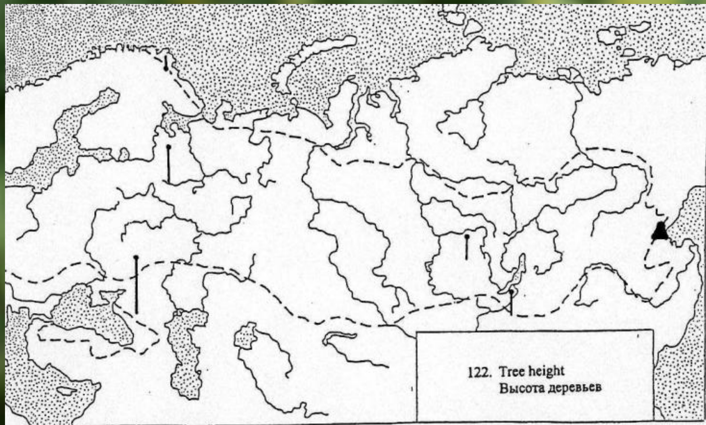


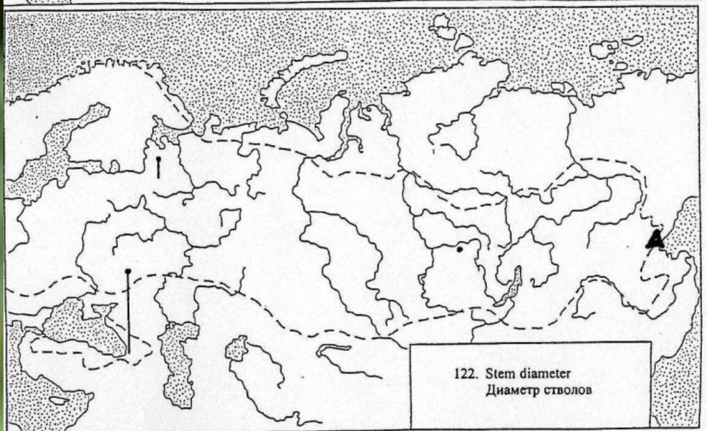
№ 86. 56°50'N, 82°20'E zone I III
Novosibirsk Prov., Suzun For. Distr., Russia

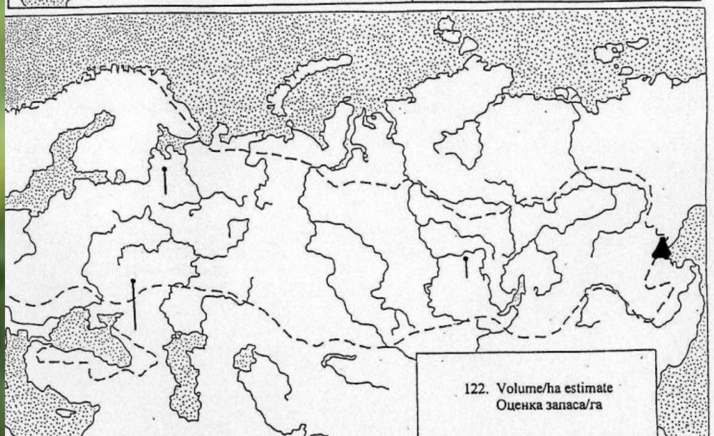
Survival and growth parameters low on western sites but improve to good ones in central regions and east of the Volga. Stems decidedly crooked.

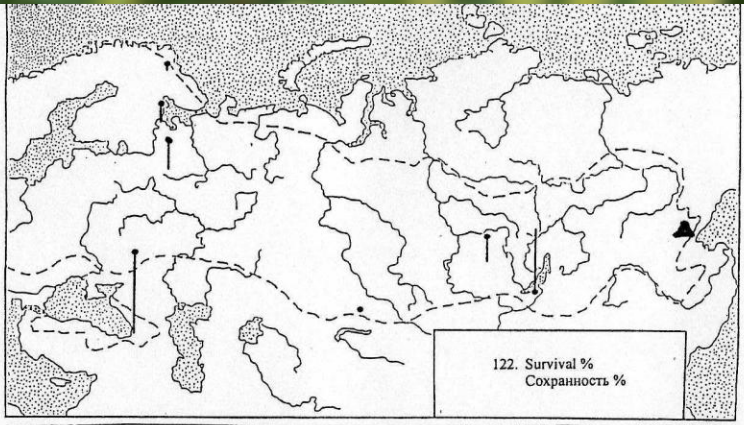
№ 86. 56° 50' N, 82° 20' E регион I III
Новосибирская обл., Сузунский лесхоз, Россия

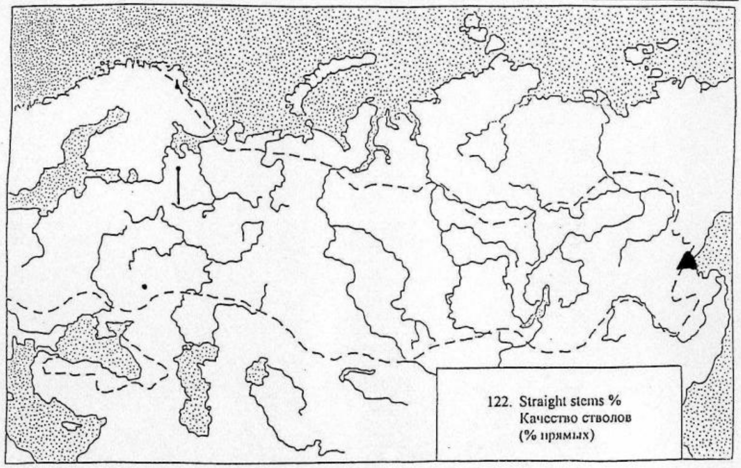
Пониженные показатели сохранности и роста в западных пунктах, увеличиваются до хороших в центральных и заволжских пунктах. Выражена кривоствольность деревьев.









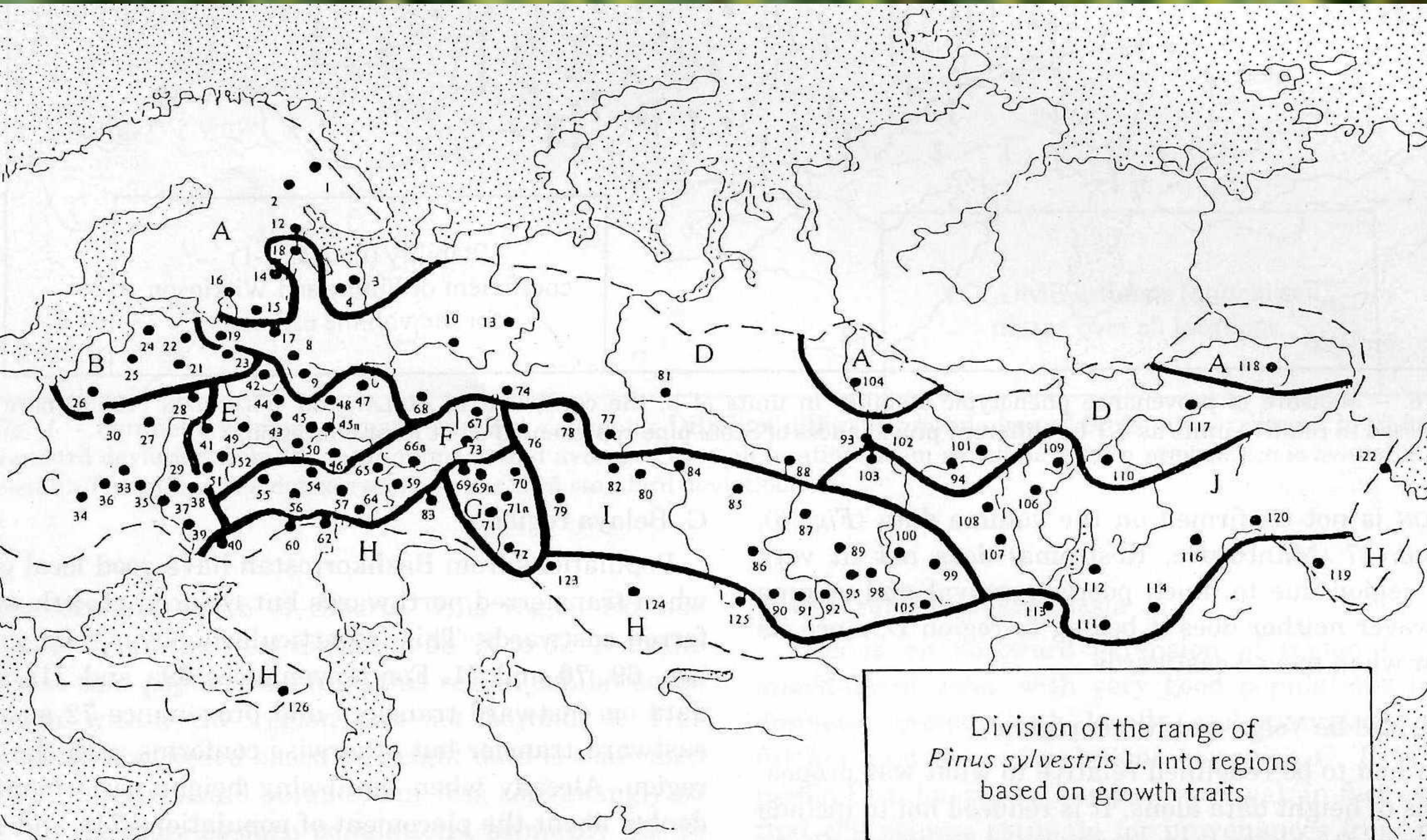


№ 122. 56°30'N, 138°00'E zone J IV
Khabarovsk region Ayan For. Distr., Russia

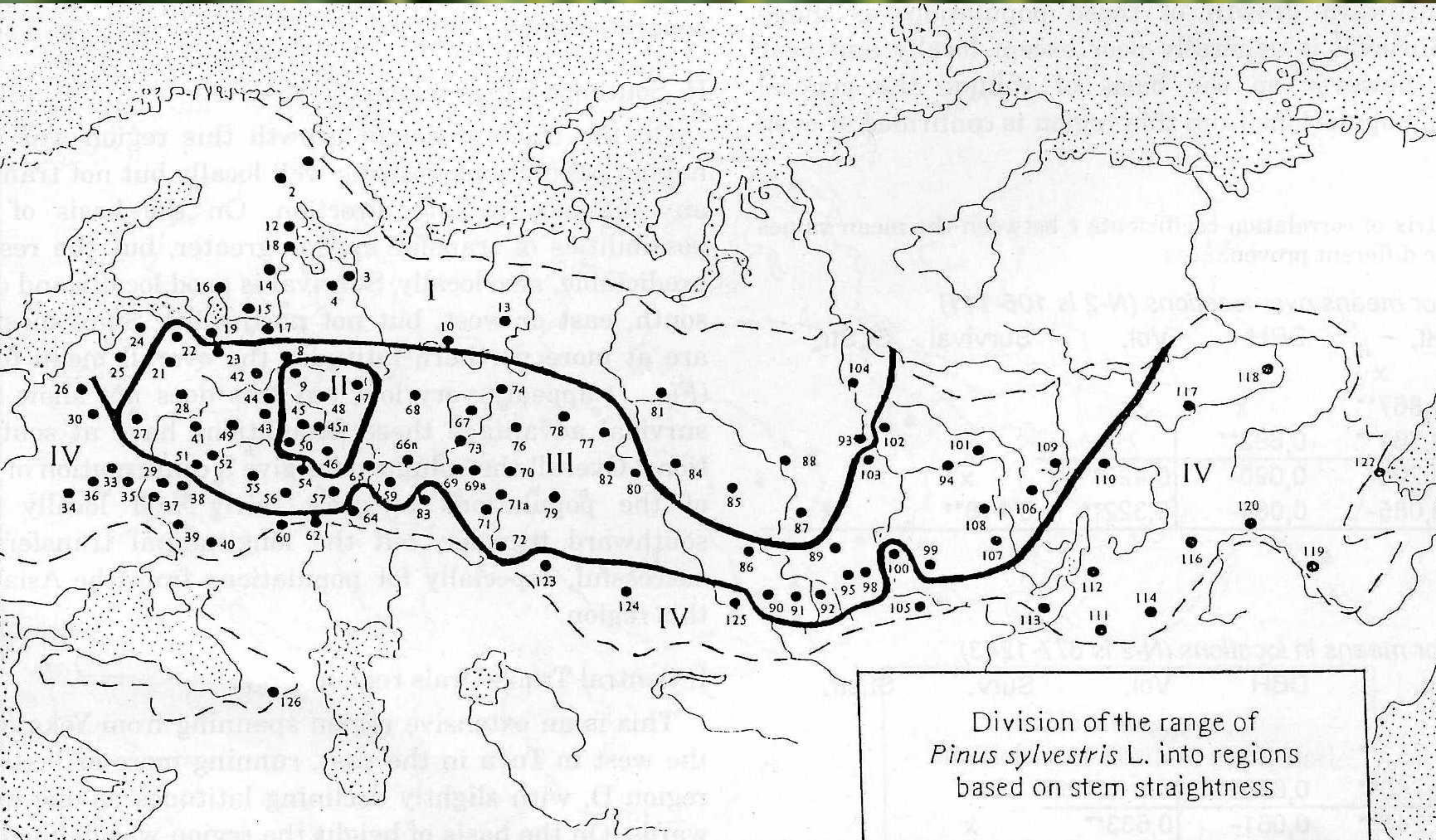
Survival everywhere poor except on the site near lake Baikal. Growth very poor everywhere. Stem straightness medium.

№ 122. 56° 30' N, 138° 00' E регион J IV
Хабаровский край, Аянский лесхоз, Россия

Сохранность везде низкая, кроме опыта в районе Байкала. Рост очень слабый. Прямизна стволов средняя.



Division of the range of *Pinus sylvestris* L. into regions based on growth traits



Division of the range of *Pinus sylvestris* L. into regions based on stem straightness

Thank you for your attention!

A joined European network of progeny trials of *Larix decidua 'polonica'*

First results (*continued*)

Pâques Luc E.

INRA-Orléans

Unité AGPF

What does large genetic field experimental network across Europe bring to the scientific community? TREEBREEDEX seminar, 22-24 June 2010, Sekocin (PL)

Objectives

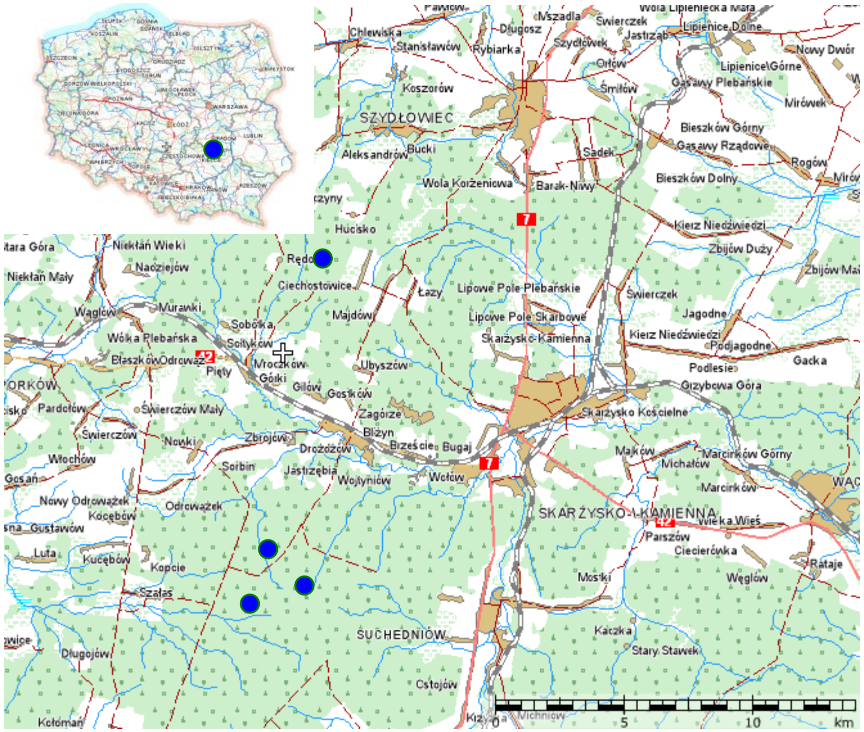
Larix '*polonica*' has shown interest in IUFRO provenance trials

- to broaden the geographic origin of provenances (Grojec),
- to confirm the interest of polish larch in terms of *adaptation*, *stem straightness*, *wood quality*,
- to examine seed transfer possibilities from East to West,
- to get a better picture on how genetic variability is structured.

- *to broaden the breeding population,*
- *to take benefits of polish larch properties in interspecific hybridization.*

Material & Methods

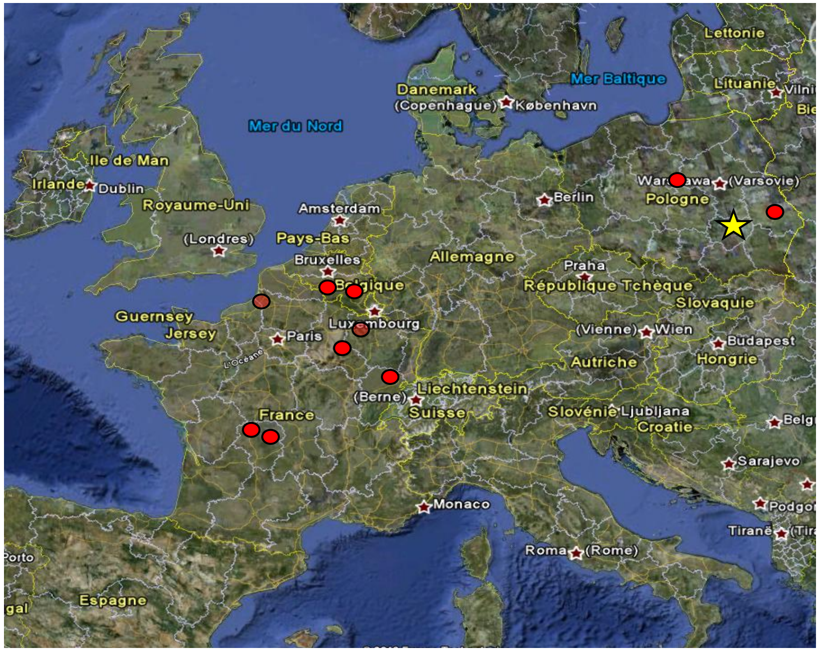
- Joined cone collection by INRA & IBL in Mont Gory Swietokezyski in Dec.1987,
- 157 open-pollinated progenies, randomly chosen (except distances and level of fructification),
- in 4 autochtonous 'stands' (mainly old natural reserves).



- material shared with IBL and SRFGx

Field trials

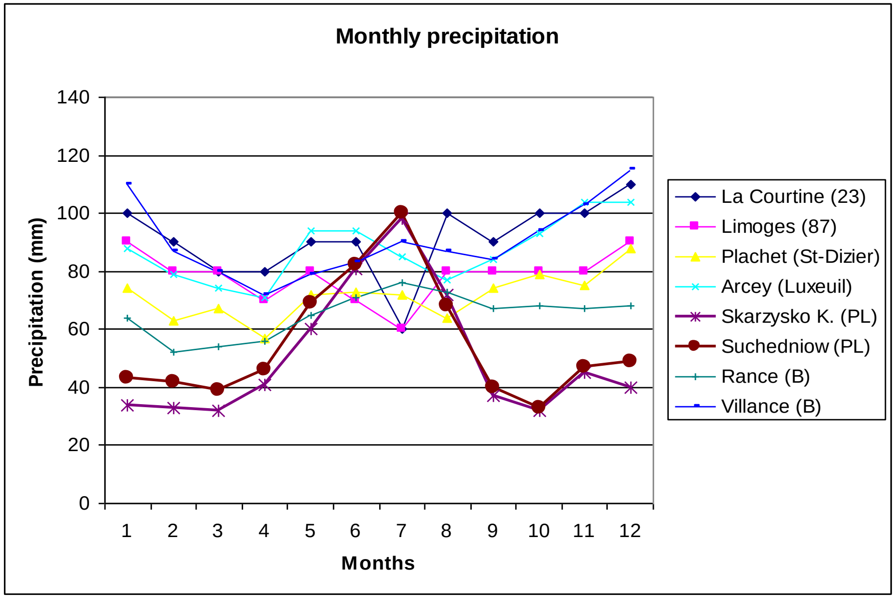
8 progeny trials + 2 conservation plots

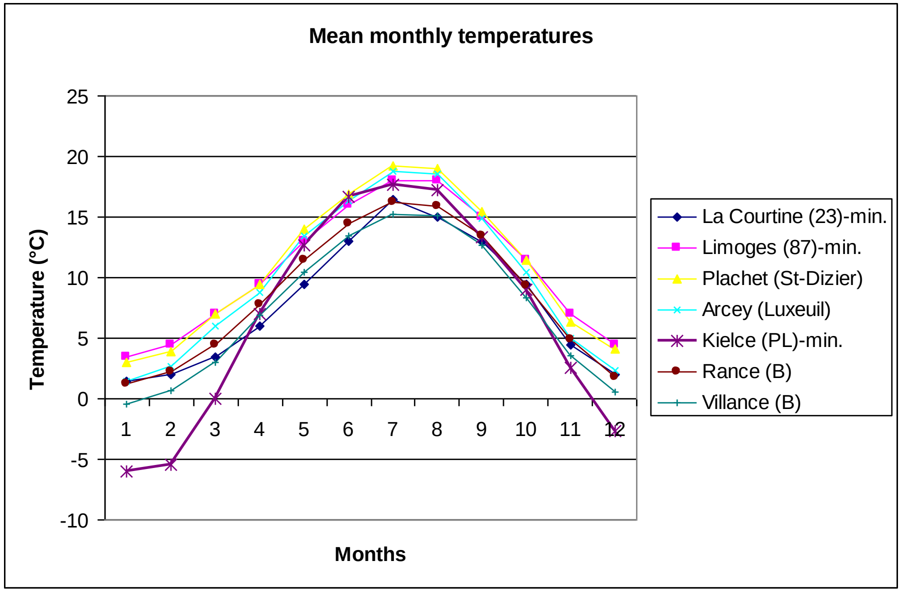


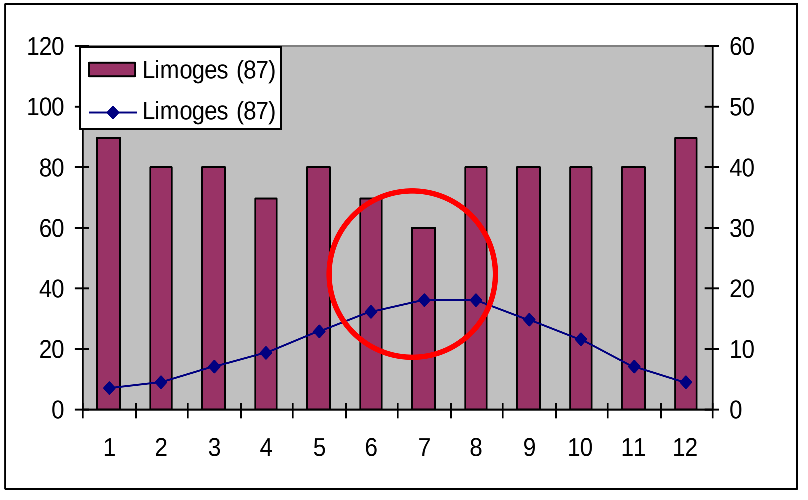
Site	Country	Region	Longitude	Latitude	Altitude (m)	Année semis	Area (ha)	Ecartements (m)	Nber of progenies	Design
FC.Arcey (25)	F	Jura	6°35’ E	47°30’ N	410	1989	5.84	2.5x2.5	157	IRBD, 1 tree plot
FD.Plachet (52)	F	Lorraine	4°59’ E	48°15’ N	320	1989	7.14	3x3	157	IRBD, 1 tree plot
Crozet (23)	F	Plateau de Millevaches	2°11’ E	45°48’ N	750	1990	5.06	3x3	157	IRBD, 1 tree plot
Bort (87)	F	Ouest Massif Central	1°20’ E	45°56’ N	350	1990	4.48	3x3	157	IRBD, 1 tree plot
FD. Apremont (55)	F	Plateau Meuse	5°37’ E	48°52’ N	350	1989	5.00	3x3	-	
FD. Eu (76)	F	Normandie	1°37’ E	49°53’ N	190	1990	1.51	3x3	-	
Kutno	PL		19°19’ E	52°16’ N		1996	1.9	2x2	157	1 tree plot
Zwierzyniec	PL		23°02’ E	50°46’ N		1998	2.2	2x2	85	1 tree plot
Rance	B	Fagne	4°15’E	50°10’ N	250	1994	1.2	3x2	93	CRBD, 8 trees raw plot
Villance	B	Ardennes	5°14’E	50°00’ N	425	1994	1.4	3x2	93	CRBD, 8 trees raw plot

Ecologically contrasting sites

- From less than 150 m up to 750 m asl.
- Constrated soils:
  - shallow (Arcey, Bort) to deep (Croze)
  - very low (Bort, Croze) up to high pH soils (Arcey, Plachet)
- Climatically different



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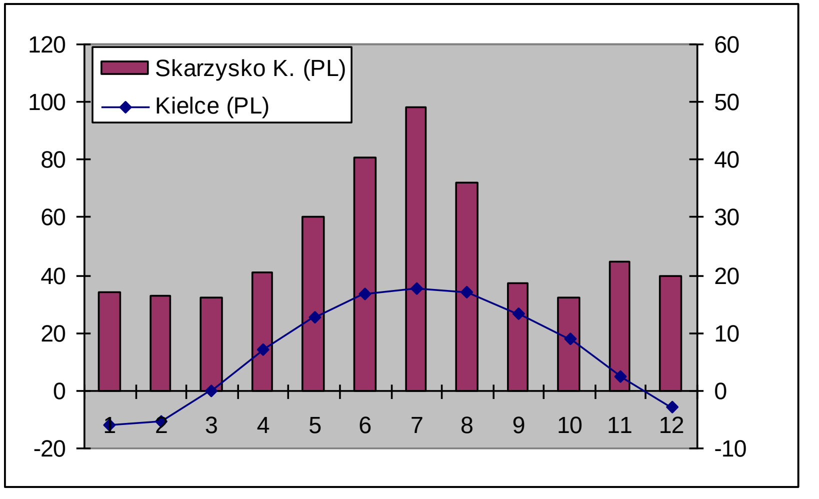
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Skarzysko K. (PL)
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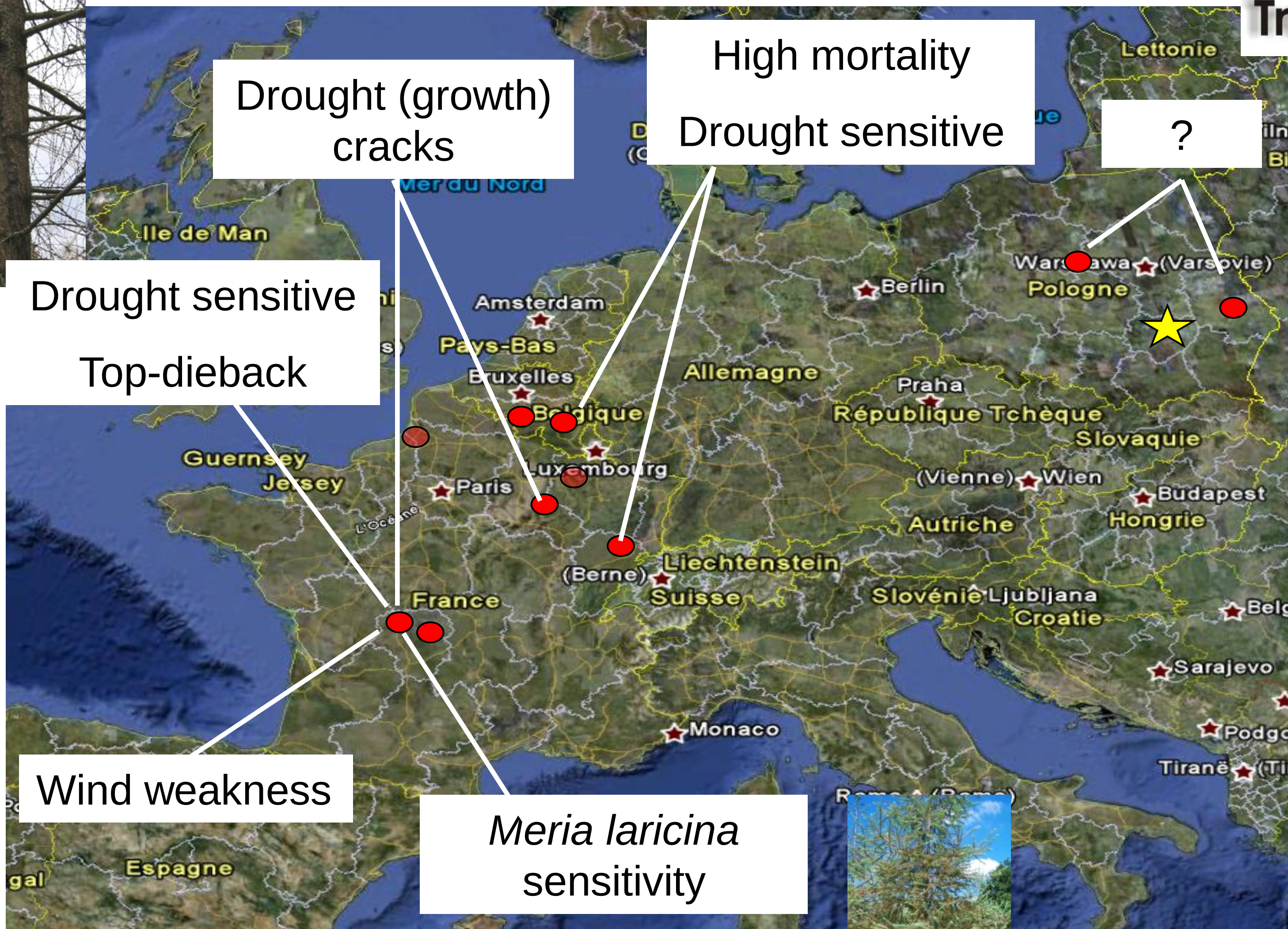
Results: 1) Adaptive traits



Results

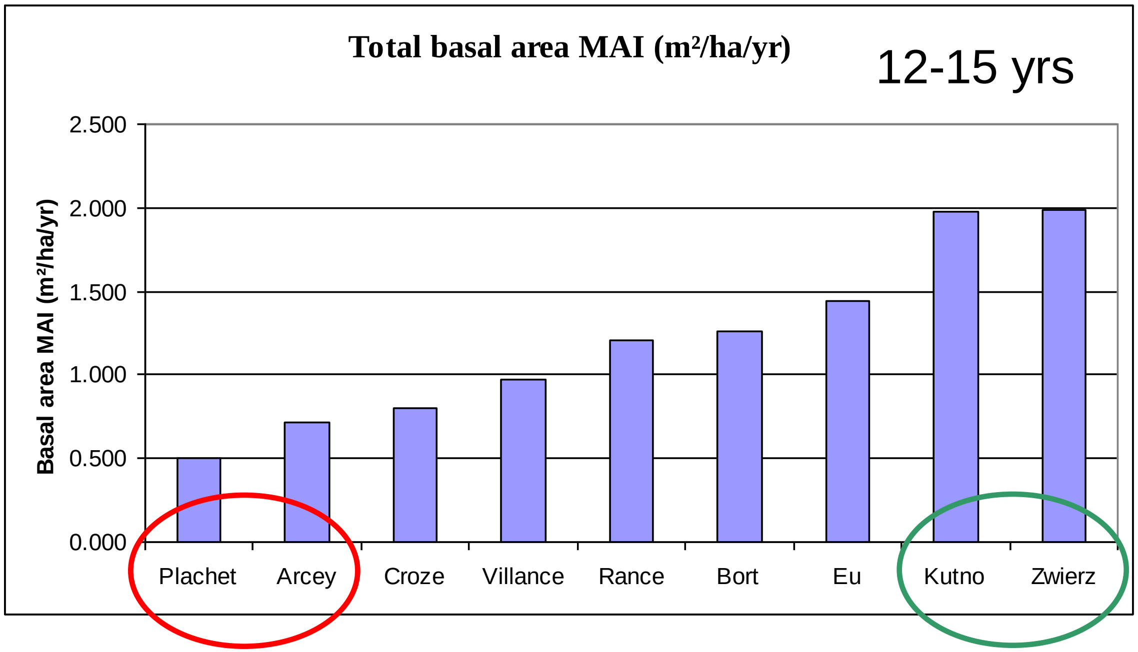
2) Growth and stem form

Field trial networks and difficulties

- Experimental design
- Site preparation
- Spacing
- Thinning
- Traits assessed and timing

		Arcey	Plachet	Bort	Croze	Eu	Rance	Villance	Kutno	Zwierzyniec
HT	1								x	
HT	2	x	x	x	x	x			x	x
HT	3								x	x
HT	4			x	x				x	x
HT	5	x		x	x		x	x		x
HT	6	x		x	x		x	x		x
HT	7	x	x				x	x		
HT	8	x	x	x	x					
HT	9	x	x	x	x					
HT	10	x	x		x					
HT	11		x	thinned						
HT	12		x						(x)	(x)
HT	13									
HT	14						(x)	(x)		
HT	15									
G	6								x	x
G	7	x								x
G	8									
G	9			x					x	x
G	10	x		x	x					
G	11			thinned						
G	12		x						x	x
G	13									
G	14						x	x		
G	15			x	x	x				
SS	4								x	
SS	5									
SS	6									
SS	7		x				x	x		x
SS	8									
SS	9			x						
SS	10	x			x					
SS	11			thinned						
SS	12		x						x	x
SS	13									
SS	14						x	x		
SS	15			x	x	x				

Site 'fertility'

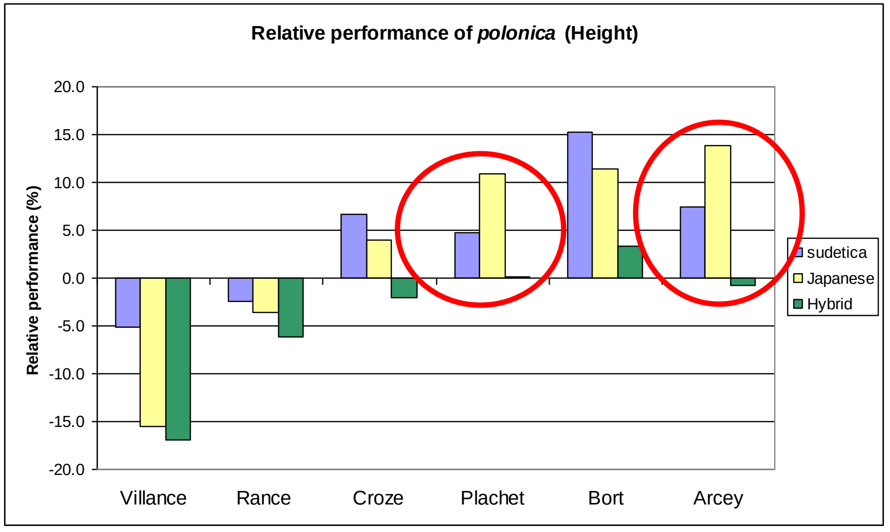


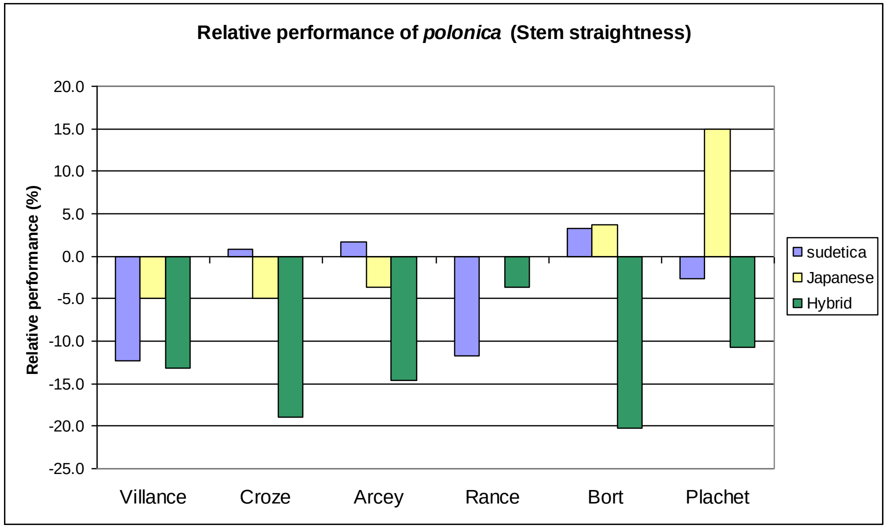
Correction for spacing/ mortality/ thinning/ age assessment

➢ *Polish sites more vigorous than FR/BE sites:*

up to 4x more BA MAI !! In France, ratio of 1 to 3 among sites.

Relative performance of *polonica* vs *sudetica* and other larch taxa





- *Even in less fertile sites in France, polonica grows better than or as well as other larch controls*
- *But stem form is worse in all sites*

5 sites **146 progenies**

		Arcey	Plachet	Croze	Bort	Kutno	Overall
h²	ah	0.109	0.140	0.255	0.248	0.325	0.099
	ac	0.136	0.190	0.262	0.380	0.225	0.139
	fl	0.296	0.300	0.384	0.343	0.109	0.254
CVA	ah	13.7	16.6	24.4	15.5	31.1	13.6
	ac	17.2	20.4	29.9	23.3	26.3	18.9
	fl	28.6	31.8	33.7	32.8	16.3	27.6

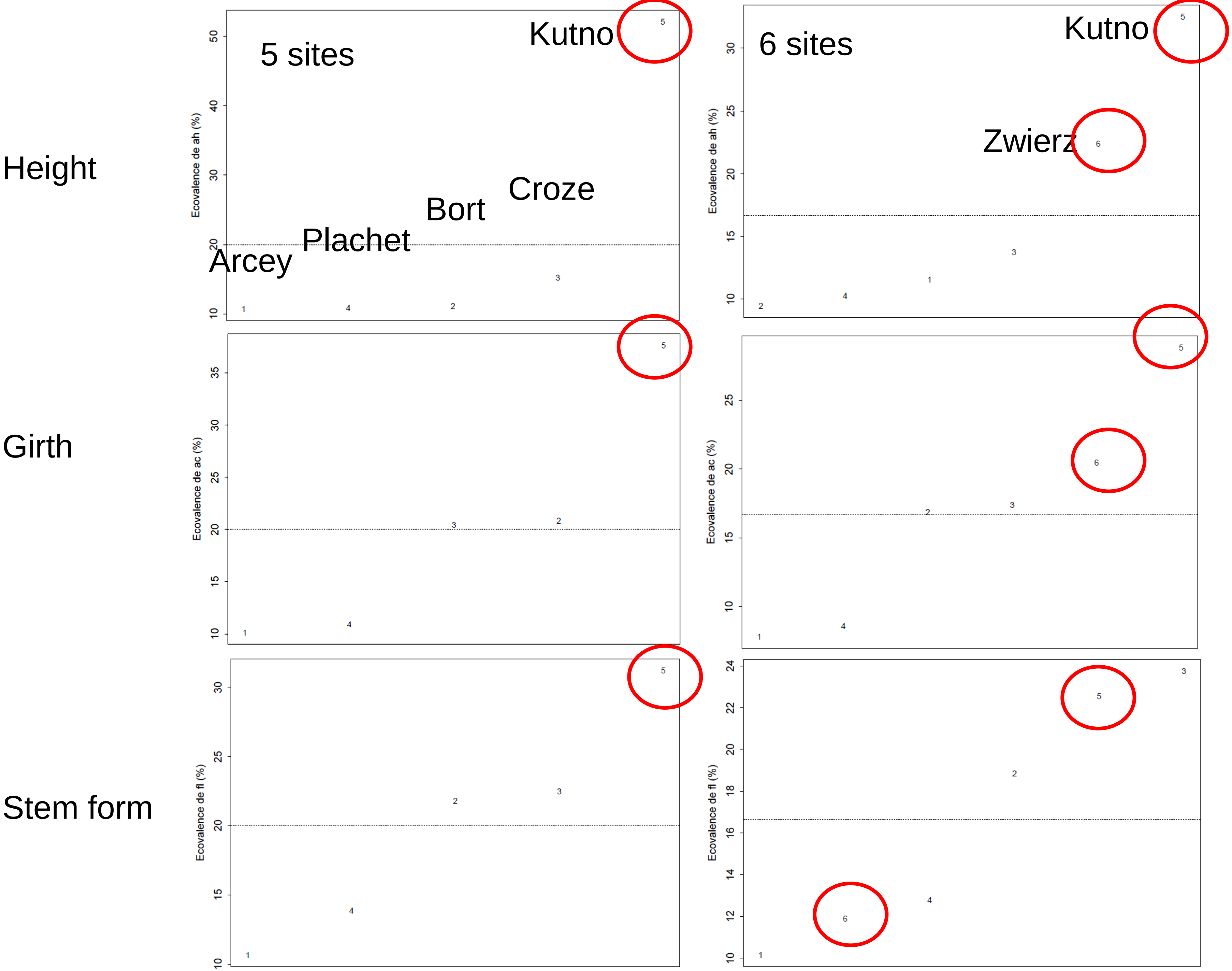
6 sites **70 progenies**

		Arcey	Plachet	Croze	Bort	Kutno	zwierz	Overall
h²	ah	0.071	0.114	0.265	0.275	0.290	0.143	0.062
	ac	0.095	0.168	0.247	0.410	0.238	0.316	0.113
	fl	0.378	0.350	0.570	0.405	0.142	0.365	0.309
CVA	ah	11.0	15.2	25.1	16.2	28.9	19.9	12.0
	ac	14.1	19.5	29.4	24.1	27.2	28.1	16.3
	fl	31.9	34.6	39.9	35.3	16.7	30.9	29.1

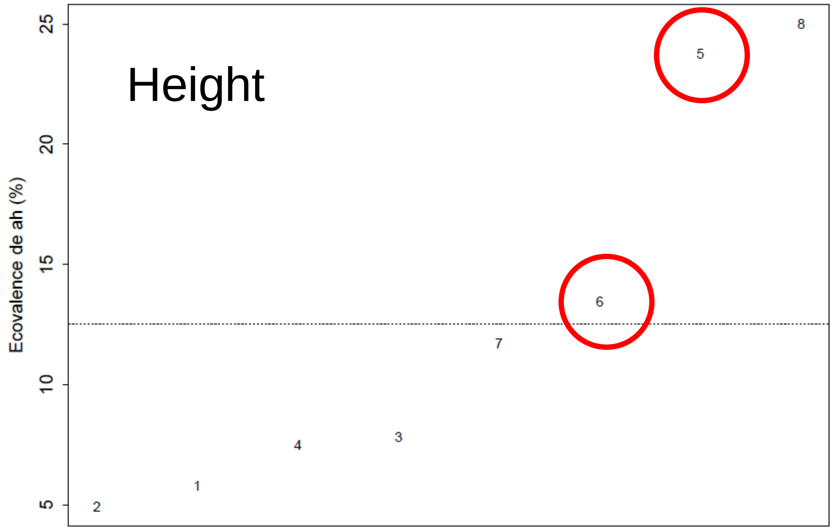
8 sites **47 progenies**

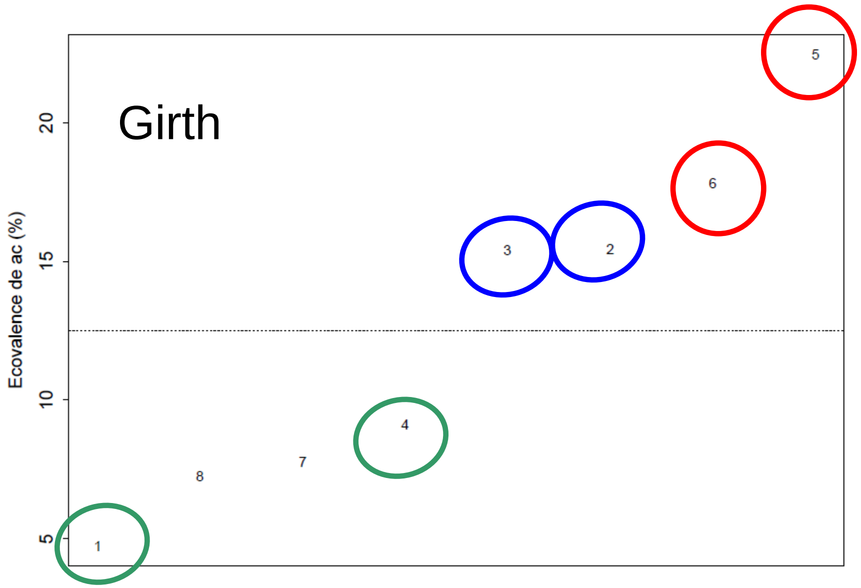
		Arcey	Plachet	Croze	Bort	Kutno	zwierz	Rance	Villance	Overall
h²	ah	0.084	0.104	0.302	0.277	0.300	0.263	0.154	0.523	0.087
	ac	0.071	0.135	0.282	0.342	0.215	0.298	0.127	0.304	0.090
	fl	0.339	0.366	0.560	0.462	0.121	0.393	0.587	0.660	0.318
CVA	ah	12.1	14.6	27.1	16.3	29.3	20.1	17.4	38.7	13.0
	ac	12.2	17.5	31.6	21.8	25.5	26.9	18.0	26.6	14.9
	fl	29.6	35.7	40.6	37.7	15.5	32.1	41.3	43.2	29.4

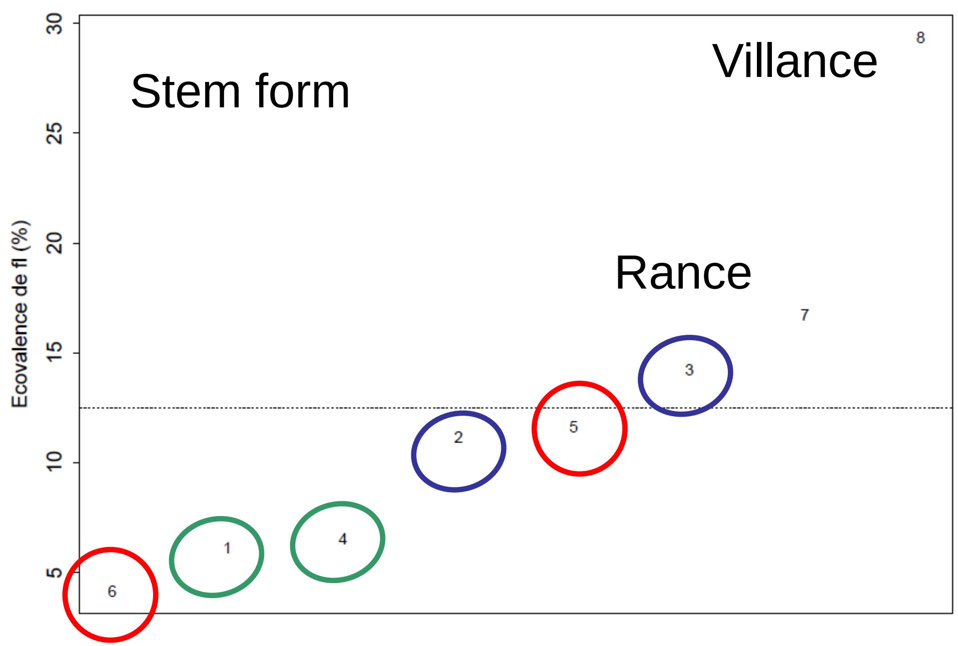
- *CV_A, h^2 : ah < ac < fl*
- *h^2 >> in good sites compared to poorest sites*


Height
Girth
Stem form
5 sites
6 sites
Kutno
Zwierz
Croze
Bort
Plachet
Arcey
Ecovalence de ah (%)
Ecovalence de ac (%)
Ecovalence de fl (%)

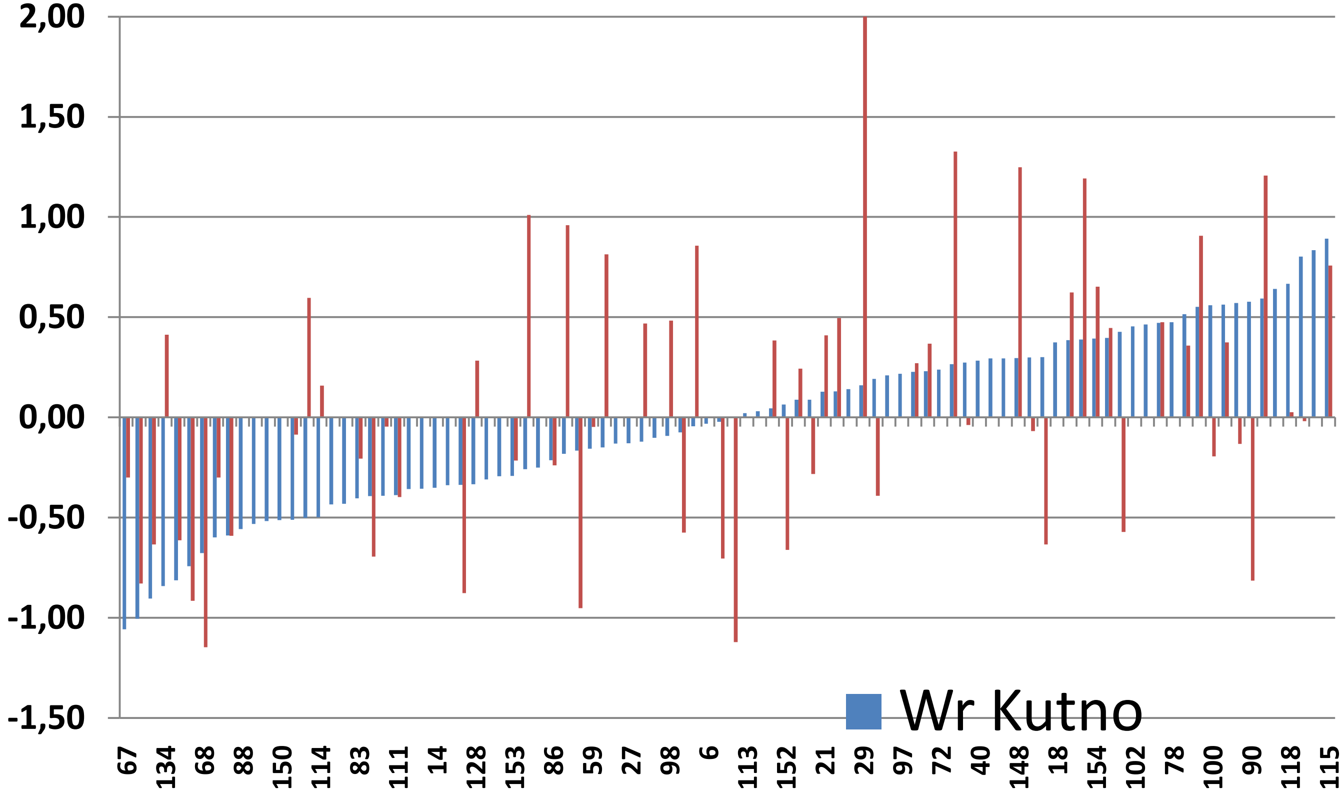
8 sites







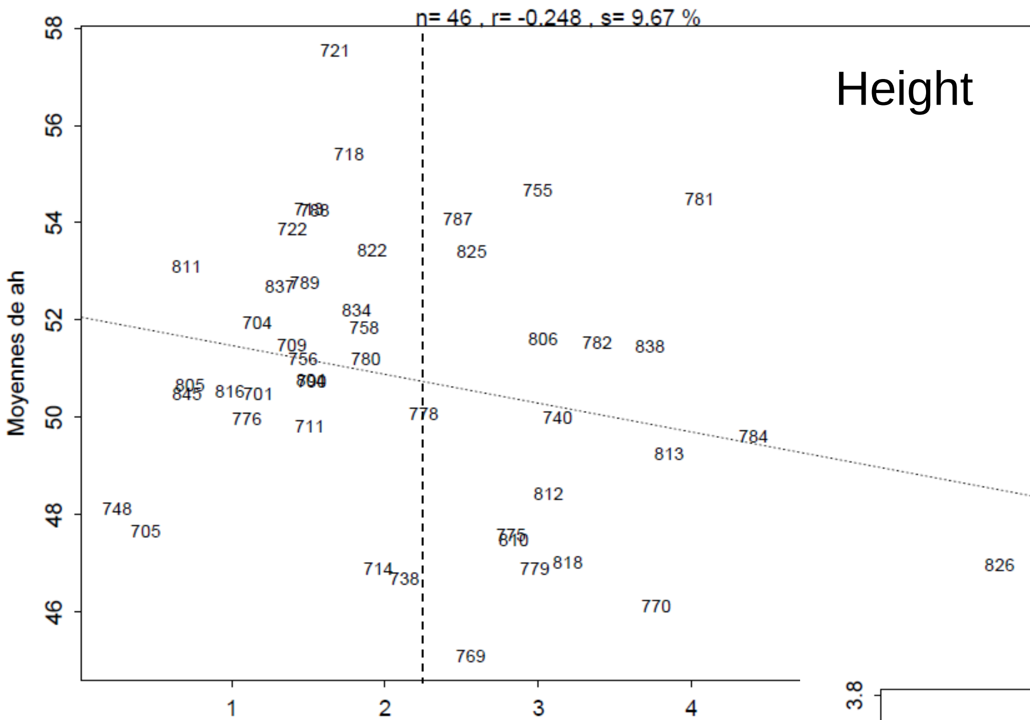
- *PL (B) sites more interactive than F sites for growth but not for stem form*
- *Low pH-soil sites in FR more interactive than high pH-soil sites*



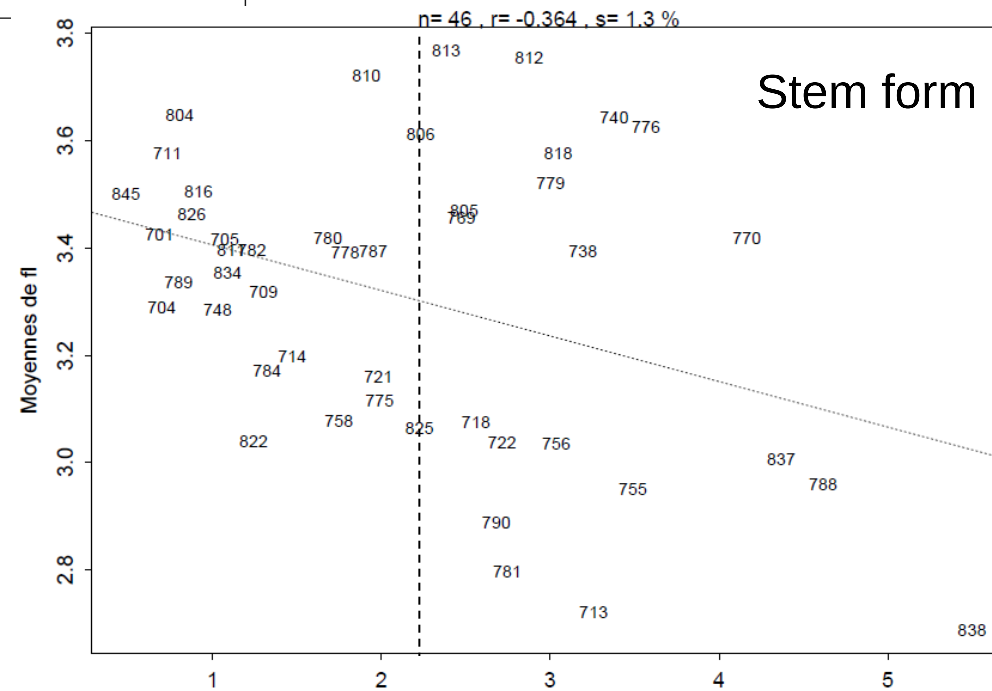
From Jan Kowalczyk (for index value), Bucharest meeting

➢ *High interactivity too among Polish sites*

Treebreedex



8 sites



- *No or negative link between ecovalence and performance*

Selection possibilities

index Height-stem form

fa	eff	index1	fa	eff	index2	fa	eff	index3	fa	eff	index4	fa	eff	index5
723	43	34.88	718	16	49.532	764	38	36.86	804	41	33.336	712	20	127.98
712	43	34.5	815	34	49.042	715	35	36.743	813	39	32.651	789	31	122.41
761	46	34.461	844	32	48.472	732	28	36.688	712	35	32.546	732	44	122.11
815	45	34.454	763	35	48.247	828	26	36.615	811	36	32.304	752	13	121.98
765	42	34.305	788	18	48.04	773	22	36.583	701	37	32.244	844	11	121.58
707	34	34.106	843	26	47.876	721	38	36.451	815	41	31.973	804	21	121.14
715	47	34.009	789	34	47.861	699	31	36.303	694	30	31.907	715	75	120.69
828	48	33.869	721	35	47.798	821	16	36.218	816	43	31.86	719	18	120.58
708	33	33.714	776	29	47.623	765	36	36.055	803	31	31.856	791	45	119.97
740	42	33.662	715	35	47.604	756	37	36.019	775	27	31.762	806	34	119.59
787	39	33.622	813	31	47.525	839	18	35.985	778	37	31.758	776	25	119
722	42	33.503	755	35	47.479	772	39	35.925	810	38	31.576	701	13	118.52
805	39	33.417	828	32	47.312	708	19	35.869	837	34	31.555	812	34	118.37
700	49	33.394	765	34	47.216	841	35	35.747	740	38	31.452	793	33	118.14
776	28	33.387	821	24	47.136	843	21	35.716	792	40	31.409	813	18	118.02
718	41	33.289	722	34	47.132	838	38	35.693	806	37	31.393	826	18	117.93
782	43	33.23	743	21	47.087	815	29	35.634	820	34	31.304	834	56	117.54
806	43	33.221	784	30	47.038	726	39	35.562	695	37	31.153	718	85	117.44
831	43	33.146	732	34	47.023	780	40	35.327	805	40	31.072	829	50	117.41
824	37	33.132	739	25	46.982	722	34	35.277	831	37	30.941	843	21	117.39
773	48	33.118	831	35	46.916	819	38	35.215	832	38	30.882	729	18	117.25
756	40	33.094	712	34	46.843	792	21	35.203	812	38	30.88	778	23	117.11
845	41	33.07	823	32	46.784	763	25	35.132	785	32	30.87	810	26	117.06
696	42	33.012	692	30	46.777	836	28	35.025	782	31	30.803	808	33	116.97
721	45	32.942	804	33	46.746	696	22	35.008	723	34	30.798	704	30	116.82
804	43	32.931	702	24	46.679	711	40	35.006	716	35	30.741	781	25	116.75
839	39	32.921	719	25	46.628	720	36	34.973	839	33	30.732	705	52	116.68
711	45	32.892	824	33	46.608	695	21	34.962	722	32	30.732	816	60	116.55
786	44	32.887	834	33	46.602	768	22	34.954	826	51	30.715	779	31	116.43
836	41	32.856	720	33	46.524	831	39	34.924	715	34	30.691	721	143	116.29

- Among the 20 best out of 146 selected in Kutno, 60% common with French sites
- more common ones at the low elevation sites (Bort)

Some conclusions

- Polish larch has an interest in FR but improvement requested for stem straightness
- High GxE interaction (but most common in larch)
- GxE interaction looks not less important within PL than within FR
- A reasonable rate of clones selected in PL may be valuable in FR but some are poor

- Should help to identify limiting ecological factors (drought in Bort, humid soil in BE? Etc) and thereby the possible range of deployment
  - *Would need information on pedo-climatic parameters of all sites*

Partners

Treebreedex

- IBL (PL)
- INRA (FR)
- CRNFB (BE)

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Elena Foffová[1], Vladimír Foff[2]

[1] National Forest Centre Zvolen

[2] LIA, Ltd.
Forestry Information Agency

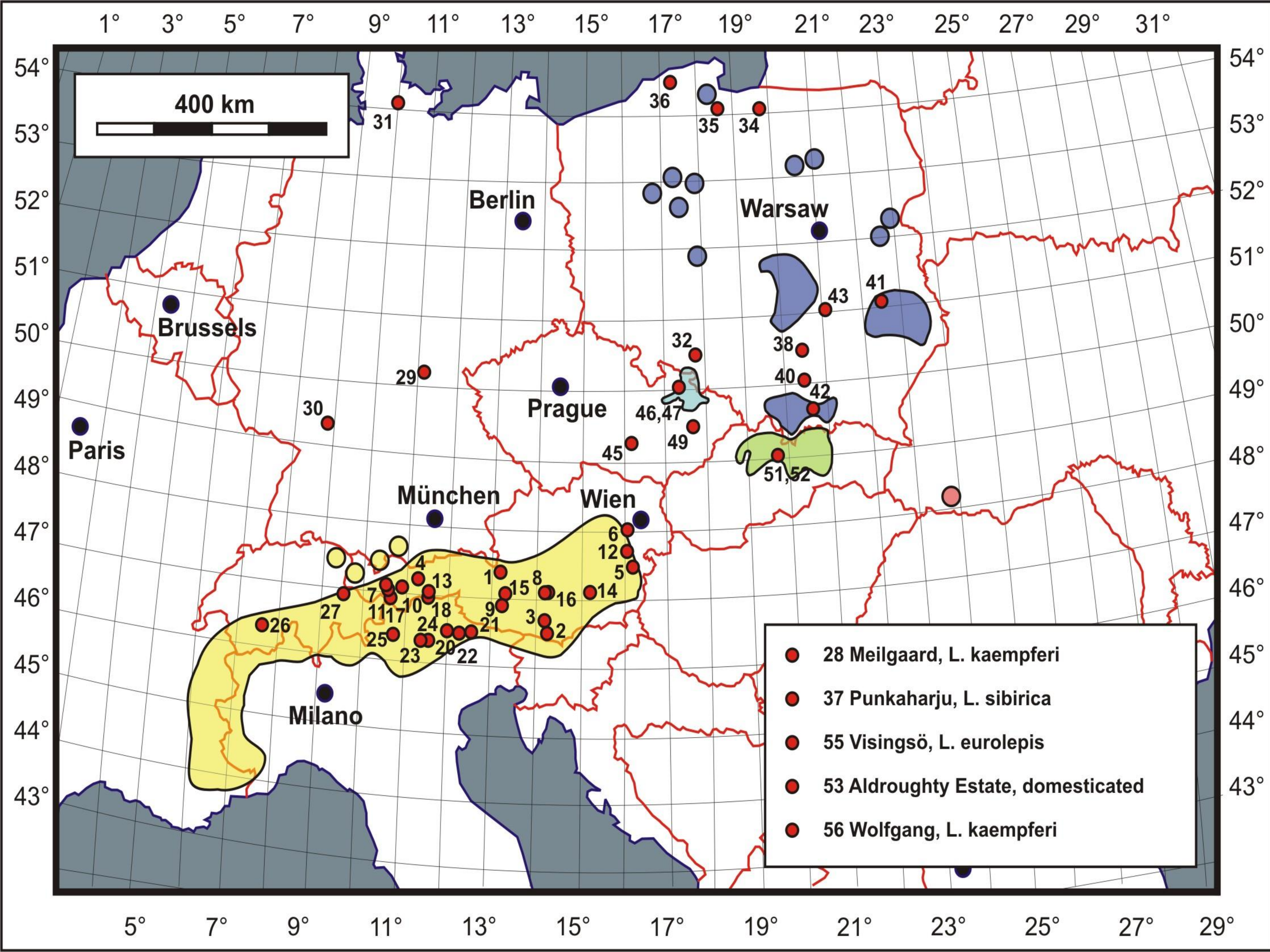
Locality of planting sites of the IUFRO 1944 European larch provenance experiment

Exp.no.	Locality	Lat. N	Long.	Alt. In m
2	Vilppula, Finland	62°00´	24°30´E	110
4	Arboretum d.l. Sivr. Nancy, France	48°45´	6°09´E	375
5	Bremervörde, Germany	55°30´	9°00´E	50
7	Drummond Hill, Perthshire, U.K.	56°34´	4°06´W	275-330
8	Savernake, Wiltshire, U.K	51°24´	1°38´W	145
9	Haugh Forest, Herfordshire, U.K.	52°01´	2°36´W	125
10	Mortimer Forest, Herfordshire, U.K.	52°19´	2°53´W	243
11	Walcot Forest, Shropshire, U.K.	52°25´	3°01´W	260
12	Wyre Forest, Worcestershire, U.K.	52°25´	2°22´W	90
13	Acguerino Forest, Pistoia, Italy	44°01´	11°05´E	950
14	Hjulenberg, Holand, Sweden	56°56´	12°44´E	175
15	Hönggerberg, Zürich, Switzerland	47°25´	8°30´E	535
16	Hillsboro, N.H., USA	43°10´	71°55´W	260
18	Podbanské, Slovakia	49°08´	19°55´E	950
19	Kolanów, Poland	49°55´	20°31´E	330

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Basic data on the provenance plot Podbanské	
Altitude:	1020 m
Latitude:	49°08´25´´
Longitude:	19°56´00´´
Inclination:	10°
N. of provenances:	42
Established:	1946
Destroyed:	November 2004


400 km
Berlin
Warsaw
Brussels
Paris
Prague
München
Wien
Milano
28 Meilgaard, L. kaempferi
37 Punkaharju, L. sibirica
55 Visingsö, L. eurolepis
53 Aldroughty Estate, domesticated
56 Wolfgang, L. kaempferi

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

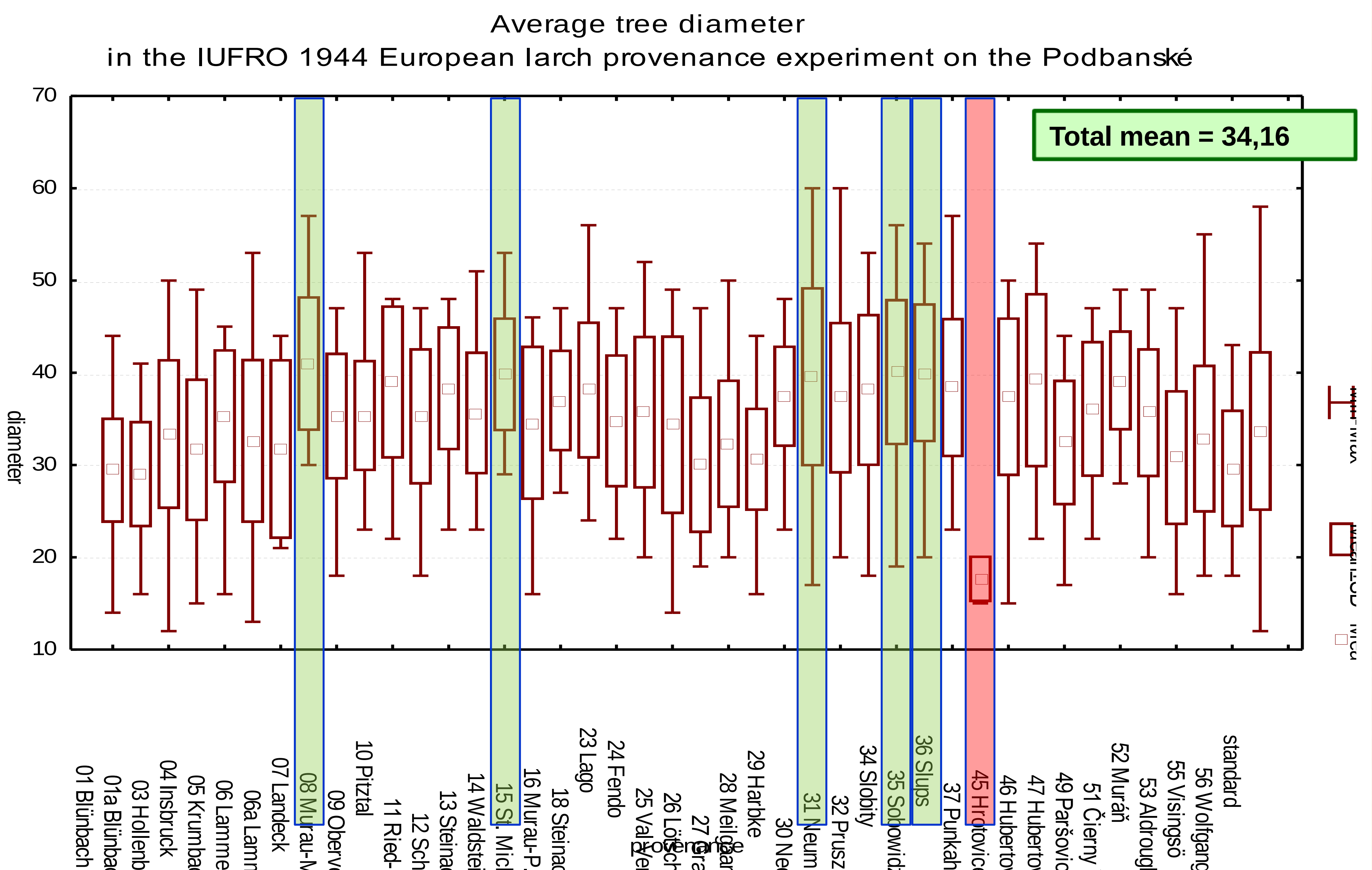
Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

European larch provenances from the IUFRO 1944 experiment used in plot Podbanské

Provenance	State	N	Altitude	Latitude	Longitude
01 Blünbach	Austria	67	600	47°29´	13°10´
01a Blünbach	Austria	74	600	46°33´	14°18´
03 Hollenburg	Austria	49	900	46°33´	14°18´
04 Insbruck	Austria	45	900	47°14´	11°23´
05 Krumbach	Austria	42	600	47°31´	16°12´
06 Lammerau	Austria	48	700	48°05´	16°10´
06a Lammerau	Austria	4	700	48°05´	16°10´
07 Landeck	Austria	25	750	47°08´	10°37´
08 Murau-M.	Austria	33	950	47°08´	14°10´
09 Obervellach	Austria	35	1100	46°55´	13°13´
10 Pitztal	Austria	9	1100	47°05´	10°50´
11 Ried-Tösens	Austria	33	1050	47°00´	10°37´
12 Schottwien-W.	Austria	35	800	47°40´	15°55´
13 Steinach-M.	Austria	42	900	47°06´	11°28´
14 Waldstein	Austria	30	550	47°14´	15°15´
15 St. Michael	Austria	33	1700	47°05´	13°39´
16 Murau-P.	Austria	21	1700	47°04	14°06´
18 Steinach-G.	Austria	40	1900	47°02´	11°30´
23 Lago	Italy	19	925	46°17´	11°23´
24 Fendo	Italy	22	1400	46°20´	11°27´
25 Val Venosta	Italy	14	1100	46°35´	10°40´
26 Lötschenthal	Switzerland	28	1500	46°23´	7°47´
27 Graubünden U.	Switzerland	33	550	46°57´	9°32´
28 Meilgaard	Denmark	88	50	56°31´	10°37´
29 Harbke	Germany	39	70	52°12´	11°03´
30 Neckargemund	Germany	30	335	49°23´	8°49´
31 Neumunster	Germany	43	50	54°05´	10°00´
32 Pruszkow S.	Poland	31	200	50°34´	17°48´
34 Slobity	Poland	30	65	54°08´	19°47´
35 Sobowidz	Poland	29	80	54°09´	18°36´
36 Slups	Poland	25	30	54°28´	17°06´
37 Punkaharju	Finland	3	85	61°48´	29°20´
45 Hrotovice	Bohemia	31	410	49°16´	16°07´
46 Hubertovo	Bohemia	10	700	50°04´	17°18´
47 Hubertovo	Bohemia	23	700	50°04´	17°18´
49 Paršovice	Bohemia	35	375	49°30´	17°42´
51 Čierny Váh	Slovakia	24	825	49°02´	19°40´
52 Muráň	Slovakia	40	1000	49°02´	19°40´
53 Aldroughty	Scotland	63	50	57°39´	3°23´
55 Visingsö	Sweden	56	100	58°02´	14°20´
56 Wolfgang	Sweden	68	500	48°15´	12°10´
standard	Slovakia	680	950	48°59´	20°20´
Total		2129			

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010



Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

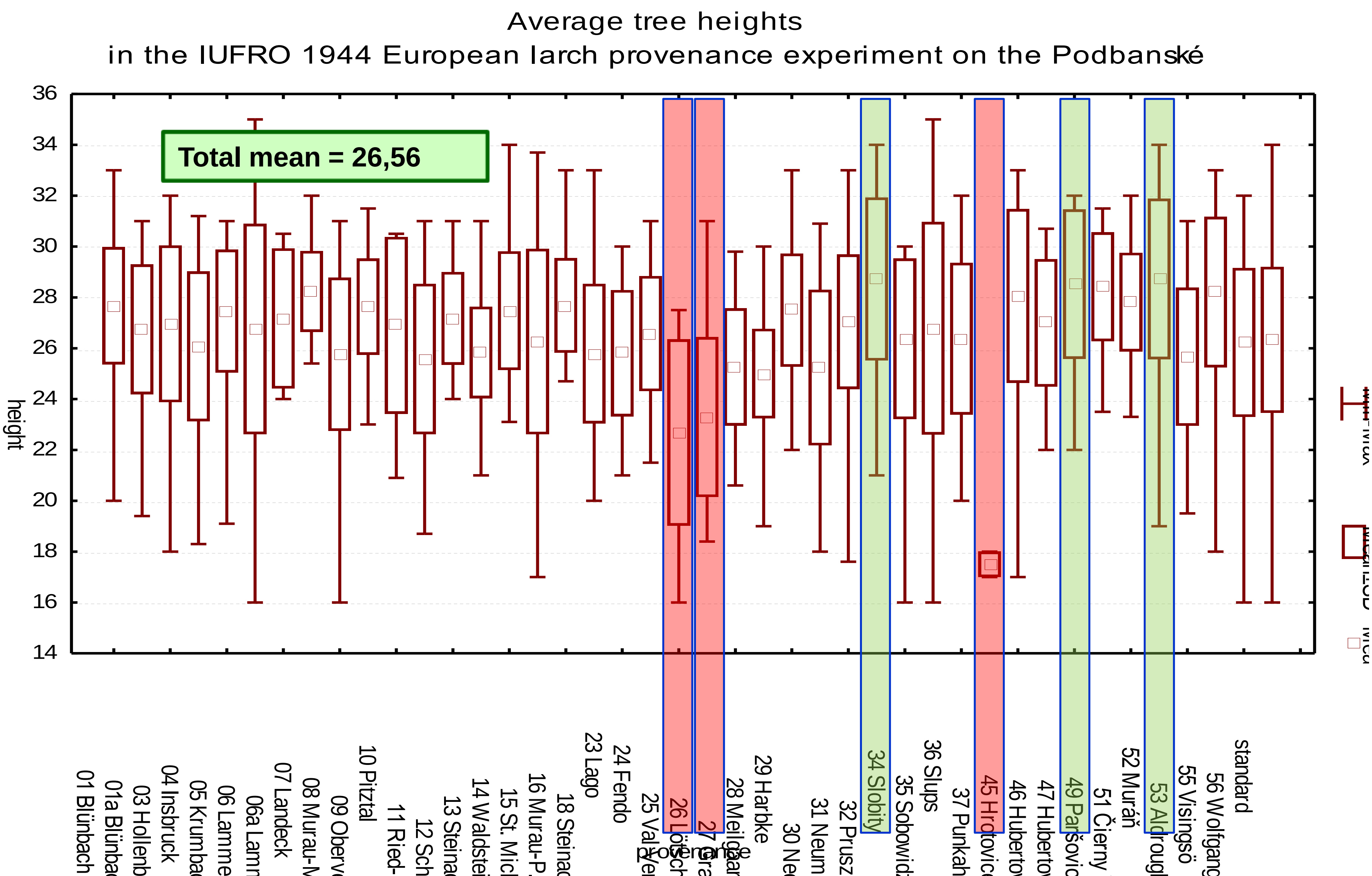
Provenance	Mean	A	B	C	D	E	F	G	H	I	J	K	L	M	N
07 Landeck	41,000	■													
34 Slobity	40,067	■	■												
35 Sobowidz	40,000	■	■												
14 Waldstein	39,833	■	■												
30 Neckargemund	39,567	■	■												
46 Hubertovo	39,200	■	■	■											
51 Čierny Váh	39,167	■	■	■											
10 Pitztal	39,000	■	■	■	■										
36 Slups	38,400	■	■	■	■	■									
12 Schottwien-W.	38,314	■	■	■	■	■	■								
32 Pruszkow S.	38,129	■	■	■	■	■	■	■							
18 Steinach-G.	38,125	■	■	■	■	■	■	■							
29 Harbke	37,462	■	■	■	■	■	■	■	■						
45 Hrotovice	37,419	■	■	■	■	■	■	■	■						
31 Neumunster	37,302	■	■	■	■	■	■	■	■	■					
16 Murau-P.	37,000	■	■	■	■	■	■	■	■	■					
49 Paršovice	36,086	■	■	■	■	■	■	■	■	■	■				
24 Fendo	35,727	■	■	■	■	■	■	■	■	■	■	■			
52 Muráň	35,675	■	■	■	■	■	■	■	■	■	■	■			
13 Steinach-M.	35,643	■	■	■	■	■	■	■	■	■	■	■			
09 Obervellach	35,371	■	■	■	■	■	■	■	■	■	■	■			
05 Krumbach	35,310	■	■	■	■	■	■	■	■	■	■	■			
08 Murau-M.	35,303	■	■	■	■	■	■	■	■	■	■	■			
11 Ried-Tösens	35,273	■	■	■	■	■	■	■	■	■	■	■			
23 Lago	34,789		■	■	■	■	■	■	■	■	■	■	■		
15 St. Michael	34,576		■	■	■	■	■	■	■	■	■	■	■	■	
25 Val Venosta	34,357		■	■	■	■	■	■	■	■	■	■	■	■	
standard	33,679			■	■	■	■	■	■	■	■	■	■	■	
03 Hollenburg	33,367				■	■	■	■	■	■	■	■	■	■	
55 Visingsö	32,857					■	■	■	■	■	■	■	■	■	
06 Lammerau	32,625						■	■	■	■	■	■	■	■	
47 Hubertovo	32,435							■	■	■	■	■	■	■	
27 Graubünden U.	32,303								■	■	■	■	■	■	
06a Lammerau	31,750								■	■	■	■	■	■	
04 Insbruck	31,644									■	■	■	■	■	
53 Aldroughty	30,810										■	■	■	■	
28 Meilgaard	30,625										■	■	■	■	
26 Lötschenthal	30,036											■	■	■	
56 Wolfgang	29,632												■	■	
01 Blünbach	29,448												■	■	
01a Blünbach	29,014													■	
37 Punkaharju	17,667														■

Analysis of variance and Duncan test for variable diameter
alpha = 0,05; mean = 34,16 cm

Effect	N	SS	MS	F	p
Provenance	41	19033,183	464,224	7,825	0,000
Error	2087	123809,288	59,324		
Total	2128	142842,471			

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010



Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

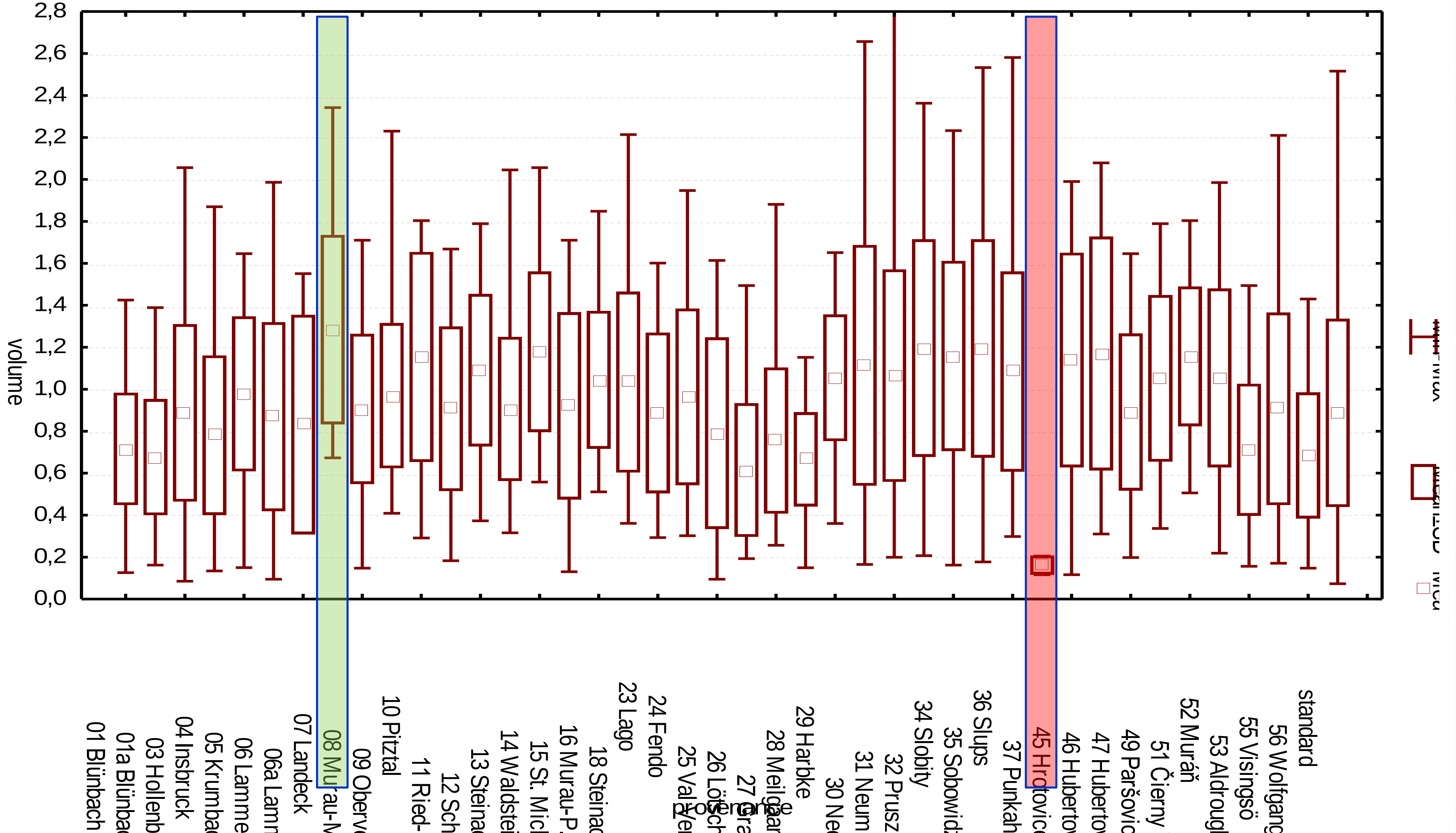
Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Provenance	Mean	A	B	C	D	E	F	G	H	I	J	K
52 Muráň	28,725	■										
32 Pruszkow S.	28,723	■										
47 Hubertovo	28,522	■	■									
49 Paršovice	28,420	■	■	■								
07 Landeck	28,236	■	■	■	■							
55 Visingsö	28,209	■	■	■	■							
45 Hrotovice	28,058	■	■	■	■	■						
51 Čierny Váh	27,817	■	■	■	■	■	■					
16 Murau-P.	27,686	■	■	■	■	■	■	■				
01 Blünbach	27,672	■	■	■	■	■	■	■				
09 Obervellach	27,634	■	■	■	■	■	■	■				
29 Harbke	27,497	■	■	■	■	■	■	■				
14 Waldstein	27,480	■	■	■	■	■	■	■				
05 Krumbach	27,462	■	■	■	■	■	■	■				
12 Schottwien-W.	27,177	■	■	■	■	■	■	■	■			
06a Lammerau	27,175	■	■	■	■	■	■	■	■			
31 Neumunster	27,044	■	■	■	■	■	■	■	■	■		
46 Hubertovo	27,000	■	■	■	■	■	■	■	■	■		
03 Hollenburg	26,957	■	■	■	■	■	■	■	■	■		
10 Pitztal	26,900	■	■	■	■	■	■	■	■	■		
35 Sobowidz	26,786	■	■	■	■	■	■	■	■	■		
06 Lammerau	26,756	■	■	■	■	■	■	■	■	■		
01a Blünbach	26,745	■	■	■	■	■	■	■	■	■		
24 Fendo	26,577		■	■	■	■	■	■	■	■		
36 Slups	26,376			■	■	■	■	■	■	■		
34 Slobity	26,370			■	■	■	■	■	■	■		
standard	26,329				■	■	■	■	■	■		
15 St. Michael	26,264				■	■	■	■	■	■		
56 Wolfgang	26,226				■	■	■	■	■	■		
04 Insbruck	26,073					■	■	■	■	■		
13 Steinach-M.	25,836						■	■	■	■		
23 Lago	25,805						■	■	■	■		
18 Steinach-G.	25,788						■	■	■	■		
08 Murau-M.	25,764						■	■	■	■		
53 Aldroughty	25,665							■	■	■		
11 Ried-Tösens	25,579							■	■	■		
27 Graubünden U.	25,264								■	■		
30 Neckargemund	25,240								■	■		
28 Meilgaard	25,005									■		
26 Lötschenthal	23,293										■	
25 Val Venosta	22,686										■	
37 Punkaharju	17,500											■

Analysis of variance and Duncan test for variable height
alpha = 0,05; mean = 26,56 m

Effect	N	SS	MS	F	p
Provenance	41	2452,097	59,807	7,688	0,000
Error	2087	16236,387	7,780		
Total	2128	18688,484			

Average volume of stem without bark
in the IUFRO 1944 European larch provenance experiment on the Podbanské



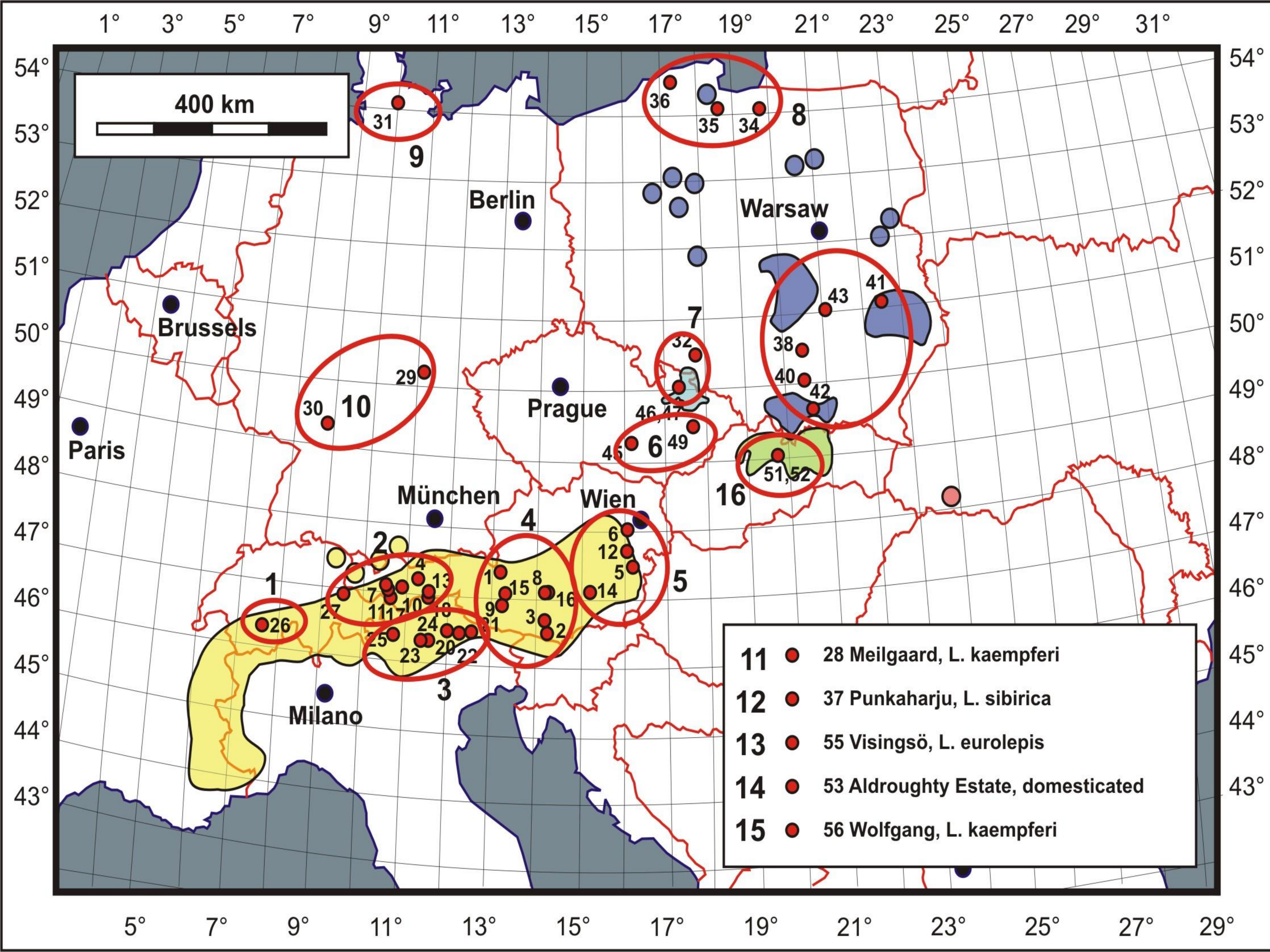
Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Provenance	Mean	A	B	C	D	E	F	G	H	I	J	K	L
07 Landeck	1,285	■											
32 Pruszkow S.	1,196	■	■										
35 Sobowidz	1,195	■	■	■									
14 Waldstein	1,178	■	■	■	■								
46 Hubertovo	1,170	■	■	■	■								
34 Slobity	1,159	■	■	■	■								
51 Čierny Váh	1,157	■	■	■	■								
10 Pitztal	1,154	■	■	■	■								
45 Hrotovice	1,140	■	■	■	■								
30 Neckargemund	1,114	■	■	■	■	■							
12 Schottwien-W.	1,091	■	■	■	■	■	■						
36 Slups	1,084	■	■	■	■	■	■	■					
31 Neumunster	1,065	■	■	■	■	■	■	■					
29 Harbke	1,054	■	■	■	■	■	■	■	■				
52 Muráň	1,054	■	■	■	■	■	■	■	■				
49 Paršovice	1,052	■	■	■	■	■	■	■	■				
16 Murau-P.	1,045	■	■	■	■	■	■	■	■				
18 Steinach-G.	1,034	■	■	■	■	■	■	■	■				
05 Krumbach	0,978		■	■	■	■	■	■	■	■			
09 Obervellach	0,969		■	■	■	■	■	■	■	■	■		
24 Fendo	0,964		■	■	■	■	■	■	■	■	■		
15 St. Michael	0,921		■	■	■	■	■	■	■	■	■		
11 Ried-Tösens	0,907		■	■	■	■	■	■	■	■	■	■	
55 Visingsö	0,907		■	■	■	■	■	■	■	■	■	■	
13 Steinach-M.	0,906		■	■	■	■	■	■	■	■	■	■	
08 Murau-M.	0,906		■	■	■	■	■	■	■	■	■	■	
47 Hubertovo	0,891		■	■	■	■	■	■	■	■	■	■	
standard	0,888		■	■	■	■	■	■	■	■	■	■	
03 Hollenburg	0,887		■	■	■	■	■	■	■	■	■	■	
23 Lago	0,887		■	■	■	■	■	■	■	■	■	■	
06 Lammerau	0,869				■	■	■	■	■	■	■	■	
06a Lammerau	0,832					■	■	■	■	■	■	■	
25 Val Venosta	0,791						■	■	■	■	■	■	
04 Insbruck	0,781							■	■	■	■	■	
27 Graubünden U.	0,755								■	■	■	■	
01 Blünbach	0,716									■	■	■	
53 Aldroughty	0,711									■	■	■	
56 Wolfgang	0,684									■	■	■	
01a Blünbach	0,676									■	■	■	
28 Meilgaard	0,666										■	■	
26 Lötschenthal	0,615											■	
37 Punkaharju	0,162												■

Analysis of variance and Duncan test for variable volume
alpha = 0,05; mean = 0,906 m^3

Effect	N	SS	MS	F	p
Provenance	41	48,698	1,188	7,091	0,000
Error	2087	349,588	0,168		
Total	2128	398,286			



400 km
Berlin
Warsaw
Brussels
Paris
Prague
München
Wien
Milano
1
2
3
4
5
6
7
8
9
10
16
11 28 Meilgaard, L. kaempferi
12 37 Punkaharju, L. sibirica
13 55 Visingsö, L. eurolepis
14 53 Aldroughty Estate, domesticated
15 56 Wolfgang, L. kaempferi

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

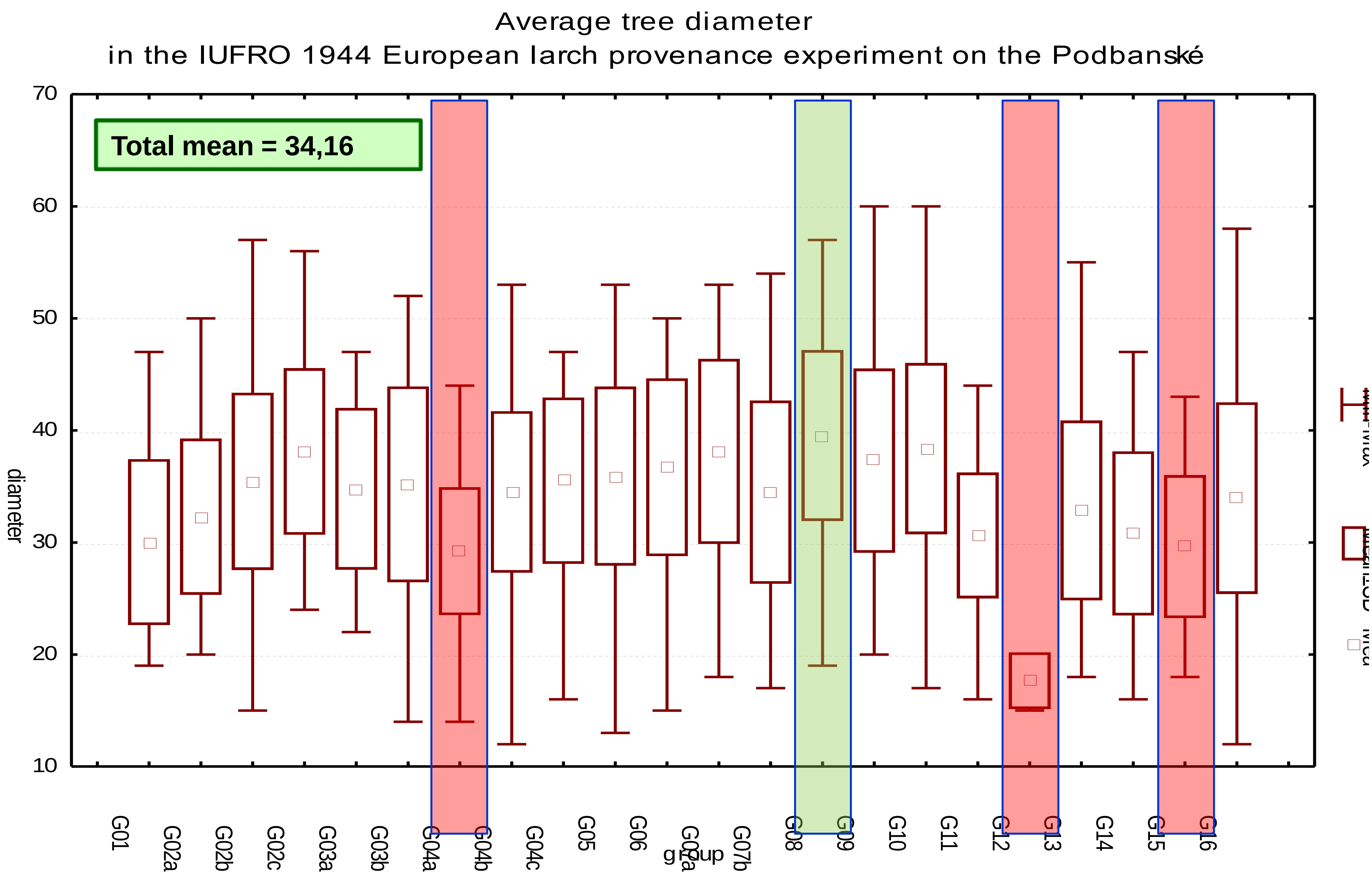
Group	Provenance	N	Altitude
G01	26 Lötschenthal	28	1500
G02a	27 Graubünden U.	33	550
G02b	04 Insbruck	45	900
	07 Landeck	25	750
	10 Pitztal	9	1100
	11 Ried-Tösens	33	1050
	13 Steinach-M.	42	900
	AVG	154	919
G02c	18 Steinach-G.	40	1900
G03a	23 Lago	19	925
G03b	24 Fendo	22	1400
	25 Val Venosta	14	1100
	AVG	36	1283
G04a	01 Blünbach	67	600
	01a Blünbach	74	600
	AVG	141	600
G04c	15 St. Michael	33	1700
	16 Murau-P.	21	1700
	AVG	54	1700

Group	Provenance	N	Altitude
G04b	03 Hollenburg	49	900
	08 Murau-M.	33	950
	09 Obervellach	35	1100
	AVG	117	973
G05	05 Krumbach	42	600
	06 Lammerau	48	700
	06a Lammerau	4	700
	12 Schottwien-W.	35	800
	14 Waldstein	30	550
	AVG	159	667
G06	45 Hrotovice	31	410
	49 Paršovice	35	375
	AVG	66	391
G07a	32 Pruszkow S.	31	200
G07b	46 Hubertovo	10	700
	47 Hubertovo	23	700
	AVG	33	700
G08	34 Slobity	30	65
	35 Sobowidz	29	80
	36 Slups	25	30
	AVG	84	60

Group	Provenance	N	Altitude
G09	31 Neumunster	43	50
G10	29 Harbke	39	70
	30 Neckargemund	30	335
	AVG	69	185
G11	28 Meilgaard	88	50
G12	37 Punkaharju	3	85
G13	55 Visingsö	56	100
G14	53 Aldroughty	63	50
G15	56 Wolfgang	68	500
G16	51 Čierny Váh	24	825
	52 Muráň	40	1000
	standard	680	950
	AVG	744	949

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010



Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Group	Mean	A	B	C	D	E	F	G	H	I	J
G08	39,548	■									
G10	38,377	■	■								
G07a	38,129	■	■								
G02c	38,125	■	■								
G09	37,302	■	■	■							
G06	36,712	■	■	■	■						
G05	35,925	■	■	■	■						
G04c	35,519	■	■	■	■	■					
G02b	35,461	■	■	■	■	■					
G03b	35,194	■	■	■	■	■	■				
G03a	34,789		■	■	■	■	■				
G04b	34,513		■	■	■	■	■	■			
G07b	34,485		■	■	■	■	■	■			
G16	33,964		■	■	■	■	■	■	■		
G13	32,857			■	■	■	■	■	■	■	
G02a	32,303				■	■	■	■	■	■	
G14	30,810					■	■	■	■	■	
G11	30,625						■	■	■	■	
G01	30,036							■	■	■	
G15	29,632								■	■	
G04a	29,220									■	
G12	17,667										■

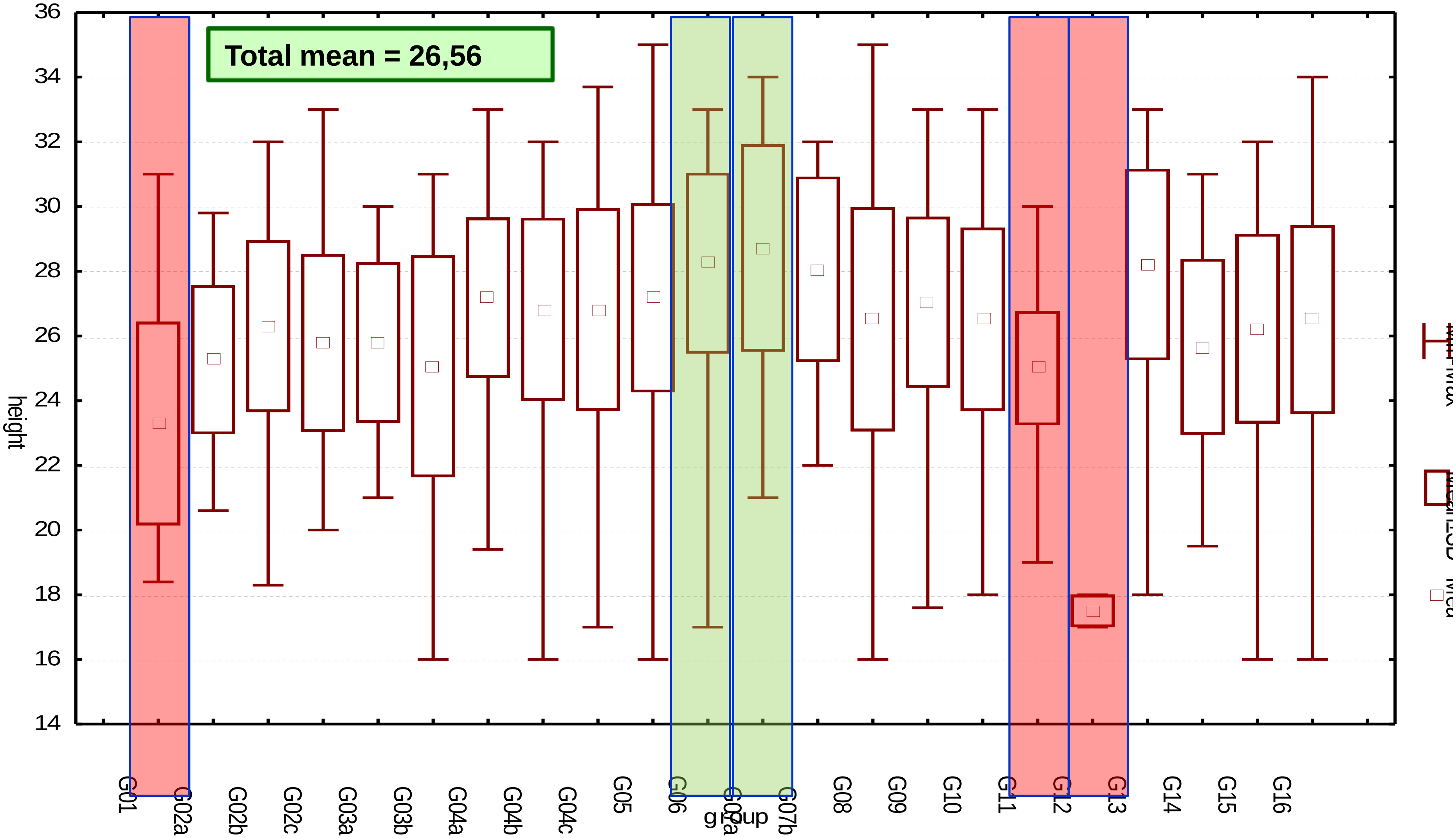
Analysis of variance and Duncan test for variable diameter
alpha = 0,05; mean = 34,16 cm

Effect	N	SS	MS	F	p
Group	21	14728,077	701,337	11,534	0,000
Error	2107	128114,394	60,804		
Total	2128	142842,471			

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Average tree heights
in the IUFRO 1944 European larch provenance experiment on the Podbanské



Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Group	Mean	A	B	C	D	E	F	G	H	I
G07a	28,723	■								
G06	28,250	■	■							
G13	28,209	■	■	■						
G07b	28,061	■	■	■	■					
G04a	27,185	■	■	■	■	■				
G05	27,182	■	■	■	■	■				
G09	27,044		■	■	■	■				
G04b	26,823		■	■	■	■	■			
G04c	26,817		■	■	■	■	■			
G10	26,516			■	■	■	■	■		
G08	26,515			■	■	■	■	■		
G16	26,506			■	■	■	■	■		
G02b	26,302					■	■	■		
G15	26,226					■	■	■		
G03a	25,805					■	■	■		
G02c	25,788					■	■	■		
G14	25,665					■	■	■		
G02a	25,264						■	■		
G03b	25,064							■		
G11	25,005							■		
G01	23,293								■	
G12	17,500									■

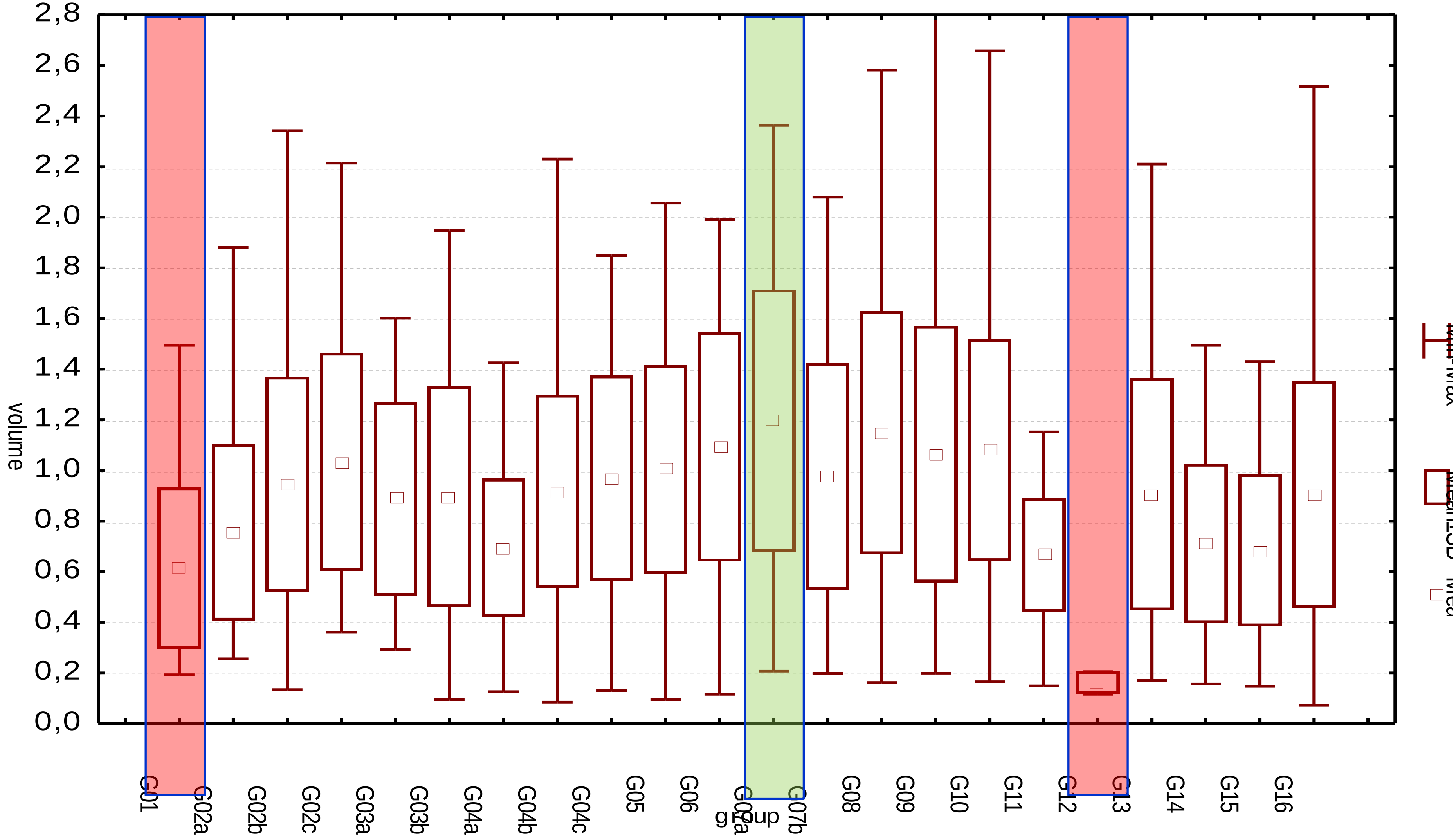
Analysis of variance and Duncan test for variable height
alpha = 0,05; mean = 26,56 m

Effect	N	SS	MS	F	p
Group	21	1697,934	80,854	10,027	0,000
Error	2107	16990,550	8,064		
Total	2128	18688,484			

Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Average volume of stem without bark
in the IUFRO 1944 European larch provenance experiment on the Podbanské



Last Evaluation of the Provenace Plot Podbanské, Slovakia (IUFRO I. Larch Series 1944)

Sękocin Stary / Warsaw, Poland, June 22.-24., 2010

Group	Mean	A	B	C	D	E	F	G	H	I
G07a	1,196	■								
G08	1,149	■	■							
G06	1,093	■	■	■						
G10	1,080	■	■	■						
G09	1,065	■	■	■						
G02c	1,034	■	■	■						
G05	1,004	■	■	■	■					
G07b	0,976	■	■	■	■					
G04c	0,969	■	■	■	■					
G02b	0,946		■	■	■	■				
G04b	0,917		■	■	■	■	■			
G13	0,907		■	■	■	■	■	■		
G16	0,905		■	■	■	■	■	■		
G03b	0,897		■	■	■	■	■	■		
G03a	0,887			■	■	■	■	■		
G02a	0,755				■	■	■	■	■	
G14	0,711					■	■	■	■	
G04a	0,695						■	■	■	
G15	0,684						■	■	■	
G11	0,666							■	■	
G01	0,615								■	
G12	0,162									■

Analysis of variance and Duncan test for variable volume
alpha = 0,05; mean = 0,906 m^3

Effect	N	SS	MS	F	p
Group	21	37,736	1,797	10,501	0,000
Error	2107	360,550	0,171		
Total	2128	398,286			


Summary:

- the height and diameter of all trees on the plot was measured
- differences in **number of survived trees** per provenance
  - high survival of the **Larix kaempferi** and **L. x eurolepis**
  - extremelly low of the **L. sibirica**)
- local standard provenance Kravany from Low Tatra – average value
- good growth (height, diameter):
  - **sudetan provenances** (including Czech allochthone populations)
  - allochthone provenances from the **North Poland** (low altitudes!)
  - **carpathian provenances** from the Low Tatra region
- not suitable provenances:
  - **Larix sibirica**
  - **Central (Western Alps), high Alpine altitudes**


Thank you for your attention

Eurasian provenance experiment of Scots Pine - trial at Sambor in Ukraine

Roman Gout,
Ukrainian National Forestry University, (UNFU), Ukraine
Jan Kowalczyk
Forest Research Institute, (IBL), Poland

Aims:

- Describe current status of the trial
- Presenting the latest results
- Comparing results with local Lvov population performance
- Looking for the growth and survival patterns

Description of the series

- In the years 1973 to 1976 Rusian Scots Pine was established with 113 provenances and 33 planting sites
- One of them is trial in Sambor near Lviv (East Roztocze region)
- Result of the series was published by Shutayev and Giertych
- In summarizing they using published results from Sambor trial after 11 years of growth
- Now we presenting data after 33 years from planting

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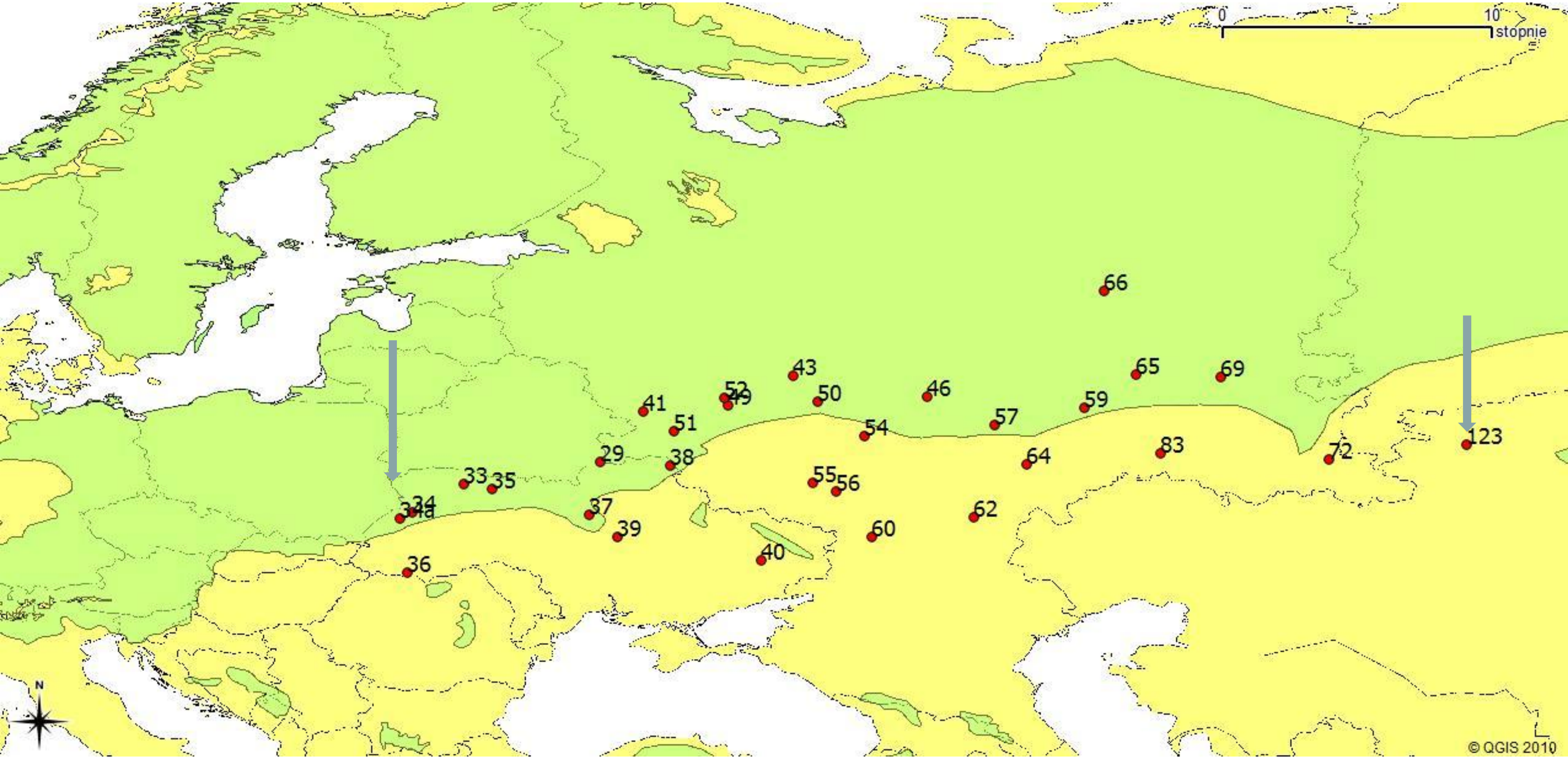
Studied populations

No	P. No	Prowenance	Name	Latitude N	Longitude E	No	P. No	Prowenance	Name	Latitude N	Longitude E
1	29	Гомельська	Gomyel	52^0 14’	31^0 40’	18	55	Воронежська	Voronyezh 1	51^0 38’	39^0 28’
2	33	Рівненська	Rovno	51^0 32’	26^0 36’	19	56	Воронежська	Voronyezh 2	$51^0$08’	$40^0$15’
3	34	Львівська (Лопатин)	Lopatyn	50^0 30’	24^0 45’	20	57	Пензенська	Pyenza	53^0 50’	46^0 00’
4	35	Житомирська	Zhitomir	51^0 14’	27^0 40’	21	59	Улянівська	Ulyanovsk	54^0 14’	49^0 35’
5	36	Ів. Франківська	Iv. Frankowsk	48^0 07’	24^0 03’	22	60	Ростовська	Rostov	49^0 36’	41^0 48’
6	37	Київська	Kiyev	50^0 21’	31^0 00’	23	62	Волгоградська	Volgograd	50^0 10’	45^0 24’
7	38	Сумська	Sumy	52^0 01’	34^0 00’	24	64	Саратовська	Saratov	52^0 05’	47^0 21’
8	39	Черкаська	Chyerkassy	49^0 37’	32^0 05’	25	65	Татарська	Tatarstan	55^0 40’	51^0 26’
9	40	Донецька	Donyetsk	48^0 50’	37^0 36’	26	66	Кіровська	Kirov	58^0 49’	50^0 06’
10	41	Смоленська	Smoliensk	54^0 00’	33^0 00’	27	69	Башкирська	Bashkortosta	55^0 30’	54^0 40’
11	43	Московська	Moskva	55^0 32’	38^0 57’	28	72	Башкирська	Bashkortosta	52^0 24’	58^0 40’
12	46	Горківська	Nizhyegorod	54^0 56’	43^0 50’	29	83	Оренбургська	Oryenburg	52^0 47’	52^0 15’
13	49	Калузька	Kaluga	54^0 25’	36^0 16’	30	86	Новосибірська	Novosibirsk	53^0 50’	82^0 20’
14	50	Рязанська	Ryazan	54^0 40’	39^0 45’	31	91	Алтайська	Altaiski Kral	51^0 32’	81^0 10’
15	51	Брянська	Bryansk	53^0 30’	34^0 15’	32	123	Кустанайська	Kustanal	52^0 80’	63^0 50’
16	52	Орловська	Oryel	54^0 50’	36^0 00’	33	125	Семипалатинсь	Syemipalatin	50^0 40’	80^0 38’
17	54	Тамбовська	Tambov	53^0 12’	41^0 20’	34	34a	Львівська	Lvov	50^0 05’	24^0 00’

Range 10° 42’ N **58° 20’E**

Studied populations

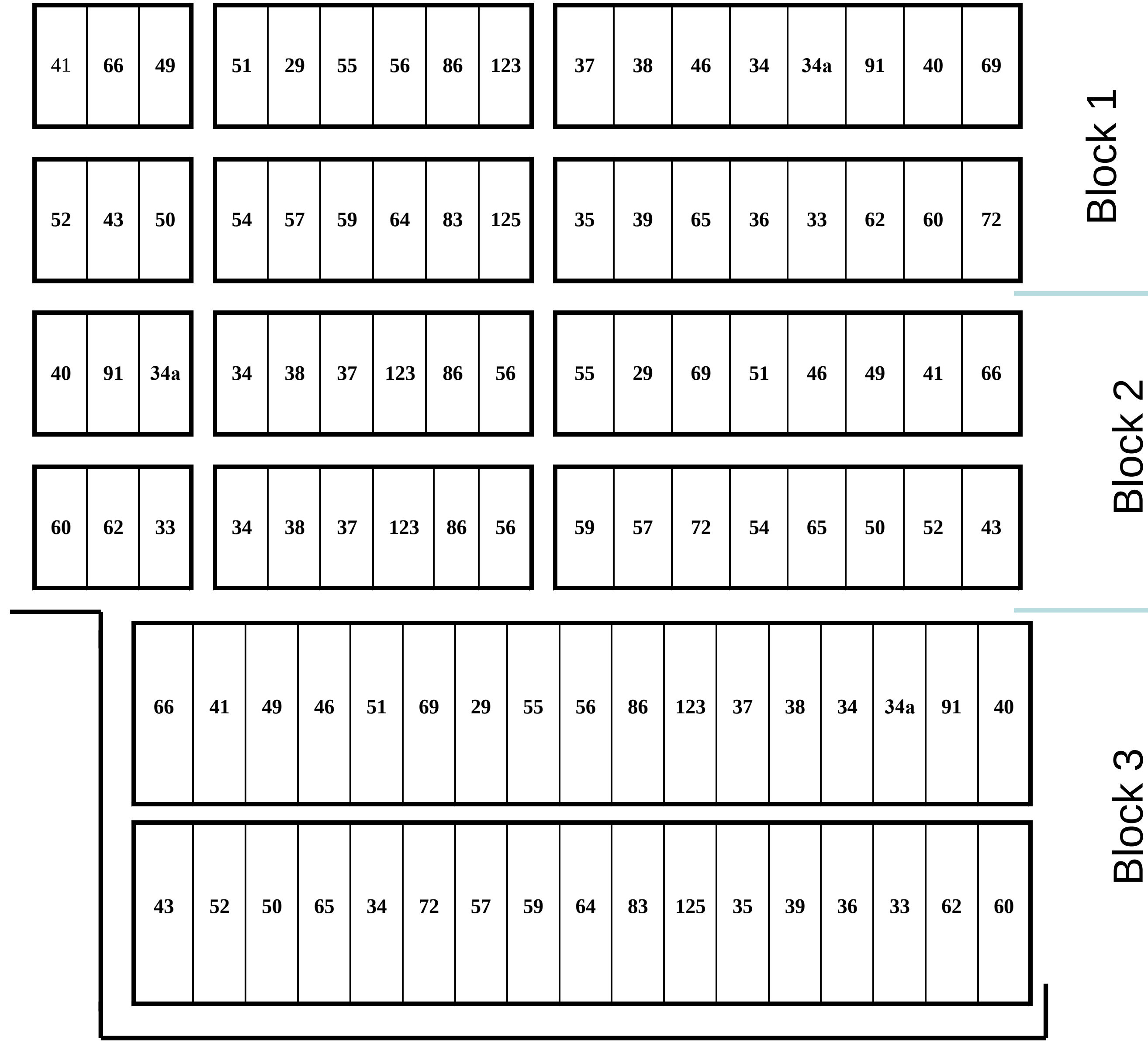


58.20 °

Experimental site description

Year of planting:1975
Spacing: 2.0 x 0.75 m
Area: 13,25 ha
Area per provenance: 0.2 , 0.3 or 0.45 ha
No of block: 3

Trial scheme



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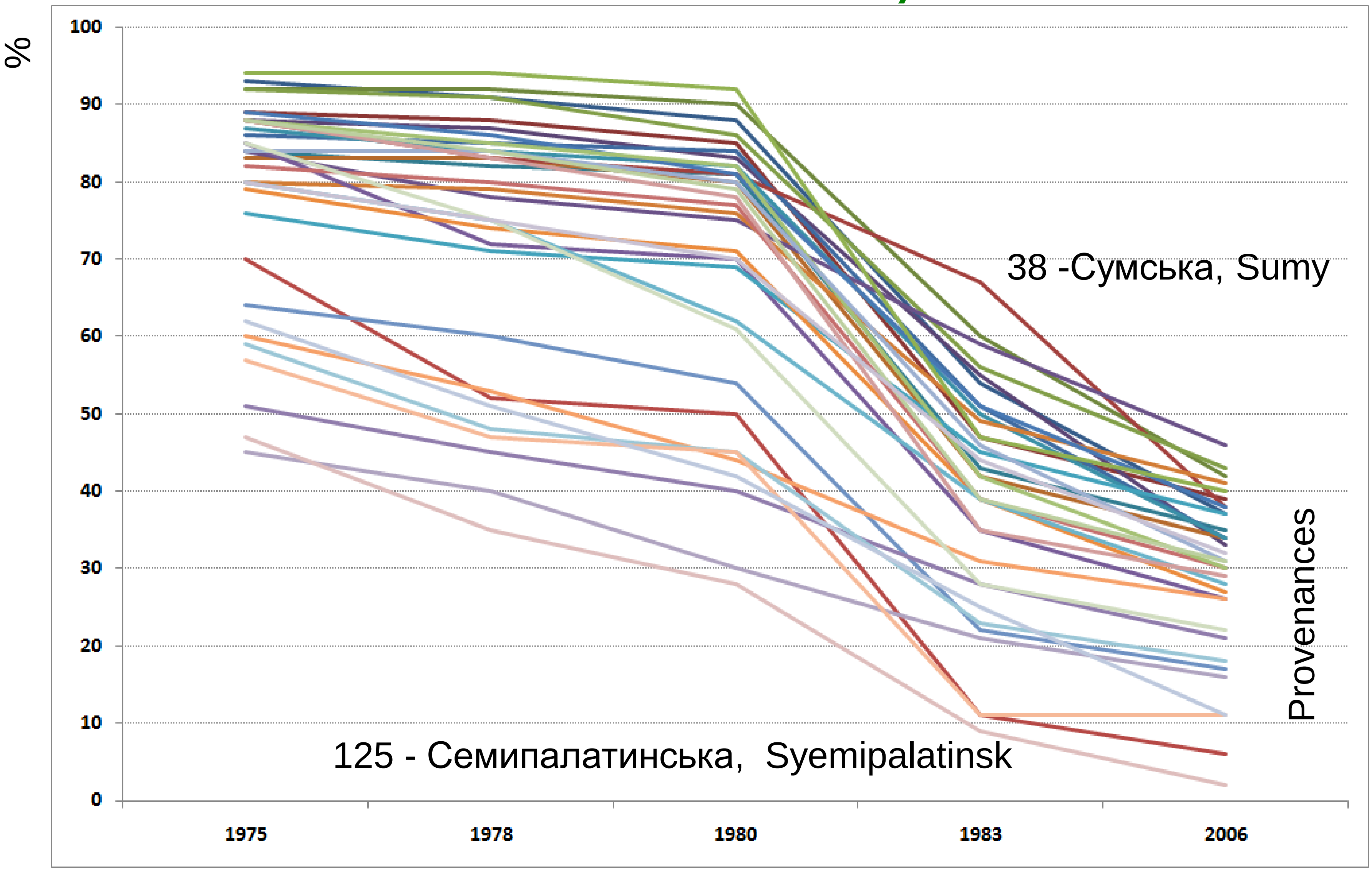
Treebreedex

Methods

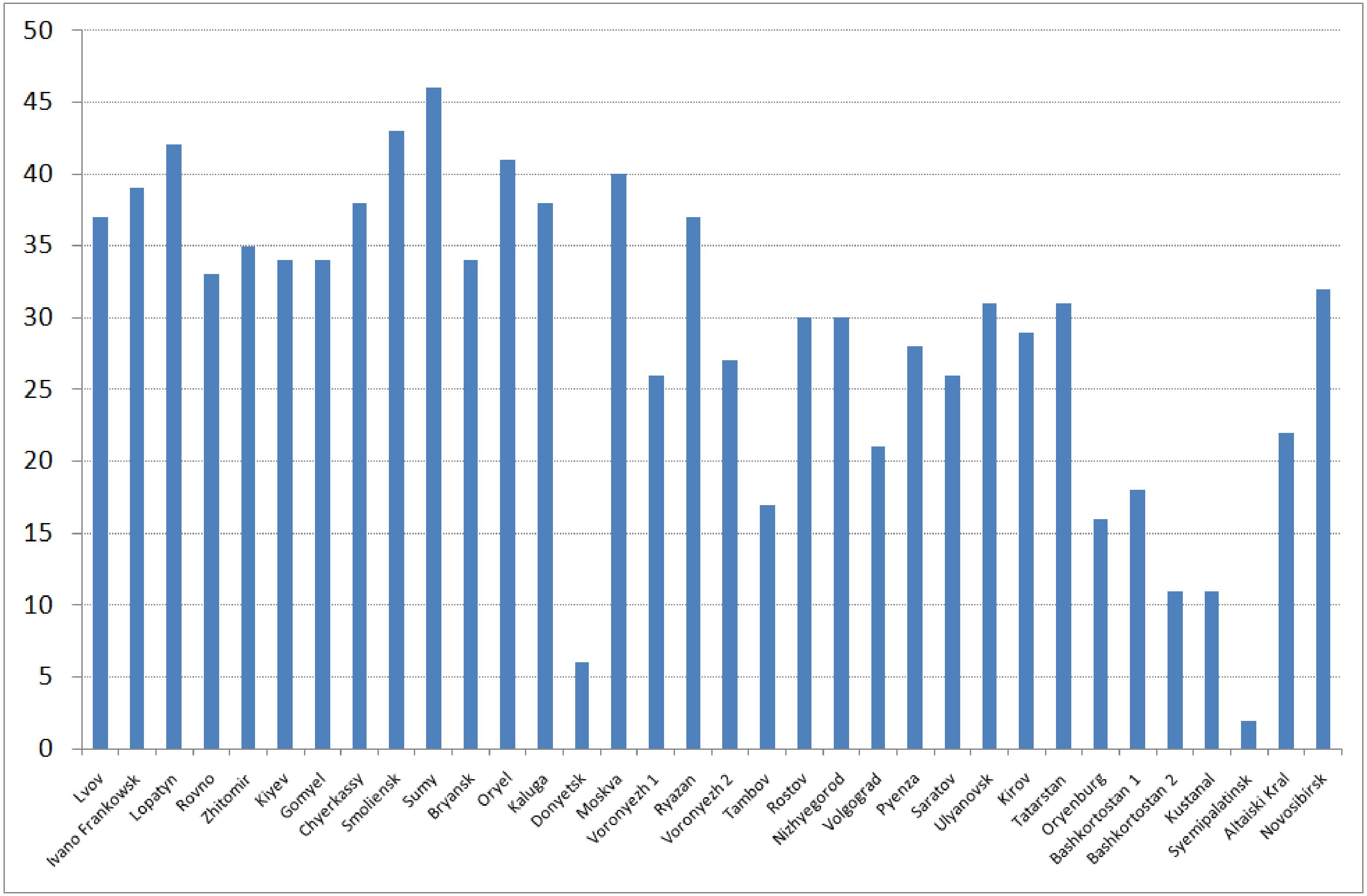
– Survival was calculated
– DBH and Height – measured
– Result are presented also on the map in standard deviation units

Survival after 33 years.



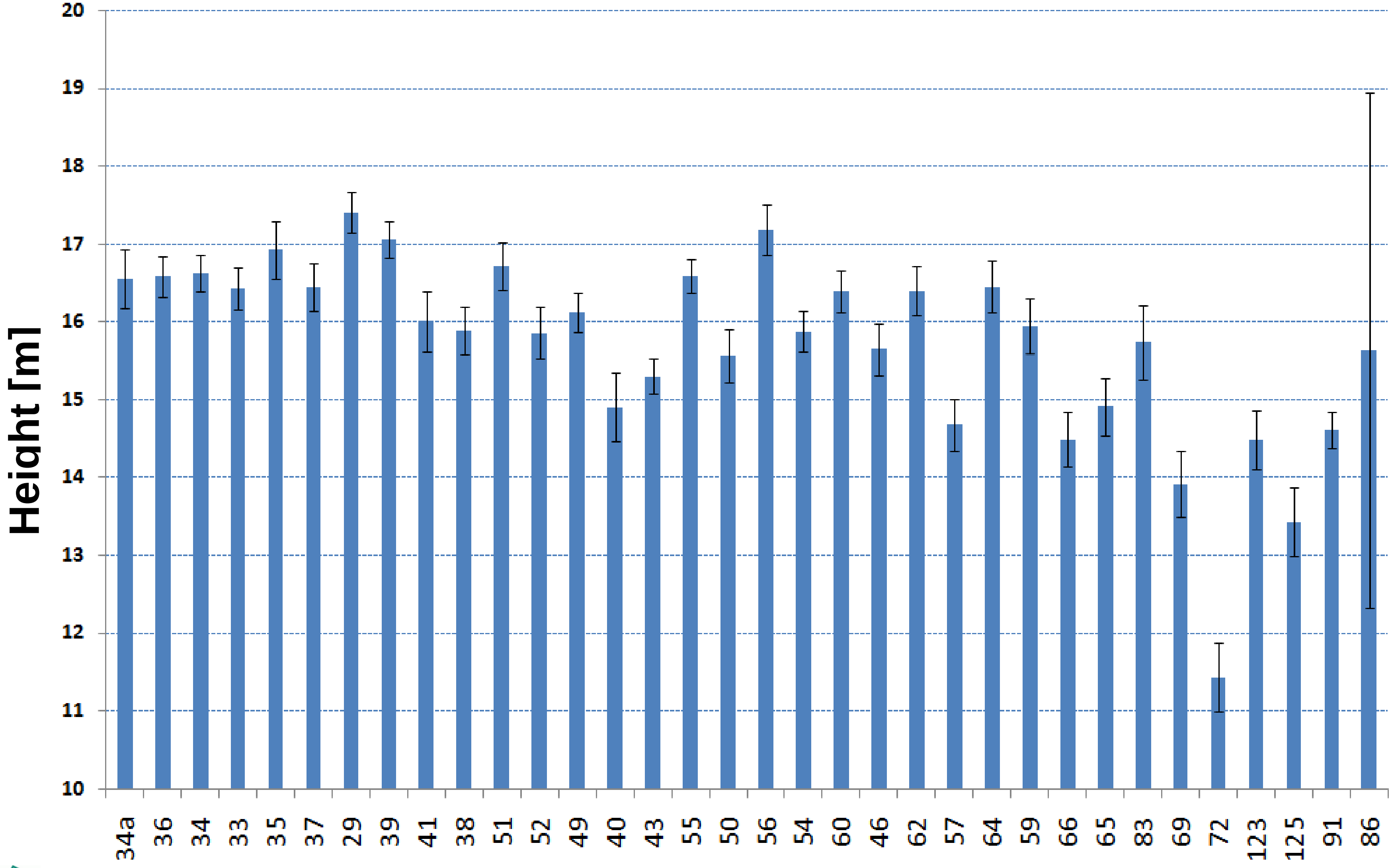
Treebreedex

Survival



50
45
40
35
30
25
20
15
10
5
0
Lvov
Ivano Frankowsk
Lopatyn
Rovno
Zhitomir
Kiyev
Gomyel
Chyerkassy
Smoliensk
Sumy
Bryansk
Oryel
Kaluga
Donyetsk
Moskva
Voronyezh 1
Ryazan
Voronyezh 2
Tambov
Rostov
Nizhyegorod
Volgograd
Pyenza
Saratov
Ulyanovsk
Kirov
Tatarstan
Oryenburg
Bashkortostan 1
Bashkortostan 2
Kustanai
Syemipalatinsk
Altaiski Kral
Novosibirsk

Growth after 33 years.



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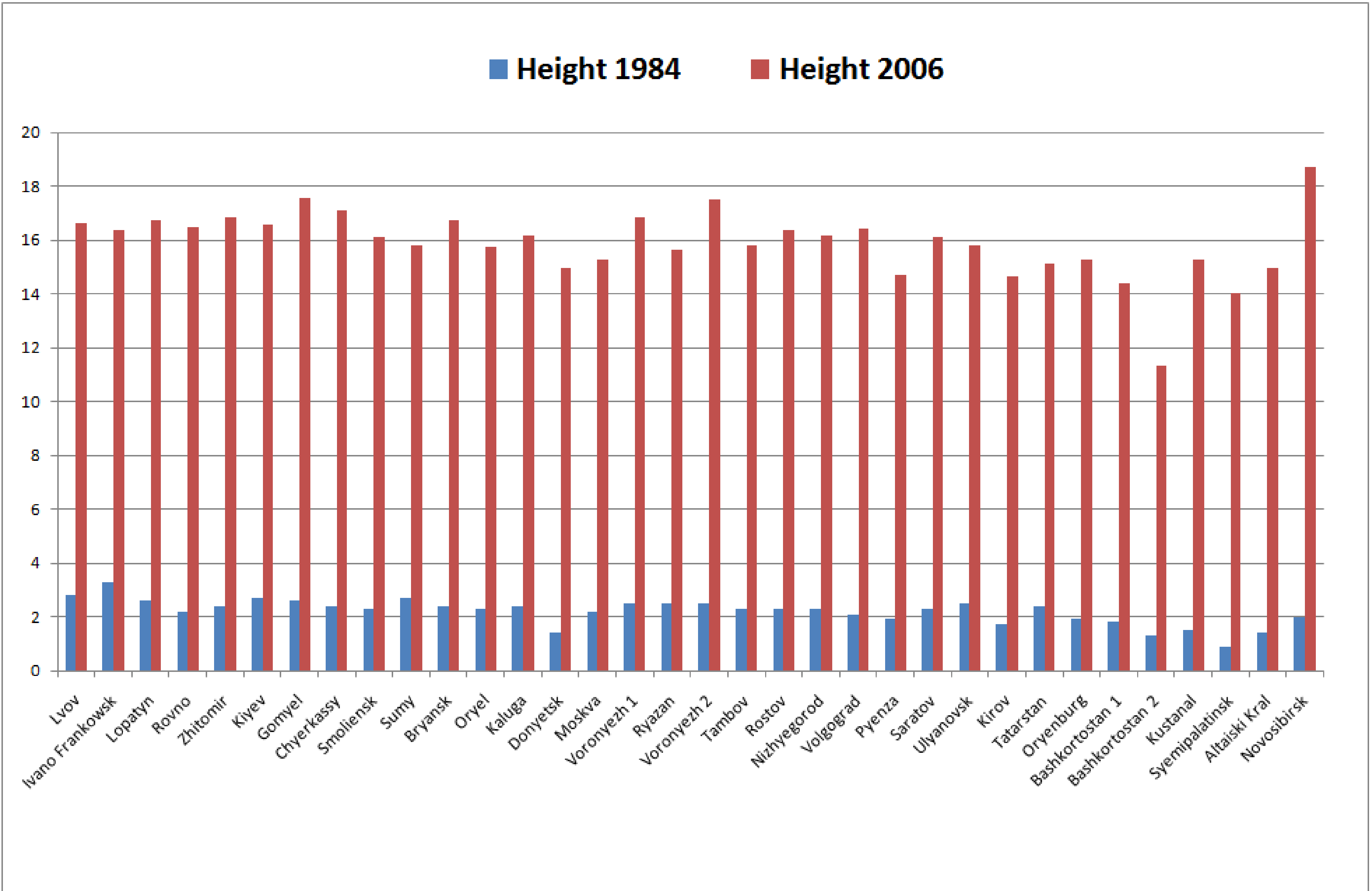
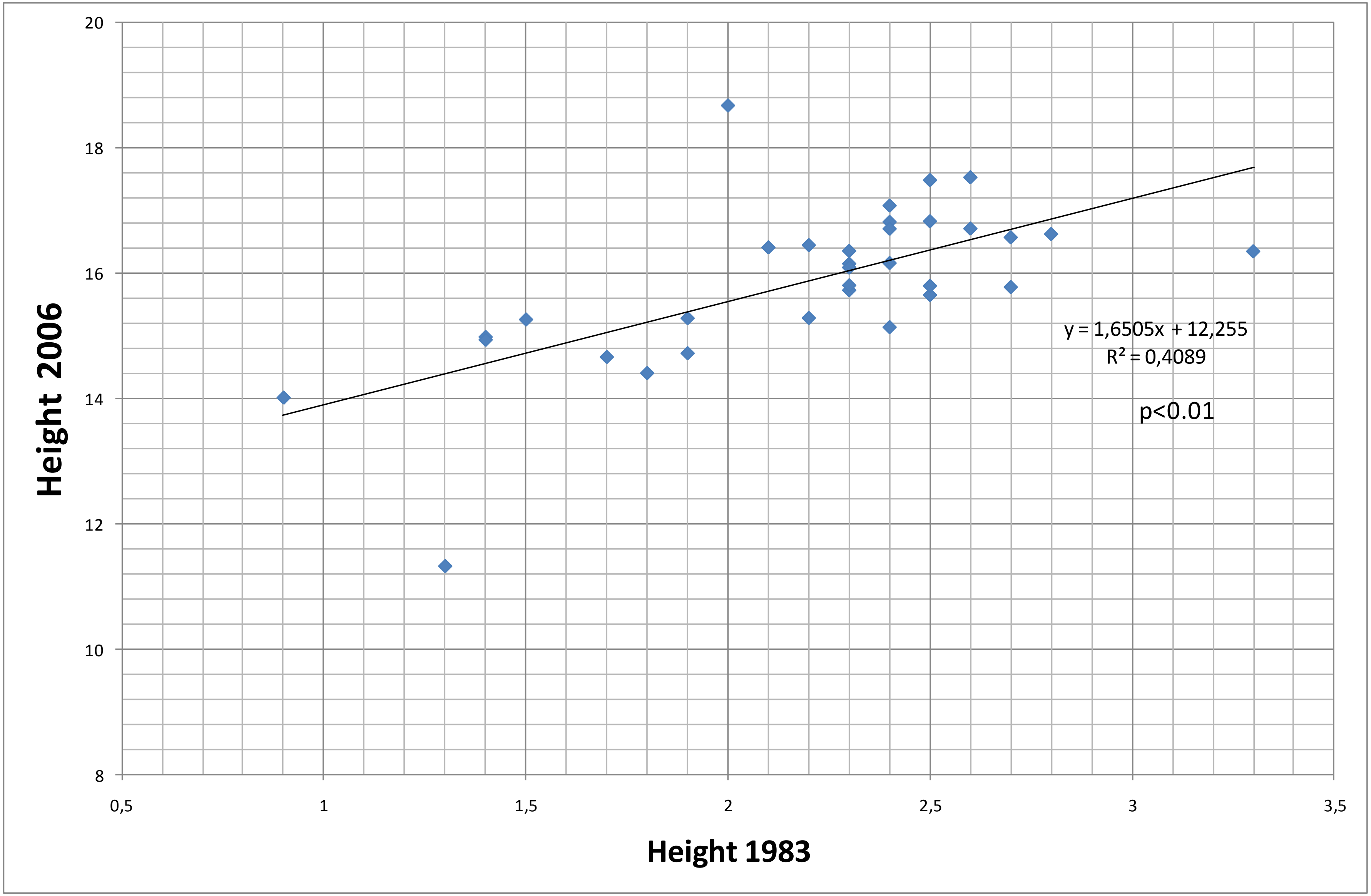
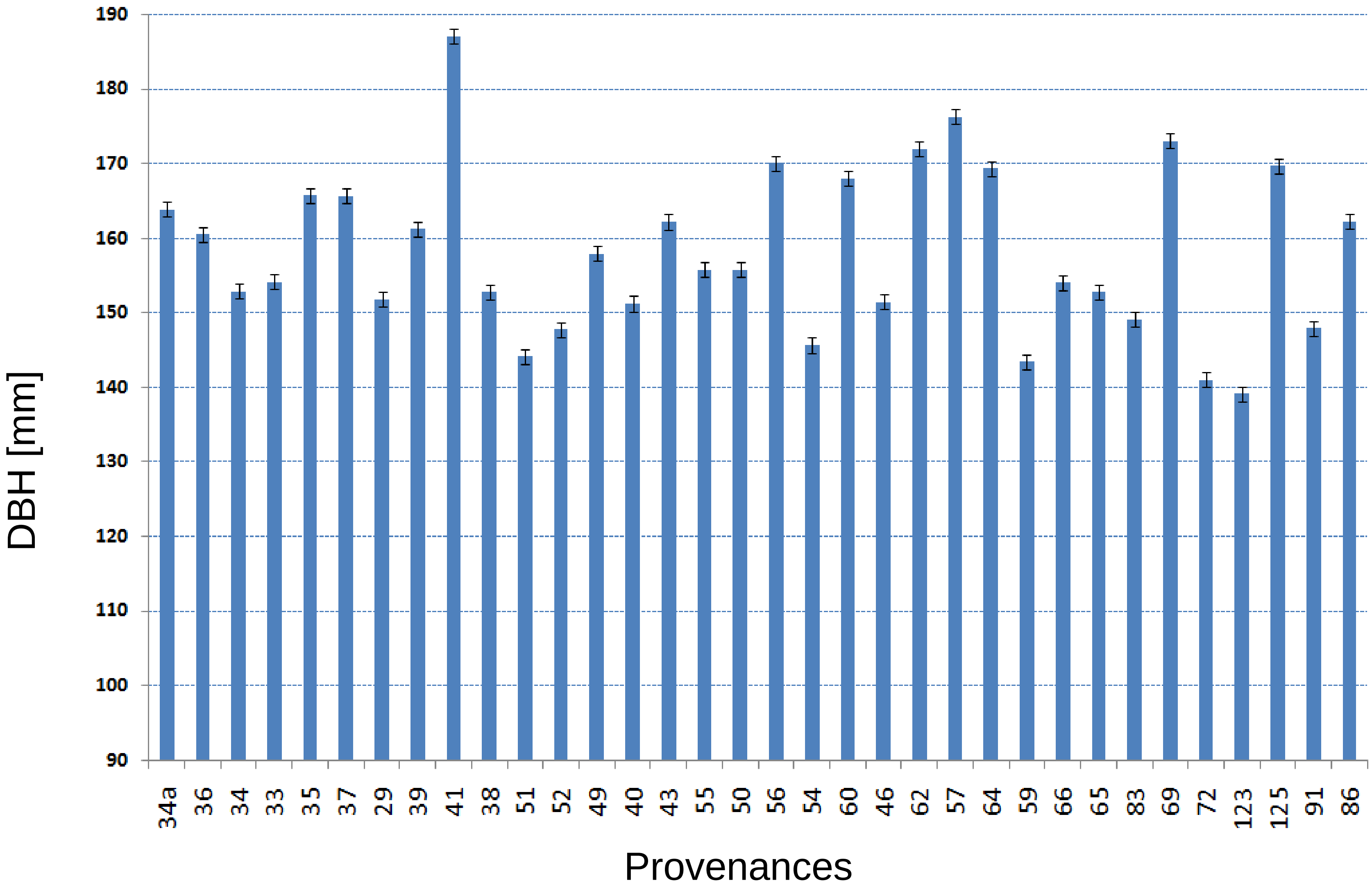


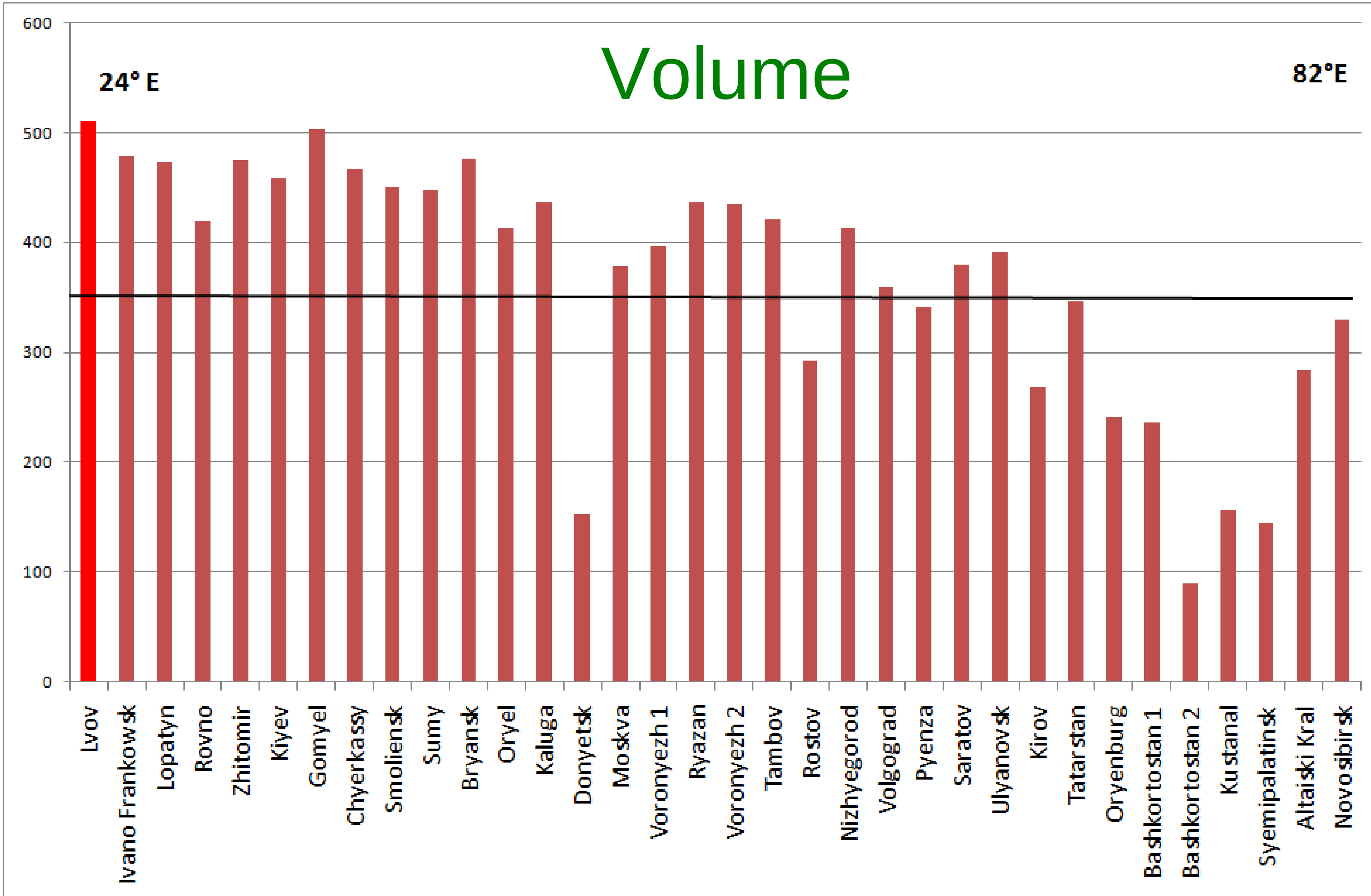
Height 1984
Height 2006
20
18
16
14
12
10
8
6
4
2
0
Lvov
Ivano Frankowsk
Lopatyn
Rovno
Zhitomir
Kiyev
Gomyel
Chyerkassy
Smoliensk
Sumy
Bryansk
Oryel
Kaluga
Donyetsk
Moskva
Voronyezh 1
Ryazan
Voronyezh 2
Tambov
Rostov
Nizhyegorod
Volgograd
Pyenza
Saratov
Ulyanovsk
Kirov
Tatarstan
Oryenburg
Bashkortostan 1
Bashkortostan 2
Kustanal
Syemipalatinsk
Altaiski Kral
Novosibirsk



20
18
16
14
12
10
8
Height 2006
0,5
1
1,5
2
2,5
3
3,5
Height 1983
y = 1,6505x + 12,255
R² = 0,4089
p<0.01

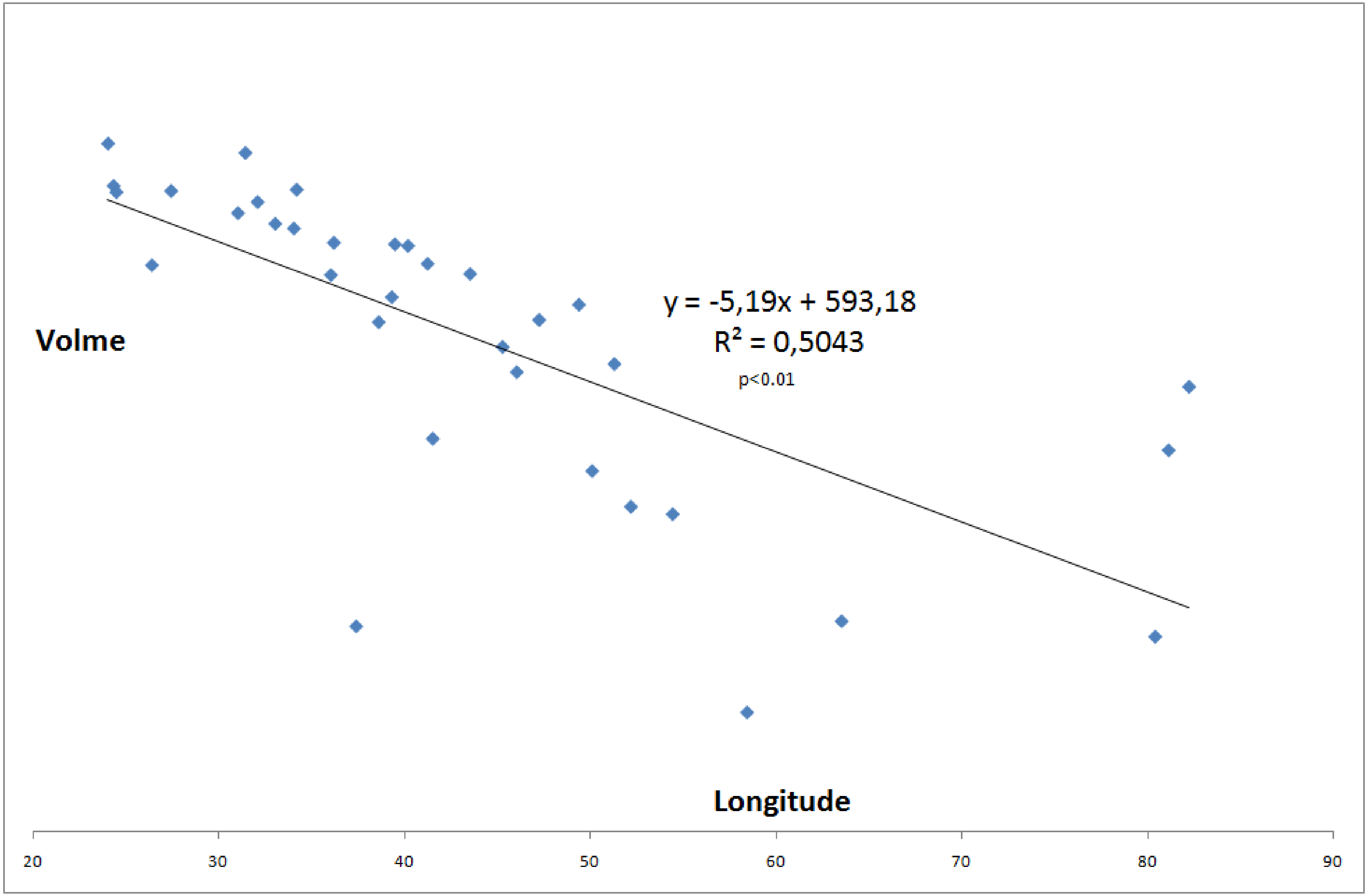
Growth after 33 years.





IBL

Treebreedex



y = -5,19x + 593,18
R² = 0,5043
p<0.01
Volme
Longitude
20
30
40
50
60
70
80
90

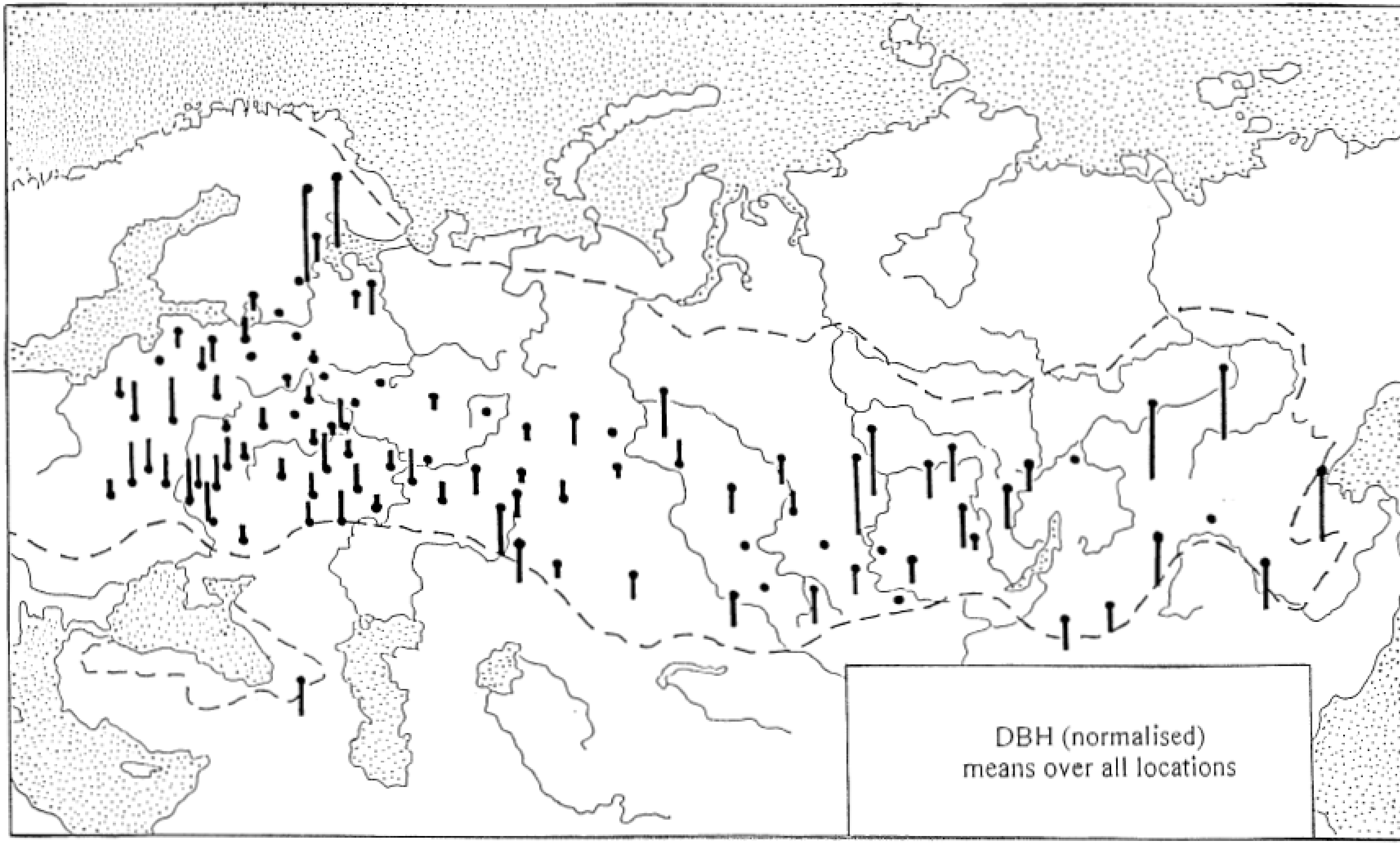


Fig. 2. – Diameter at breast height (DBH) of different provenances of Scots pine expressed in units of standard deviation from the location mean and averaged over all locations from which data for a provenance is available (at least 3). The radius of a dot corresponds to ± 0.15 standard deviations.

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Genetic Subdivisions of the Range of Scots Pine (*Pinus sylvestris* L.) Based on a Transcontinental Provenance Experiment

By A. M. SHUTYAEV[1]) and M. GIERTYCH[2])[3])

(Received 16th February 2000)

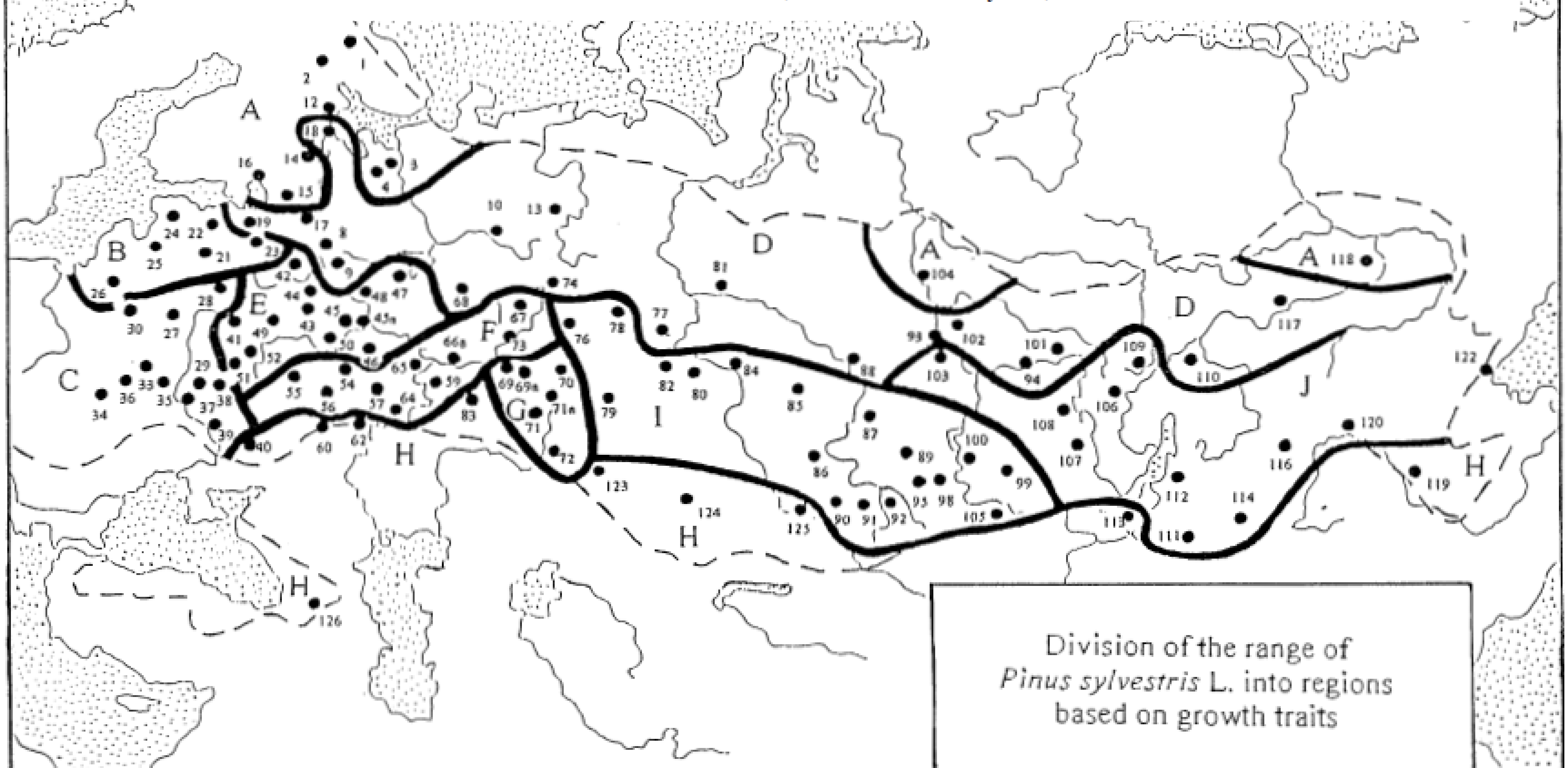


Fig. 7. – Proposed division of the range of Scots pine in the former USSR on the basis of growth traits as observed on 113 sample populations tested at 33 locations.

Heritability

DBH | | **Volume**

$variances:	$variances:	$variances:
Prov Residuals	Prov Residuals	Prov Residuals
116.9974 2089.656	116.9974 2089.656	0.0008270825 0.01146277
$sd.variances:	$sd.variances:	$sd.variances:
Prov Residuals	Prov Residuals	Prov Residuals
0 9602.431	0 9602.431	1.059522e-012 6.498451e-011
$BS.heritability:	$Genotypic.heritability:	$Genotypic.heritability:
BS.herit sd.herit	Genotypic.herit sd.herit	Genotypic.herit sd.herit
0.2120811 0.922888	**0.7132209** 0.004474393	**0.9780172** 0.2008099

Treebreedex

Discusion

- Missing data about quality traits
- In Ukraine parallel plots exist from this series, to make some common conclusion common evaluation is needed
- The correction of the data is needed in some cases because of different spacing caused by mortality

Summary

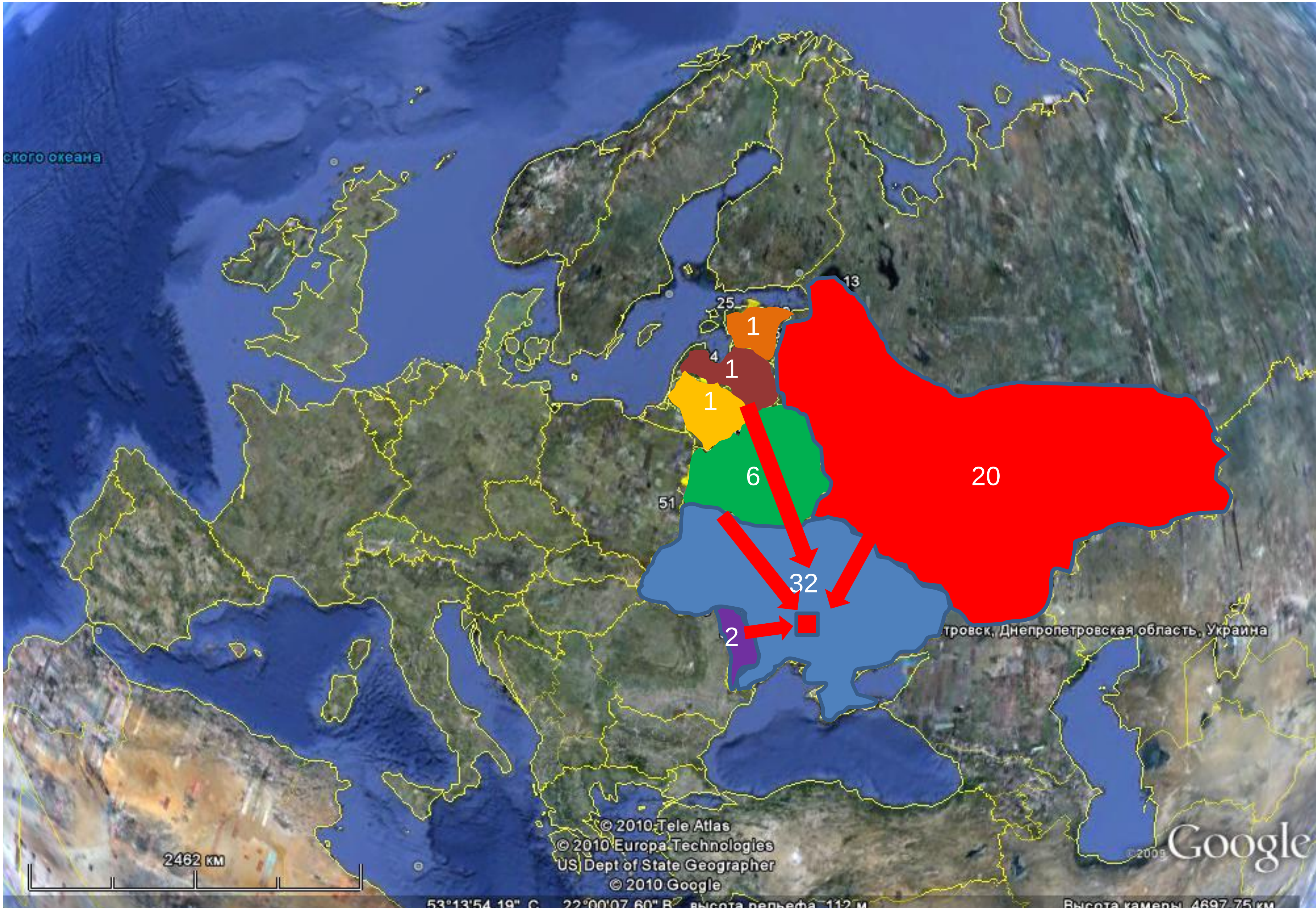
- Longitude - strong influence on growth
- Local provenance is the best in terms of growth
- Based on the results from the series transfer from East to West is not recommended

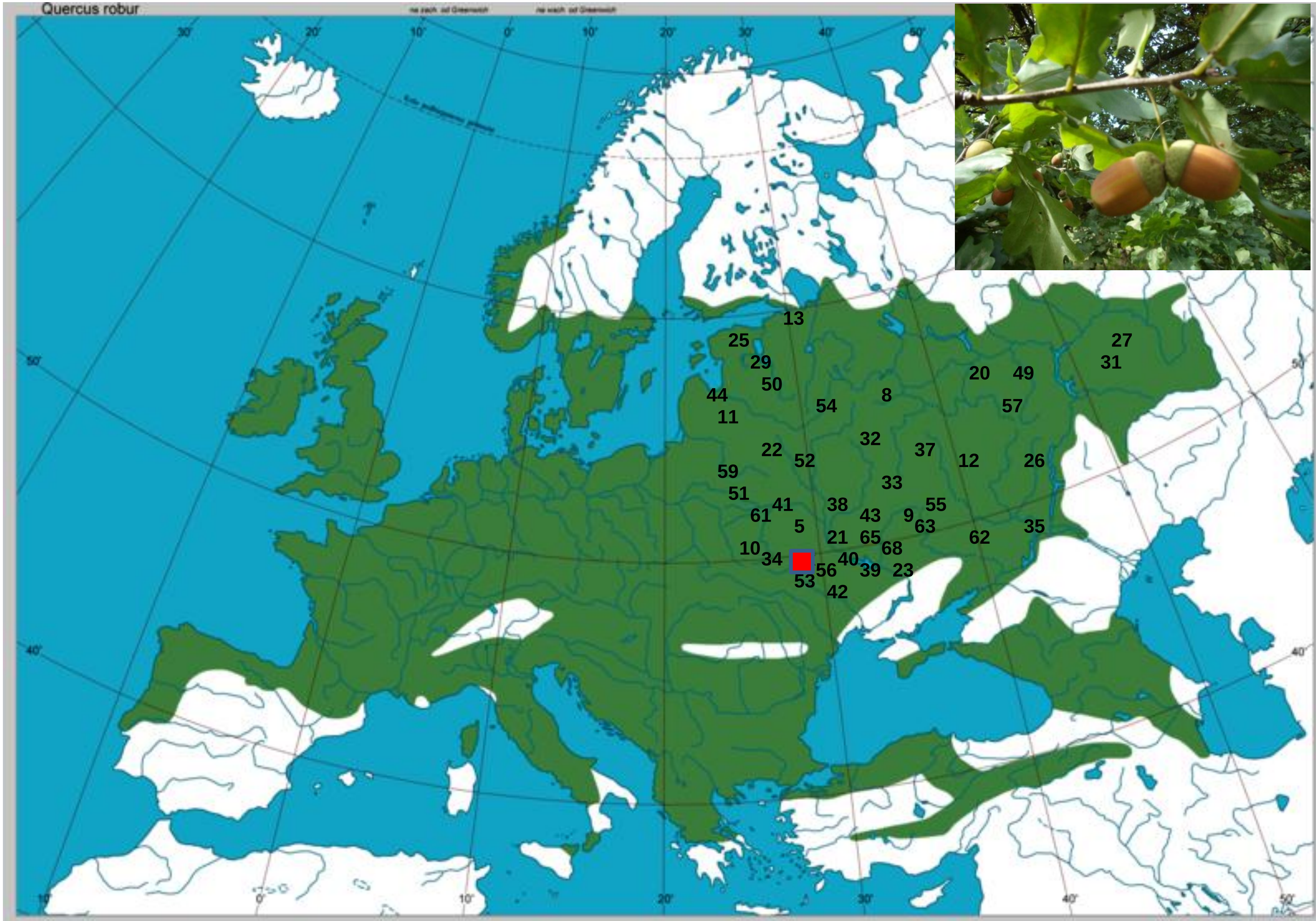
Thank you for your attention

Adaptability of oak (Quercus robur L.) ecotypes in condition of climate change

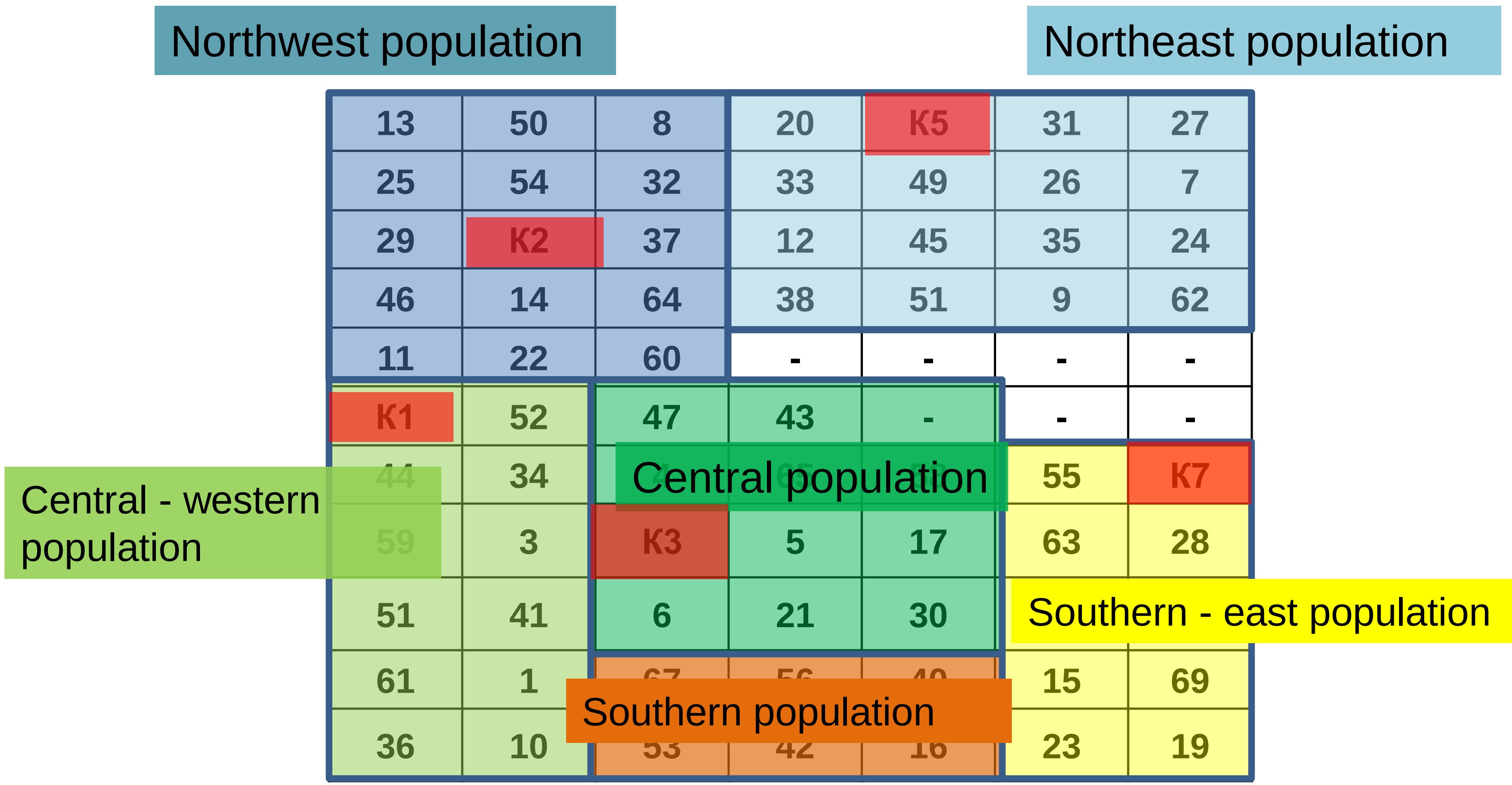
Ihor Neyko

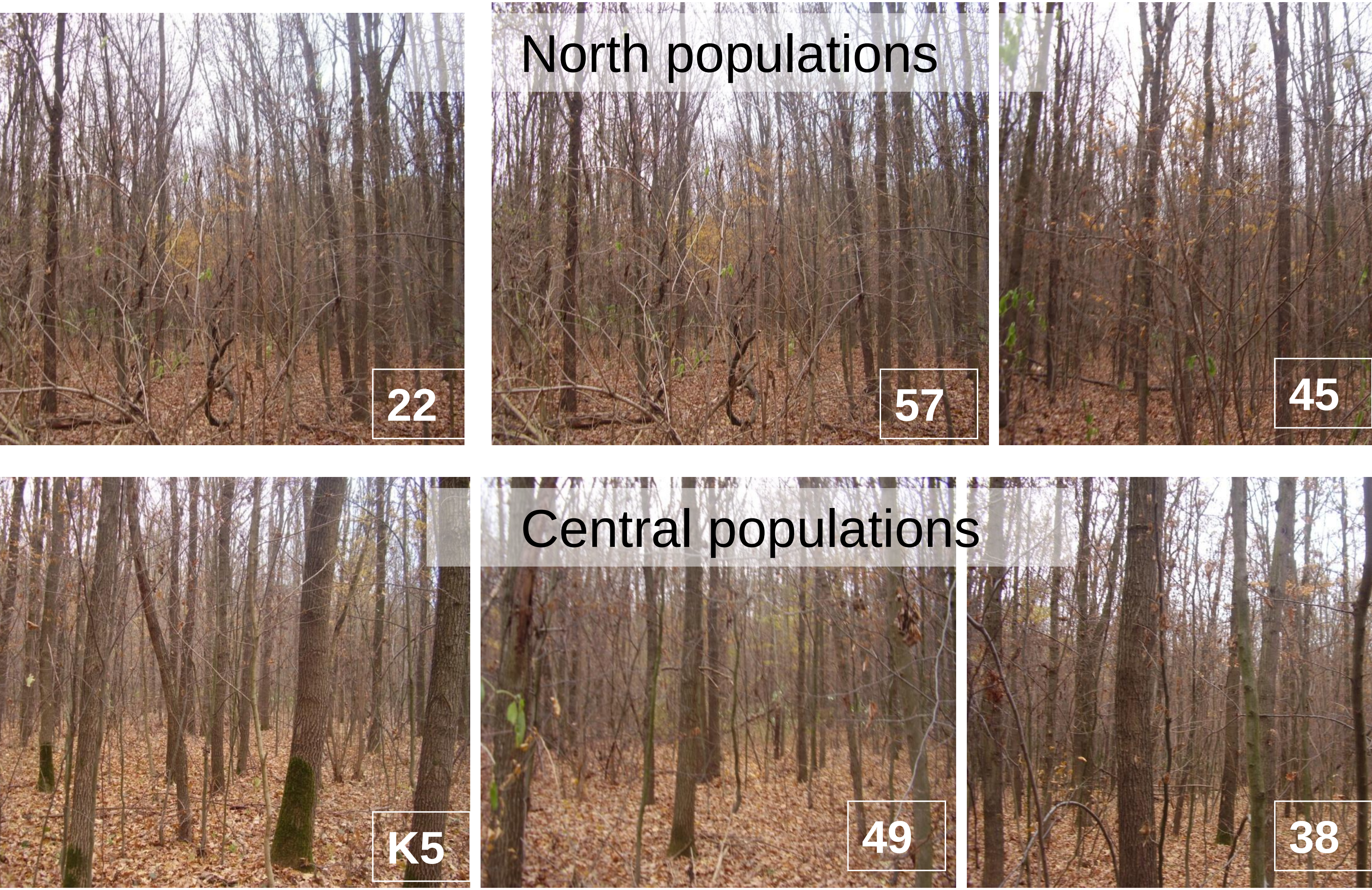
Vinnitsya National Agrarian University, Vinnitsya, Ukraine


ского океана
13
25
1
1
1
4
6
20
51
32
2
тровск, Днепропетровская область, Украина
© 2010 Tele Atlas
© 2010 Europa Technologies
US Dept of State Geographer
© 2010 Google
2462 км
53°13'54.19" С 22°00'07.60" В высота рельефа 112 м
Высота камеры 4697.75 км
Google

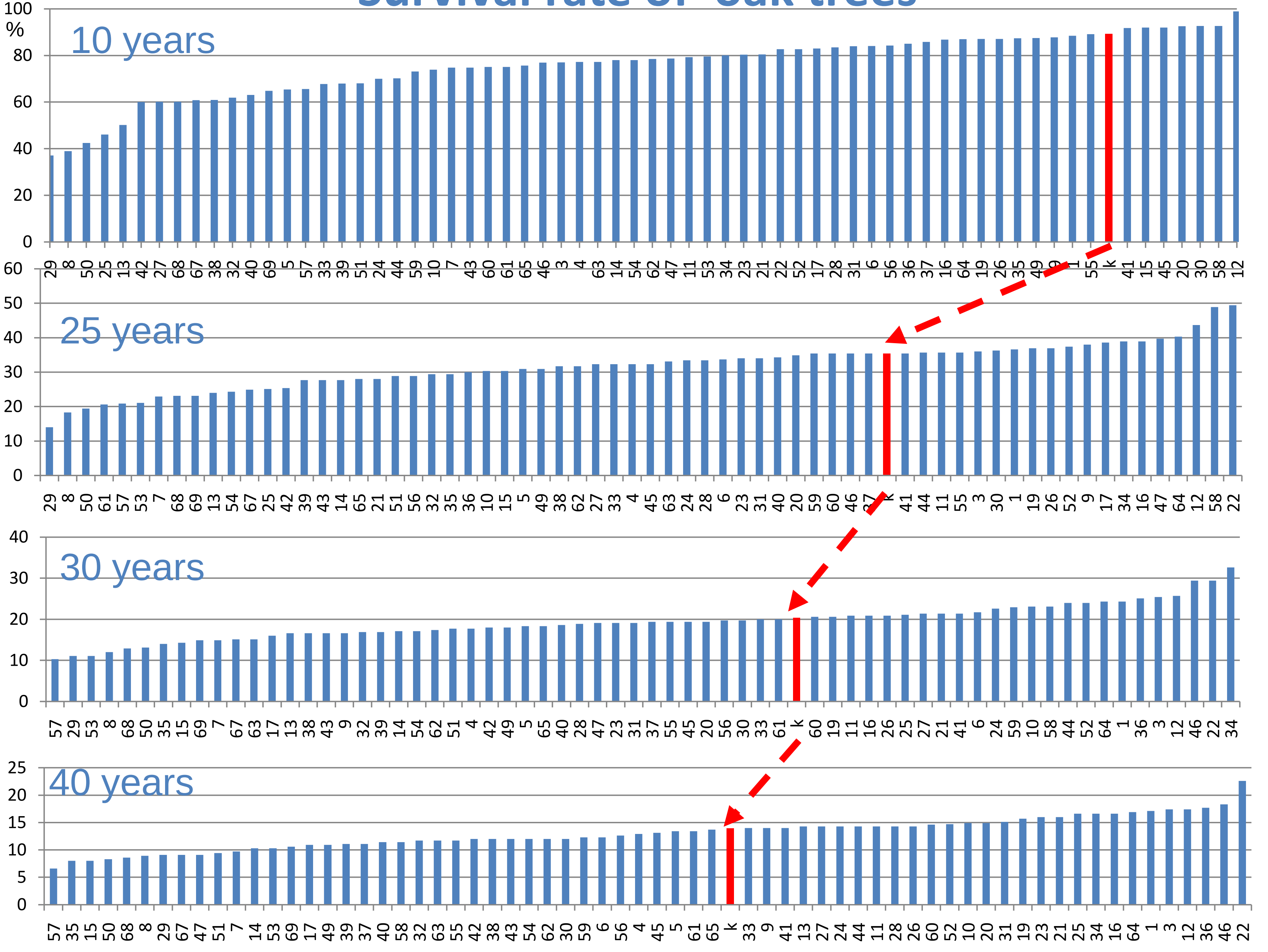

Quercus robur
13
25
27
29
31
20 49
50
44
8
54
57
11
32
22
37
52
12
26
59
33
51
41
38
55
61
43
9
5
63
35
21
65
62
10
68
34
40
56
39
23
53
42

Scheme of Quercus robur provenance tests (Vinnitsya, Ukraine)

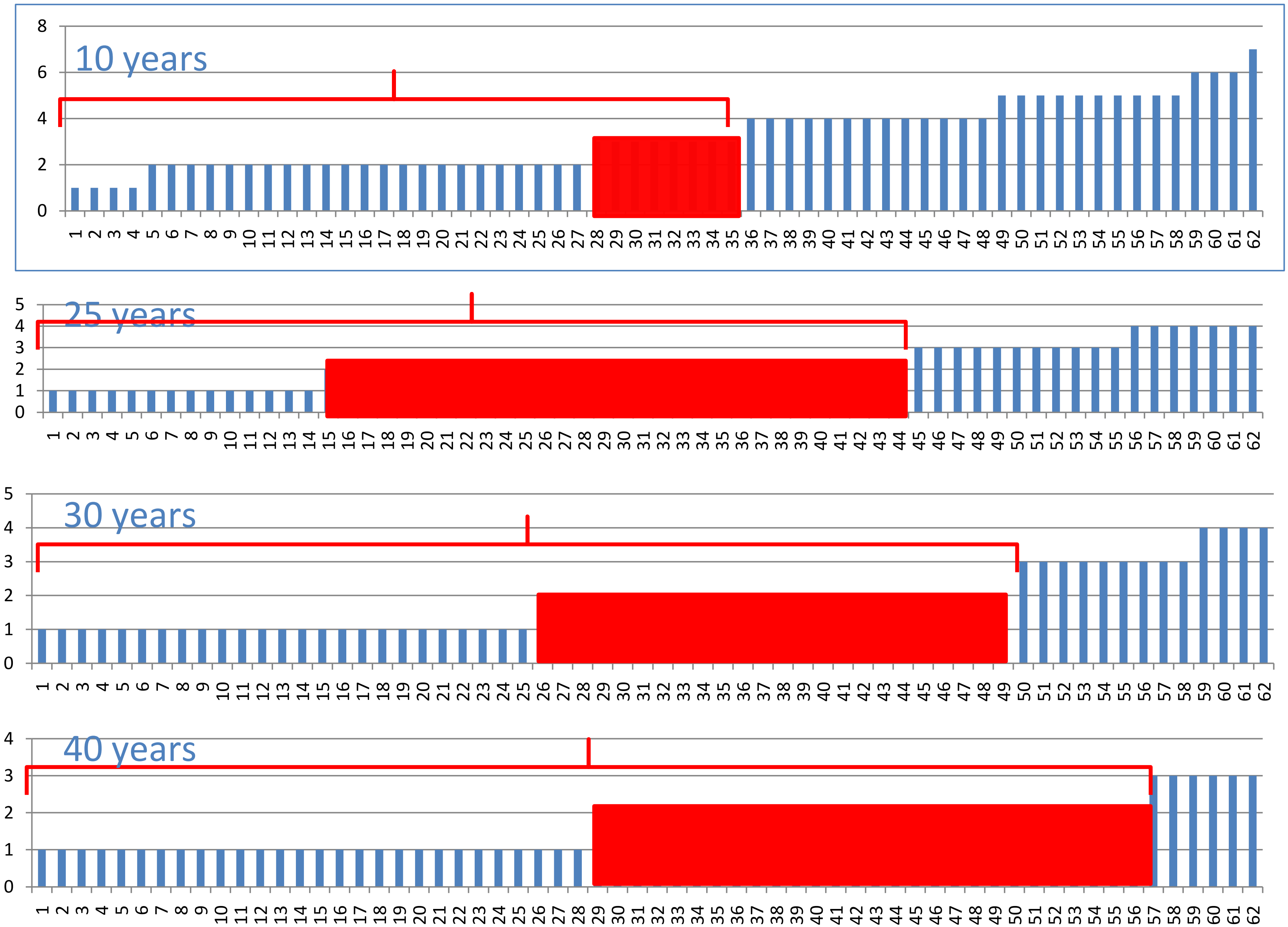



North populations
22
57
45
Central populations
K5
49
38

Survival rate of oak trees



Changes of heights ranks



The data analysis of 1964-2010 specifies essential ecological and geographical influence of seeds origin, phenological forms on the growth and productivity of climatic ecotypes as well as on selection and quality indicators.

The worst seed germination intensity was characteristic for the most remote northern and north-east ecotypes: Moscow, Volgograd, St.-Petersburg, Chuvash, Estonian, Bashkir, Latvian, and Pskov. But it is necessary to note that some remote ecotypes had tendencies for the improvement of adaptability and decrease of tree dying intensity (some populations from Estonian, Bryansk, Brest, Latvian and Minsk ecotypes).

CONCLUSION:

✓ Progeny of the ecotypes of the most remote northern, northeast and east regions (Moscow, Tambov, St.-Petersburg, Bashkiria, Estonian, Chuvashia ecotypes) are marked by the slowest growth in height and diameter.

✓ Analysis of the results on the growth dynamics of oak ecotypes testifies that the greatest differentiation in height was marked at the initial stages of growth.

✓ Up to 10-year age the difference of growth intensity in height was more than 60 %. At the age of 25 - 40 there was a tendency towards activization of growth intensity of the northern and north-east ecotypes (Estonian, Tula, Tatarstan ecotypes).

✓ Intensity increase of the growth processes specifies the increase of adaptability of the remote ecotypes. Acclimatization of the remote geographical oak ecotypes makes up about 20-30 years.

Thank you!

PLANTACOMP

Genetic experimental network of the French National Institute for Agricultural Research

Christel ANGER
INRA Orléans (FRANCE)

Activity 5 seminar

« What do large genetic field experimental networks across Europe bring to the scientific community? »
June 22–24, 2010, Sękocin Stary (Poland)

Introduction to PlantaComp

Definition and history

- « Comparative trials » : genetic experiments which are implanted in diverse ecological conditions and make it possible to compare several genetic units
- First trials of the French network installed 40 years ago by genetic breeders
- Initial aims :
  - To analyse expression of genetic variability
  - To study genetic parameters

❯ Selection of improved varieties

Introduction to PlantaComp

Experiments involved

- The network collates trials enabling comparisons between :
  - Species
  - Provenances
  - Progenies
  - Clones

Many species tested to differing degrees :
Larix, Quercus, Populus, Pseudotsuga, Picea, Pinus, Abies, Cedrus, …

~1000 trials
~2000 ha

Introduction to PlantaComp

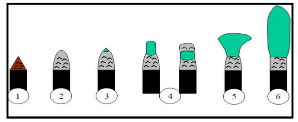
↳ Main strength

- Inter and intra specific diversity → natural variability representation
- Unique spatio-temporal dimension
  - Long-term follow-up
  - Identical genetic units installed in various environments or clines

  } Analysis of genotype * environment interactions

- Repeated and statistically rigourous experimentations
- Many traits studied by
  - Standardised observation
  - Sampling





Introduction to PlantaComp

Main difficulties

- Lack of organisation of network data between the different managing units
- Insufficient financing to assure a permanent follow-up of the whole network

  Ex : Only ten permanent people to manage trials

- Difficulties in qualifying correctly the ecology of experimental stations (in particular for soil characteristics)

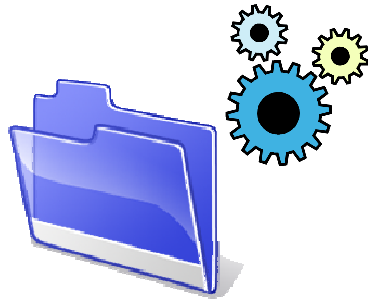
Objectives of PlantaComp's action

- 1 post created in October 2009
  - Missions : coordination, animation, valorisation of the network
  - Collaboration with all network teams
- Main objectives :
  - Improvement of the management of the network
  - Valorisation of these experimentas by new collaborations and new projects

Objectives of PlantaComp's action

Improvement

- Improvement of data management



  - Inventory of all the experiments and their status
  - Evaluation of data
  - Definition of standart data organization
  - Implementation of an information system collating all information on the network
  - Interoperability with other databases : opening-up to partners
  - Insertion of ecological databases and geographical referencing tools

Objectives of PlantaComp's action

Valorisation

PLANTACOMP NETWORK

Inter-specific diversity	Intra-specific diversity	Spatial iterations	Long-term follow-up

- Auto-ecology of species
- Conservation of genetic diversity
- Adaptation to environmental strains
- Long-term impact of climat
- Search for new forestry material
- Genetic improvment and selection of adapted material
- Other thematics : forestry pest invasion, interactions with biogeophysical cycles, etc.

Adaptation to environmental changes

In concertation with partners of several disciplines, on a national and international scale

Objectives of PlantaComp's action

Communication

- Emphasis on the necessity of communication
  - With scientists to highlight the potential of the network and encourage the setup of new projects;
  - With the whole forestry community to inform of the results of our studies.


Thank you for
your attention

6th framework programme
Research Infrastructures Action
Integrating activity

Treebreedex

Large forest tree provenance experimental networks: their advantages, limitations and importance for future experiments

Mirko Liesebach (vTI), Heino Wolf (SBS)

vTI

Sachsenforst
Wald braucht Zukunft

Table of contents

1. History of provenance research

- Since middle age deforestation, exploitation and devastation of forests in Central Europe
- Development of sustainable forestry and reforestation
- Large scale seed transfer with no consideration of the origin of seed esp. Norway spruce, Scots pine

➔ Decrease of yield, poor quality, high susceptibility to pest and diseases

➔ Ban on different species

➔ Consideration of local seed sources

➔ Increasing interest in provenance research

History of provenance research

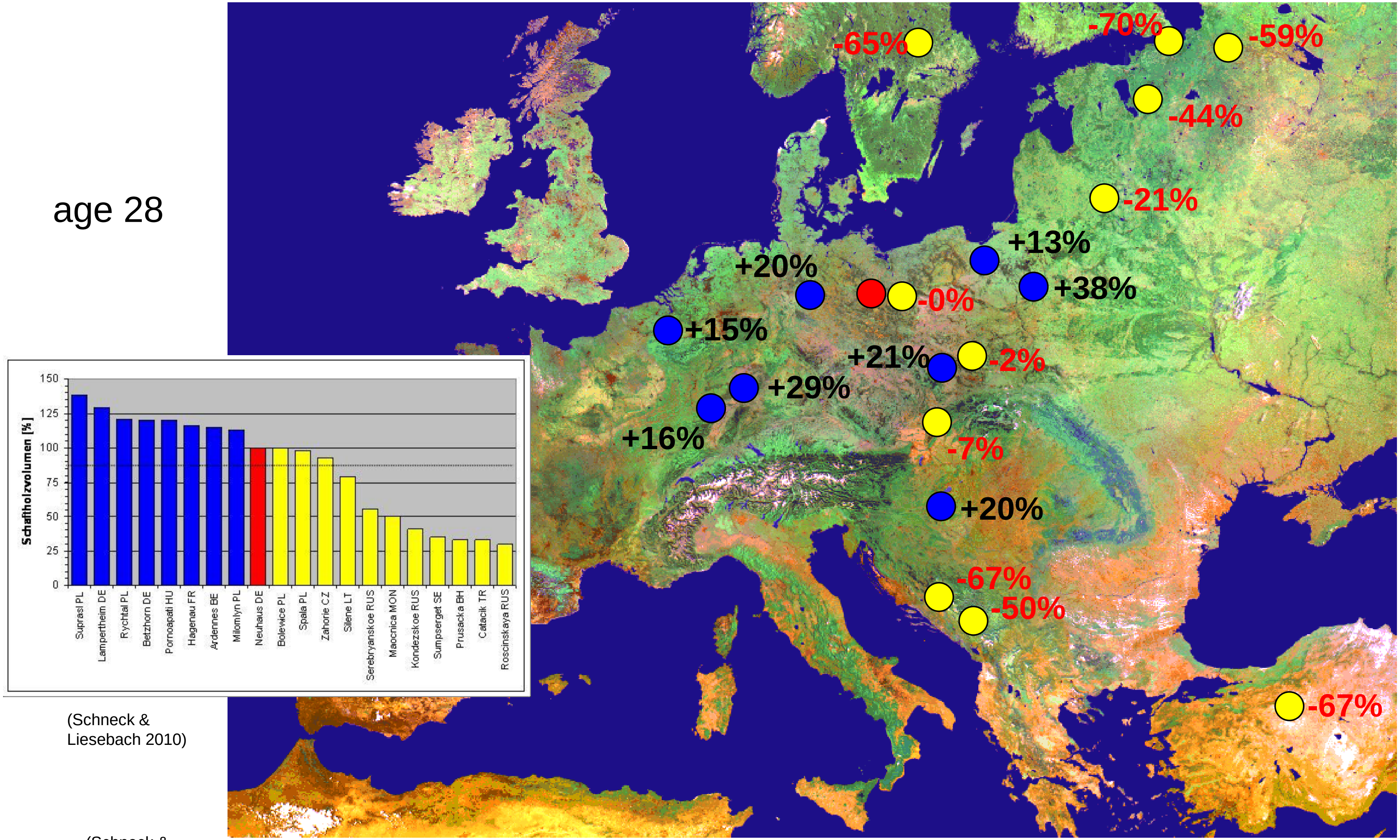
- 18th century:
  - Observations on correlations between provenance and site or provenance and quality respectively (Duhamel du Monceau)
- 19th century :
  - 1821: First provenance trials established in France (A. de Vilmorin)
  - 1893: IUFRO-congress in Vienna „Importance of seed origin in silviculture"
- 20th century :
  - 1906: Conference of German Forest Association in Dansk „Significance and obtaining of good forest seeds and plants"
  - 1907: Establishment of the first international provenance trial with Scots pine

2. Examples: IUFRO-Provenance experiments

Species	Year	Number of seed-lots	Number of trial plots	Participating countries
Pinus sylvestris (Giertych, Oleksin 1992)	1907	13	20	7
	1938	55	25	12
	1939	23	2	2
	1982	20	11	5
Picea abies (Krutzsch 1992)	1938/39	36	26	14
	1964/1968	1.100	20	13
	1972	20	43	10

IUFRO-Scots pine provenance experiment 1982

age 28



(Schneck & Liesebach 2010)

(Schneck & Liesebach 2010)

Two IUFRO-Norway spruce provenance tests

(Krutzsch 1992)

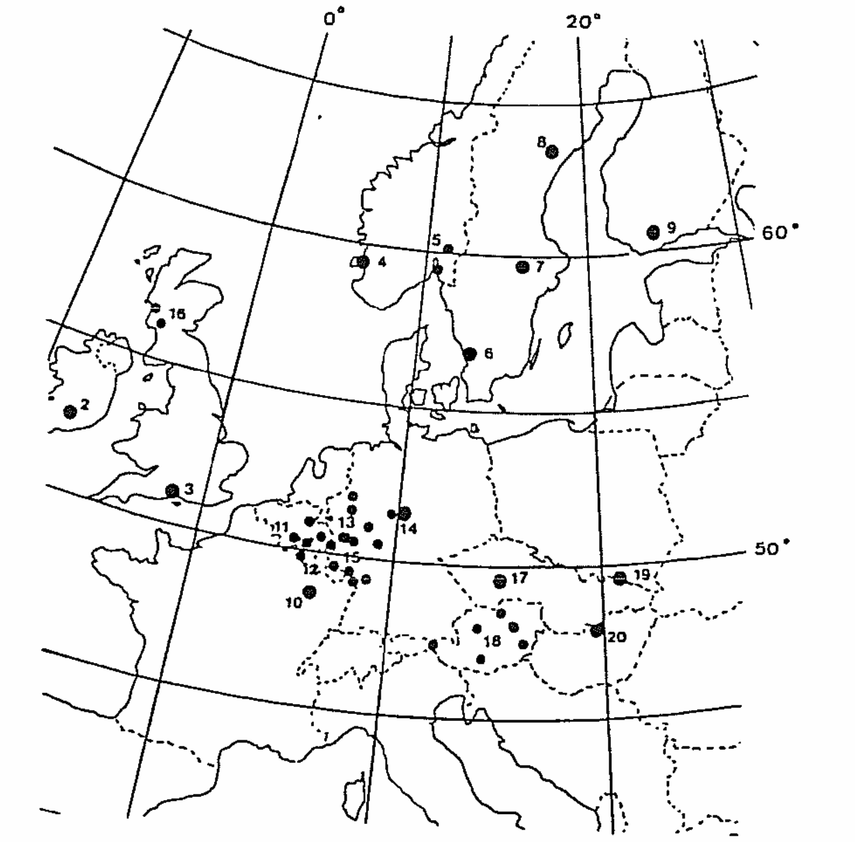


Figure 2. — International Provenance Test with Norway spruce IUFRO 1964/1968, Test sites.

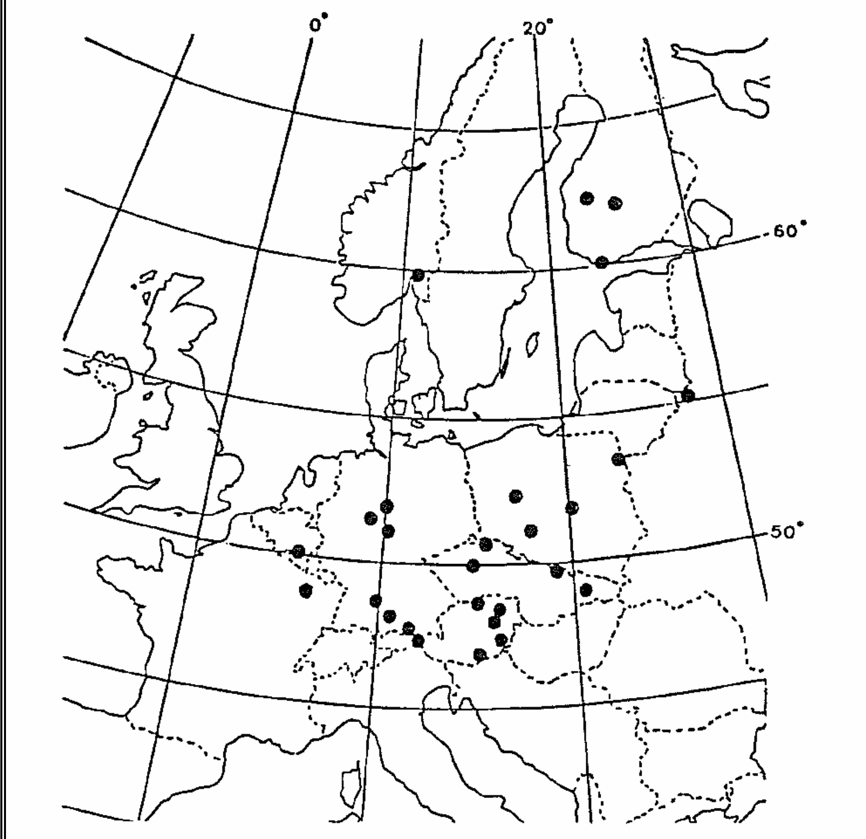


Figure 3. — International Provenance Test with Norway spruce IUFRO 1972, Test sites.

IUFRO-Provenance experiments

Species	Year	Number of seed-lots	Number of trial plots	Participating countries
Larix decidua (Weisgerber, Sindelar 1992)	1944	48	23	12
	1957/58	63	75	15
Pseudotsuga menziesii (Kleinschmit, Bastien 1992)	1973/78	182	60	36

3. Research in IUFRO-provenance tests

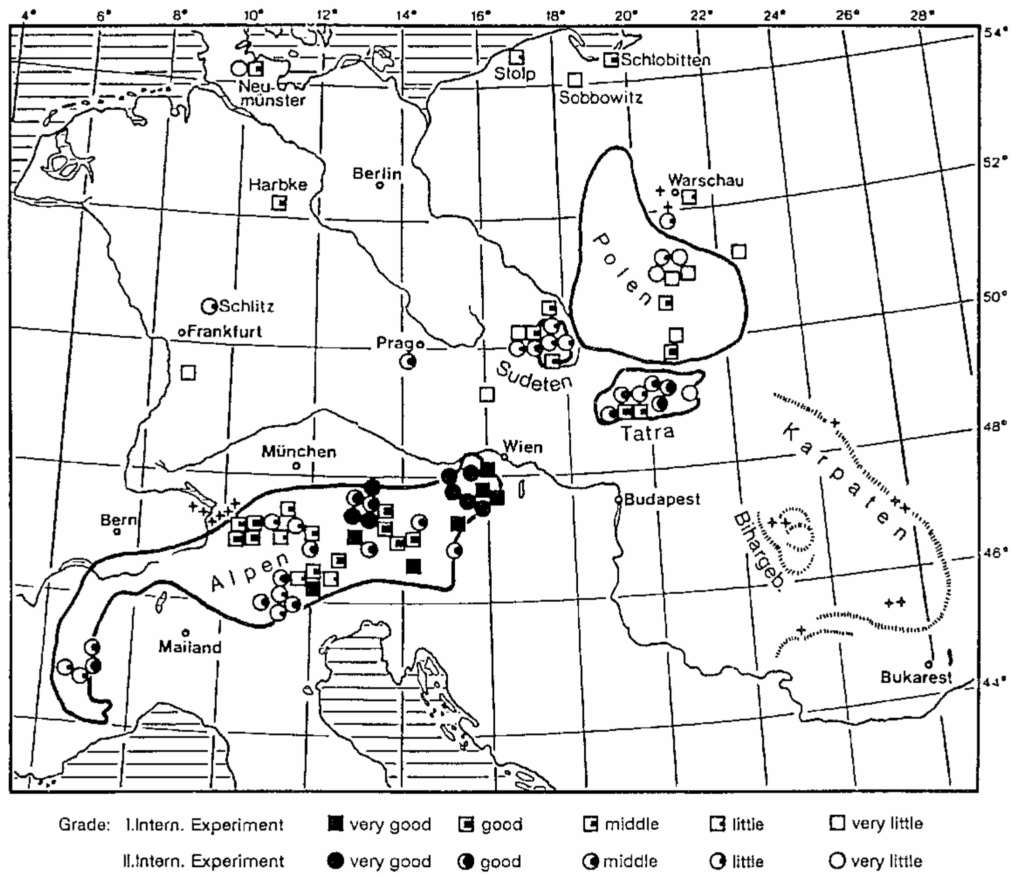


Figure 2. — Stem shape of provenance samples of European larch. From the 1st International Trial, sub-trial Neuhof, at age 23 and also as the mean of 24 sub-trials of the 2nd International Trial at the age of up to 20 years. Proportion of straight and slightly bent stems (1st Trial) and straight stems (2nd Trial) in the total number of stems, according to grades (from SCHOBER, 1981, 1985).

European larch

Traits:

- Growth
- Stem straightness
- Larch cancer
- Cultivation value

Stem shape of provenance samples of European larch (Weisgerber, Sindelar 1992)

EU-Provenance/progeny experiments

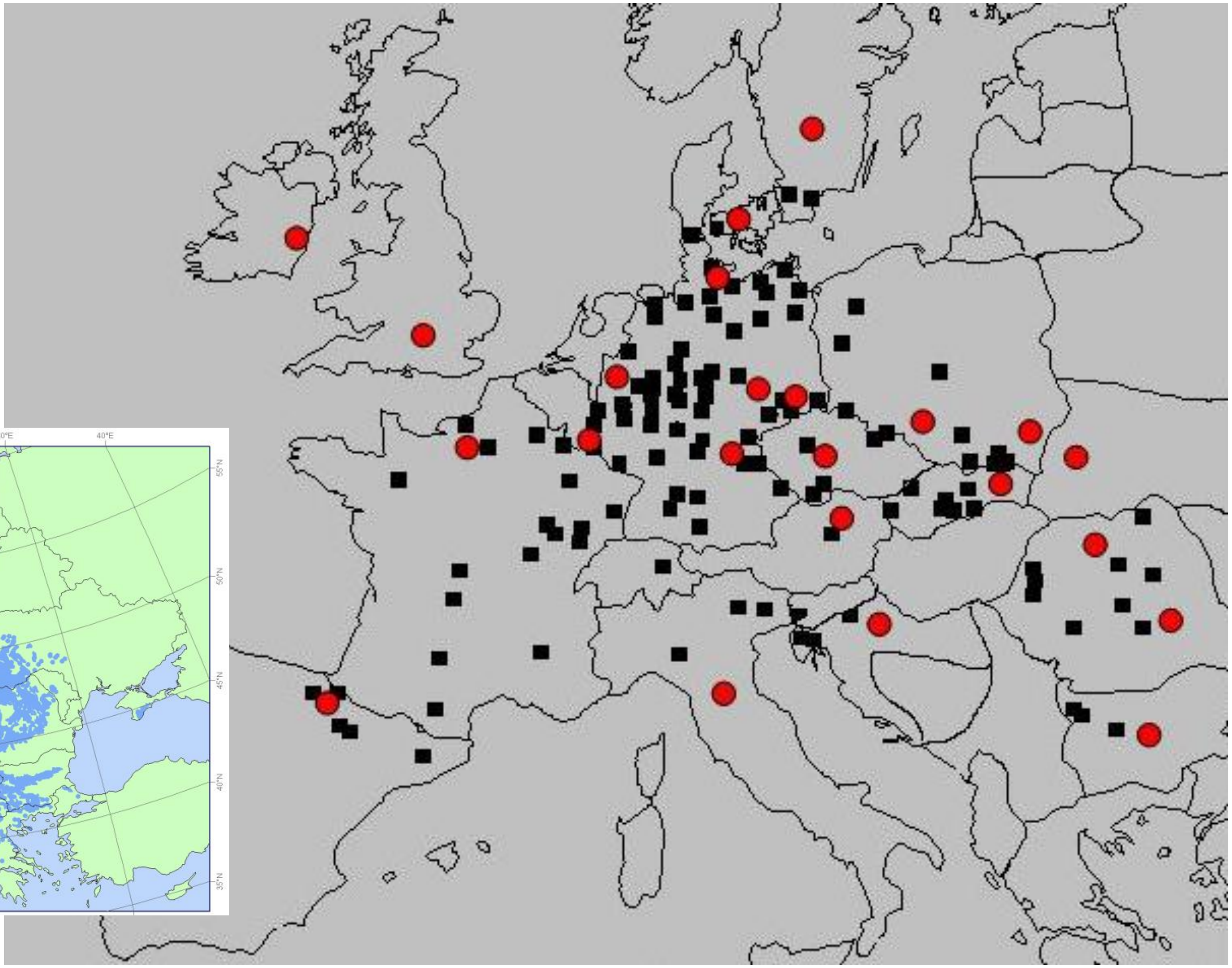
Species	Year	Number of seed-lots	Number of trial plots	Participating countries
Fagus sylvatica	1993/95	126	23	18
	1996/98	61	26	17
Larix eurolepis, *Larix lepteuropea*, *Larix* sp.	1999	25	18	7
…				

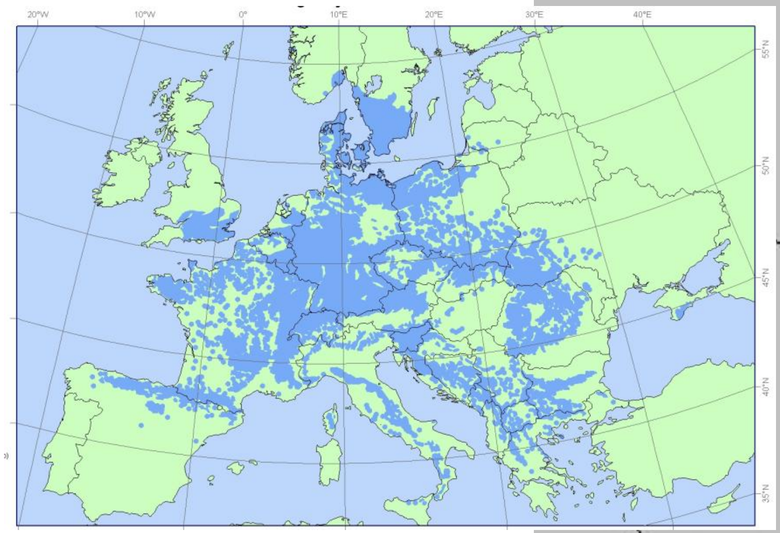
International Beech Provenance Experiment 1993/95

23 trial sites

126 provenances

(26) 36-49 or 100 provenances per site





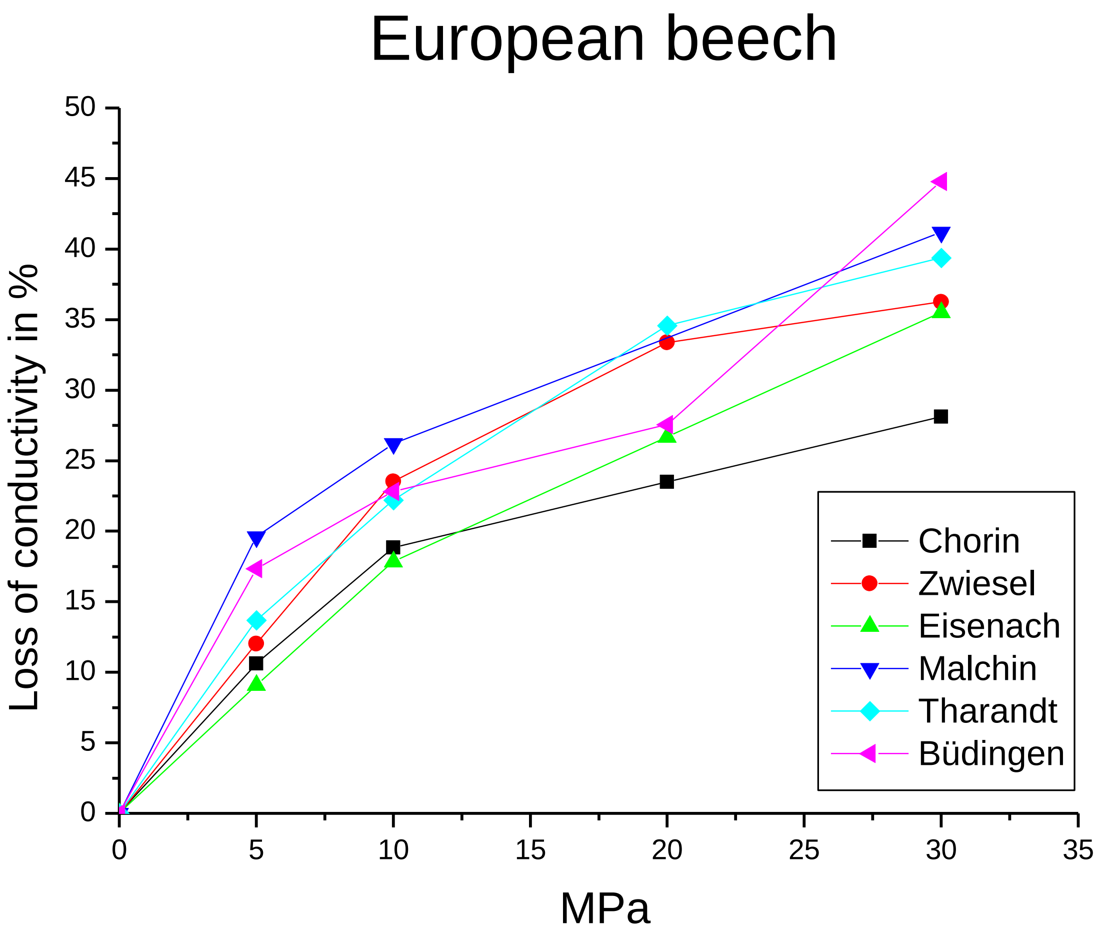
Research in IUFRO-provenance tests

- Scots pine
  - Evaluation of provenances` growth
  - Relations to climate of origin
  - Correlation with geographic coordinates
- Norway spruce
  - Genecological studies
  - Time of flushing and bud cessation
  - Growth capacity
- Douglas fir
  - Cone and seed morphology
  - Phenology
  - Frost sensitivity
  - Growth capacity and quality

Research in EU-provenance tests

- European beech
  - Survival
  - Growth and quality
  - Morphological and anatomical traits
  - Physiological traits
- Larch-hybrids
  - Survival
  - Growth and quality
  - Wood quality

Research in EU-provenance tests



Assessment of loss of conductivity 2005 using provenances of Malter trial plot (DE-SN)

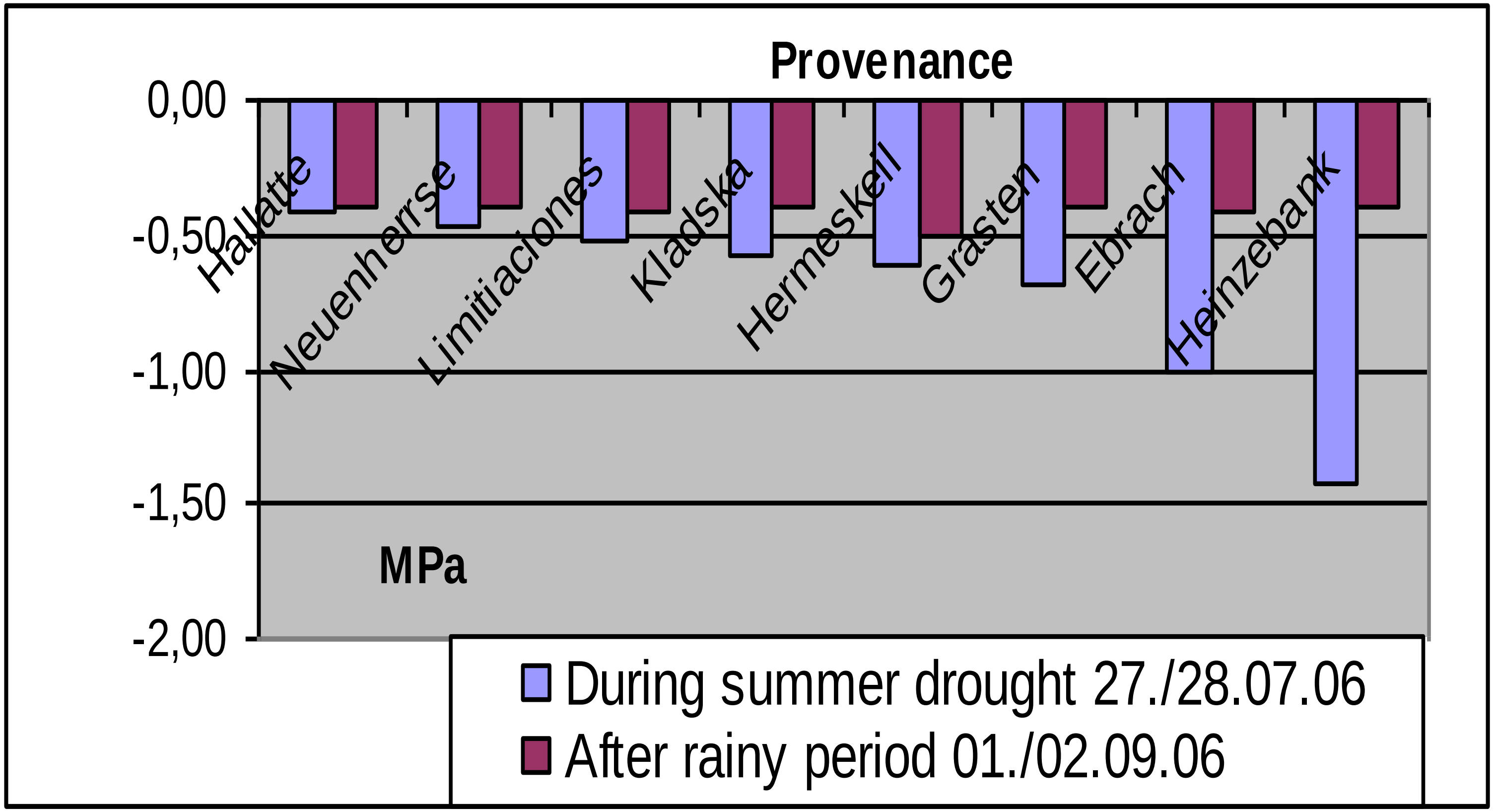
Significant correlation between "Colouring" in Graupa and PLC30 in Malter:

rs=0,943

Research in EU-provenance tests

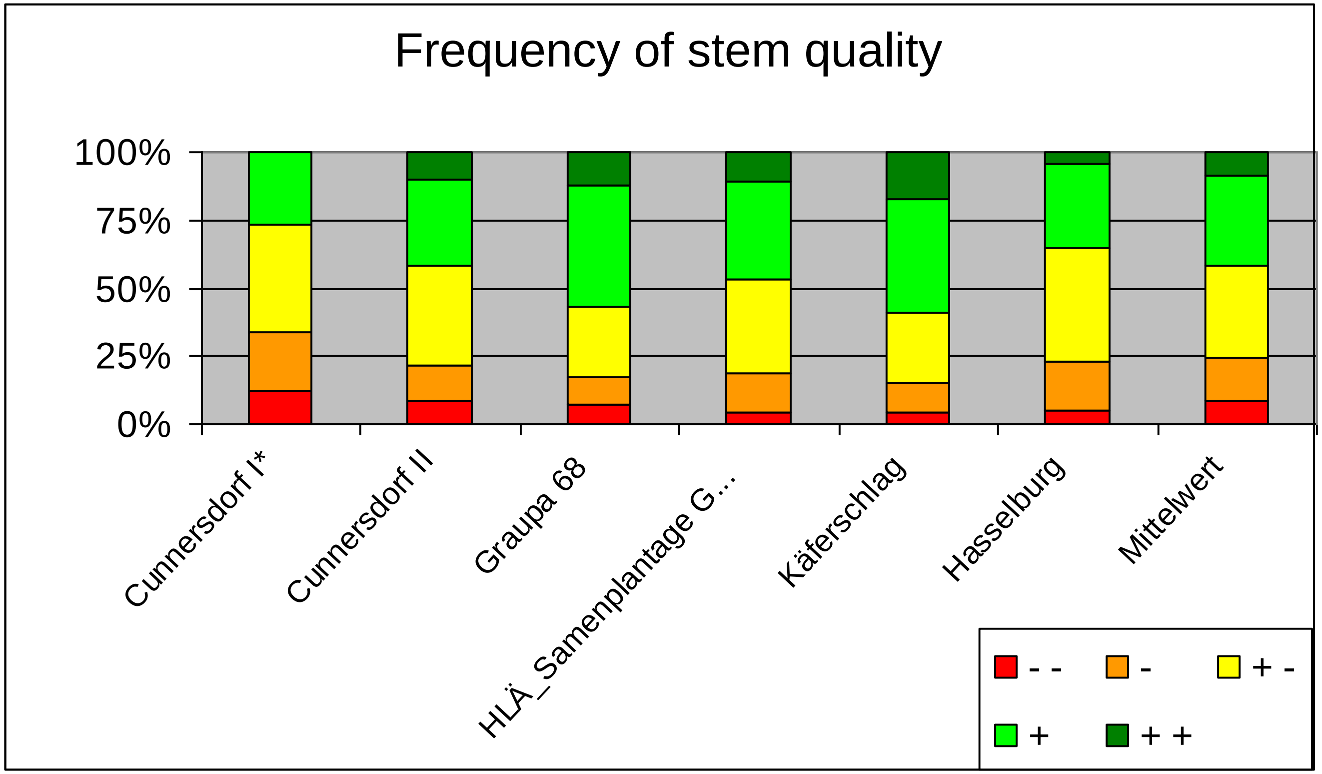
European beech

Assessment of predawn water potential 2006 using provenances of Malter trial plot



Research in EU-progeny tests

Hybrid-larch progeny test 1999



Research results - credit

- Main conifer species and broadleaved species covered by provenance tests
- Assessment of cultivation value with main emphasis on growth, quality and resistance
- More or less sound knowledge on the variation of provenances of species investigated under existing climate conditions
- Systematic screening of material approved as tested on European level just started with Hybrid-larch

Research results - <u>debit</u>

- Rare and/or valuable tree species under-represented
- Related to participation still regional gaps where no direct results are available
- Assessment of morphological, anatomical or physiological traits related to adaptability to climate change done more or less accidentally
- Material approved as tested on regional level can be traded on European level without constraints
- General approach for systematic screening of material on the European level e. g. Poplar still to be developed

4. Advantages and limitations

- Practical approach to study the variation of provenances as well as genecological and clinal correlations
  - Survival
  - Morphological, phenological, physiological traits
  - Growth, quality, resistance traits
- Scientific base for the delineation of regions of provenance
- Practical approach to develop recommendations for the use and the planting of provenances
- Scientific base for the delineation of deployment and breeding zones

Advantages and limitations

- Representivity of experiments depends on
  - Selection of provenances in relation to natural distribution area
  - Balancing dissimilarities in flowering and fruiting among regions
  - Set of standard provenances
  - Number of participating countries
  - Distribution of trial plots in relation to soil and climate
- Reliability of experiments depends on
  - Comparable seed collection procedures (intensity of flowering and fruiting, number of trees, distances among mother trees, amount of seeds collected per tree)
  - Comparable spacing, planting, tending and thinning procedures
  - Comparable assessment methods

Advantages and limitations

- Continuity of experiments depends on
  - Stability of institutional infrastructure
  - Availability of labour and finances
  - Long term accessibility of trial plots
- Analysis of experiments depends on
  - Reliable data collection
  - Completeness of data
  - Long term data storage
  - Data accessibility
  - Ability to cope with missing values

5. Importance for future experiments

- Research on the response of species and their provenances to changing climate
  - Growth response of provenances
  - Change of productivity of provenances
  - Suitability of emerging species and provenances
- Advanced breeding work
  - Systematic testing of improved and approved material in different environments as the test environment
  - Development of breeding zones
  - Selection of trees and their vegetative propagation by TC
  - Provenance and species crossing

Importance for future experiments: Example "Growth response to changing climate"

Pinus contorta Dougl. ex Loud. provenances (Wang et al. 2006)

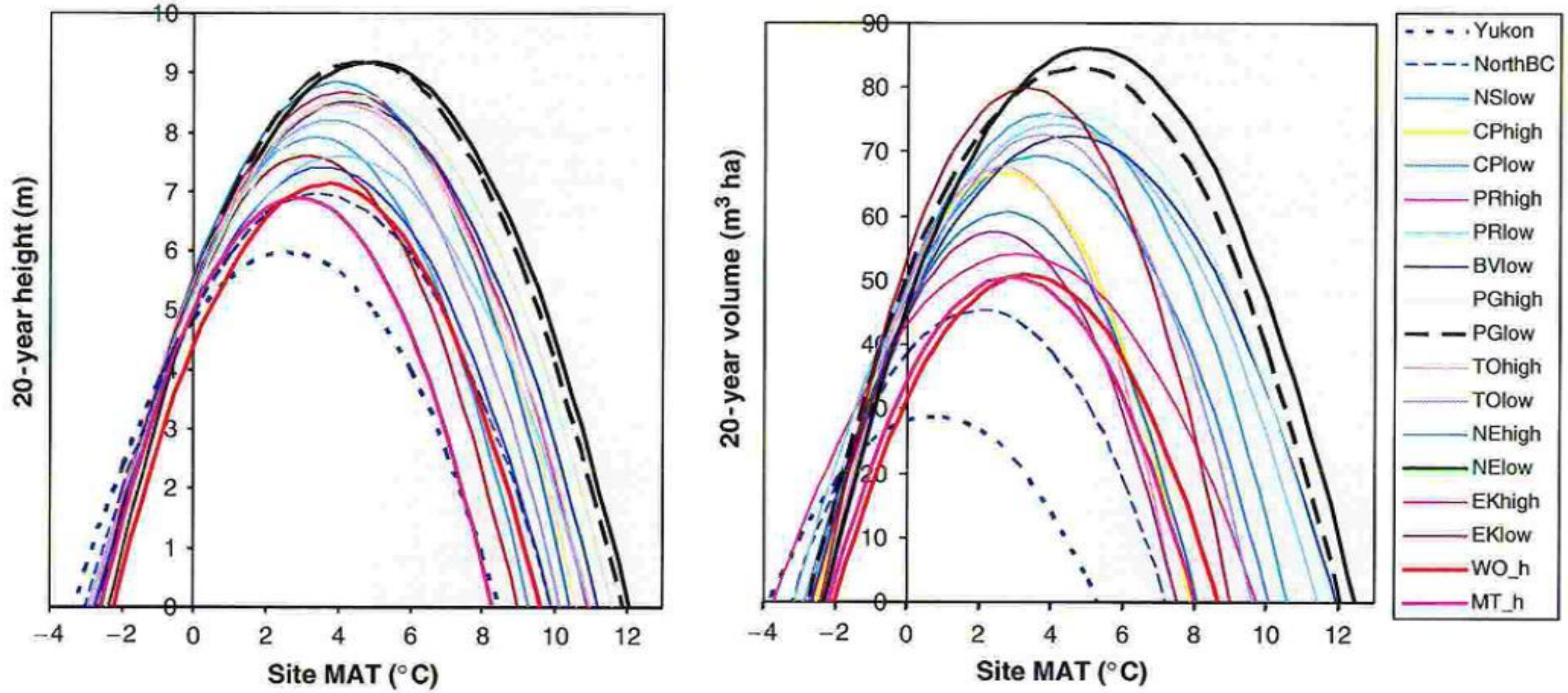


Fig. 6 Growth response curves of seed planning unit populations and regions for 20-year height and volume per hectare against mean annual temperature (MAT) at each population's optimum annual heat:moisture index (AHM). Shaded areas are extrapolations beyond the MAT range of test sites.

Importance for future experiments:
Example "Growth response to changing climate"

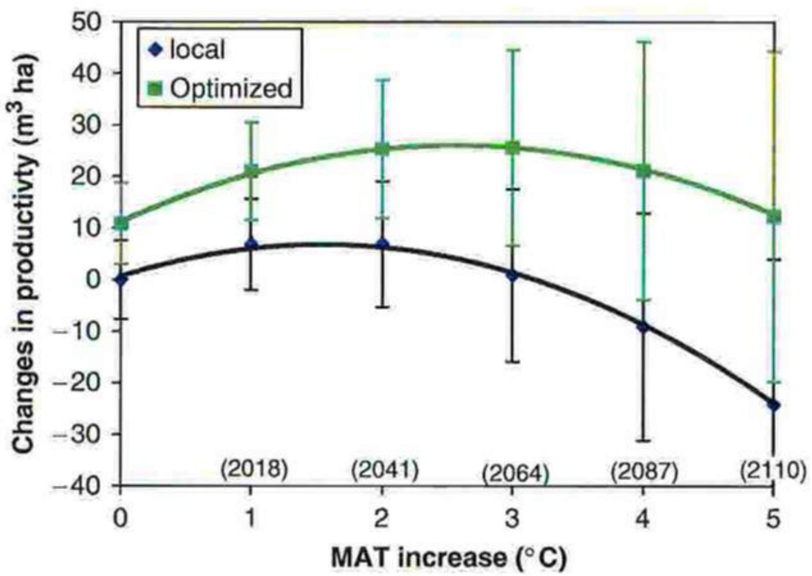


Fig. 8 Predicted changes in productivity of lodgepole pine across all seed planning units in BC for local seed vs. most productive seed source for future climates. Each increase of 1 °C in mean annual temperature (MAT) is accompanied by an increase of 1.8% increases in mean annual precipitation. Error bars indicate the 90% confidential interval for predicted means.

Pinus contorta Dougl. ex Loud. provenances

(Wang et al. 2006)

6. Conclusions

- Large forest tree provenance experimental networks
  - Source for basic and general knowledge on the variation as well as on the cultivation value of provenances of species investigated in existing climate conditions
  - Base for on-going research on the adaptability of the material in question under climate change
  - Important tool for the assessment of cultivation value of emerging species and their provenances under existing climate conditions as well as under future climate conditions
- Tools for the assessment of cultivation value of material in question in climate change to be improved and made suitable for systematic screening

Conclusions

- Large forest tree provenance experimental networks
  - Difficult to manage in the long term
  - Time and labour consuming
  - Full of problems related to every step of the experiment as well as related to the involvement of different institutions with different mentalities, different background, different budgets

- However, it is the only and practical way to explore the possibilities and limitations of genetic resources until something better is developed.

Thank you for your attention!