15.12.2011. LVMI “Silava”

Starptautiska zinātniska konference “Adaptīvo pazīmju ģenētiskā variācija” (Genetic variations of adaptive traits)

No 2011. gada 30. novembra līdz 1. decembrim LVMI “Silava” organizēja starptautisku zinātnisko konferenci “Adaptīvo pazīmju ģenētiskā variācija” (Genetic variation of adaptive traits).

Konferences darbā iesaistījās 24 dalībnieki no 3 Baltijas valstīm, pārstāvot 5 zinātniskās institūcijas. Tika prezentēti galvenokārt ESF finansēta pētījuma “Ģenētisko faktoru nozīme adaptēties spējīgu un pēc koksnes īpašībām kvalitatīvu mežaudžu izveidē” 2010. un 2011. gada iegūto rezultātu apkopojums, ietverto šādus jautājumu blokus:

- koku radniecība audzes ietvaros, tās noteikšanas metodes un potenciālā ietekme uz adaptāciju;
- dažādu sugu koku augstuma pieauguma veidošanās sezonālā dinamika, saikne ar meteoroloģiskajiem faktoriem un atšķirības starp dažādu genotipu kokiem;
- introducētas koku sugas (Klinškalna priede) produktivitāte un to ietekmējošie faktori Baltijas valstīs;
- ģenētisko faktoru un atjaunošanas/kopšanas ietekme uz jaunaudžu parametriem;
- koksnes īpašības un to ģenētiskā nosacītība dažādu sugu kokiem;
- koku noturība pret biotisko un abiotisko faktoru ietekmi, genotipu atšķirības un molekulārās ģenētikas metožu pielietošana šo atšķirību cēloņu analīzē prognozēšanā;
- apšu hibrīdu pazemes biomasas un klonu atšķirības šajā aspektā.

Detalizēta konferences darba kārtība (angļu val.) pievienota relīzes pielikumā.

Iegūtie rezultāti liecina, ka koku ģenētikai ir būtiska loma, nosakot to augšanas sezonālos procesus, atbildes reakciju uz meteoroloģiskajiem apstākļiem, kā arī noturību pret dažādiem nelabvēlīgiem vides faktoriem un koksnes īpašības. Tas jāņem vērā, plānojot meža atjaunošanu sagaidāmo klimata izmaiņu kontekstā.

Konferences prezentācijas (angļu valodā, pievienotas relīzes pielikumā):

- Zeps M. Annual shood development dynamics of hybrid aspen: results of 2010, 2011;
- Jansons Ā. Annual shoot development dynamics of Scots pine (genetic differences);
- Lībiete-Zālīte Z. Climate impacts on lodgepole pine (Pinus contorta var. latifolia) height growth in a provenance experiment some preliminary results
- Irbe I., Grīnfelds U., Šāble I., Verovkins A., Vīķele L., Horste B., Treimanis A., Škute M., Jansons Ā. Differences in wood trials between Norway spruce
- Kānberga-Siliņa K. Genetic determination of wood traits in Scots pine – analysis of candidate genes influencing wood quality
- Zeps M. Genetic diversity with aspen stands: phenology observations and molecular analysis
- Danusavicius D., Jansons Ā. Genetic variation in annual height growth of Latvian Norway spruce OP families
- Voronova A., Ruņģis D., Jansons Ā. Genome plasticity of Scots pine (Pinus sylvestris L.) under different stress conditions
- Irbe I. Spruce. Natural durability
- Maaten T. Within stand relatedness and genetic diversity
- Zeps M., Grīnfelds U. Wood trait differences of Hybrid aspen clones

Konferences ietvaros diskutēti pētījumu metodiskie aspekti un nepieciešamie papildus paraugu ievākšanas vai apstrādes darbi, lai visus iegūtos rezultātus būtu iespējams sagatavot zinātnisku publikāciju formātā. Tāpat analizēti rezultātu praktiskās izmantošanas aspekti.

Genetic variation of adaptive traits

Salaspils, LSFRI Silava, 30.11.2011.

9:00 Predicted climatic changes and possibilities for adaptation
9:40 Within-stand relatedness and genetic diversity: review
10:00 Genetic diversity with aspen stands: phenology observations and molecular analysis
10:20 prospects of further analysis – discussion
11:00 break
11:20 annual shoot development dynamics of hybrid aspen: results of 2010, 2011
11:40 annual shoot development dynamics of Scots pine
12:00 annual shoot development dynamics of Norway spruce
12:20 climatic factors and annual height growth development of *Pinus controta*: preliminary results
12:40 break
13:40 productivity of *Pinus contorta* in Lithuania
14:00 traits of *Pinus contorta* in Latvia and Estonia
14:20 influence of genetic factors and regeneration method on Scots pine productivity
14:40 influence on thinning and genetic factors on productivity and quality of young Silver birch stands
15:00 break
15:20 genetic differences in wood traits of hybrid aspen
15:40 below-ground biomass of hybrid aspen
16:00 genetic differences in stress resistance
16:20 genetic determination of wood traits
16:40 differences in wood traits between Norway spruce clones
17:00 discussion, closing remarks,
departure to Jaunkalsnava

Jaunkalsnava, 1.12.2011

9:00 genetic differences among Scots pine families in resistance again needle cast
9:20 genetic and environmental factors determining occurrence of lamas growth of Scots pine
9:40 differences among Scots pine families in resistance against root rot
10:00 differences among Norway spruce clones in resistance against wood decay fungi
10:20 prospects of further analysis – discussion
10:40 break
11:00 departure to trials
15:30 closing of the conference

ESF project “Importance of Genetic Factors in Formation of Forest Stands with High Adaptability and Qualitative Wood Properties” (No 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)

EUROPEAN UNION

INVESTMENT IN YOUR FUTURE

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Annual shoot development dynamics of hybrid aspen: results of

2010, 2011.

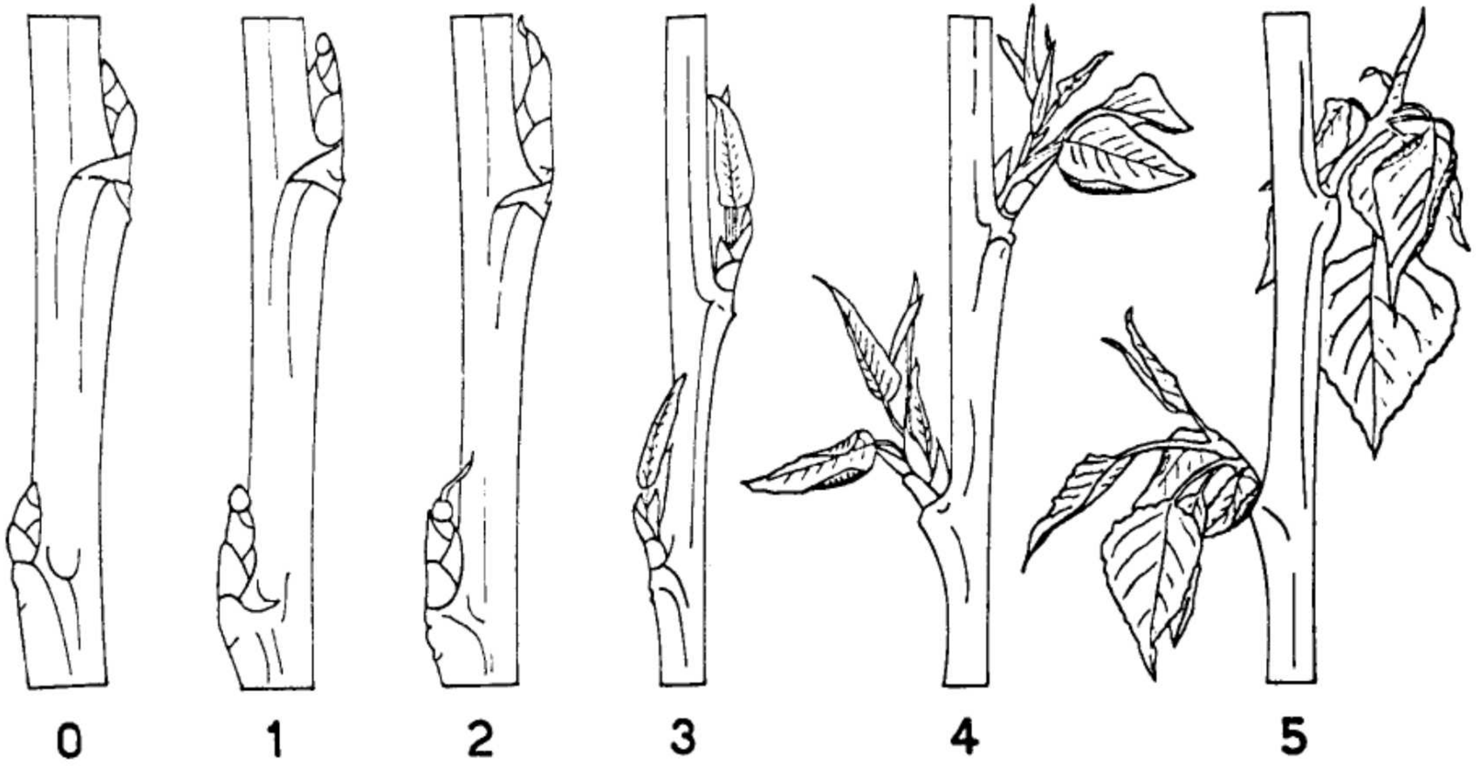
Mārtiņš Zeps

martins.zeps@silava.lv

Materials and method

Progeny trial No. 620 with 15 hybrid aspen clones, represented by 25 ramets with initial spacing 3 x 3 m, has been established in former agricultural land in central part of Latvia. Inventory of phenology and measurements have been carried out in 4th and 5th growing season, starting from middle of April, with an interval of 1 week on average.

Materials and method



UPOV 1981.

Leaf prosperity phases

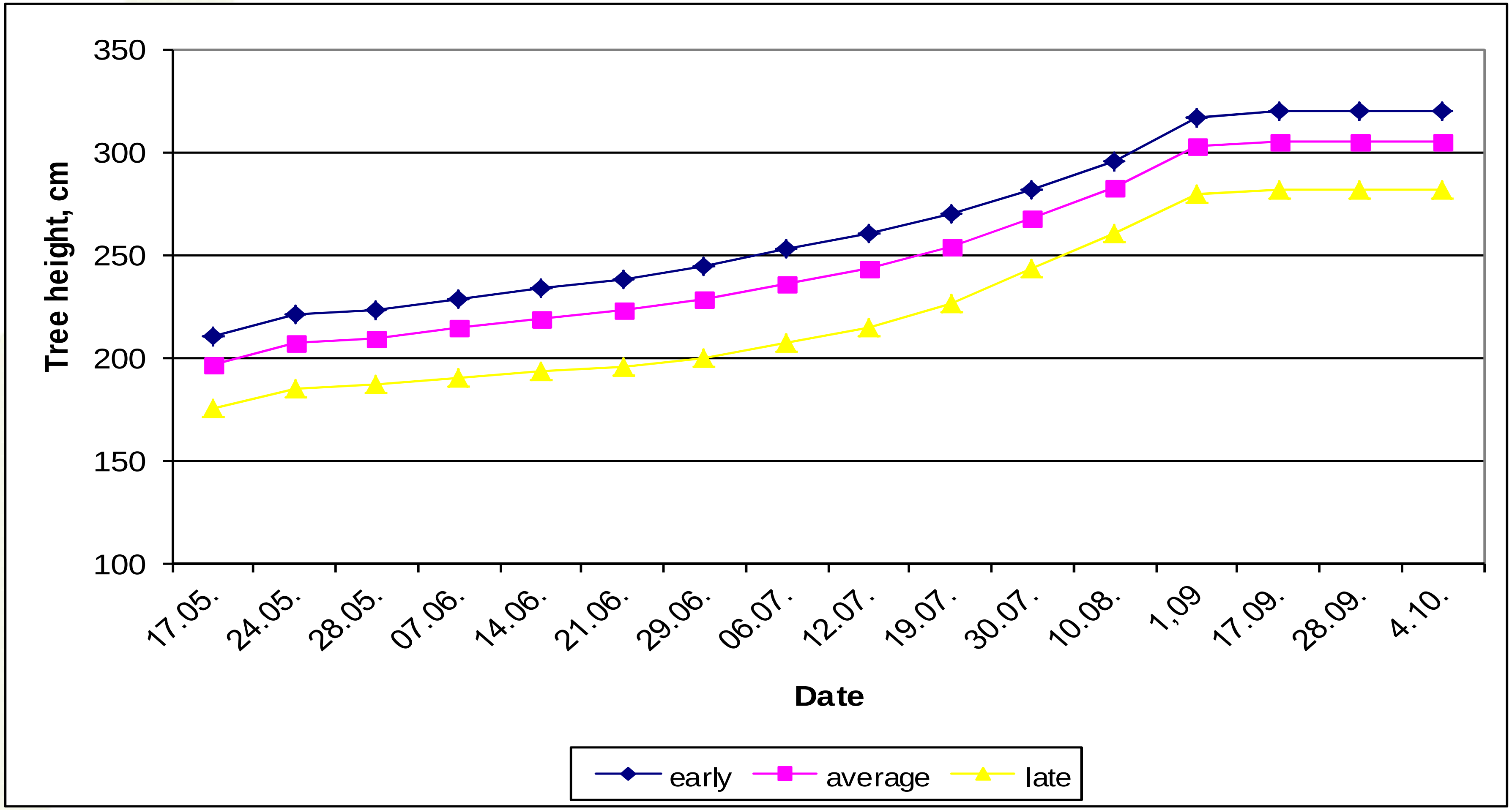
Differences between leaf prosperity was 12 day in phase 2 in 2010

But in 2011. only 2 days.

Differences between leaf prosperity was 4 days in phase 5 in 2010

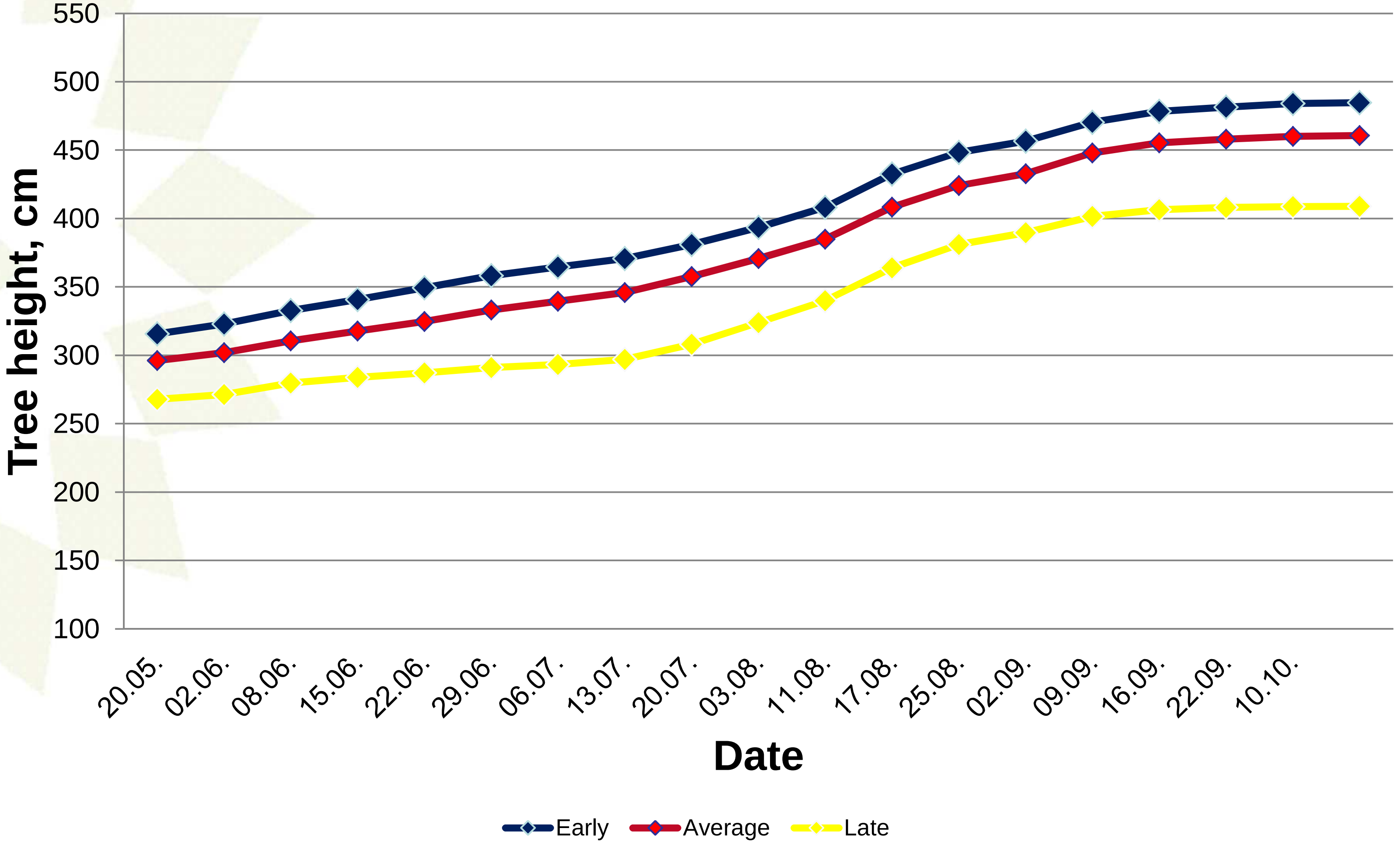
But in 2011. 7 days.

Development of tree height increment with different bud burst phenology pattern 2010



INVESTMENT IN YOUR FUTURE

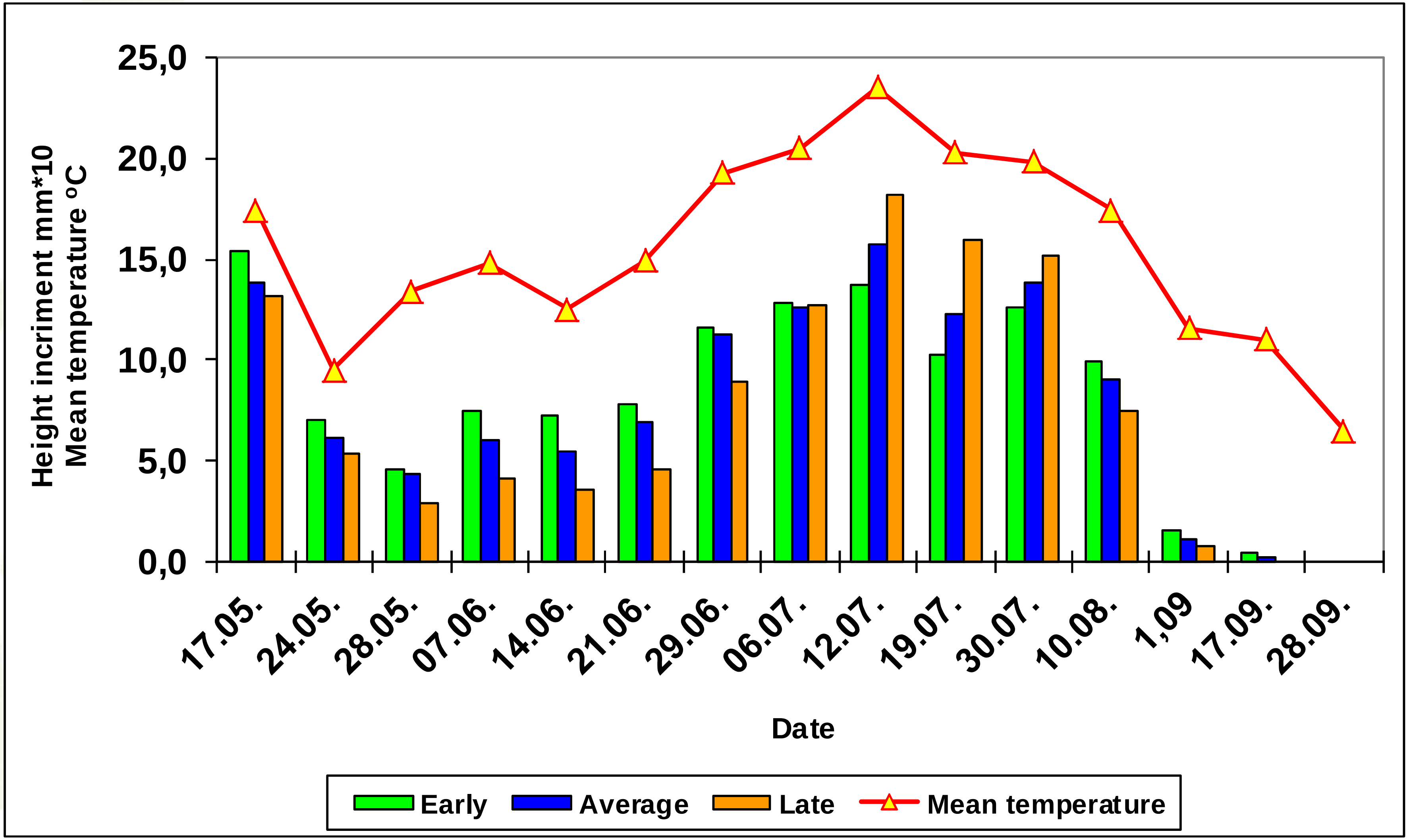
Development of tree height increment with different bud burst phenology pattern 2011



Funded by the European Union

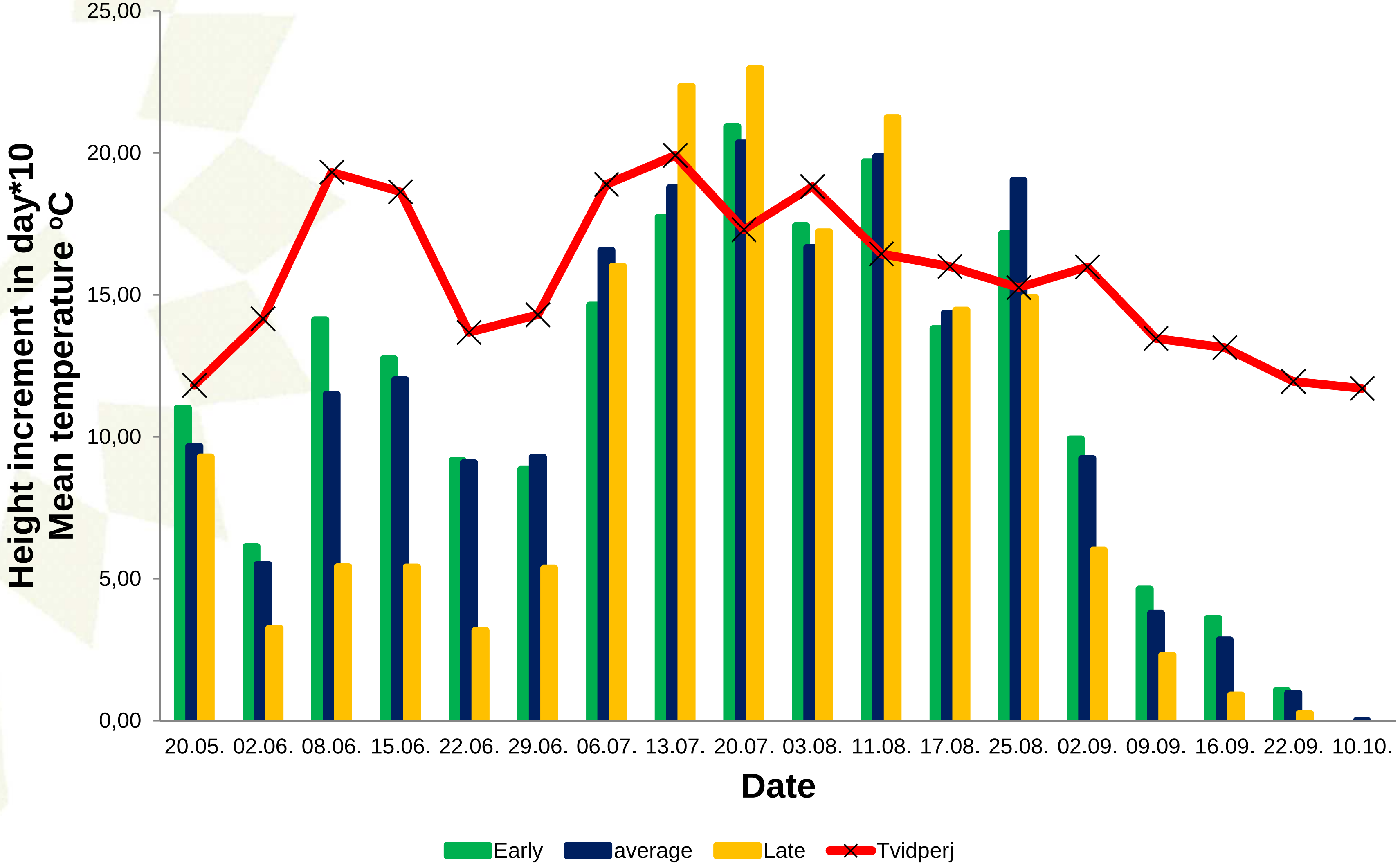
INVESTMENT IN YOUR FUTURE

Intensity of height growth per day, mm *10, of clones with different bud burst and mean temperature ºC 2010.



INVESTMENT IN YOUR FUTURE

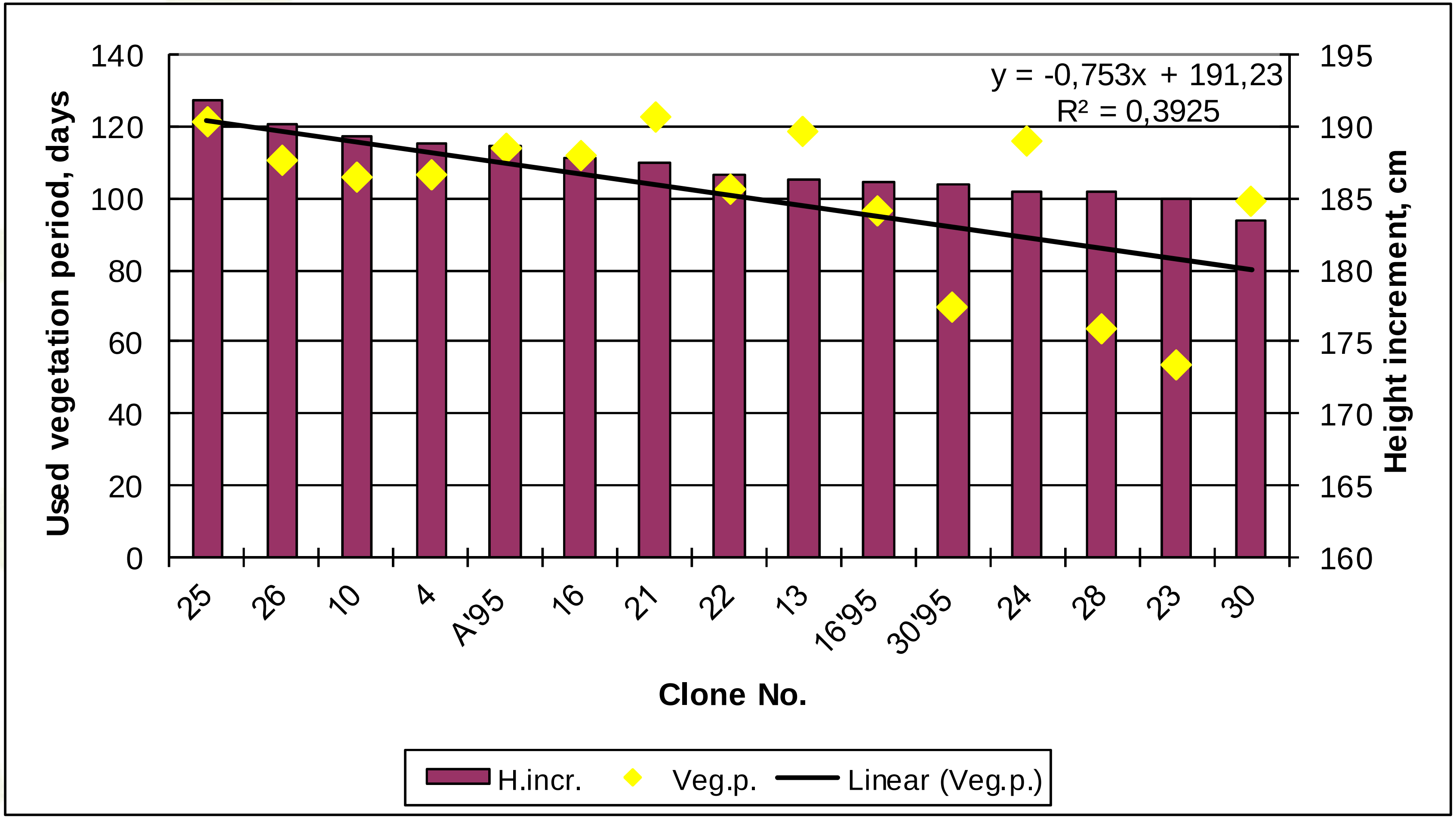
Intensity of height growth per day, mm *10, of clones with different bud burst and mean temperature ºC 2011



Funded by the European Union

INVESTMENT IN YOUR FUTURE

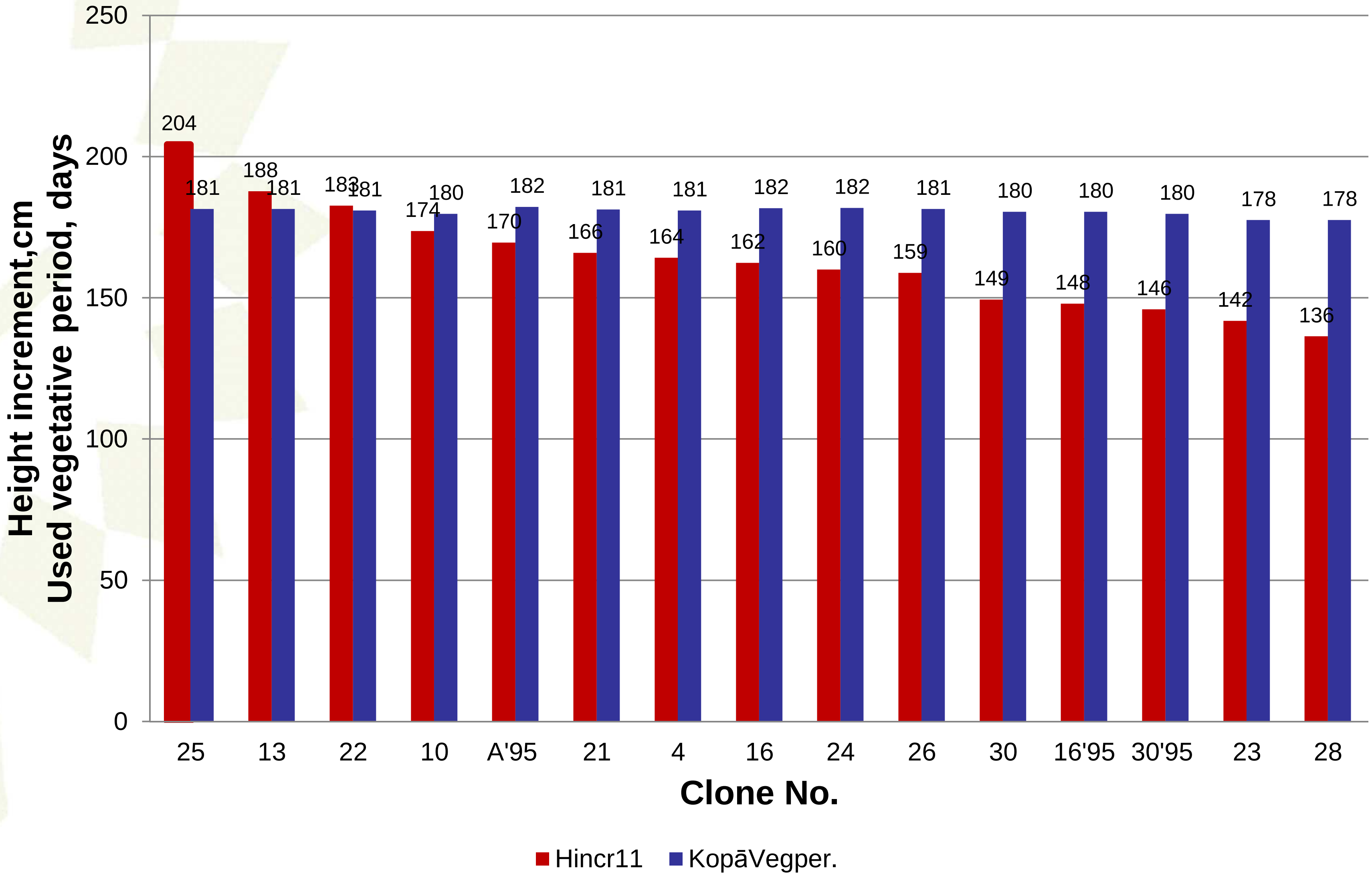
Total length of height increment and length of used vegetation period for particular hybrid aspen clones 2010



Funded by the European Union

INVESTMENT IN YOUR FUTURE

Total length of height increment and length of used vegetation period for particular hybrid aspen clones 2011



Conclusions

- Hybrid aspen clones have 2 height increment culminations – end of May and middle of July;
- Height increment have strong correlation this average temperature of day;
- Clone who have longer used vegetation period have bigger height increment;
- Growing intensity have bigger influence to total height increment of middle of July in 2010, but in 2011 midle of June.

Thank You for attention!

SILAVA

ESF

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Nr. 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Annual shoot development dynamics of Scots pine

(genetic differences)

aris.jansons@silava.lv

Materials & Methods

Repeated measurements of height carried out in 3 trials:

- Grafted seed orchard, age 10 years
- In total 72 clones, represented by 4 ramets (copies) each
- Mean height 4.1 m, diameter 7.2 cm
- Height differences for 95% or ramets does not exceed 0.4 m from mean and have no significant influence to annual height increment (r^2=0.03) or height growth intensity (r^2=0.02)
- Measurements carried out in year 2008

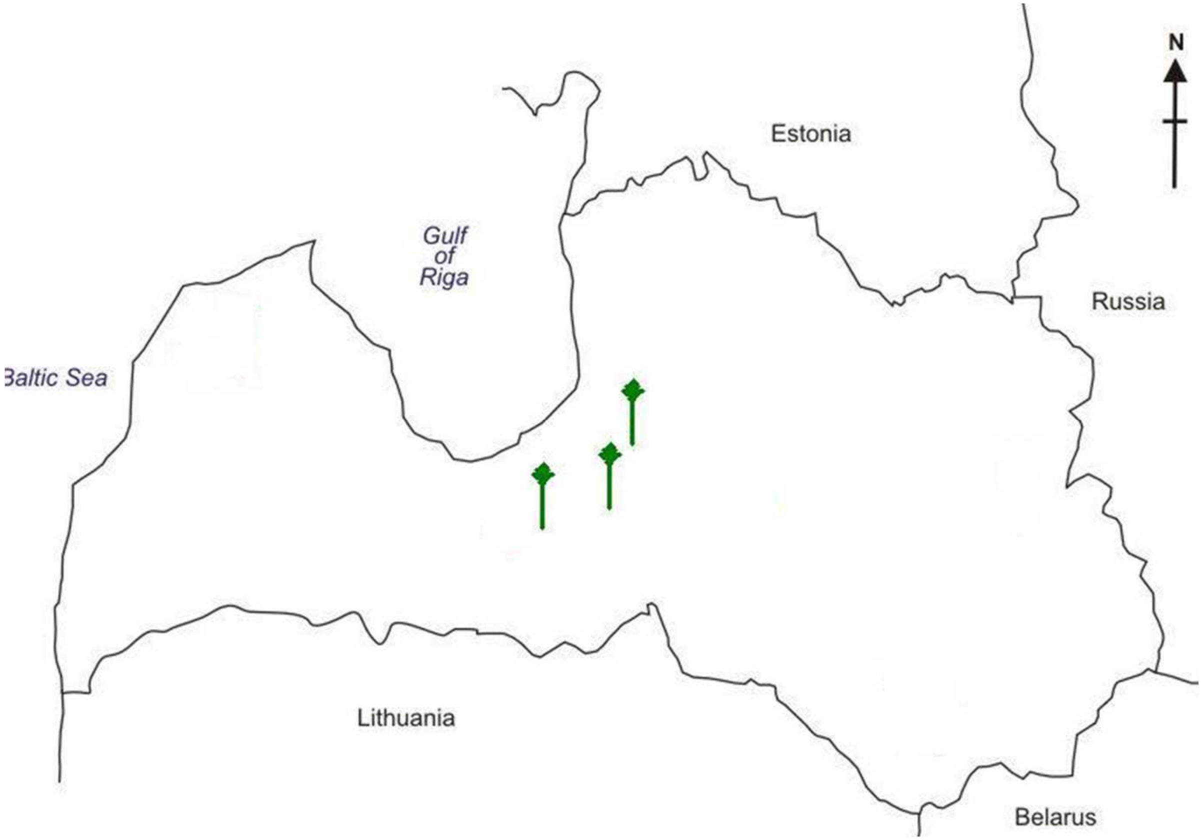
Materials & Methods

Funded by the European Union
INVESTMENT IN YOUR FUTURE

- Open pollinated progeny trials (experiments No. 352 and 441) at the age of 4 and 6 years (in year 2008 and 2010)
- Progenies of 61 tree and 4 control lots
- Mean height at the beginning of 6th vegetation period in exp. No. 352 was 110.5 cm and in exp. No. 441 – 64.0 cm.

Materials & Methods

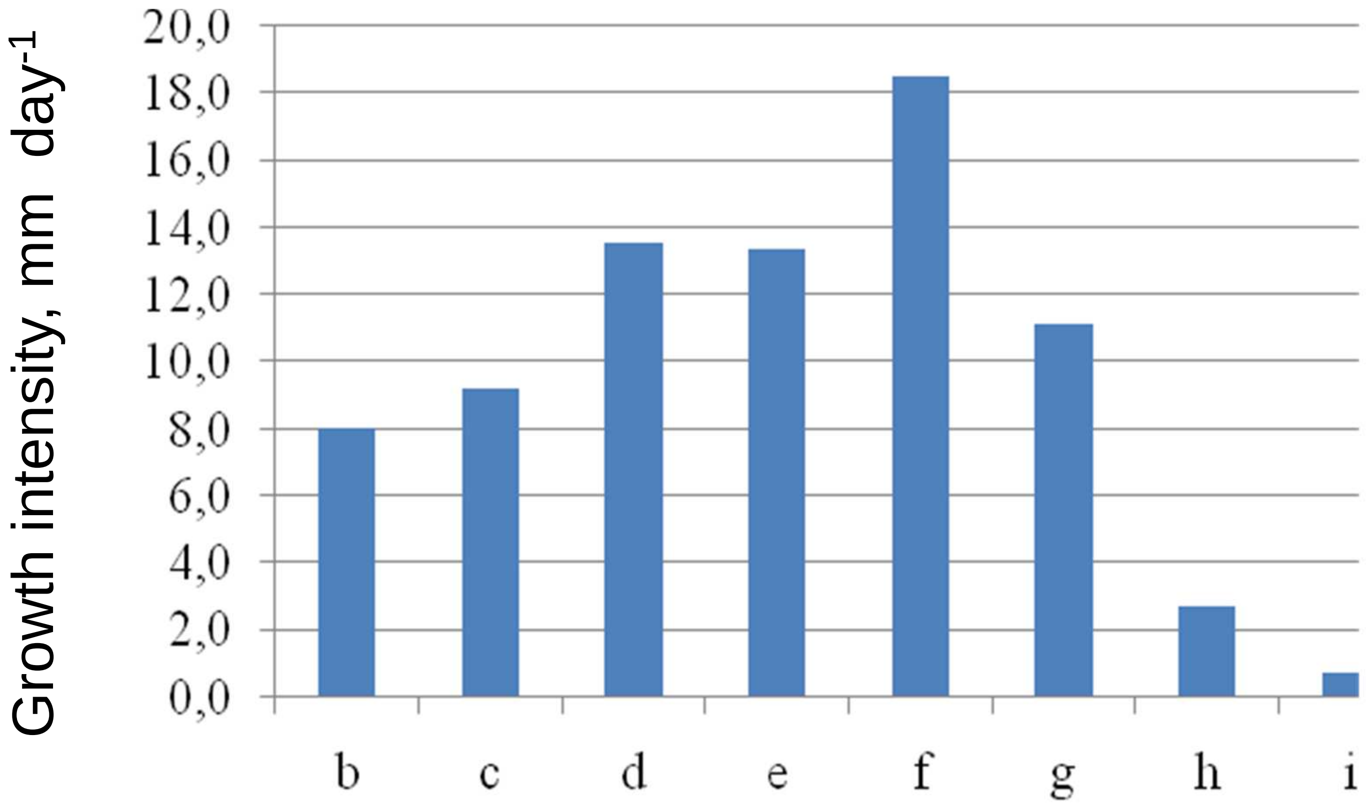
- All experiments located in poor sandy soil, *Vacciniosa* forest type in relative similar climatic conditions, surrounded by Scots pine stands



Results
Seed orchard

INVESTMENT IN YOUR FUTURE

- Average height increment reached 70 cm

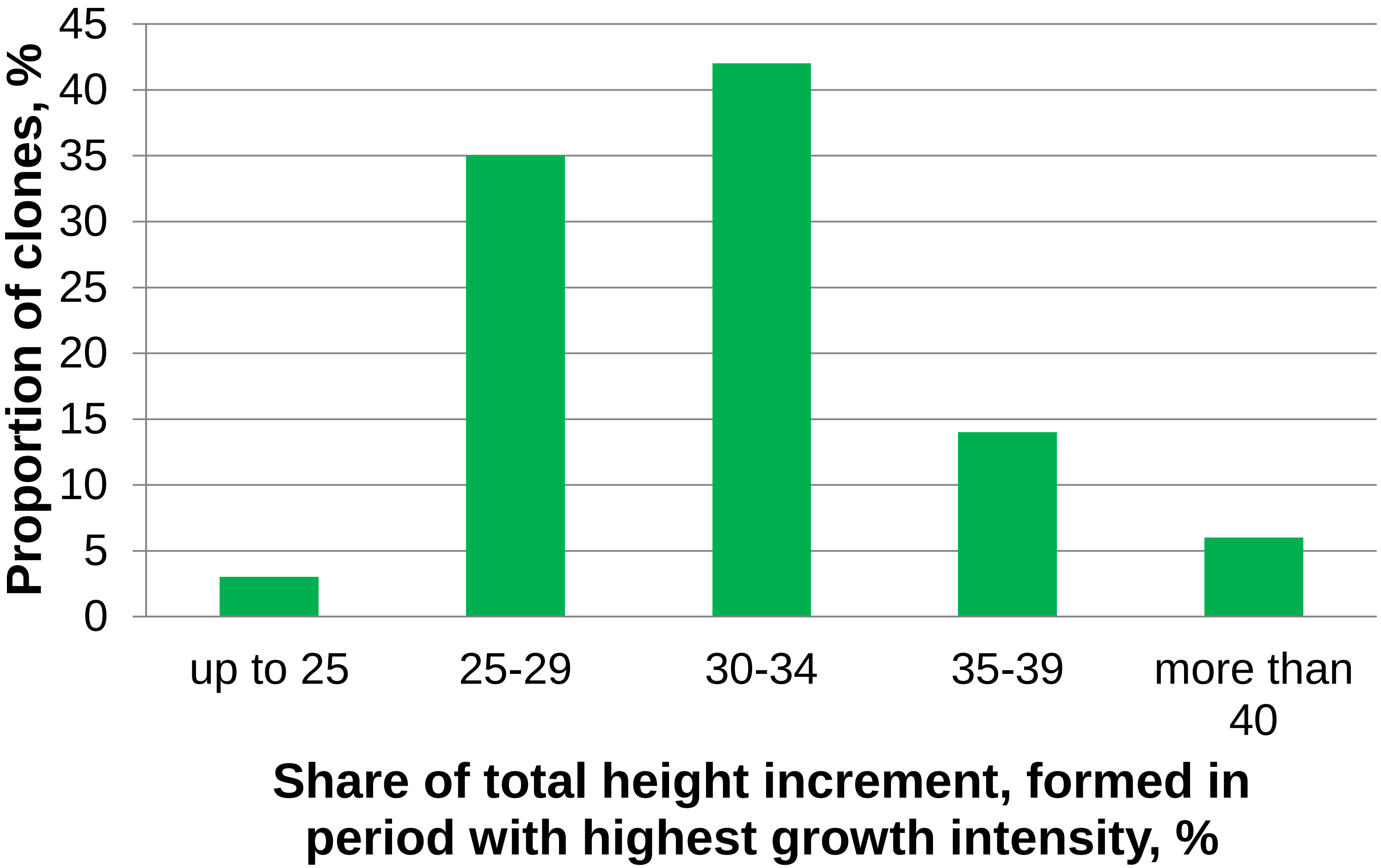


Growth period

Growth period: a- 27.04.-04.05.; b-05.05.-10.05.; c-11.05.-16.05.; d-17.05.-22.05.; e-23.05.-30.05.;f-31.05.-4.06.;g-5.06.-11.06.; h-12.06.-24.06.; i-25.06.-02.07.

Results
Seed orchard

Funded by the European Union
INVESTMENT IN YOUR FUTURE



Share of total height increment, formed in period with highest growth intensity, has moderate heritability (H^2=0,30), similar to that of growth intensity on average (H^2=0.29)

Results
Seed orchard

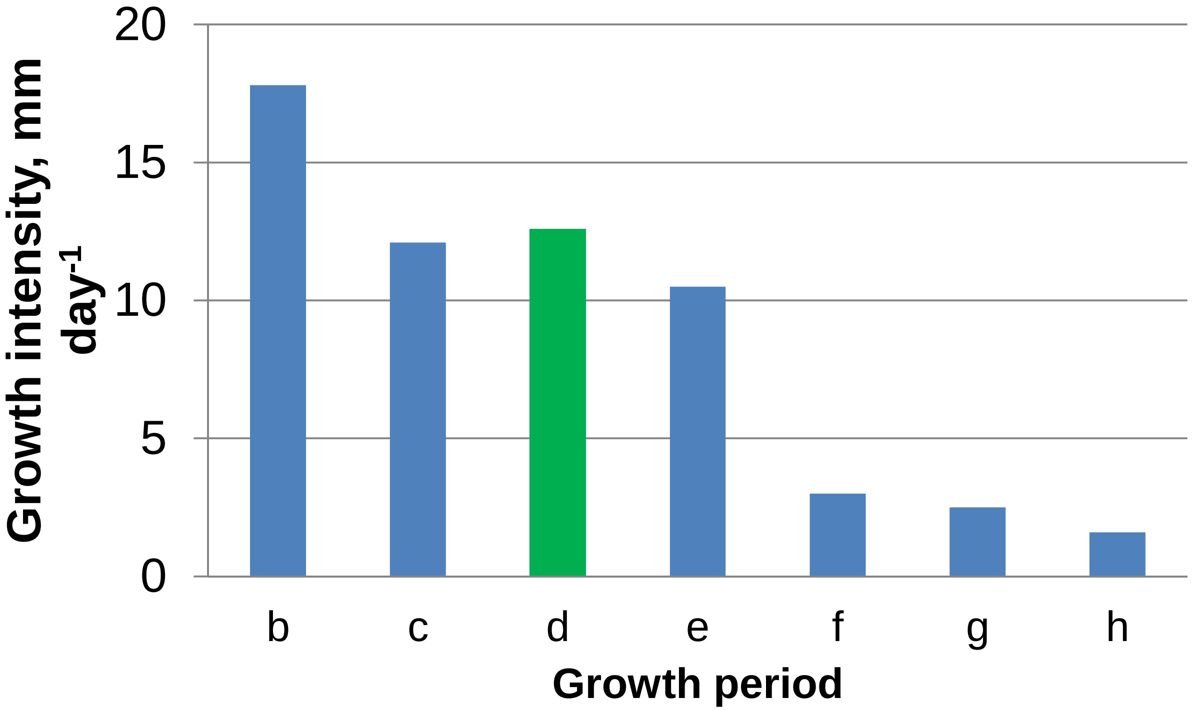
Funded by the European Union
INVESTMENT IN YOUR FUTURE

- On average 32% of height increment is formed during the period of highest growth intensity (end of May- beginning of June).
- Correlation between share of height increment, formed in period with highest growth intensity and total length of height increment is negative, non-significant and week (r=-0.22).
- It is possible to select clones, forming more than 35% of total length of height increment during relative short period (15-20% of total height growth period) and still heaving average or high total length of height increment.

Results
O.p. progeny trials

INVESTMENT IN YOUR FUTURE
Funded by the European Union

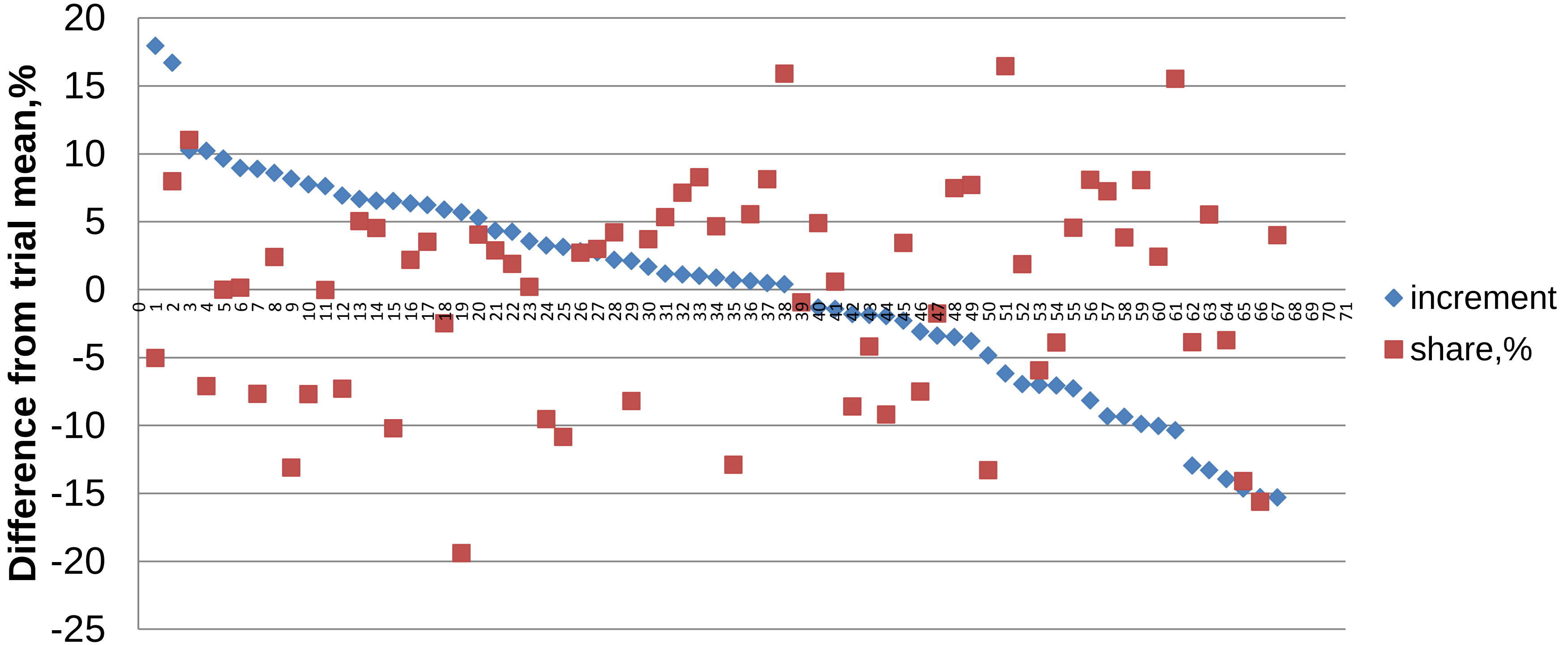
- Tree height have a relative large influence to height increment: correlation with total length of increment r=0.56 at the age of 4 years and r=0.48 at the age of 6 years.
- Average height increment reached 48 cm in exp. No. 352 and 23 cm in exp. No. 441.



Results
O.p. progeny trials

INVESTMENT IN YOUR FUTURE

- In both trials and ages total length of height increment was weakly related to share of total height increment, formed in period with highest growth intensity (on average r=-0.22 at individual tree and r=-0.07 at family mean level).



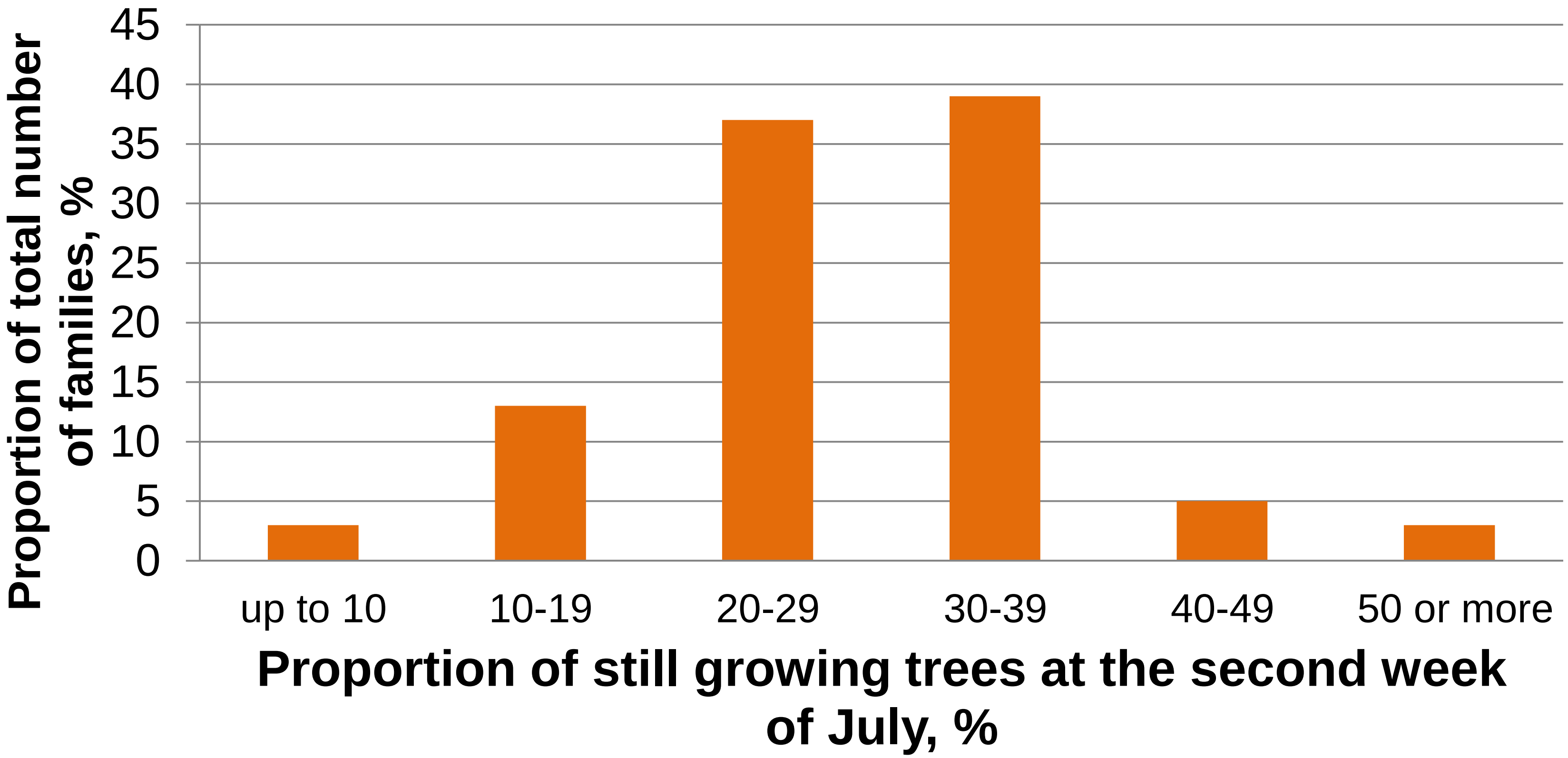
share,% - share of total height increment, formed in period with highest growth intensity

Results
O.p. progeny trials

INVESTMENT IN YOUR FUTURE

Funded by the European Union

- Length of used growing season at family mean level was weakly related with total length of height increment (r=-0.05) and share of total height increment, formed in period with highest growth intensity (r=-0.13)



Funded by the European Union

Conclusion

Main conclusion – it is possible to select genotypes, forming relative large proportion from total increment in short period of time (1-2 weeks, corresponding to 15-20% of height growth period),

but

selections especially for this trait needs to be carried out; ordinary selection based on tree height would not yield the result

Parts of the studies have been funded by:
- Forest Development Fund (2009)
- ESF project “Importance of Genetic Factors in Formation of Forest Stands with High Adaptability and Qualitative Wood Properties” (No. 2009/0200/1DP/1.1.1.2.0/ 09/APIA/VIAA/146)

Thank You!

aris.jansons@silava.lv

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Climate impacts on lodgepole pine (*Pinus contorta* var. *latifolia*) height growth in a provenance experiment-some preliminary results

Zane Libiete-Zalite, LSFRI “Silava”

Some theoretical background (1)

- Lodgpole pine (*Pinus contorta*, including all subspecies) is widely spread throughout western North America, growing between the latitudes 30° and 64°N.
- Lodgepole pine has a wide ecological amplitude, its varieties being adapted to maritime, continental and subalpine conditions and capable of growing on any type of site.
- There are three main varieties: a coastal form (var. *contorta*), a southern inland form (var. *murrayana*) and a northern inland form (var. *latifolia*).
- The *latifolia* variety has proved useful in northern European conditions, combining fast and straight growth with sufficient climatic hardiness; around 1970 large-scale introduction of these species was started in Sweden.

Some theoretical background (2)

According to results of Scandinavian experiments,

- The wood quality of lodgepole pine is comparable to that of Scots pine (*Pinus sylvestris* L.)grown under similar conditions;
- Lodgepole pine has slightly lower wood density, lower bark proportion in stem volume, higher proportion of heartwood and better stem form than Scots pine;
- Lodgepole pine is estimated to produce up to 36% more yield than Scots pine, irrespective of the site index; the optimum rotation is 10-15 years shorter;
- Survival during the initial stand development is higher for lodgepole pine than for Scots pine;
- Lodgepole pine plantations are less stable and lose more biomass due to wind and snow damage than Scots pine.

Consequently...

- Lodgepole pine might be of interest for production of energy wood, pulpwood and perhaps also saw-timber in plantation forestry in Latvia

Understanding tree growth-climate relationships

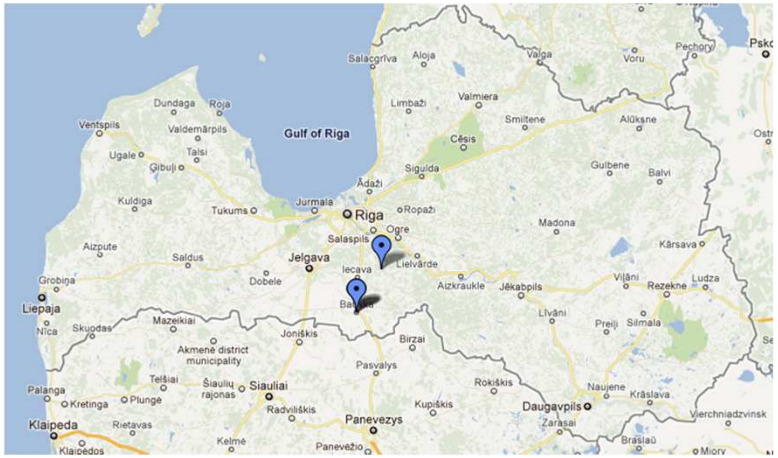
- Before any recommendations for the use of lodgepole pine in Latvian forestry can be made, it is essential to understand how the tree growth is affected by weather and climate variables in Latvian conditions ➔ ADAPTATION
- The most common way to analyze responsiveness of the growth to the climate variables is the analysis of radial growth patterns (tree-rings)
- Several studies suggest that height growth is more suitable for examining the effects of climatic variations, less frequent use of this variable is most likely associated with more laborious gathering of the data

Objective

- The objective of the study was to analyze the effects of climate variables (temperature, precipitation) on the height growth of lodgepole pine (*Pinus contorta* Dougl. var. *latifolia* Engelm.) trees from three various provenances

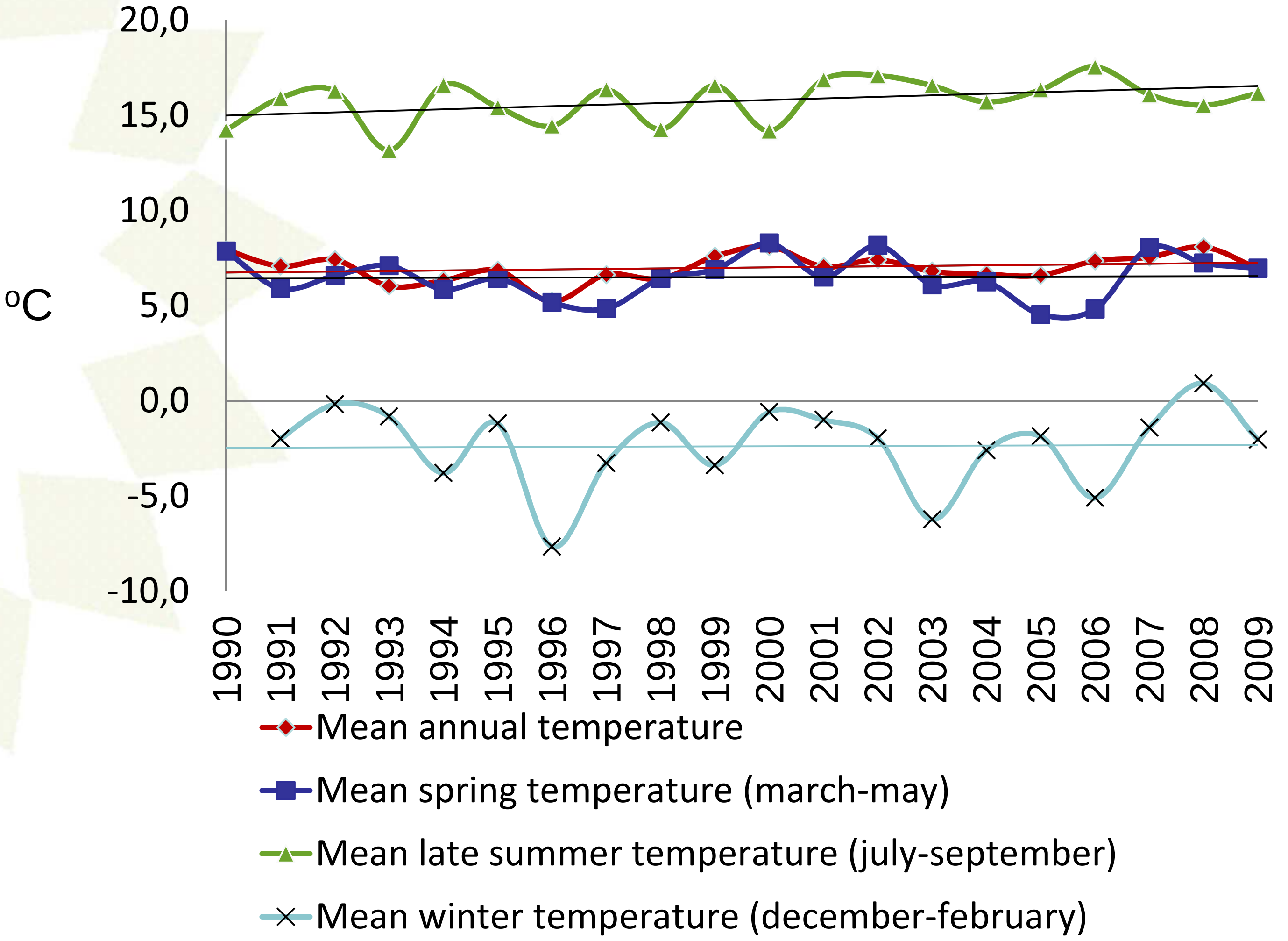
Study material

- Information on annual height growth (cm) of 297 lodgepole pine trees of 3 proveniences – Pink Mountain, Fort Nelson, Summit Lake
- Location of plantation – Zvirgzde
- Year of plantation establishment – 1985
- Information about mean monthly temperature and monthly precipitation amounts from meteostation Bauska

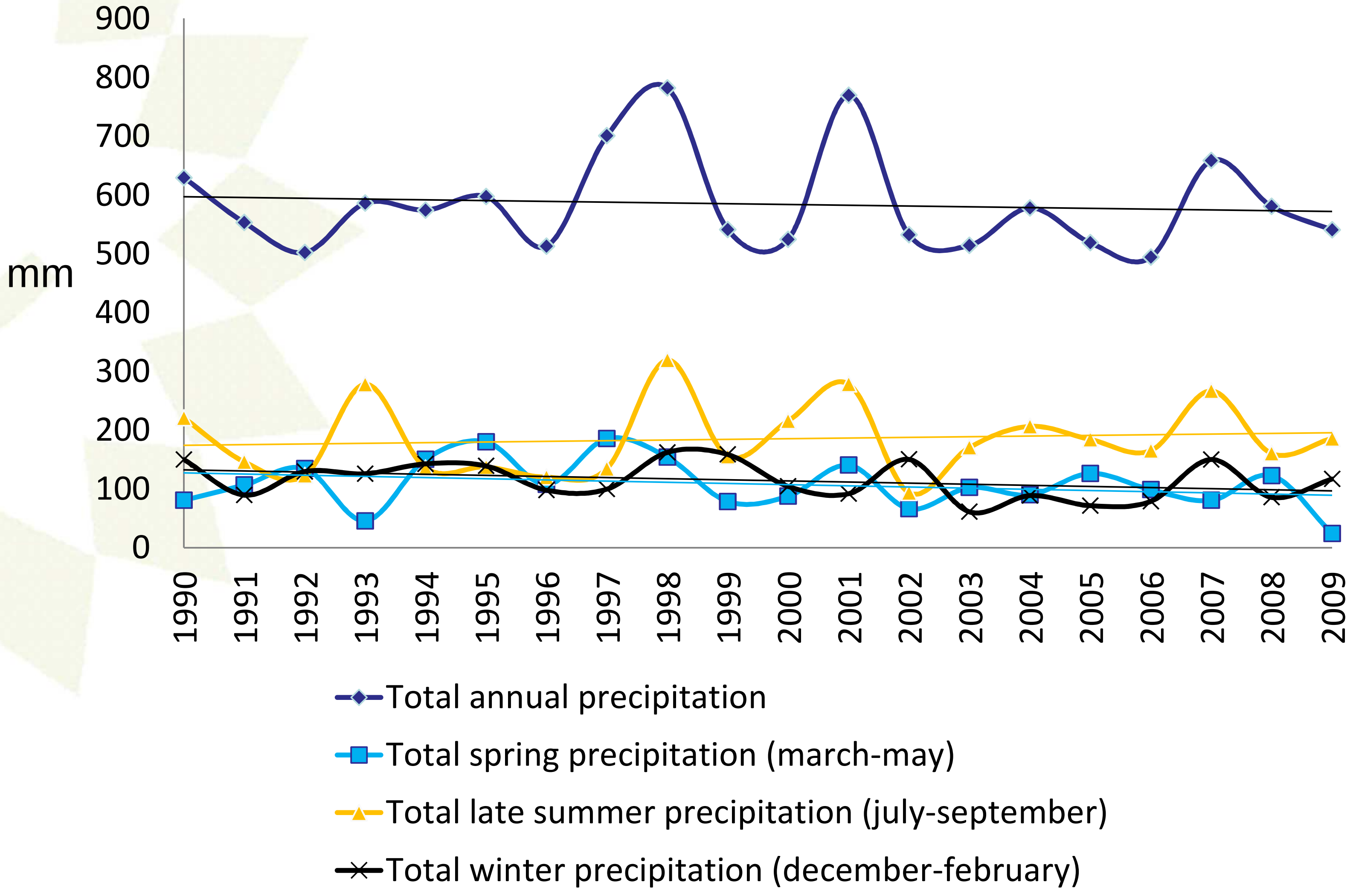


Provenance	Geographical		
	latitude	longitude	altitude a.s.l.
Pink Mountain	57°00'	122°15'-45'	850
Fort Nelson	58°38'	122°41'	495
Summit Lake	54°24'	122°37'	813

Temperature change



Precipitation change



Climate variables

Temperature variables

- Mean annual temperature
- Mean annual temperature of the previous year
- Mean late summer temperature of the previous year (July-September)
- Mean temperature from previous October to April of the current growing season
- Mean temperature of previous November-December

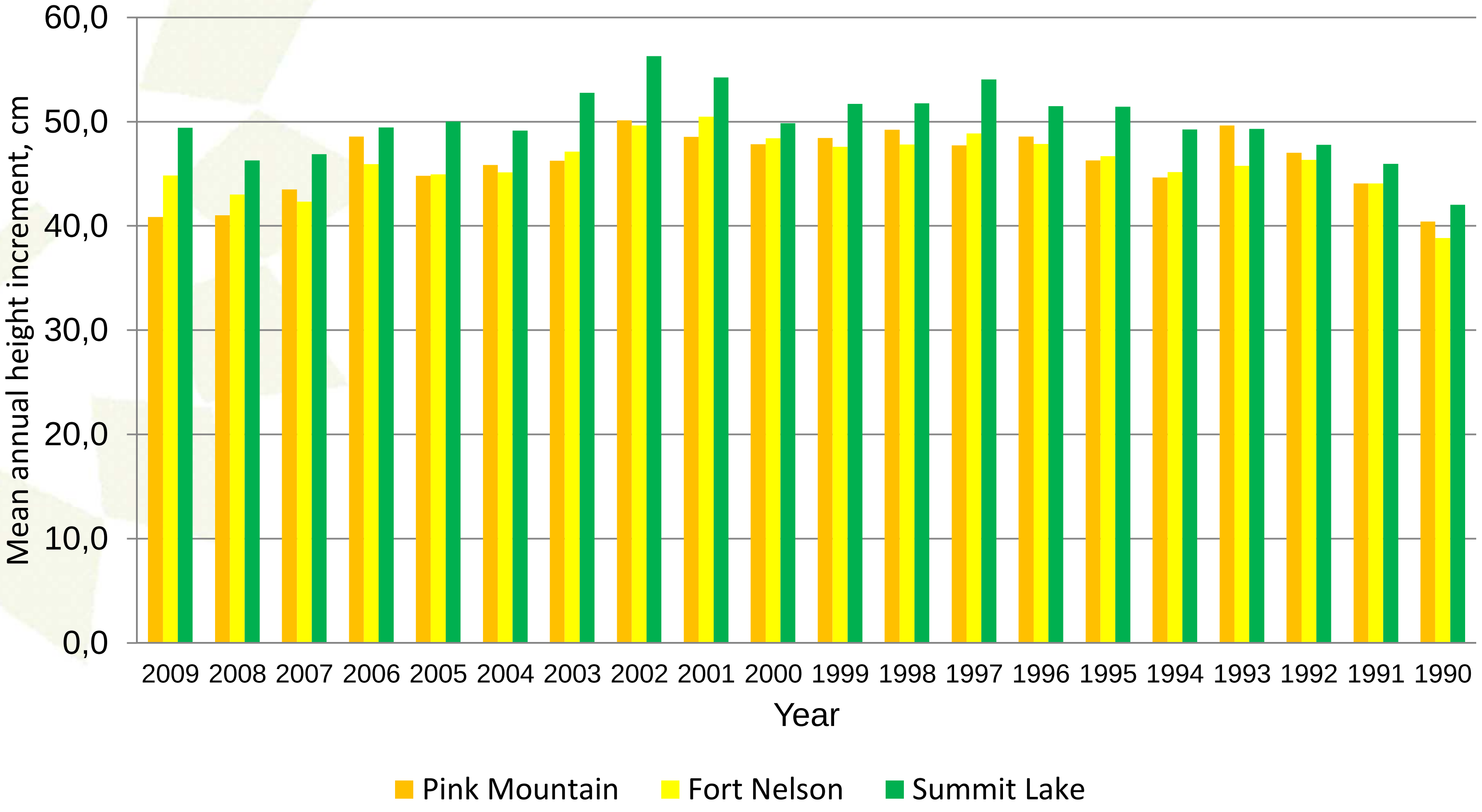
Precipitation variables

- Total annual precipitatipon
- Total annual precipitation of the previous year
- Total precipitation from previous October to April of the current growing season
- Total late summer precipitation of the previous year (July-September)
- Total precipitation from previous December to February
- Sum of total precipitation of previous and current growing season (May-August)

Analysis

- All tree height increment values prior to 1990 were excluded from the analysis to remove establishment-related growth effect
- Linear regression analysis was used to determine possible relationships between annual height growth and climate variables
- Analysis was performed separately for each provenance

Results – mean annual height increment



Results – correlation with climate variables – Pink Mountain

Climate variable	**R**	**R^2**	**F**	**p**
Mean t°	0.078	0.006	11.264	0.001
Mean t° of the previous year	0.087	0.008	13.912	0.000
Mean late summer (July, August, September) t° of the previous year	0.018	0.000	0.606	0.436
Mean t° from previous October to April	0.080	0.006	11.702	0.001
Mean t° of previous November and December	0.069	0.005	8.603	0.003
Total annual precipitation	0.015	0.000	0.420	0.517
Total annual precipitation of the previous year	0.011	0.000	0.235	0.628
Total precipitation from previous October to April	0.017	0.000	0.528	0.467
Total late summer (July, August, September) precipitation of the previous year	0.015	0.000	0.398	0.528
Total precipitation from previous December to February	0.016	0.000	0.459	0.498
Total precipitation of the previous and current growing seasons combined (May-August)	0.060	0.004	6.635	0.010

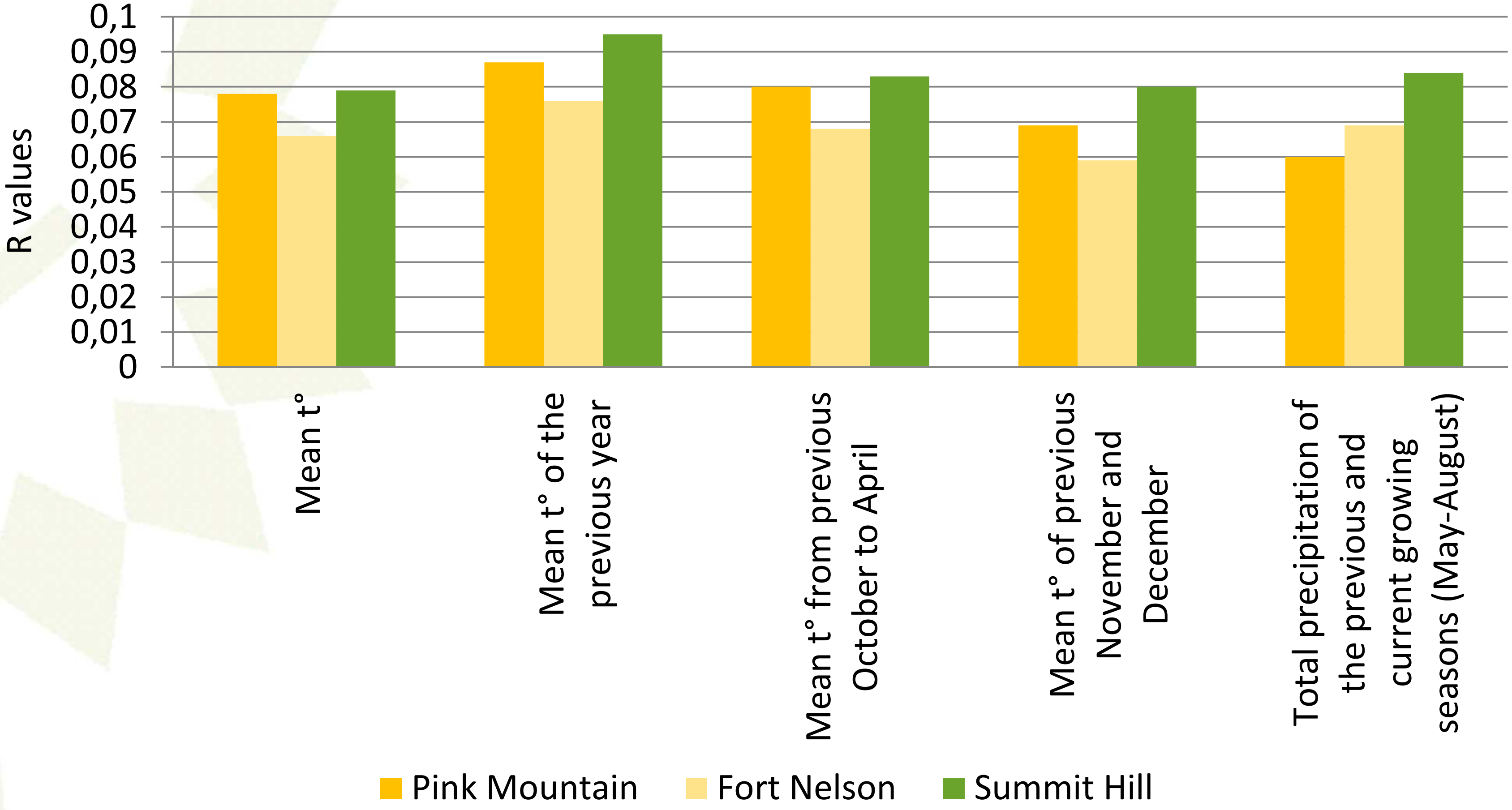
Results – correlation with climate variables – Fort Nelson

Climate variable	R	R^2	F	p
Mean t°	0.066	0.004	8.943	0.003
Mean t° of the previous year	0.076	0.006	11.653	0.001
Mean late summer (July, August, September) t° of the previous year	0.012	0.000	0.273	0.602
Mean t° from previous October to April	0.068	0.005	9.254	0.002
Mean t° of previous November and December	0.059	0.003	7.009	0.008
Total annual precipitation	0.025	0.001	1.251	0.263
Total annual precipitation of the previous year	0.011	0.000	0.232	0.630
Total precipitation from previous October to April	0.016	0.000	0.544	0.461
Total late summer (July, August, September) precipitation of the previous year	0.004	0.000	0.036	0.849
Total precipitation from previous December to February	0.024	0.001	1.175	0.278
Total precipitation of the previous and current growing seasons combined (May-August)	0.069	0.005	9.670	0.002

Results – correlation with climate variables – Summit Lake

Climate variable	**R**	**R^2**	**F**	**p**
Mean t°	0.079	0.006	13.121	0.000
Mean t° of the previous year	0.095	0.009	19.137	0.000
Mean late summer (July, August, September) t° of the previous year	0.004	0.000	0.033	0.855
Mean t° from previous October to April	0.083	0.007	14.649	0.000
Mean t° of previous November and December	0.080	0.006	13.675	0.000
Total annual precipitation	0.033	0.001	2.240	0.135
Total annual precipitation of the previous year	0.026	0.001	1.461	0.227
Total precipitation from previous October to April	0.017	0.000	0.605	0.437
Total late summer (July, August, September) precipitation of the previous year	0.009	0.000	0.158	0.691
Total precipitation from previous December to February	0.014	0.000	0.406	0.524
Total precipitation of the previous and current growing seasons combined (May-August)	0.084	0.007	14.793	0.000

Results – comparison of correlation coefficients



Things to do next

- Get meteodata from a closer location, if possible;
- Extend the analysis, including combined climate variables of temperature and precipitation
- Compare the climate responsiveness of the lodgepole pine height growth to that of the Scots pine in Latvia

Thank You for Your attention!

European Social Fond project (No. 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Differences in wood trials between Norway spruce

Ilze Irbe, Uldis Grīnfelds,

Inese Šāble, Anrijs Verovkins,

Laura Vīķele, Baiba Horste,

Arnis Treimanis, Mārīte Škute,

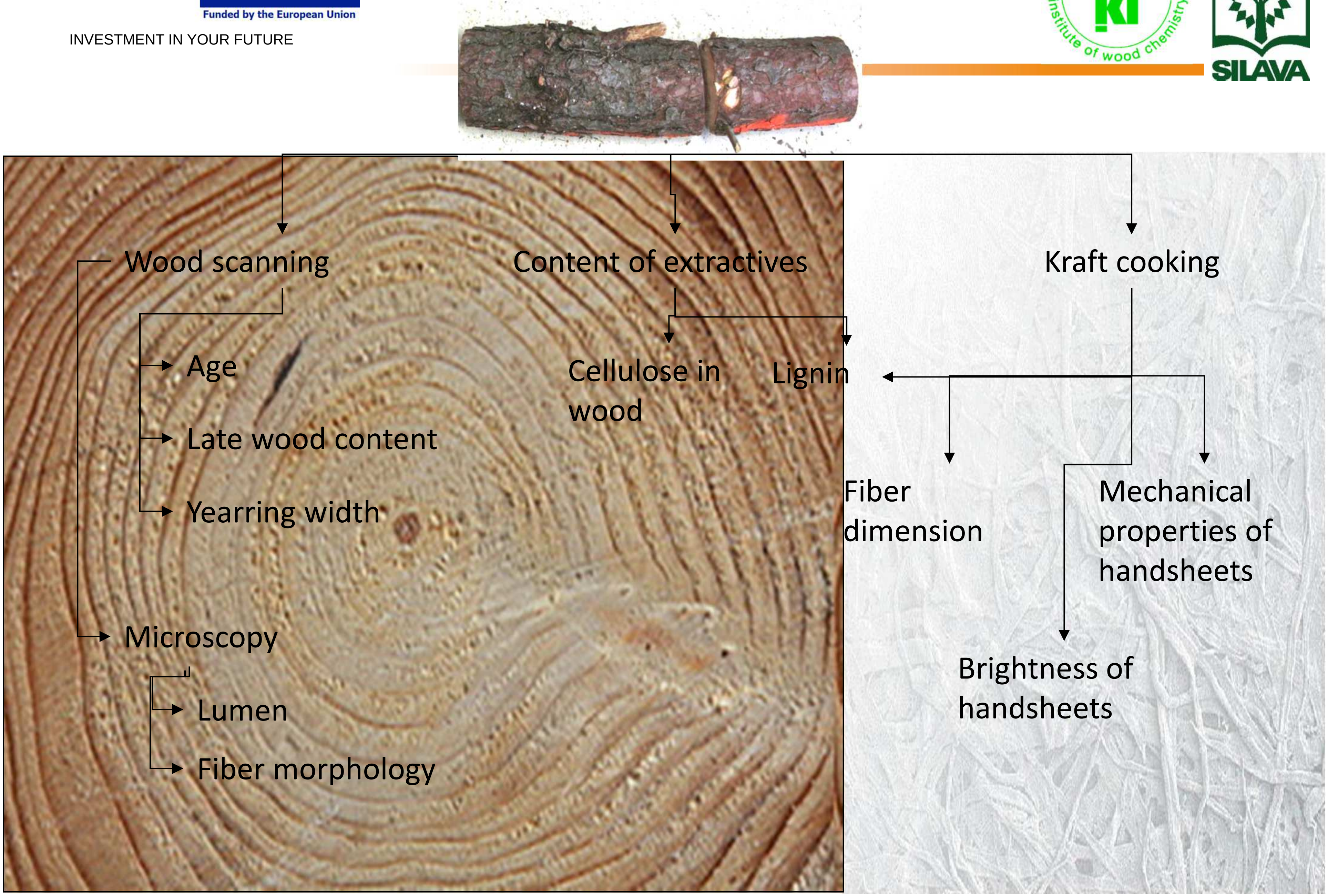
Āris Jansons e.t.c.

Backgraund

Sample trees cut at age 21 in one site – Madona region
Wood used for analysis of the trunk from 0.5 to 1.3 meters in height from the ground.

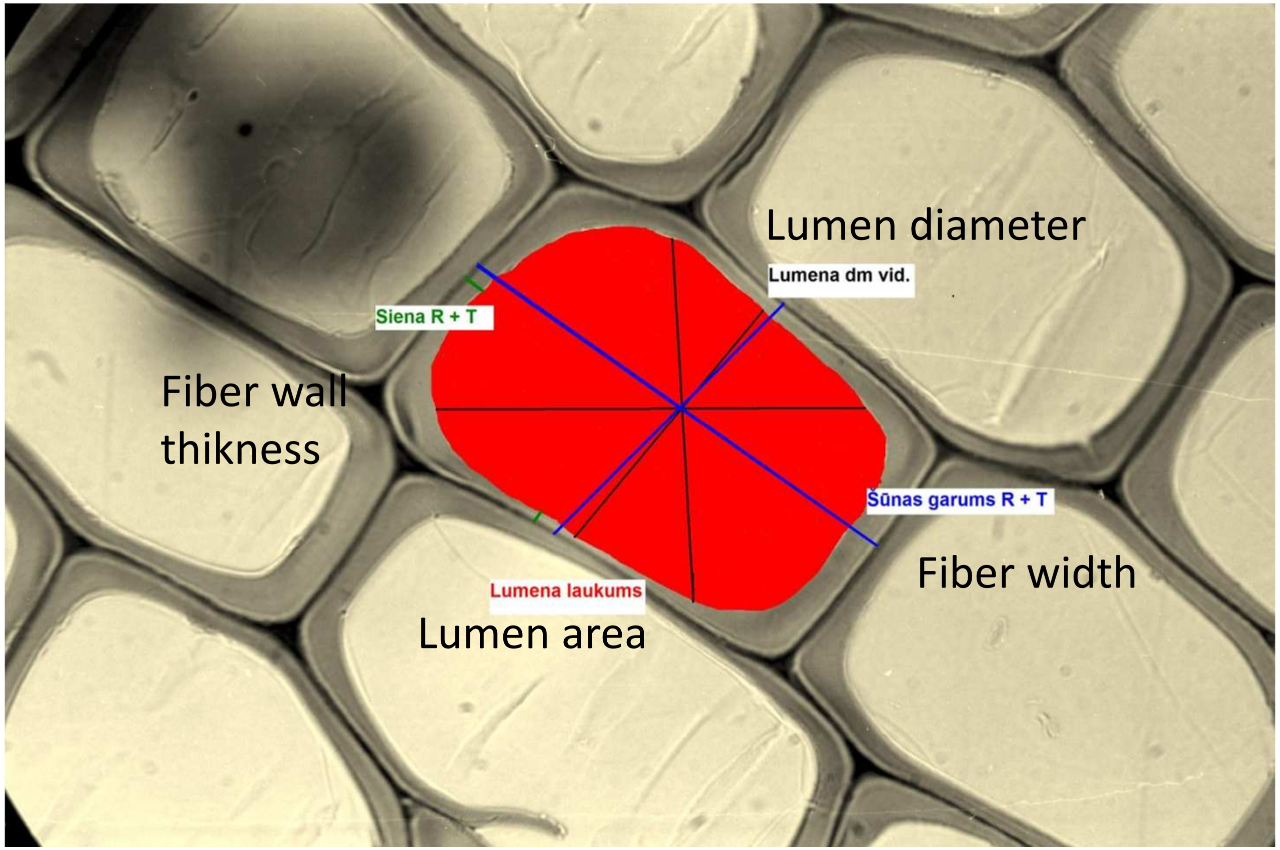
Clone	Count of trees
26	3
31	4
A10	3
A15	3
A7	2
B10	3
B15	3
B6	4
KR13	3
V7	3
V9	3

Materials and method



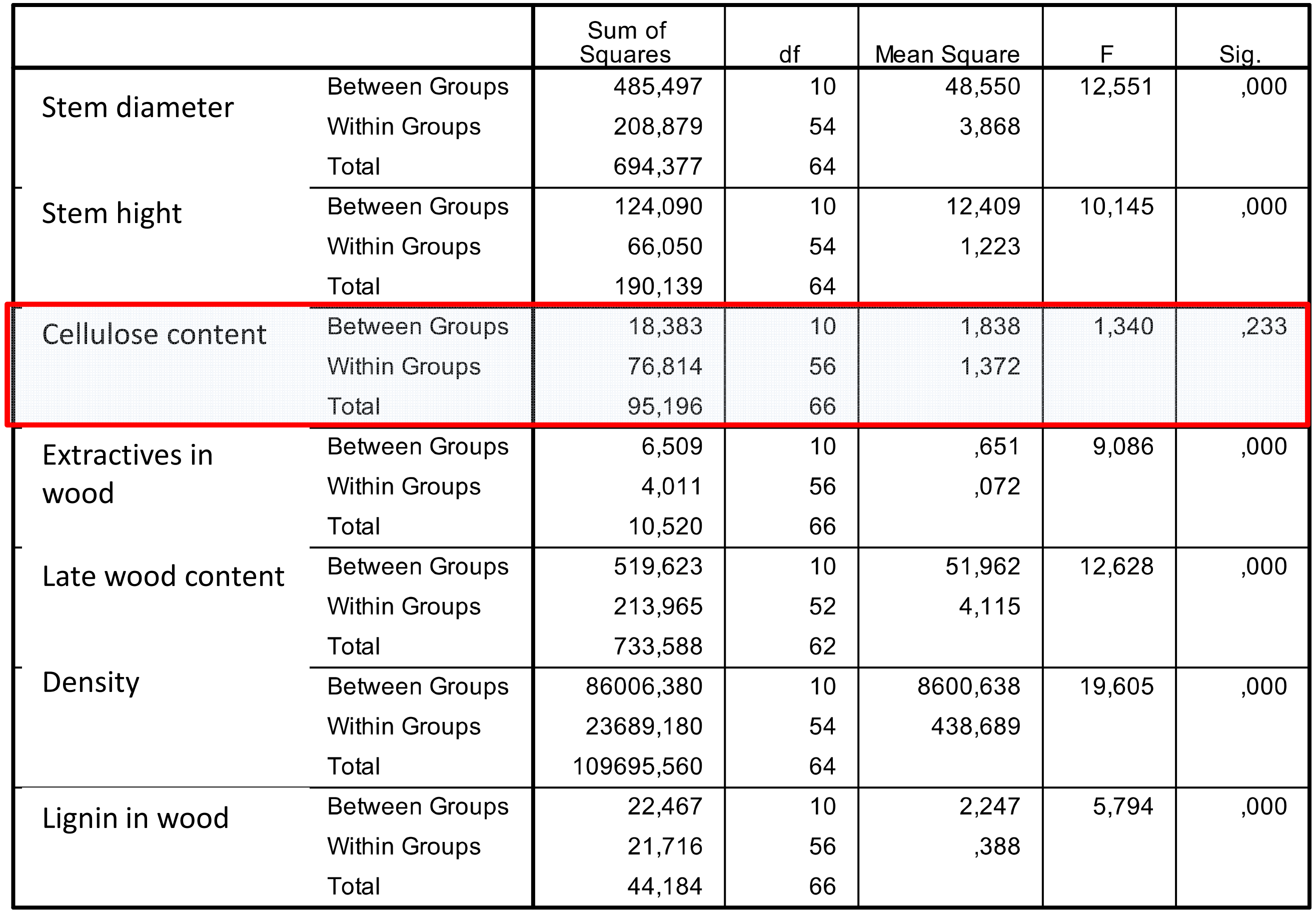
- Wood scanning
  - Age
  - Late wood content
  - Yearring width
- Microscopy
  - Lumen
  - Fiber morphology
- Content of extractives
  - Cellulose in wood
  - Lignin
- Kraft cooking
  - Lignin
  - Fiber dimension
  - Mechanical properties of handsheets
  - Brightness of handsheets

Microscopy


Lumen diameter
Lumena dm vid.
Siena R + T
Fiber wall thikness
Šūnas garums R + T
Fiber width
Lumena laukums
Lumen area

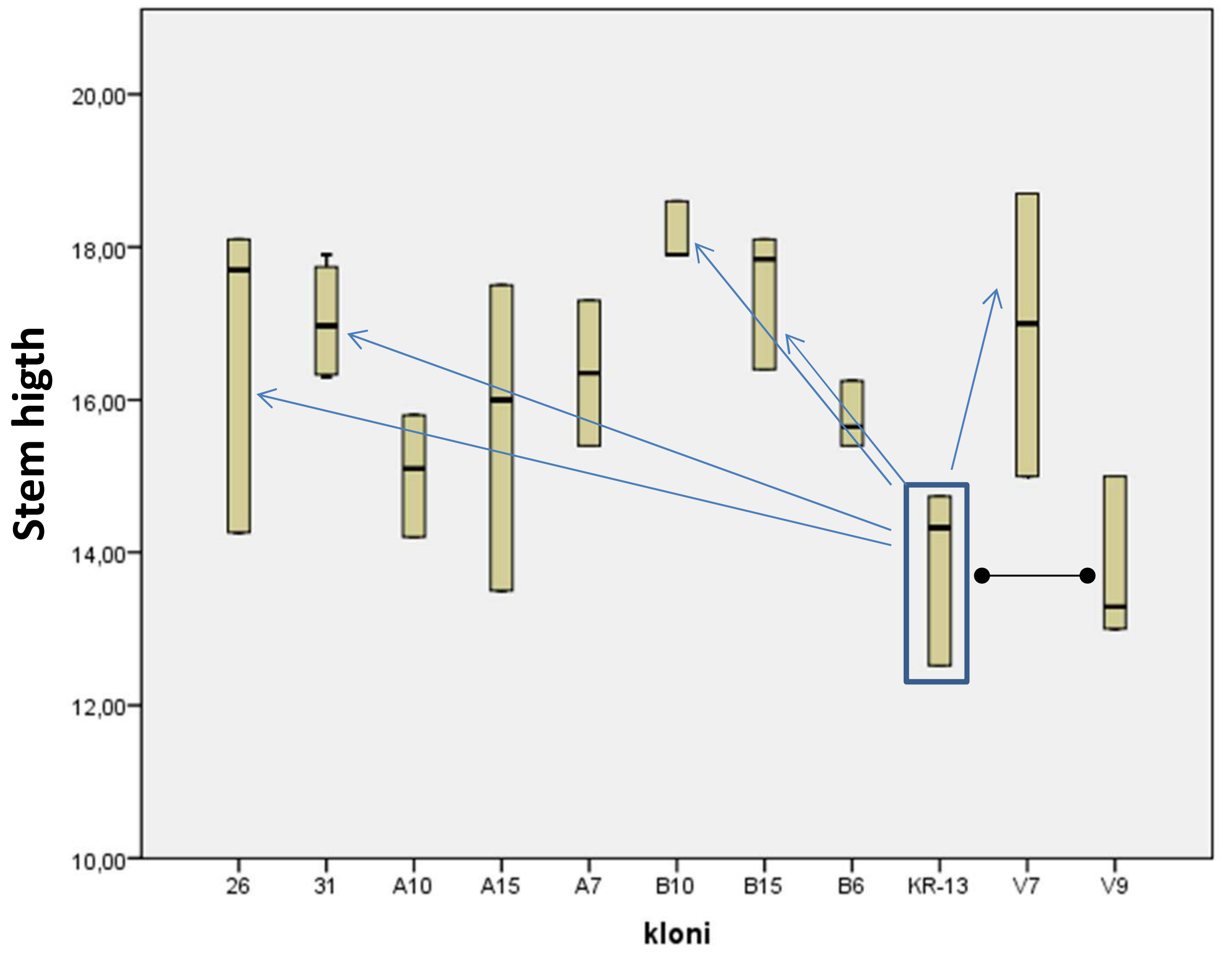
Results

ANOVA

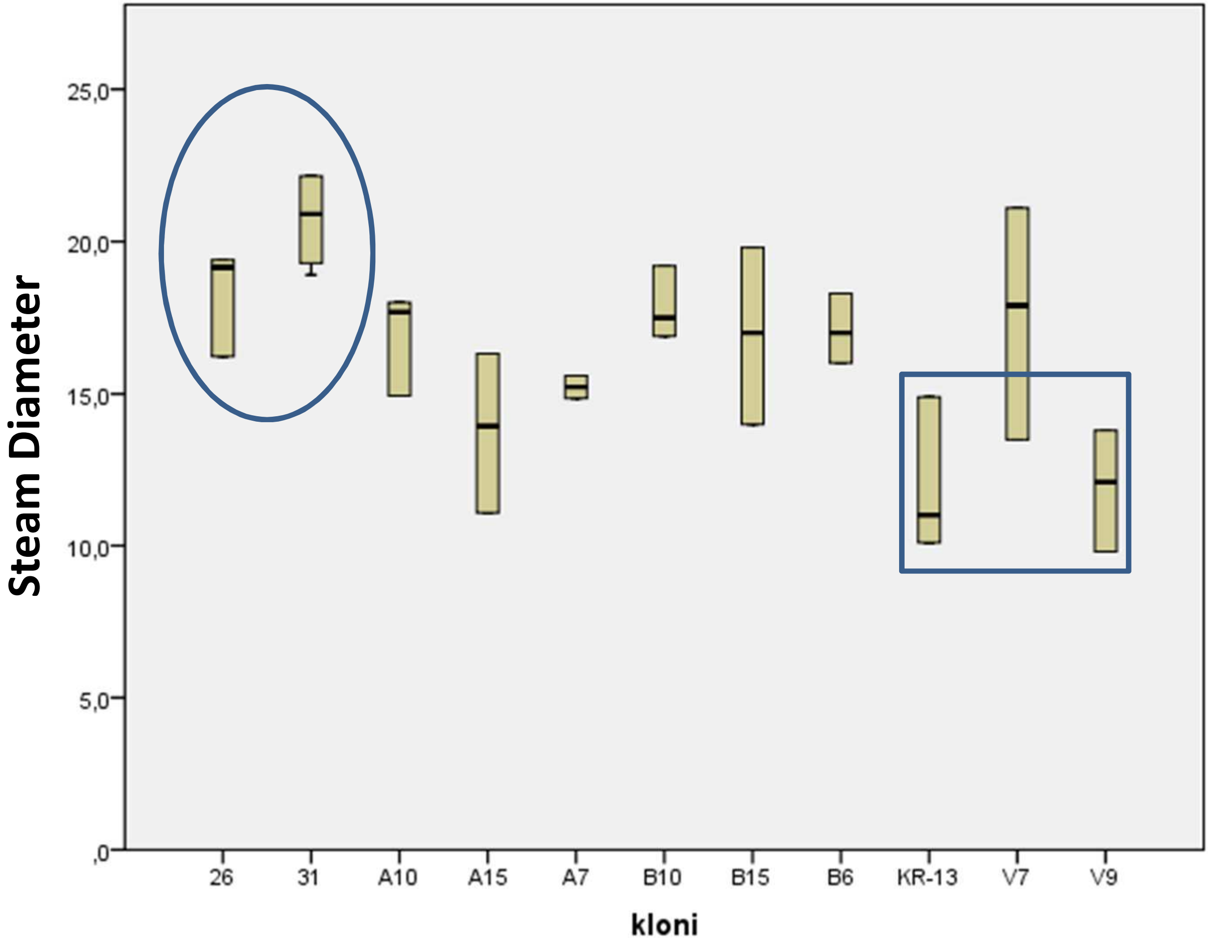


		Sum of Squares	df	Mean Square	F	Sig.
Stem diameter	Between Groups	485,497	10	48,550	12,551	,000
	Within Groups	208,879	54	3,868		
	Total	694,377	64			
Stem hight	Between Groups	124,090	10	12,409	10,145	,000
	Within Groups	66,050	54	1,223		
	Total	190,139	64			
Cellulose content	Between Groups	18,383	10	1,838	1,340	,233
	Within Groups	76,814	56	1,372		
	Total	95,196	66			
Extractives in wood	Between Groups	6,509	10	,651	9,086	,000
	Within Groups	4,011	56	,072		
	Total	10,520	66			
Late wood content	Between Groups	519,623	10	51,962	12,628	,000
	Within Groups	213,965	52	4,115		
	Total	733,588	62			
Density	Between Groups	86006,380	10	8600,638	19,605	,000
	Within Groups	23689,180	54	438,689		
	Total	109695,560	64			
Lignin in wood	Between Groups	22,467	10	2,247	5,794	,000
	Within Groups	21,716	56	,388		
	Total	44,184	66			

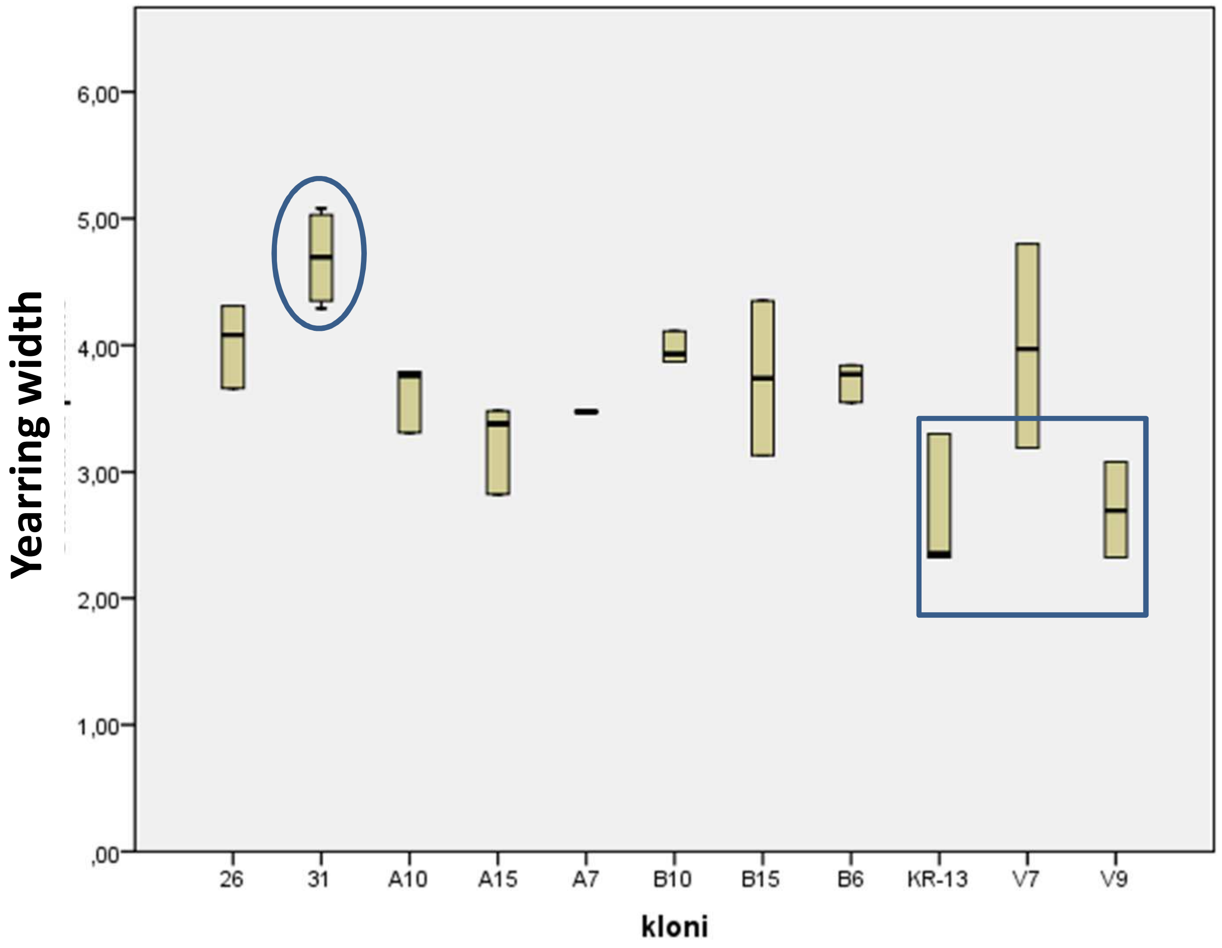
Results


Stem higth
20,00
18,00
16,00
14,00
12,00
10,00
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9
kloni

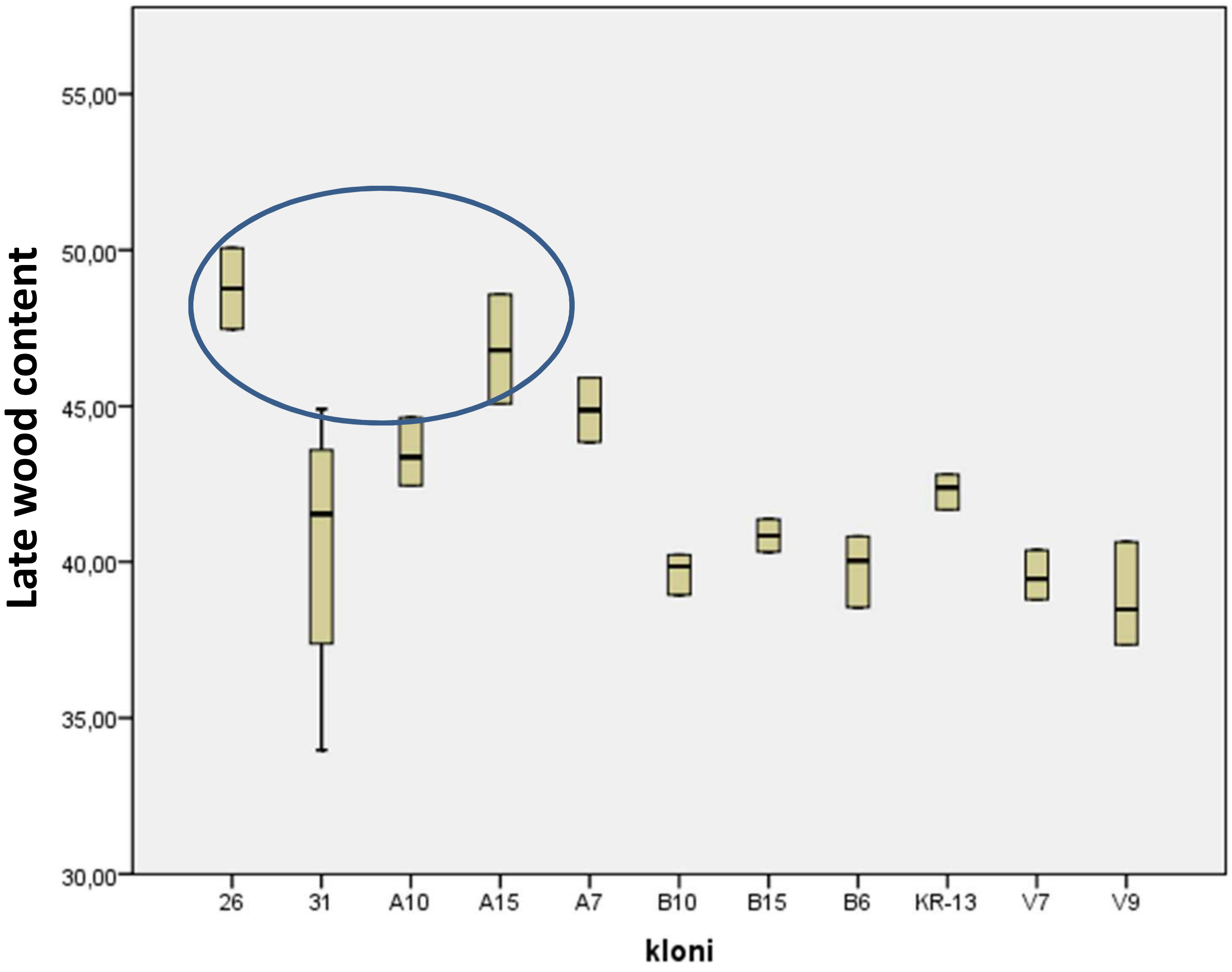
Results


Steam Diameter
25,0
20,0
15,0
10,0
5,0
,0
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9
kloni

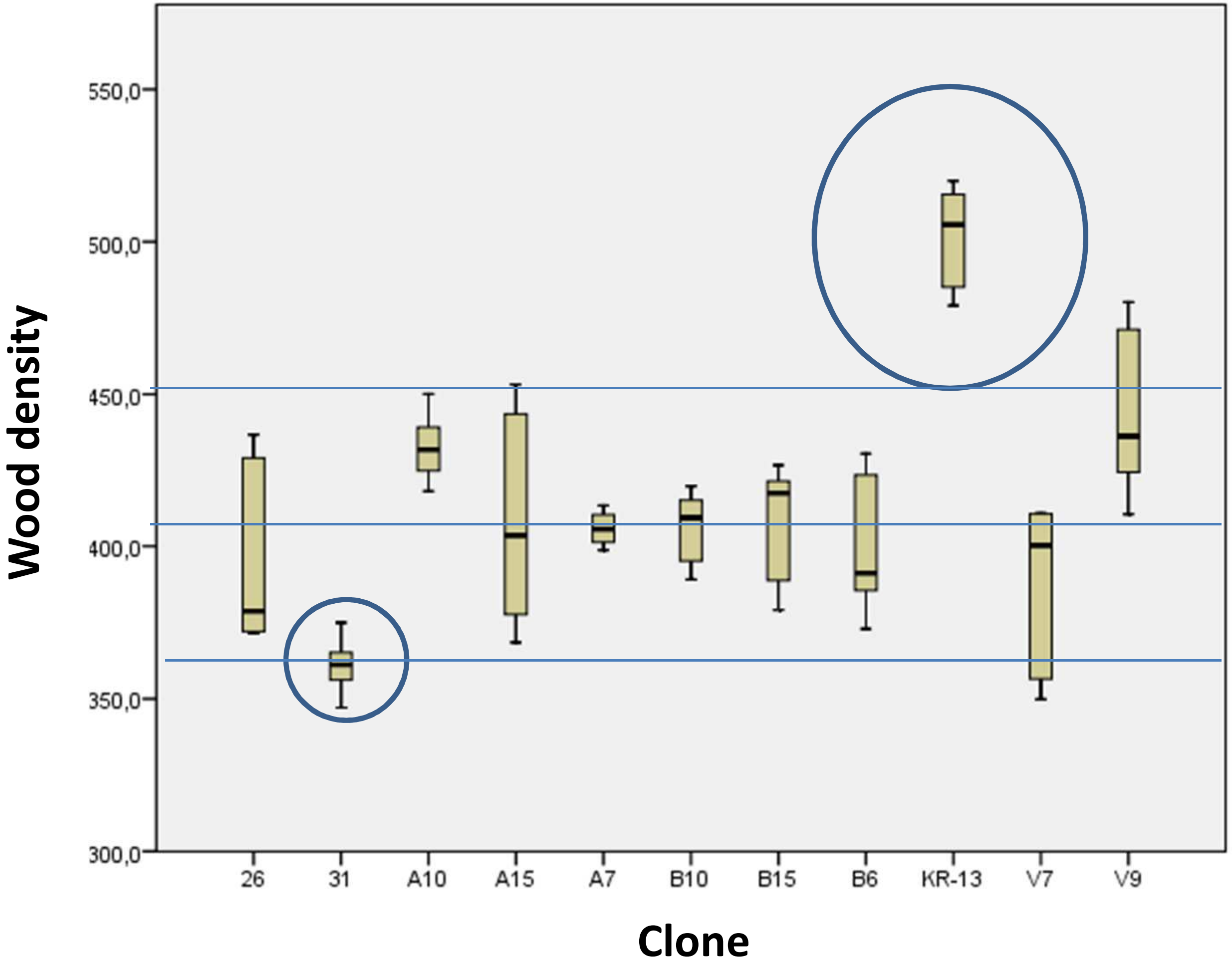
Results


Yearring width
6,00
5,00
4,00
3,00
2,00
1,00
,00
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9
kloni

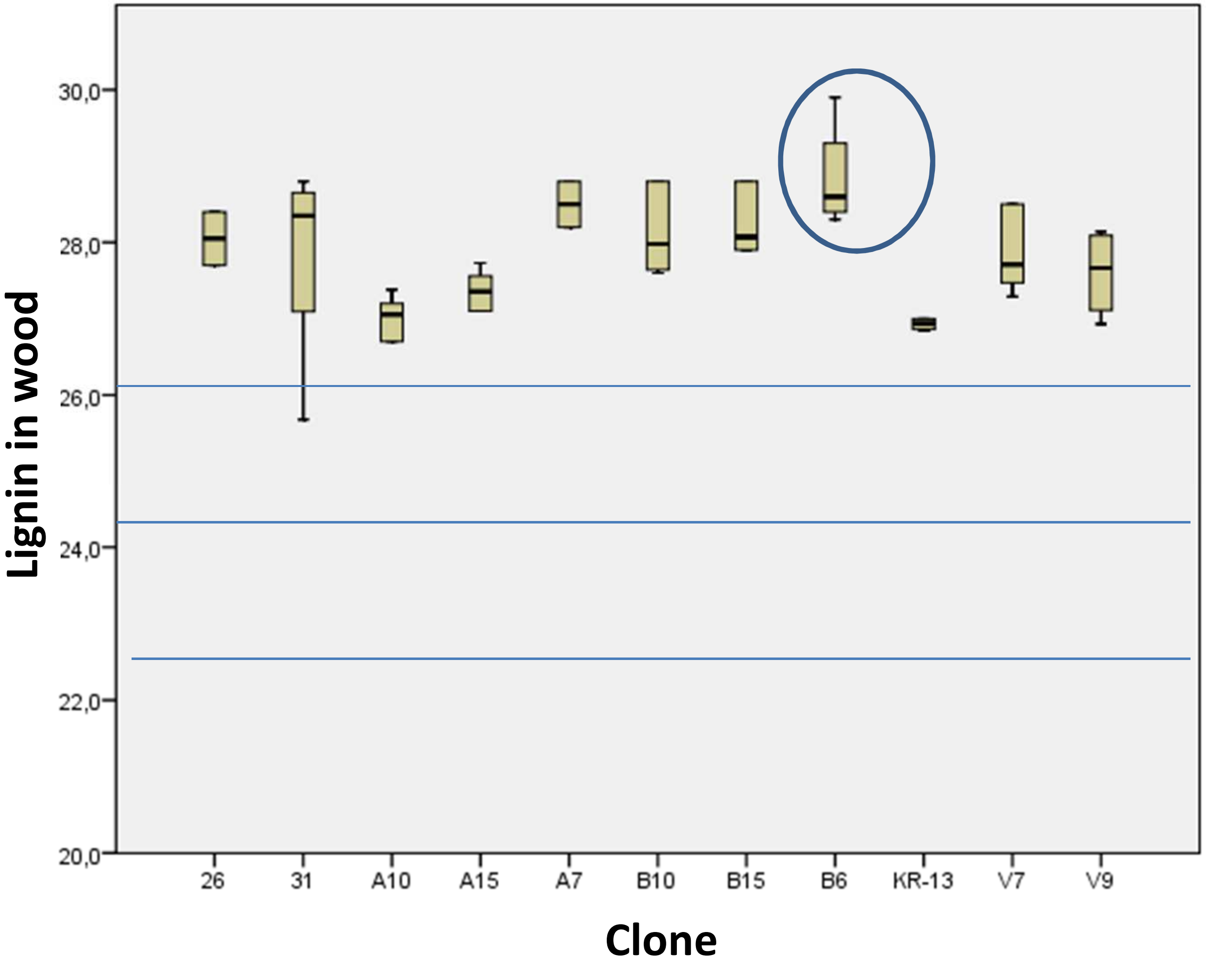
Results


Late wood content
55,00
50,00
45,00
40,00
35,00
30,00
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9
kloni

Results


Wood density
550,0
500,0
450,0
400,0
350,0
300,0
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9
Clone

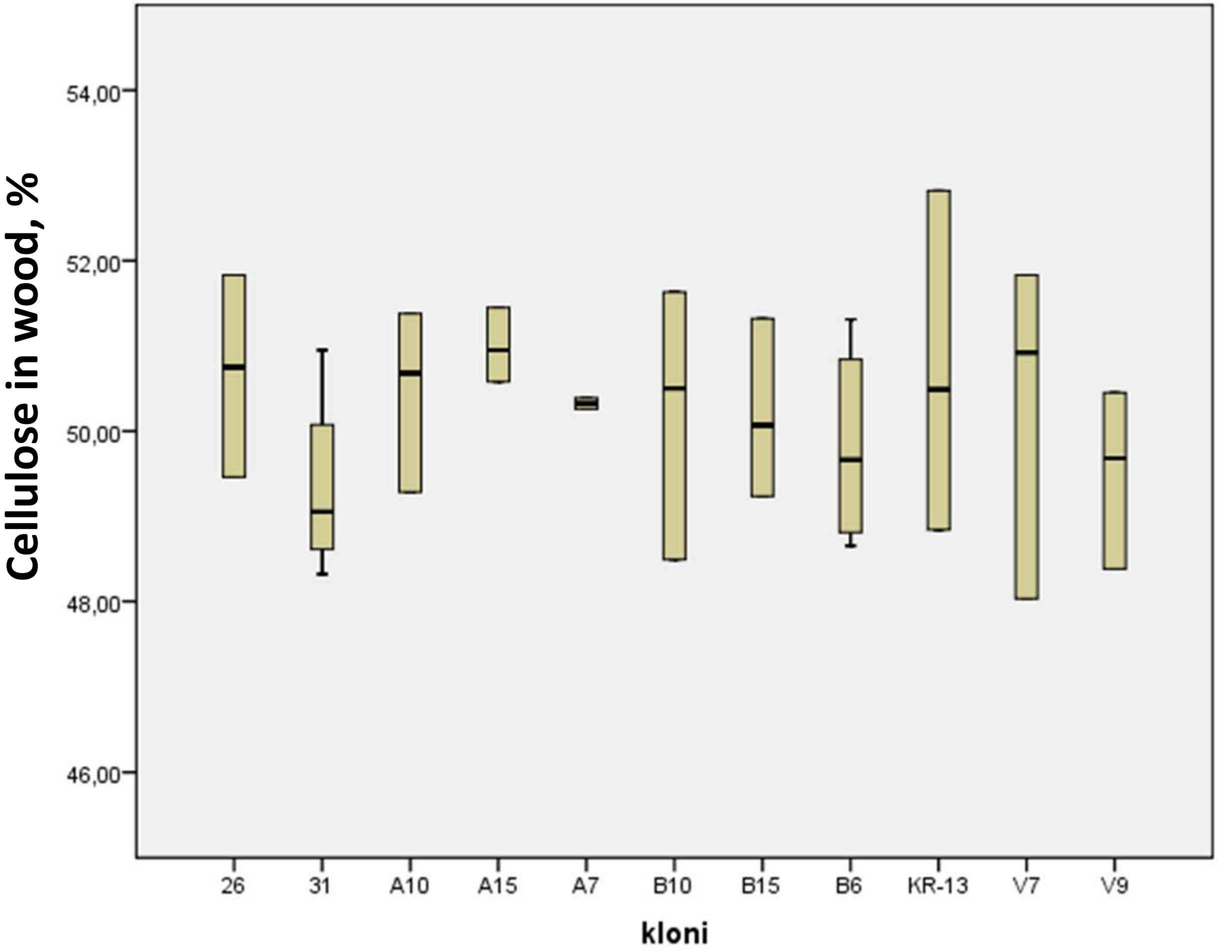
Results


Lignin in wood
30,0
28,0
26,0
24,0
22,0
20,0
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9
Clone

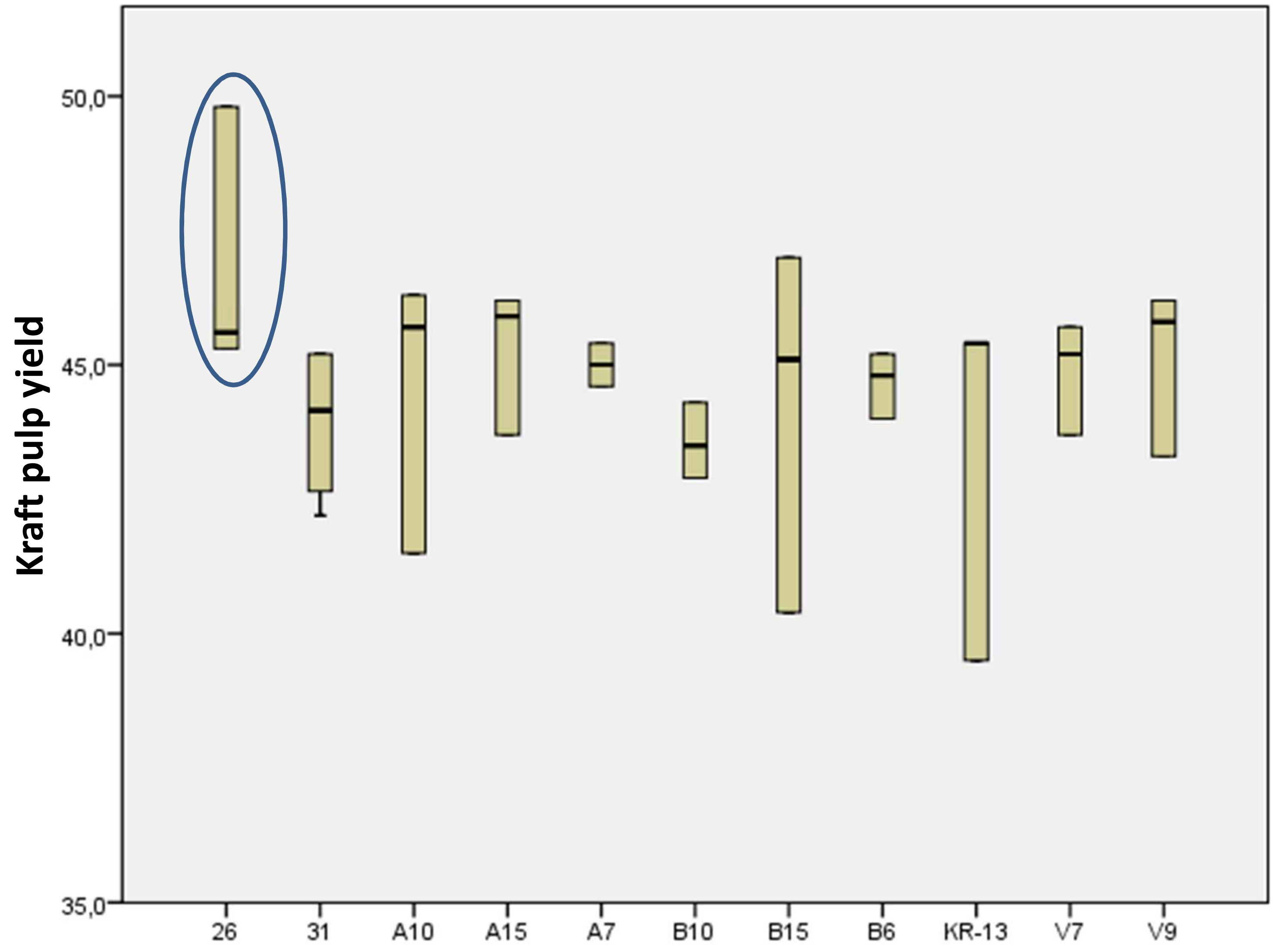
Funded by the European Union

INVESTMENT IN YOUR FUTURE

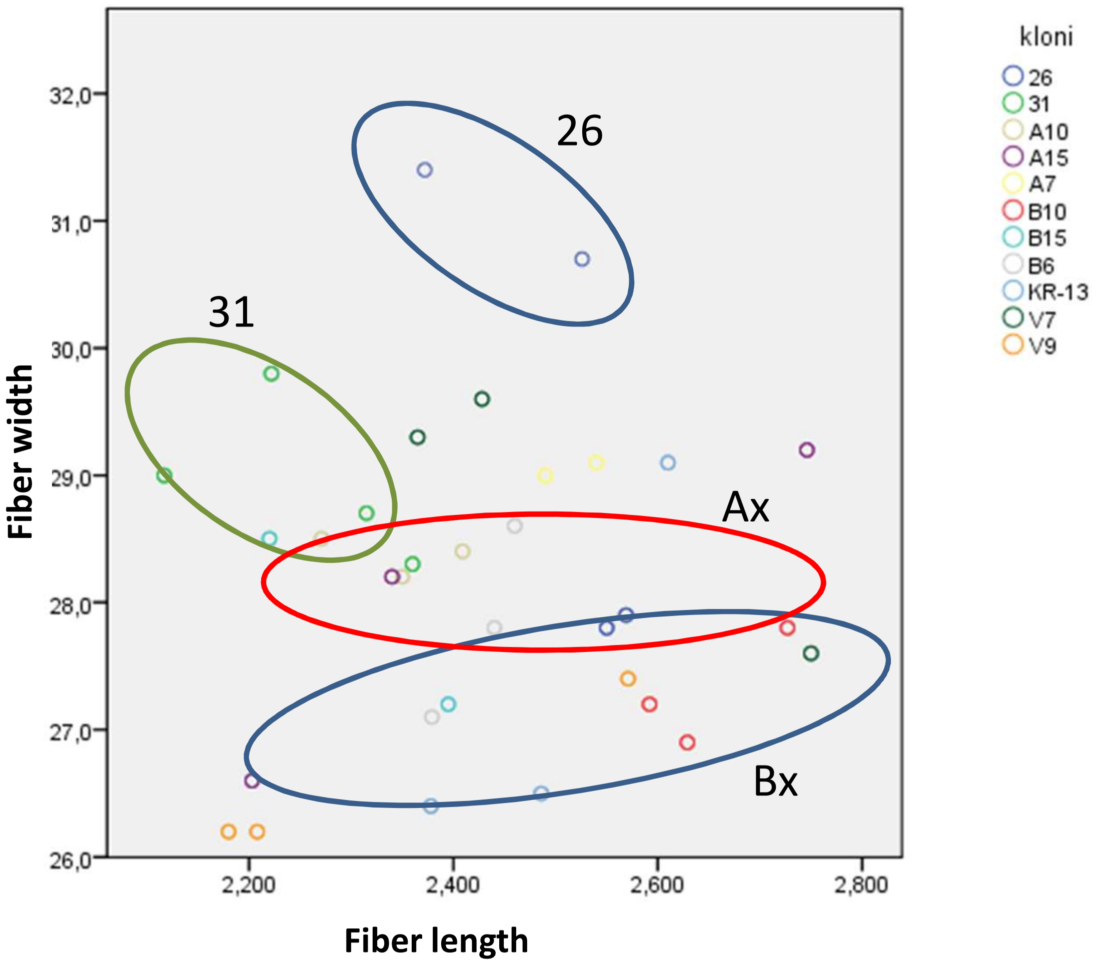
Results



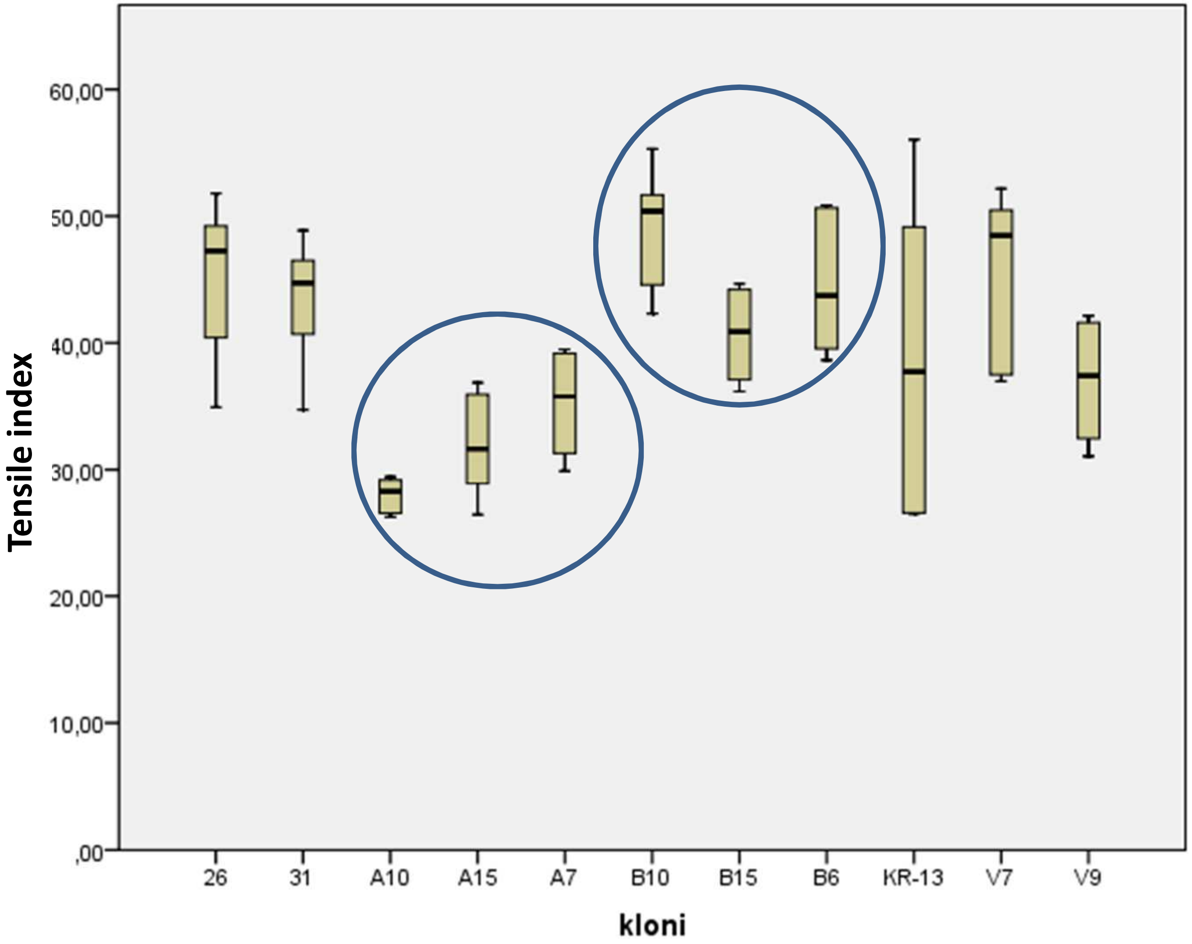
Results


Kraft pulp yield
50,0
45,0
40,0
35,0
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9

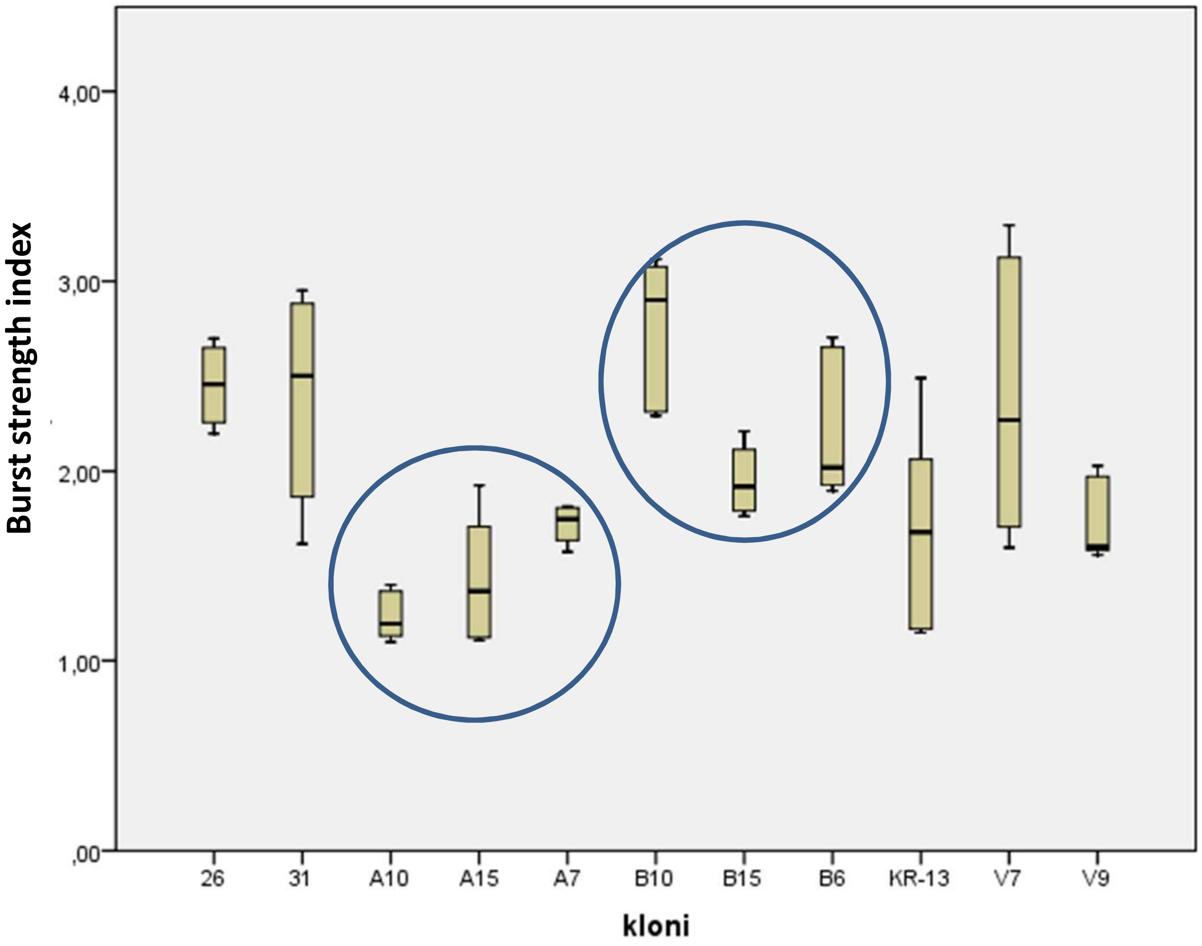
Results


26
31
Ax
Bx
32,0
31,0
30,0
29,0
28,0
27,0
26,0
2,200
2,400
2,600
2,800
Fiber width
Fiber length
kloni
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9

Results


Tensile index
60,00
50,00
40,00
30,00
20,00
10,00
,00
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9
kloni

Results

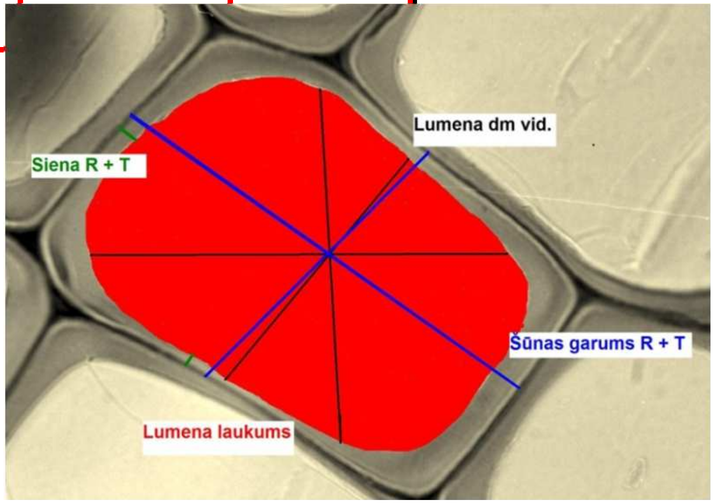

Burst strength index
4,00
3,00
2,00
1,00
,00
26
31
A10
A15
A7
B10
B15
B6
KR-13
V7
V9
kloni

Funded by the European Union
INVESTMENT IN YOUR FUTURE

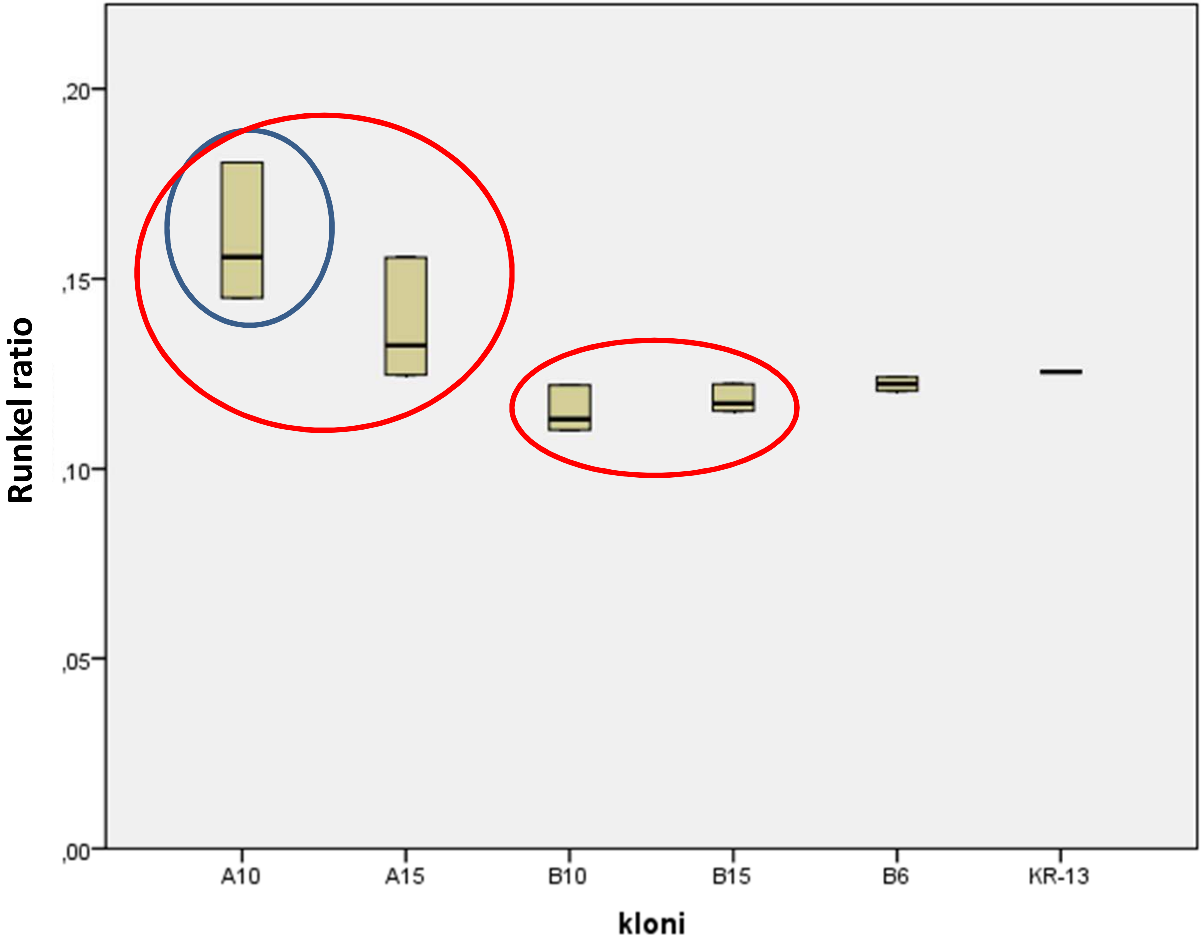
Results

		Fiber length	Fiber width	Runkel l.w.	Runkel e.w.
Tensile index	Pearson Correlation	,185	-,117	-,305	-,645**
	Sig. (2-tailed)	,151	,364	,114	,000
	N	62	62	28	28
Burst index	Pearson Correlation	,150	,037	-,274	-,625**
	Sig. (2-tailed)	,243	,776	,158	,000
	N	62	62	28	28
Breaking length	Pearson Correlation	,203	-,110	-,315	-,650**
	Sig. (2-tailed)	,114	,396	,102	,000
	N	62	62		

Runkel ratio = 2x fiber wall thickness / lumen diameter



Results



Conclusion

1. More wood produce 26, 31, B10, V7 Sitka spruce clones

2. Kraft pulp yield doesn't differ significant, but more pulp is possible to produce from clone #26.

3. No signficant differences found in fiber length, but is found significant differences in fiber width between clones

4. Is significant difference in paper tensile strength between Ax and Bx spruce clones. Bx shows higher results compare to Ax.

5. Fiber morphology microscopy measurments shows, that Runkel ratio in earlywood effect mechanical properties than fiber latewood.

Study has been partly funded by:

ESF project "Importance of Genetic Factors in Formation of Forest Stands with High Adaptability and Qualitative Wood Properties"

(No 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)

koksnes ķīmijas institūts • institute of wood chemistry •

SILAVA

ESF

Funded by the European Union

INVESTMENT IN YOUR FUTURE

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE
SILAVA

Genetic determination of wood traits in Scots pine - analysis of candidate genes influencing wood quality

Krista Kānberga–Siliņa
Latvian State Forest Research Institute «Silava»

Salaspils 2011

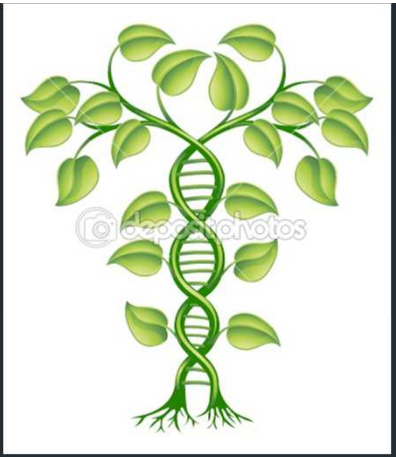
Introduction

- **With a few exceptions, little is known about the cellular, molecular, and developmental processes that underlie wood formation.**
- **Wood formation is controlled by exogenous (photoperiod and temperature) and endogenous (phytohormones) factors and by interaction between them.**
- **Wood (secondary xylem) formation four major steps : cell division, cell expansion (elongation and radial enlargement), cell wall thickening (involving cellulose, hemicellulose, cell wall proteins, and lignin biosynthesis and deposition) and programmed cell death.**
- **Wood density is one of main characteristics of wood quality.**

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Genetic aspects



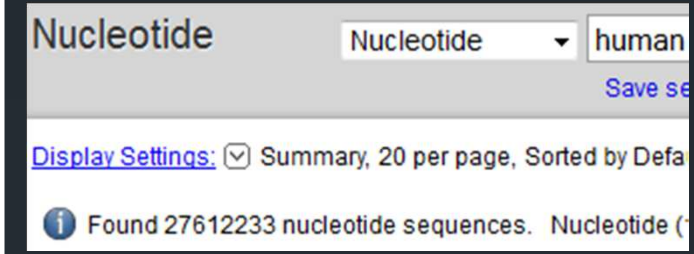
- Wood formation is driven by the coordinated expression of numerous structural (some of known function) and regulatory genes (mostly unknown).
- The very large genomes of all *Pinus* species, long life cycle, large multigenic families and high metabolistic elasticity are some of the reasons why pines were less studied at molecular level.
- Now there are linkage maps, EST databases and gene expression data available for *P.taeda* and *P.radiata* so comparative genomics approach can be used for information transfer to other important pine species.
- Gene copy number variation (CNV) is type of genetic variation. In human genomes CNV affects gene expression. In *Arabidopsis thaliana* and *Sorghum bicolor* gene duplications altered ion transport.

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Aim

- To find out if it is possible to find link between wood density and genetic parameters in Scots pine
- For future dream- marker assisted selection for Scots pine.
- Taking in consideration one genetic variation types –CNV.

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE



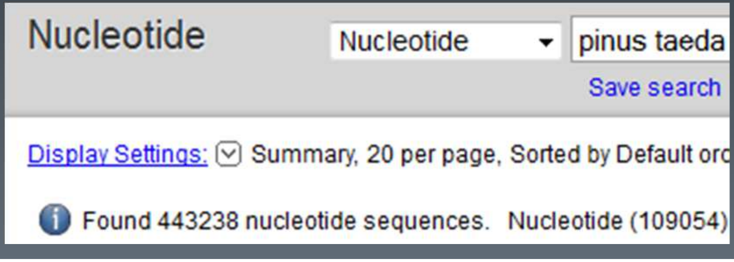
human

Display Settings: Summary, 20 per page, Sorted by Defa

Found 27612233 nucleotide sequences. Nucleotide (

Methods

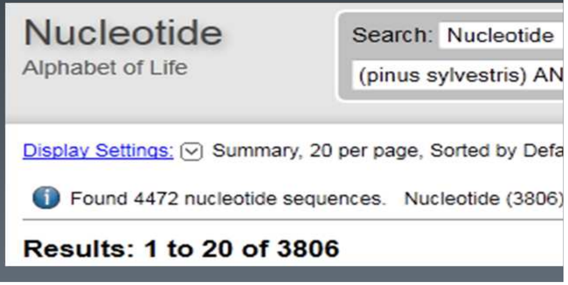
- Wood density measured with Pilodyn instrument.
- Selected 25 trees with higher wood density and 25 with lower, belonging to different tree families.
- Literature analysis and searching in databases for candidate genes.
- Sample gathering (Spring and Autumn), DNA, RNA extracting, purification, PCR, Real time PCR optimization.
- Quantitative RT PCR for detecting gene copy number variation.
- Relative standart curve RT PCR for gene expression analysis.
- Data analysis



pinus taeda

Display Settings: Summary, 20 per page, Sorted by Default orc

Found 443238 nucleotide sequences. Nucleotide (109054)



(pinus sylvestris) AN

Display Settings: Summary, 20 per page, Sorted by Defa

Found 4472 nucleotide sequences. Nucleotide (3806)

Results: 1 to 20 of 3806

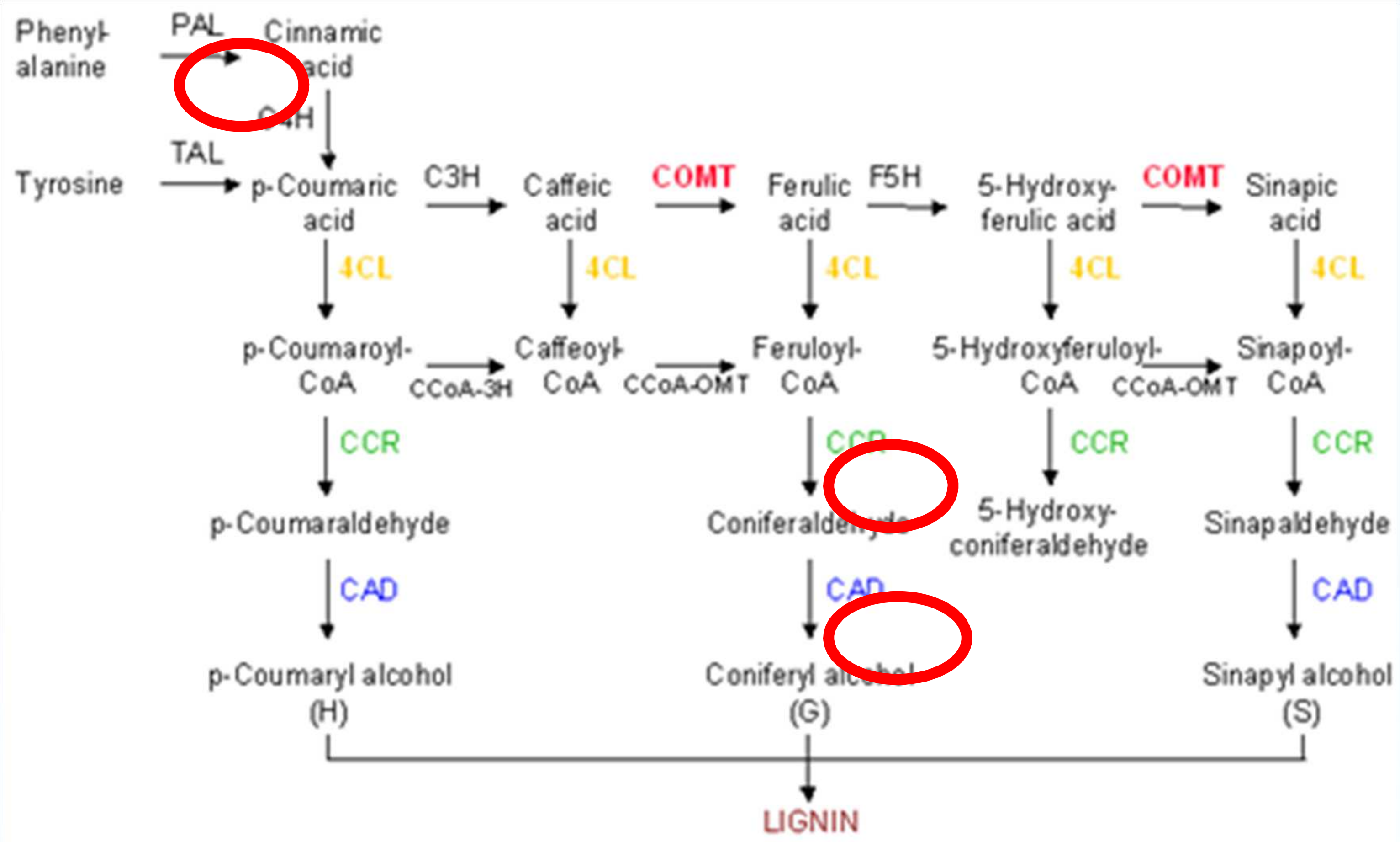
Candidate genes

- At first nine genes were taken in consideration (*CAD1, CESA1, CESA7, CESA4, AGP1, aquaporin like, aquaporin gene, Susy1*).
- Candidate genes were selected of which three are involved in lignin biosynthesis – phenylalanine ammonia-lyase gene (*PAL1*), cinnamyl alcohol dehydrogenase gene (*CAD1*), Cinnamoyl-CoA reductase gene (*CCR1*);

sucrose synthase gene (*Susy1*) in sucrose metabolism ; Aquaporin like gene (*Aqual1*) involved in water transport, in attempts to reveal whether link can be established between candidate gene expression, gene copy number and wood density .

Funded by the European Union
INVESTMENT IN YOUR FUTURE

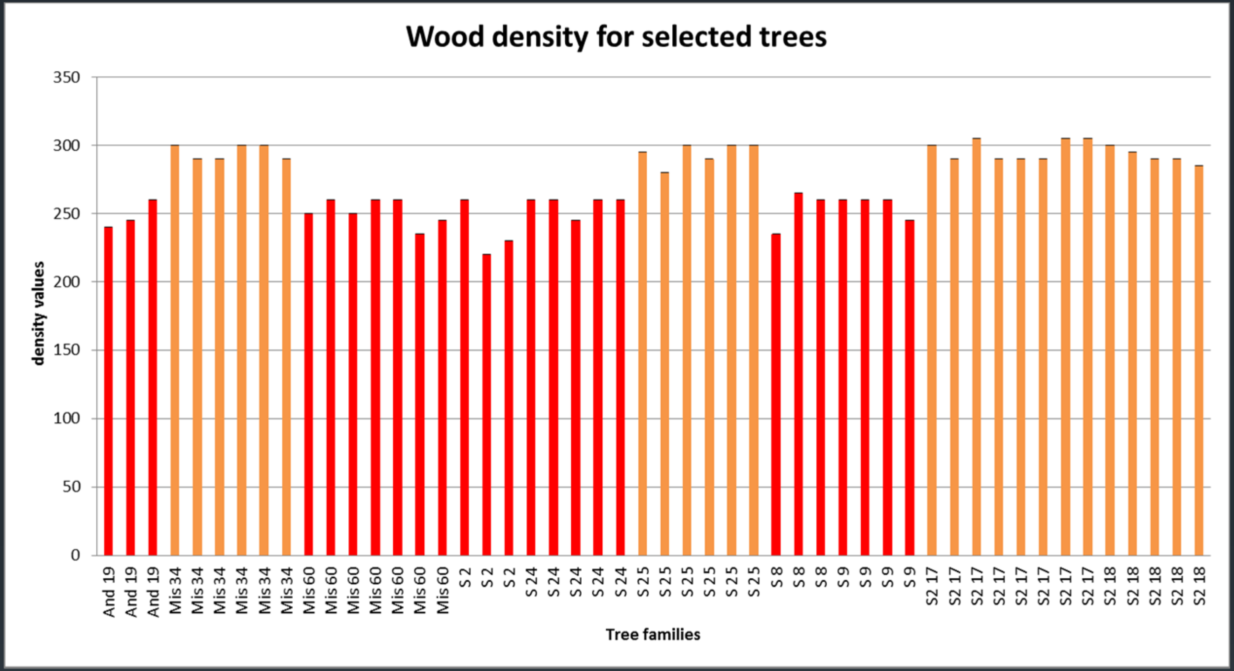
Lignin biosynthesis



Funded by the European Union

INVESTMENT IN YOUR FUTURE

Wood density



Orange - trees with higher wood density

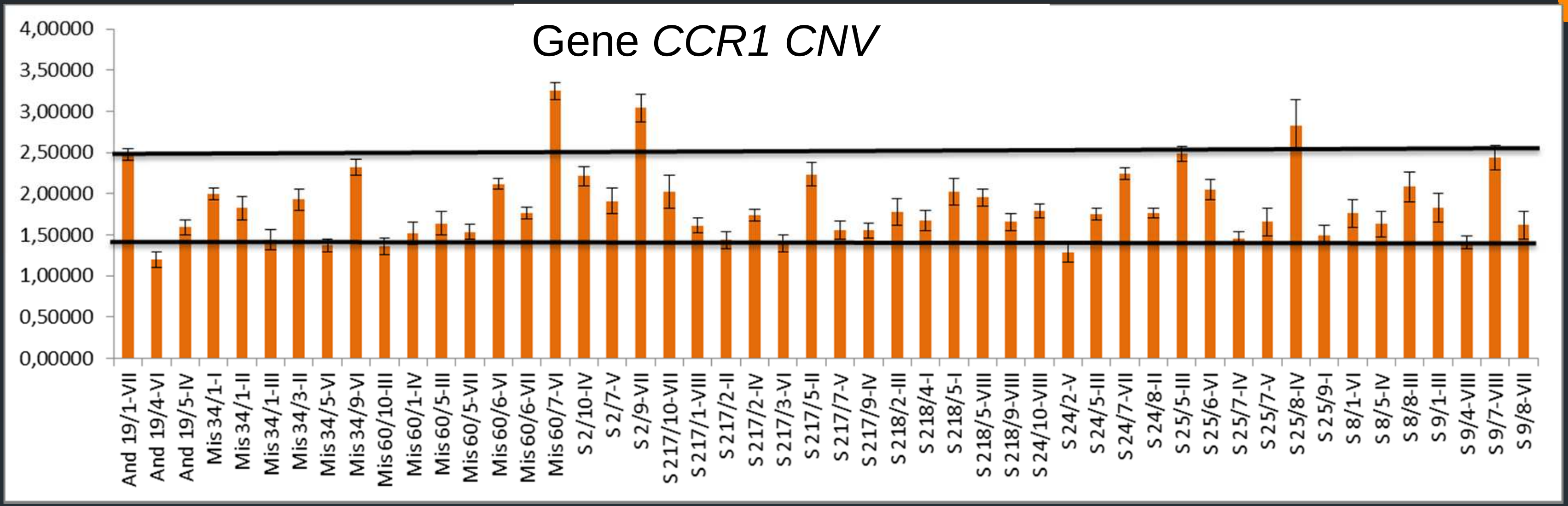
Red - with lower wood density

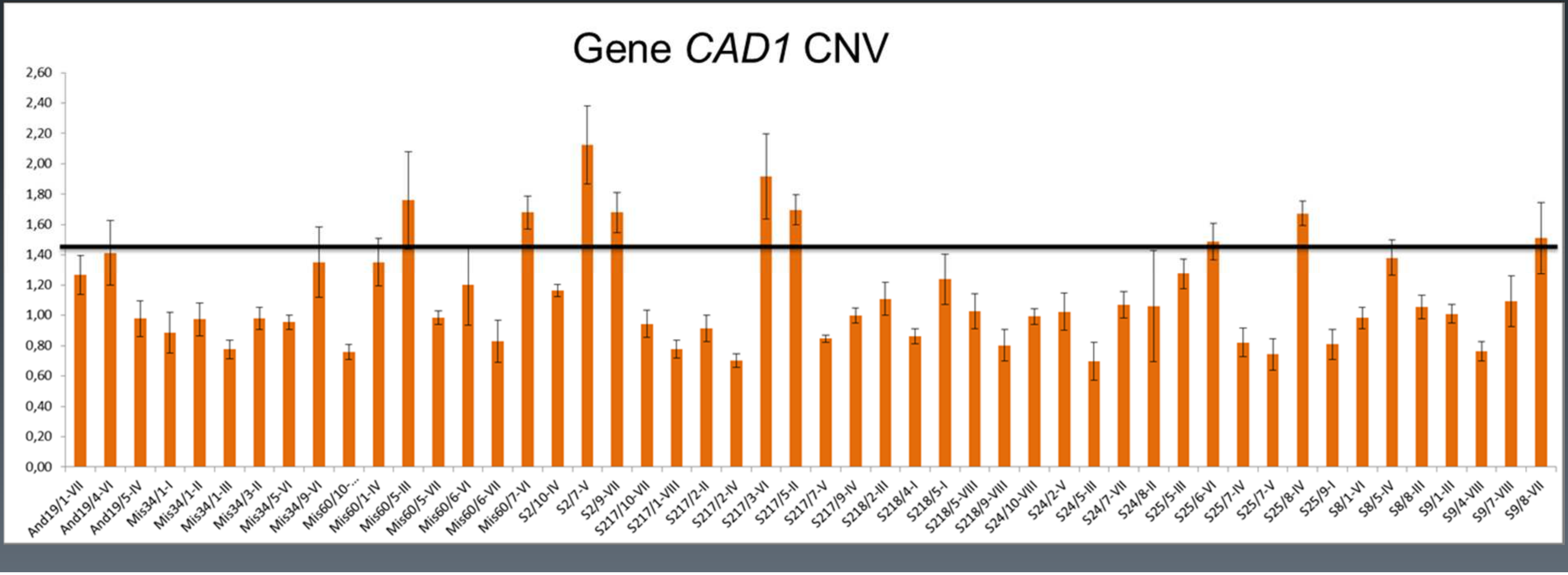
Funded by the European Union

INVESTMENT IN YOUR FUTURE

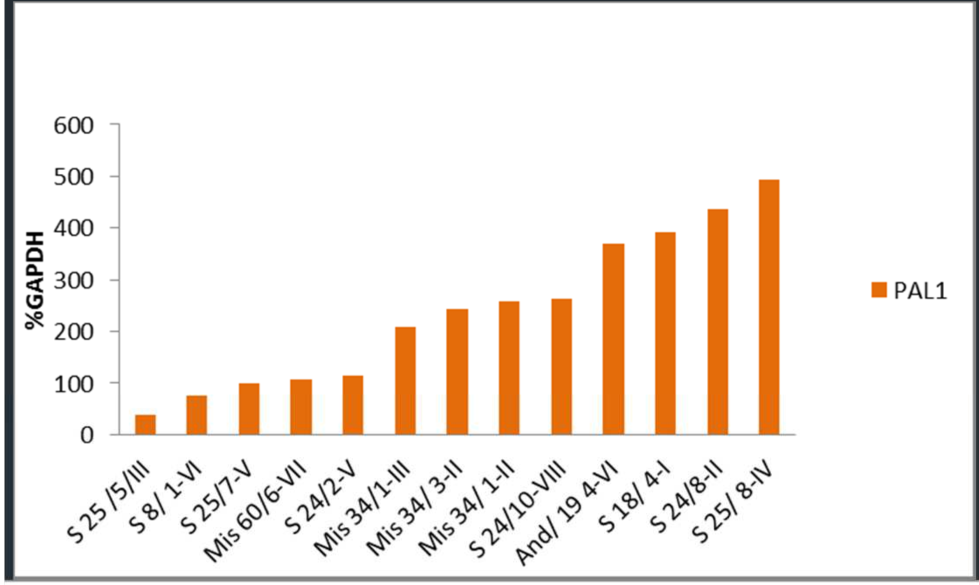
Copy number variation of gene *CCR1* and *CAD1*

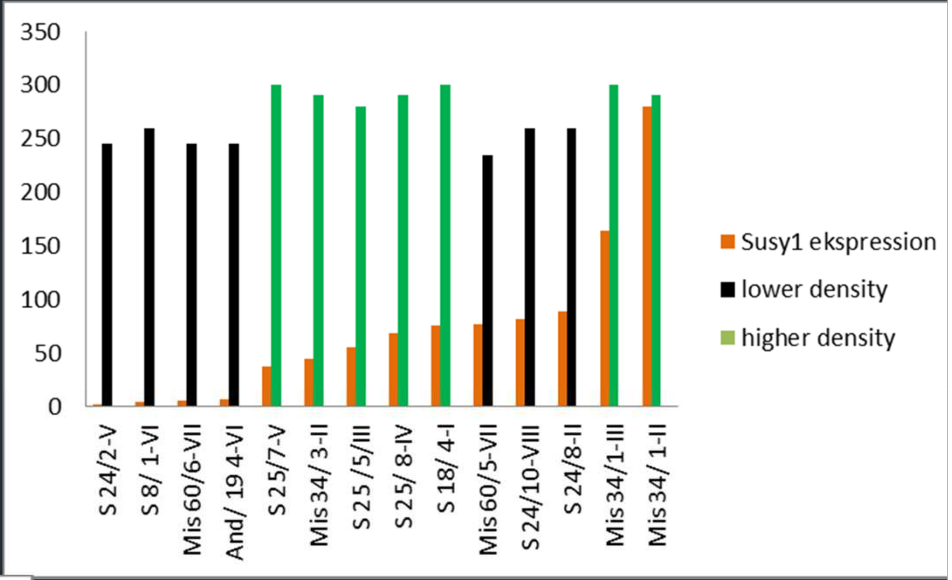
|Z| < 2

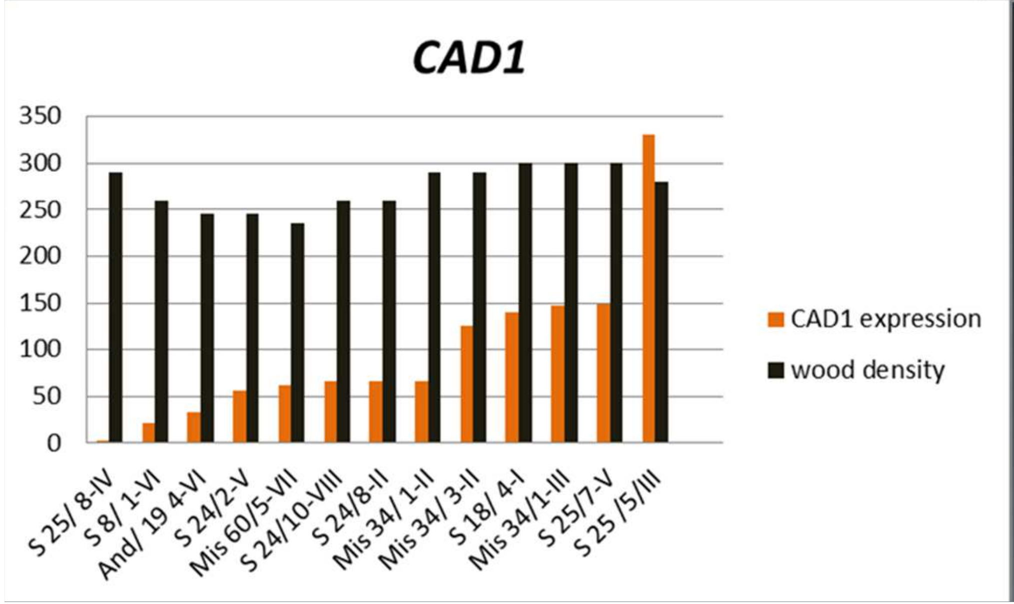




Gene *PAL1, CAD1, Susy1* expression(spring)

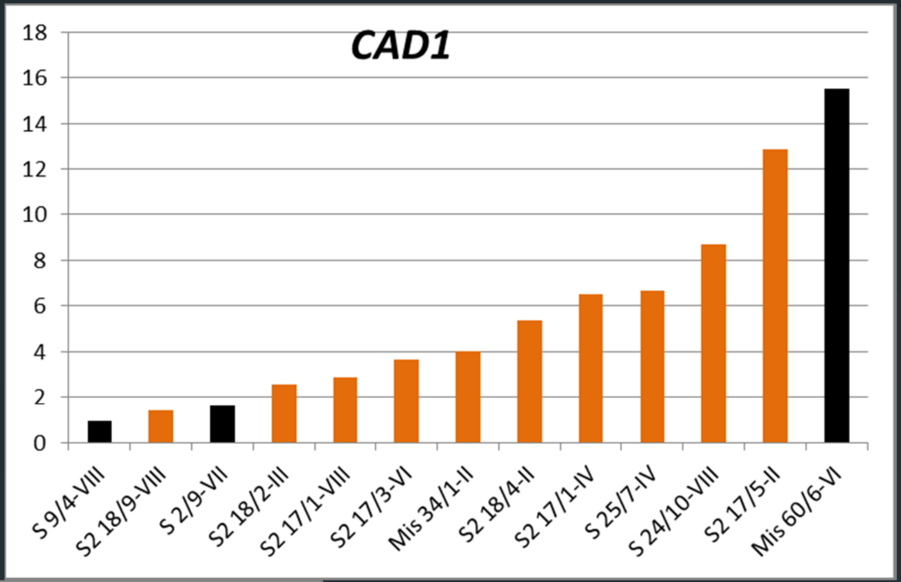


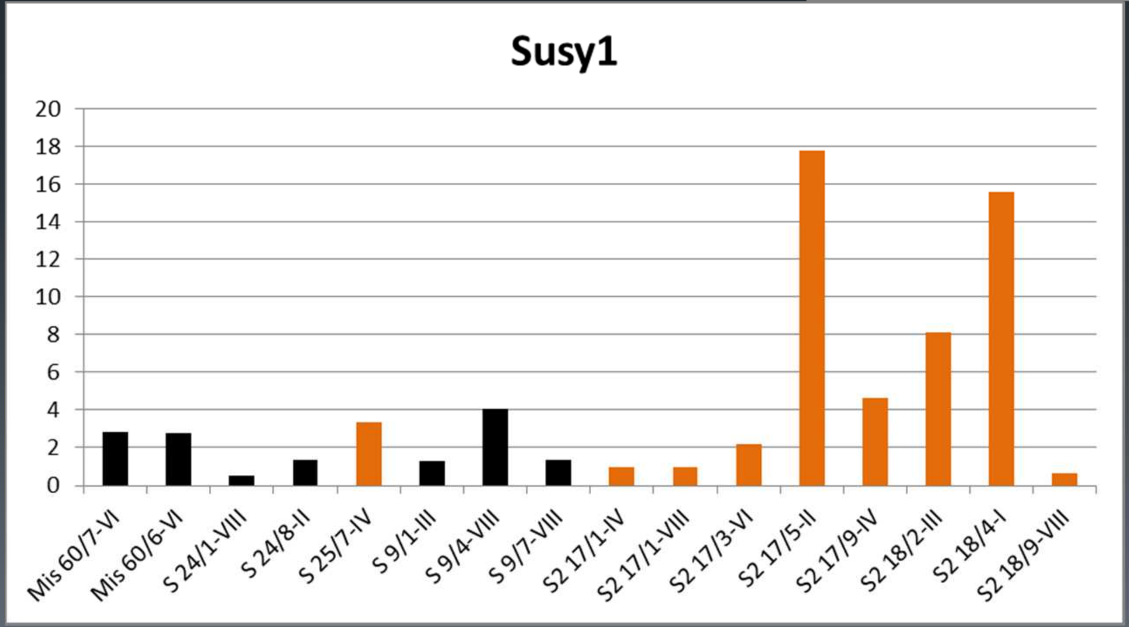




ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

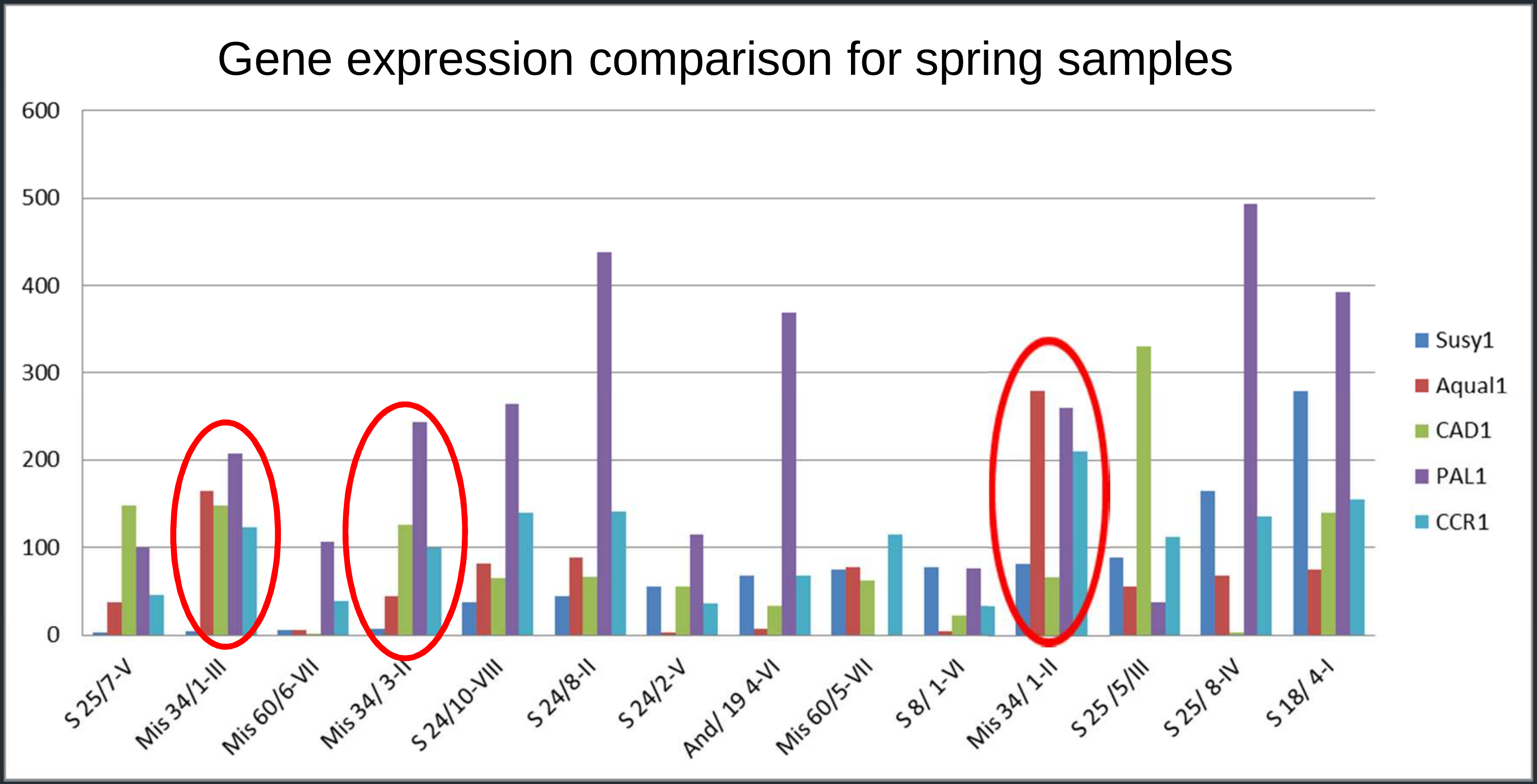
Autumn





Funded by the European Union

INVESTMENT IN YOUR FUTURE



PAL1 ekspression higher 2x than for others
Mis 34 perspective

	Susy1	***Aqual1***	***CAD1***	***PAL1***	***CCR1***
Susy1	1				
Aqual1	0,063774	1			
CAD1	0,043073	0,11905	1		
PAL1	0,4313	0,205608	-0,3006	1	
CCR1	0,400035	0,838829	0,166369	0,492318	1

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Some conclusions

- Quantitative RT PCR can be used to determine gene copy number variation for *P.sylvestris.*
- CNV data confirms sugestions about genes PAL1 and CAD1- that there are single functional gene copy in pines.
- There are positive regression between gene *SuSy1* and *CAD1* expression in spring and wood density, so ve can assume thatearly wood density is affected significantly by carbohydrate availabilty and last step of monolignol biosynthesis .
- Between genes *CCR1* and *Aqual1* exists strong correlation for spring samples, which my indicate about gene interraction im wood formation process.

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Future research plans

- Continue gene expression determination for genes *CAD1, PAL1, Aqual1,Susy1,CCR1* for all samples and possibly more.
- Analyse more candidate genes, for example transcription factors *MYB1*, *MYB2.* Search for genes envolved in monolignol transportation (coniferyl alcohol glucosyltransferase).
- Microscopic evaluation of celulose/lignin content, cell wall thickness. Or at least earlywood/latewood proportion measurment.
- Sequencing in hope to find gene regions suitable for marker development

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Conferences and result presentations

- 69. Annual Scientific Conference of University of Latvia, Plant Biology section, 22 february, 2011 (Oral Presentation).

- Scientific conference «Advances in plant biotechnology in Baltic Sea Region» , 30-31 March, 2011, Lithuania, Abstract book p.53-54, (Poster) .

- 2011. Master degree in Biological Sciences in University of Latvia.

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Research funding

European Social Fund’s Project “Importance of Genetic Factors in Formation of Forest Stands with High Adaptability and Qualitative Wood Properties” (No 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)

ESF

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Thank you for attention!

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Genetic diversity with aspen stands: phenology observations and molecular analysis

Mārtiņš Zeps

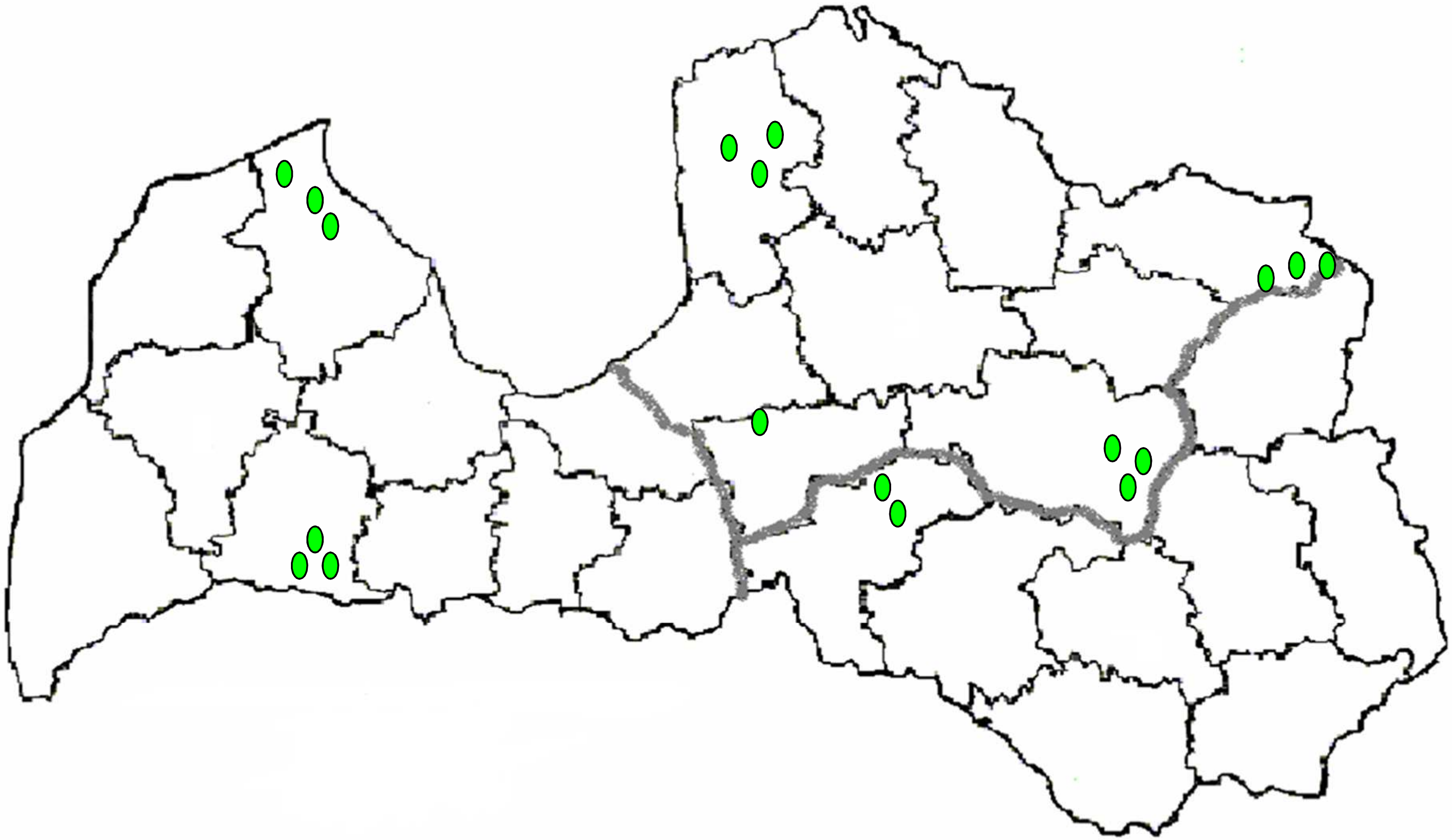
martins.zeps@silava.lv

Funded by the European Union
INVESTMENT IN YOUR FUTURE

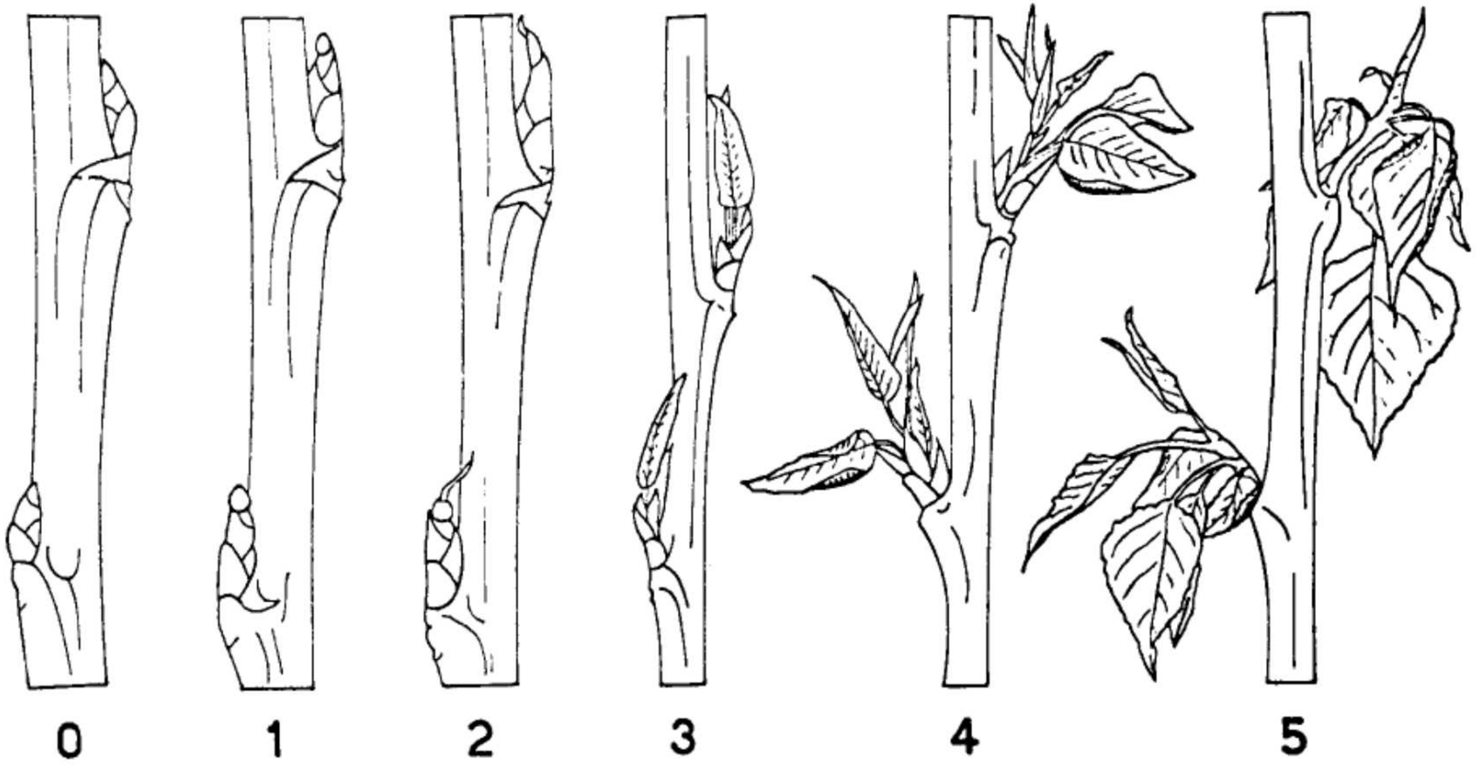
Background

The European aspen (*Populus tremula*) is thought to reproduce mostly asexually. Thus aspen forms clones, in which several ramets belong to one genetically defined genet. We compared the clonal structure of aspen in managed forests in 6 populations in Latvia. In every population selected 3 stands aproxametely 5 to 10 years old, naturally regenereted this srpouts. Clones were identified using morphological characters and 3+3 microsatellite loci originally developed for *Populus remuloides*.

Materials and method

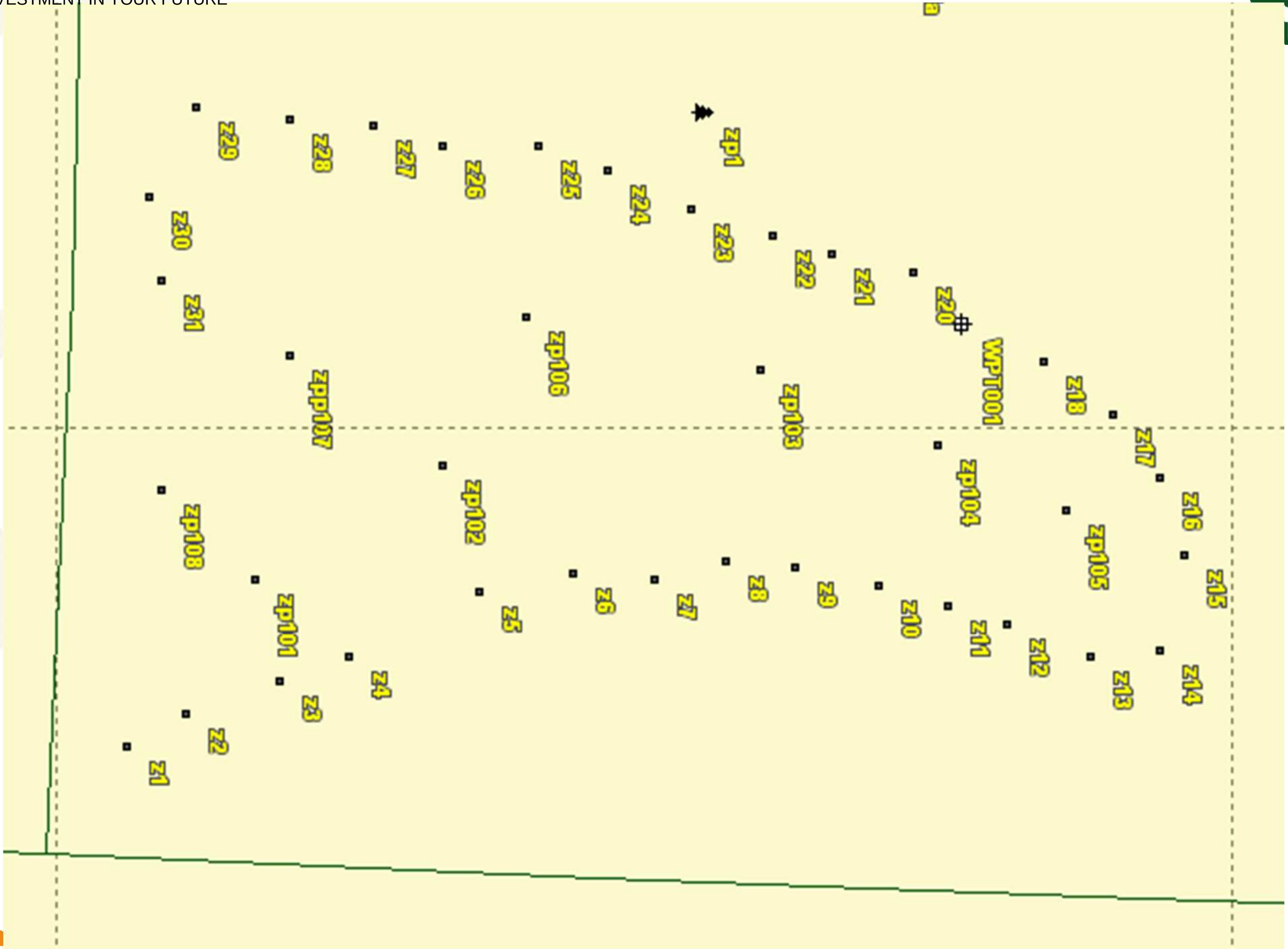


Materials and method



UPOV 1981.

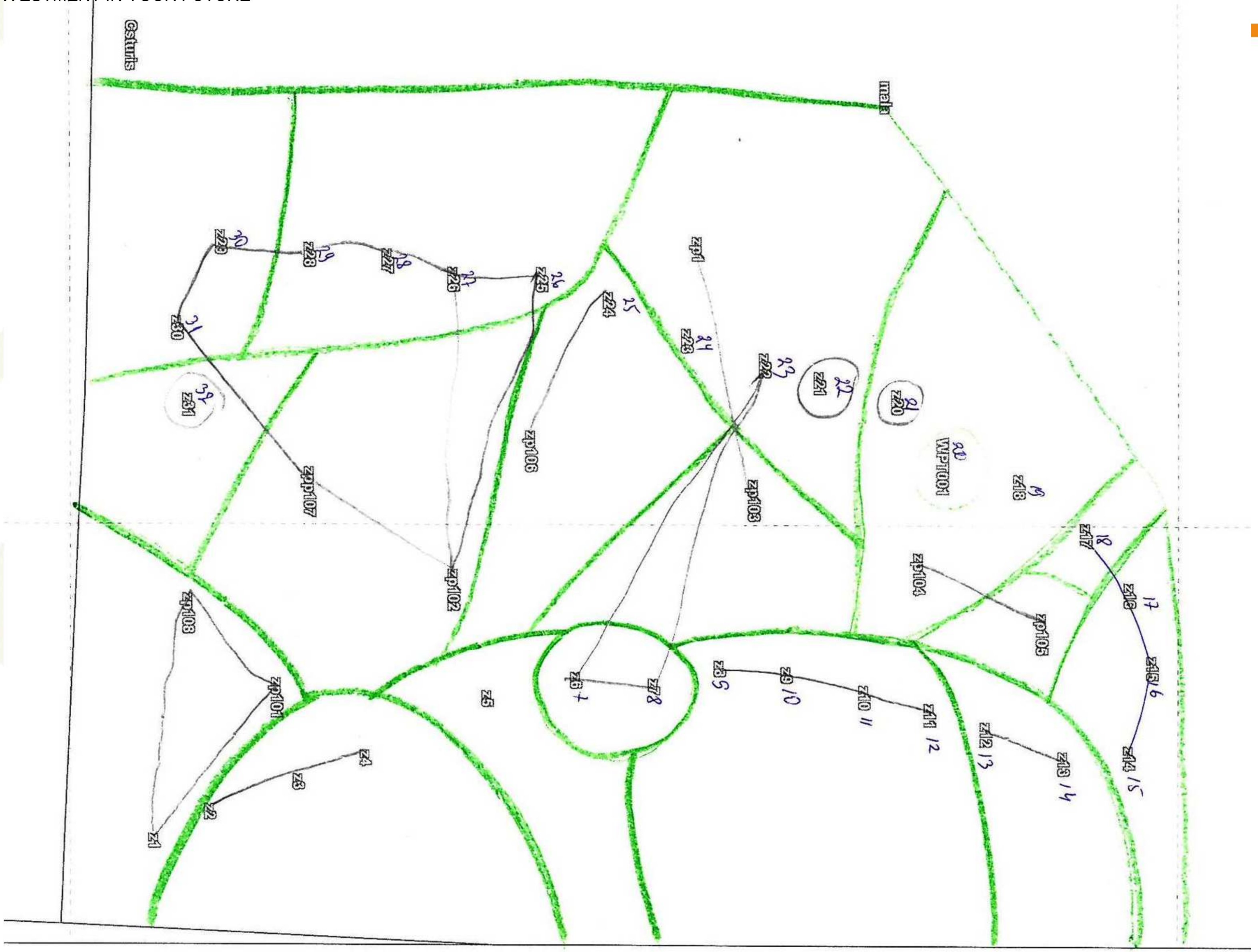
Results


z29
z28
z27
z26
z25
zp1
z24
z30
z23
z22
z21
z20
z31
zp106
WPT001
z18
zpp107
zp103
z17
zp104
zp108
zp102
z16
zp105
z15
zp101
z5
z6
z7
z8
z9
z10
z11
z12
z13
z14
z4
z3
z2
z1

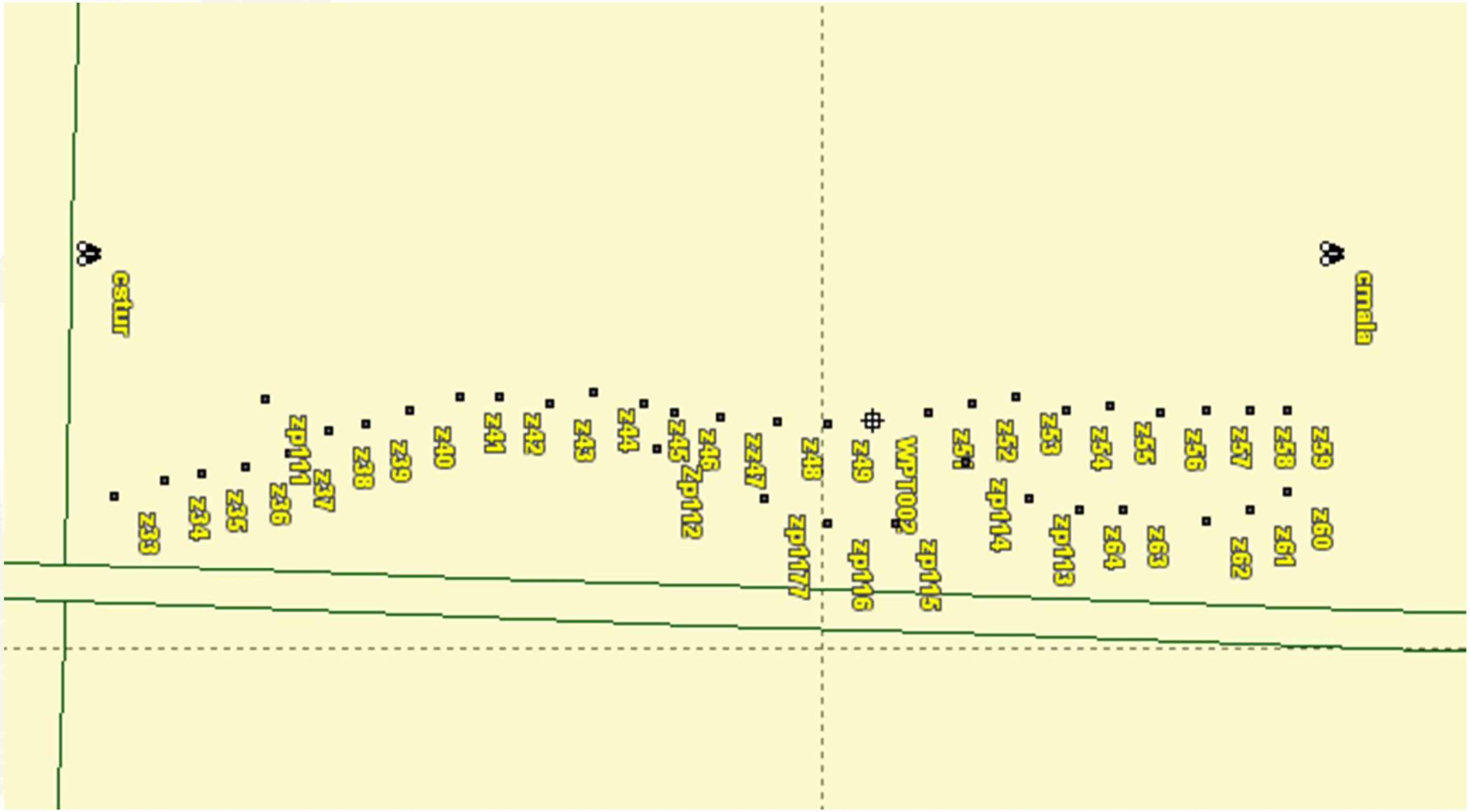
Funded by the European Union

INVESTMENT IN YOUR FUTURE

Results

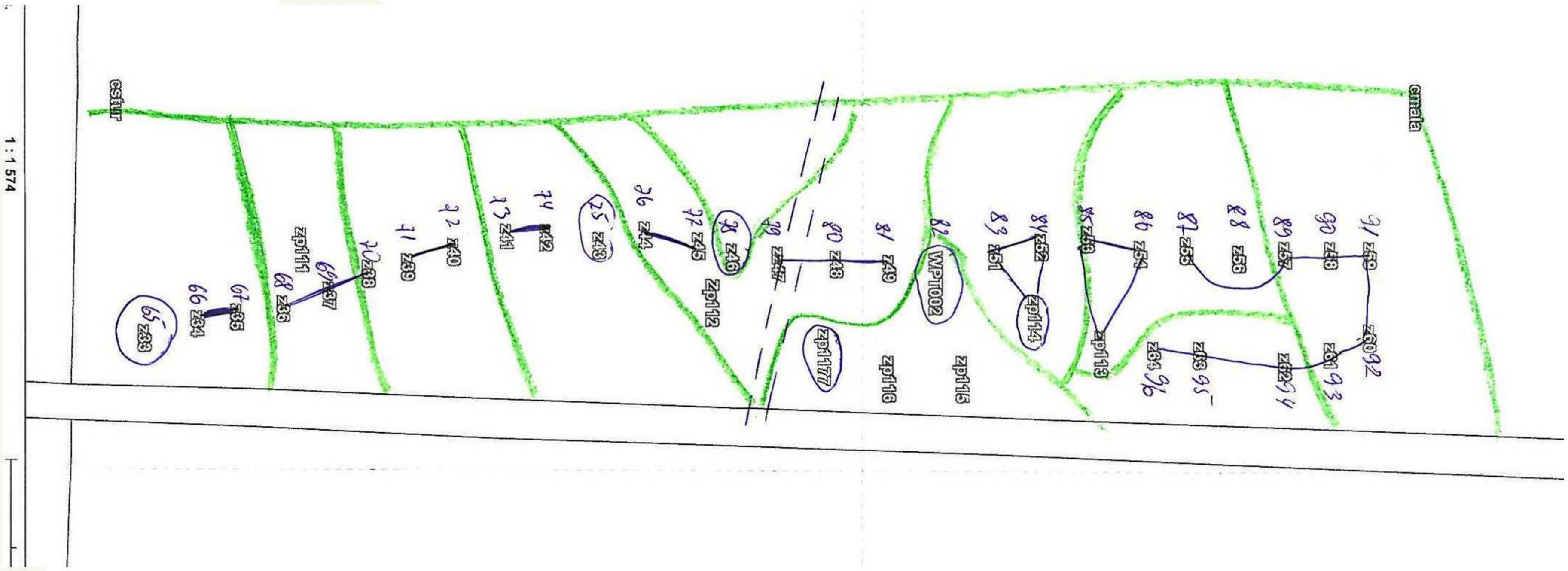


Results


cstur
cmala
z33
z34
z35
z36
zp111
z37
z38
z39
z40
z41
z42
z43
z44
z45
z46
zp112
zz47
z48
zp1177
z49
zp116
WPT002
zp115
z51
z52
zp114
z53
zp113
z54
z64
z55
z63
z56
z57
z62
z58
z61
z59
z60

Funded by the European Union

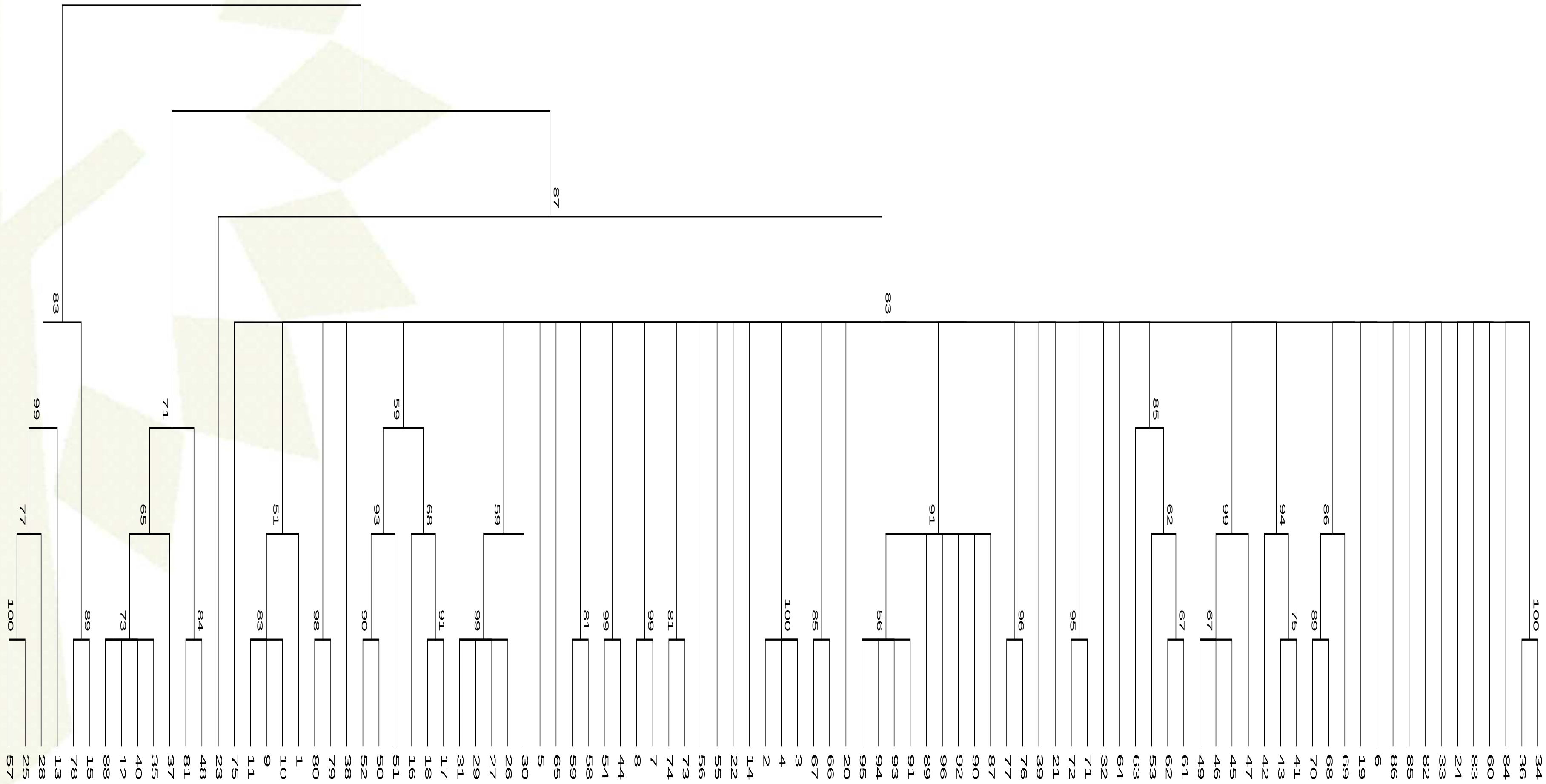
INVESTMENT IN YOUR FUTURE



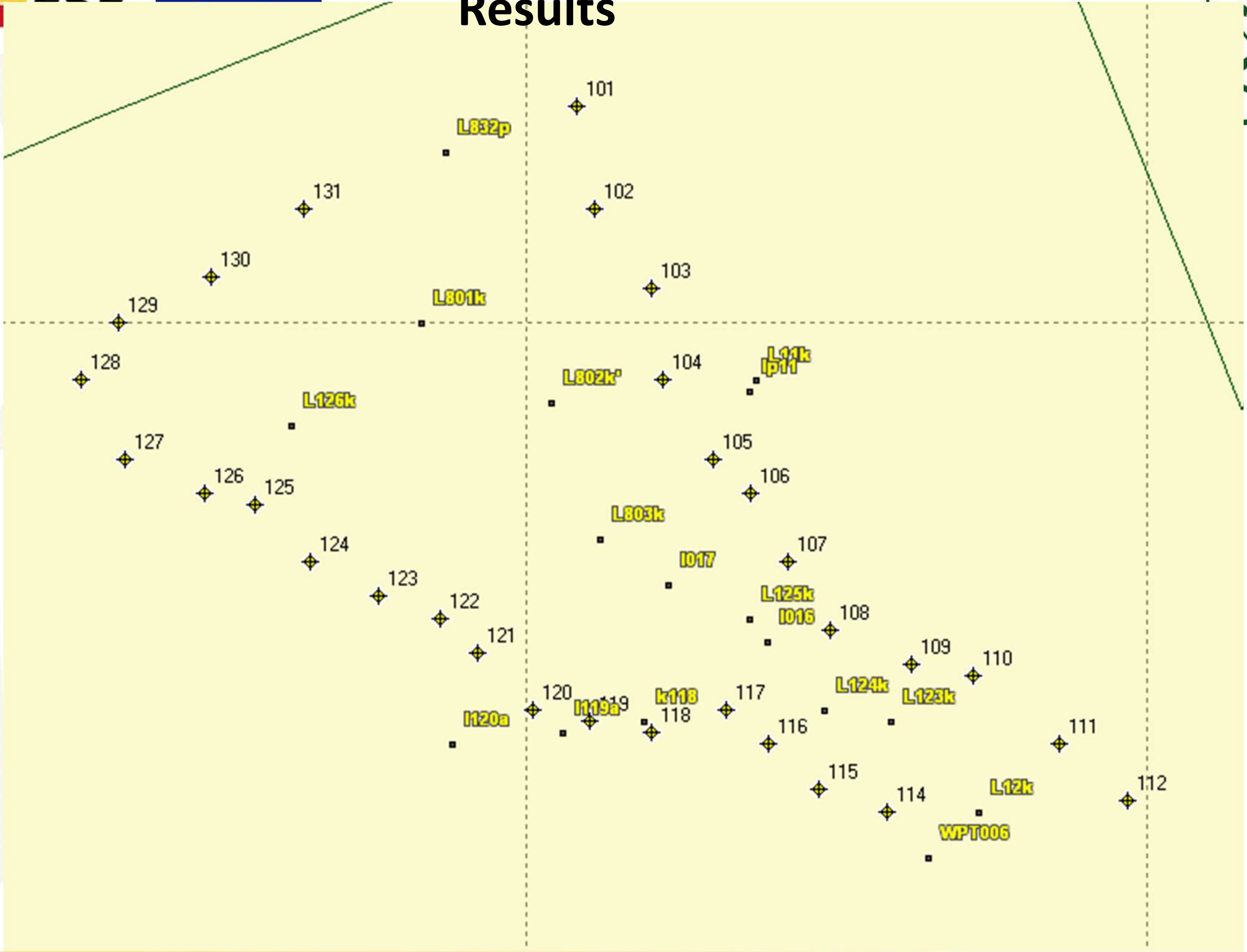
Funded by the European Union

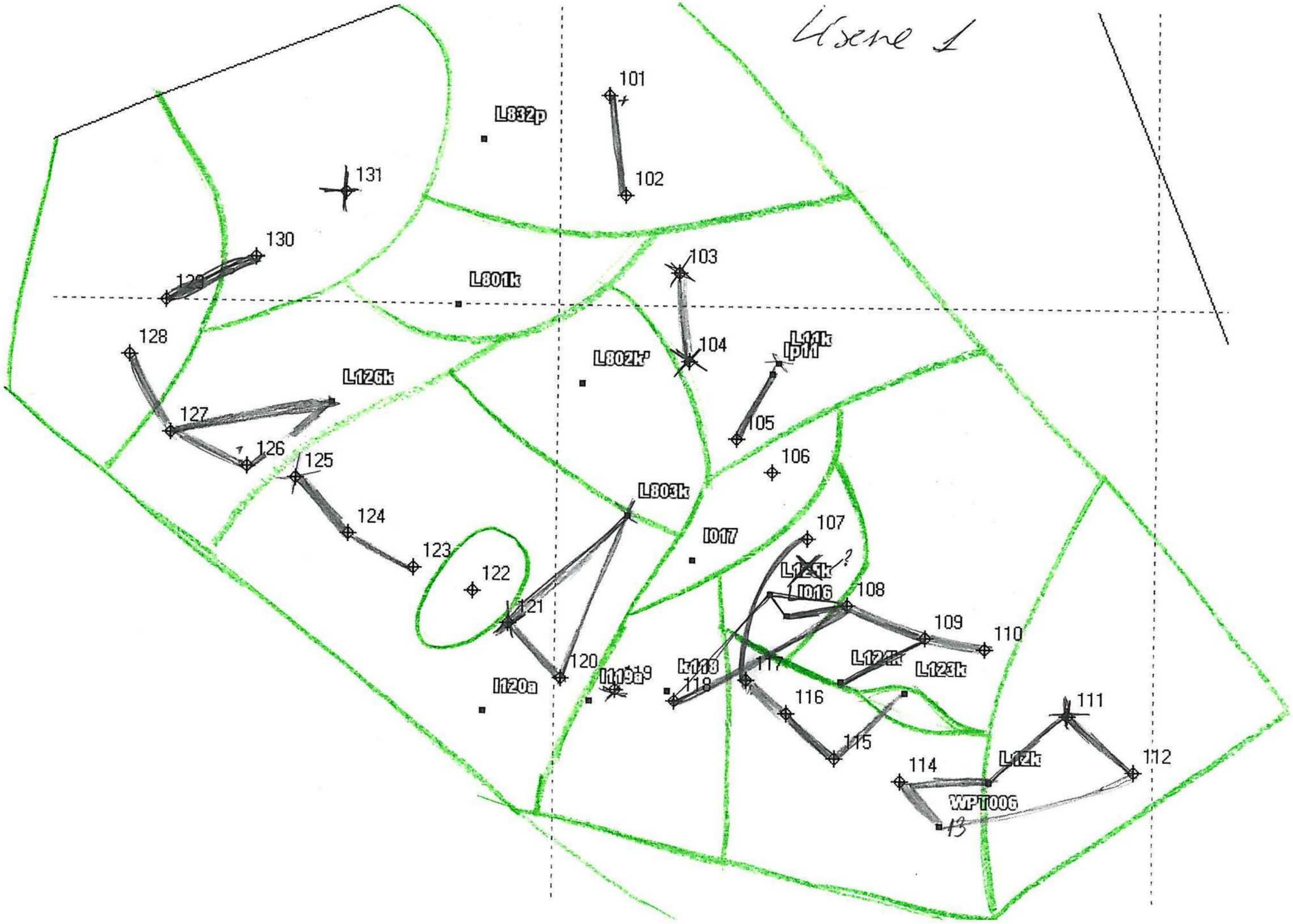
INVESTMENT IN YOUR FUTURE

Results



Results

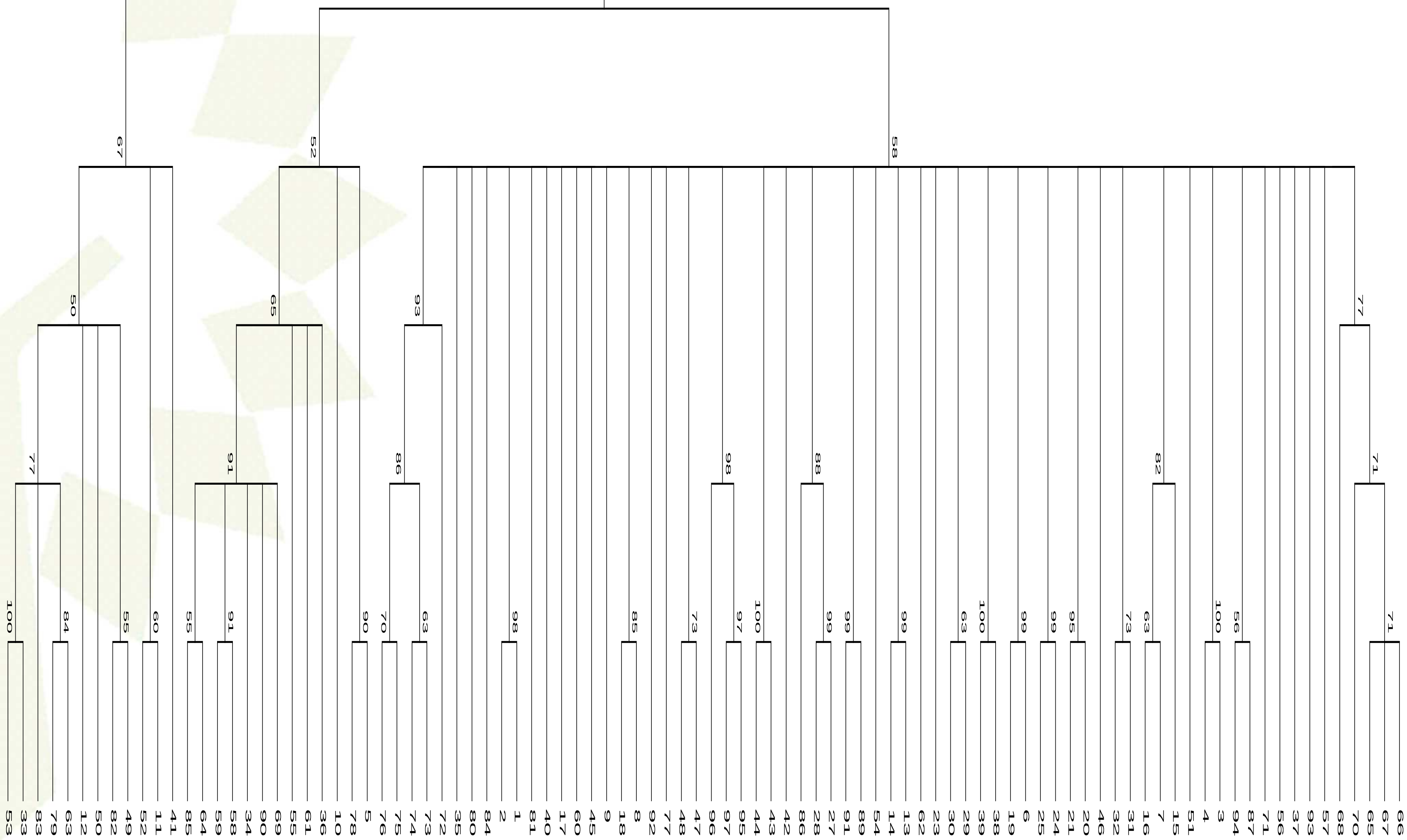

101
L832p
131
102
130
103
L801k
129
128
L802k'
104
L11k
lp11
L126k
127
105
126
125
106
L803k
124
107
l017
123
L125k
122
l016
108
121
109
110
120
l119a
119
k118
117
L124k
L123k
l120a
118
116
111
115
114
L12k
112
WPT006


Lisene 1
101
102
L832p
131
130
129
L801k
103
104
128
L802k'
L11k
lp11
L126k
127
105
106
126
125
L803k
124
123
I017
107
122
L125k ?
I016
108
121
109
110
120
I119a
119
k118
118
117
L124k
L123k
I120a
116
111
115
L12k
112
114
WPT006
13

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Results



Conclusions

- ✓ The numbers of clones that were identified with microsatellites were larger than morphological characters.
- ✓ On average clone size in population was 1,6 ramets
- ✓ Only one ramets average in population was 22 ramets
- ✓ The average number of clones per hectare was 11,3.

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Thank You for attention!

Study has been funded by:
ESF project "Importance of Genetic Factors in Formation of Forest Stands with High Adaptability and Qualitative Wood Properties" (No 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)

Genetic variation in annual height growth of Latvian Norway spruce OP families

Darius Danusevicius, ASU, LT

Aris Jansons, Silava, LV

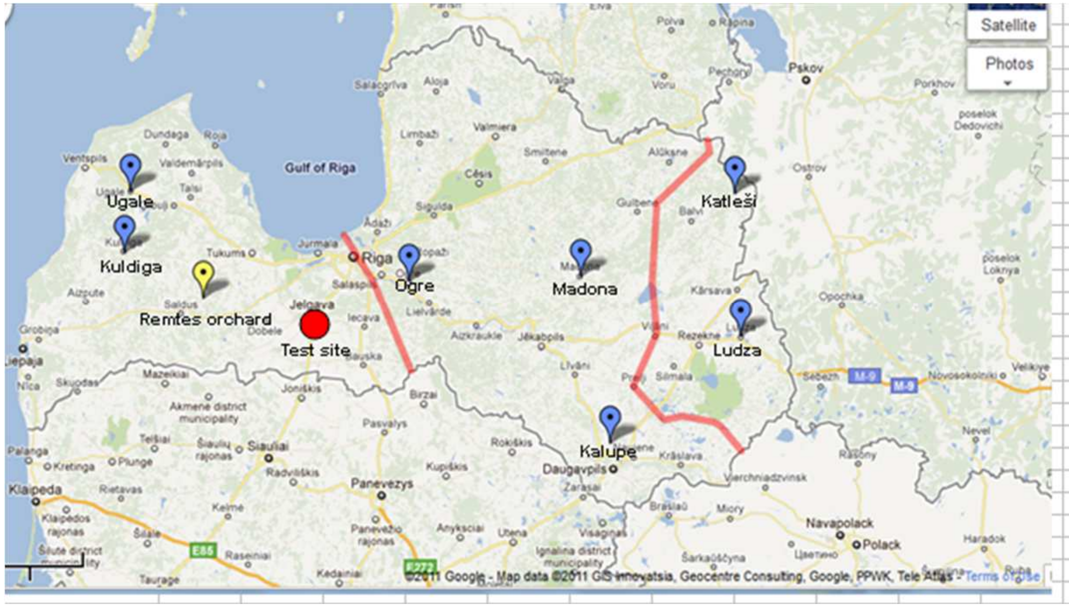
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Objectives

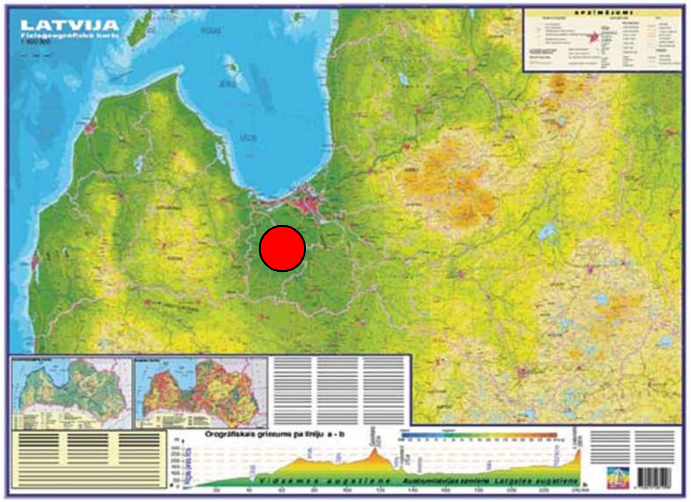
- Assess H growth to reveal adaptive environments and transfer effect within LV
- Patterns of genetic parameters during the growth period

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Material

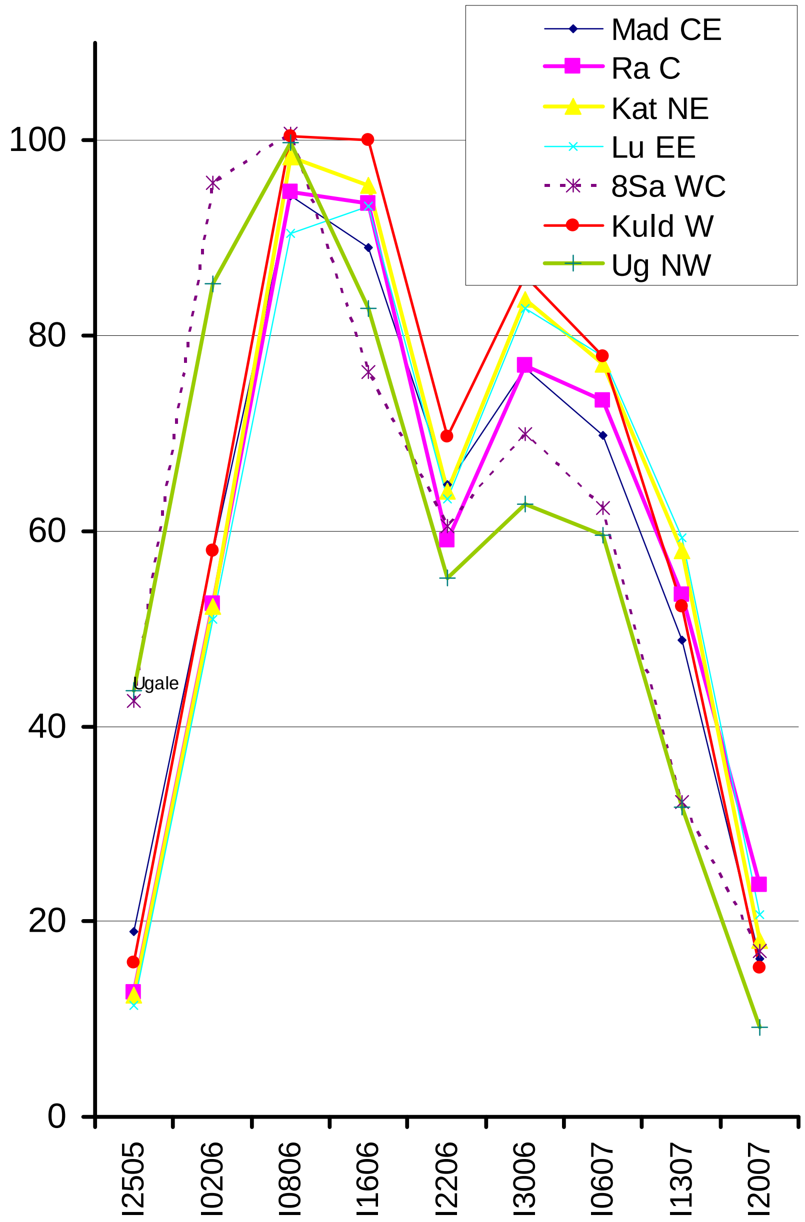


- 56 OP fam.s from 8 pop.s from 3 zones
- All moved from “cooler” to warmer (see altitude)
- 3 pop.s moved from CONT to MARITME



Funded by the European Union

INVESTMENT IN YOUR FUTURE



Funded by the European Union

INVESTMENT IN YOUR FUTURE

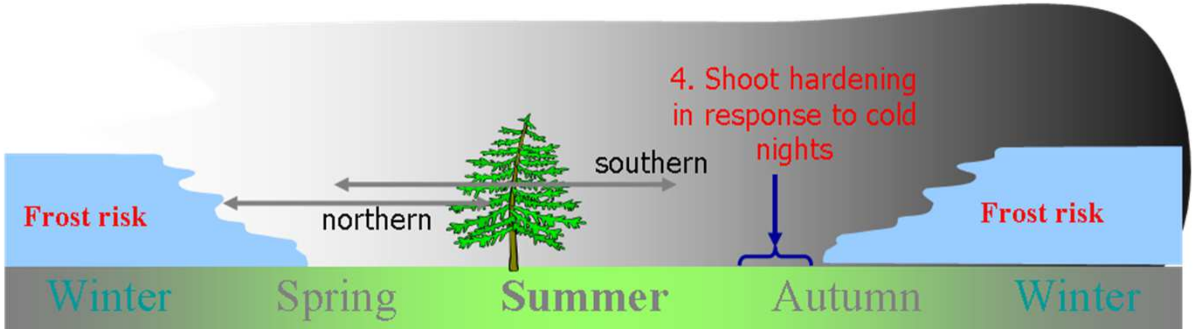
Basic theory

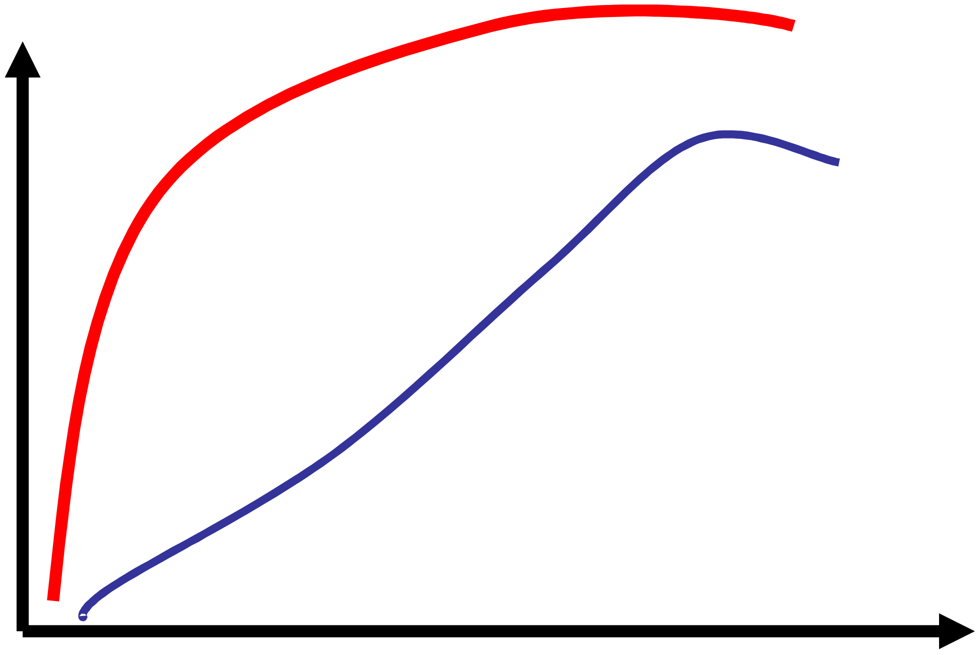
Funded by the European Union
INVESTMENT IN YOUR FUTURE

3 major components of shoot length

1. Transfer effect = growth rhythm

↕ May be connected?





2. Growth vigor (fam effect)

3. Free growth (sea –continent)

Damage

Funded by the European Union
INVESTMENT IN YOUR FUTURE

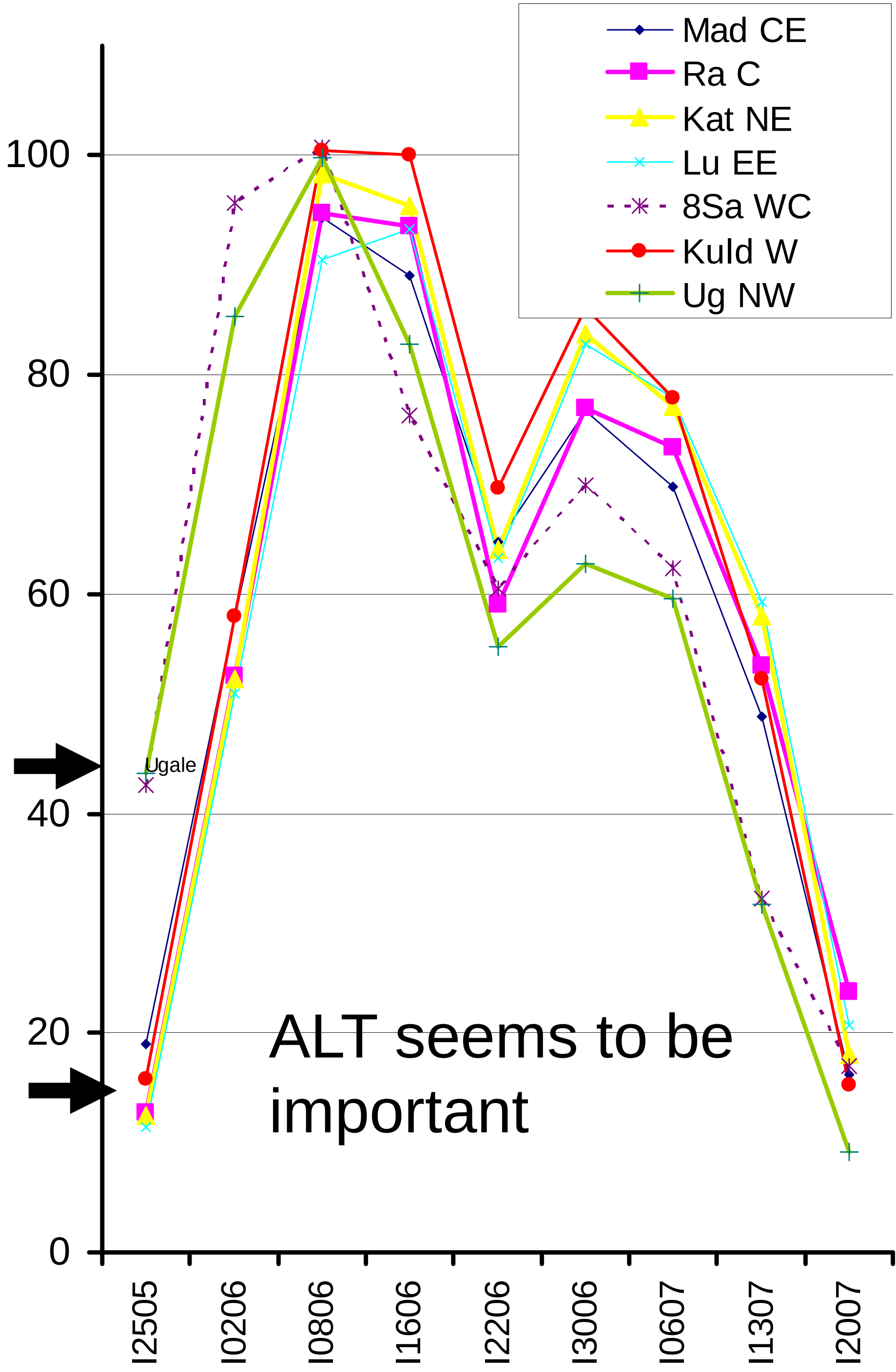
Results

- Population and transfer effect
- Correlations (early start means early end?)
- Genetic parameters and genetic variation at various stages
- Response to stress in June

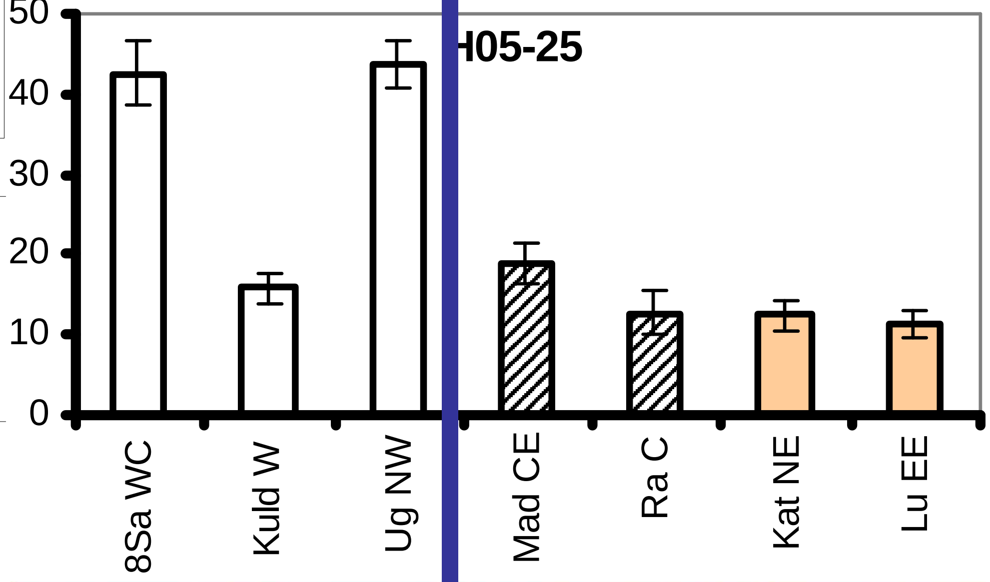
Population (transfer) effect

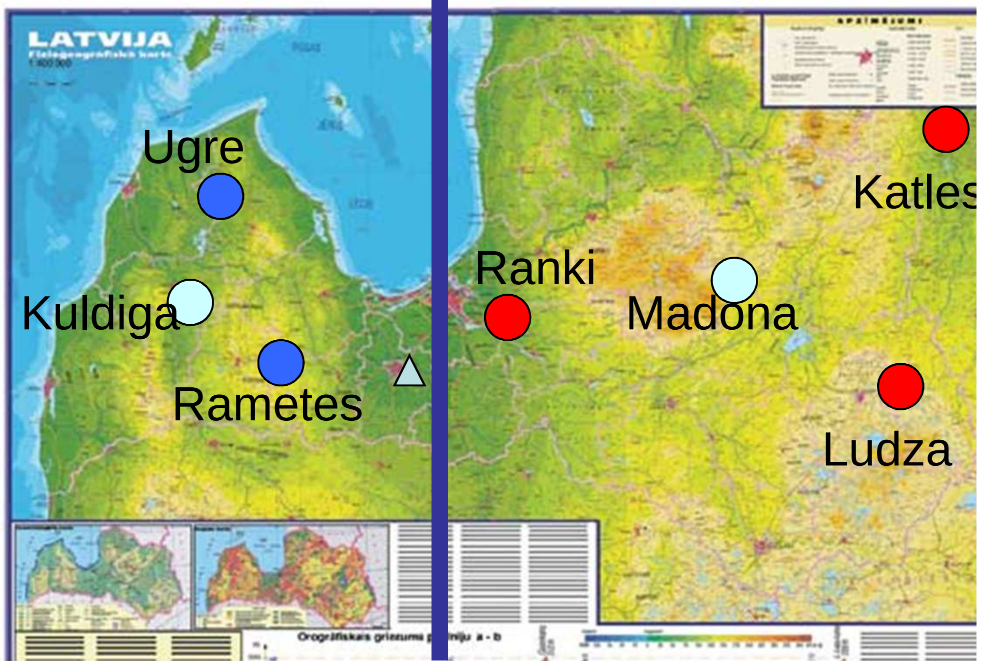
Bandomuosiuose želdiniuose

Start of GP



ALT seems to be important

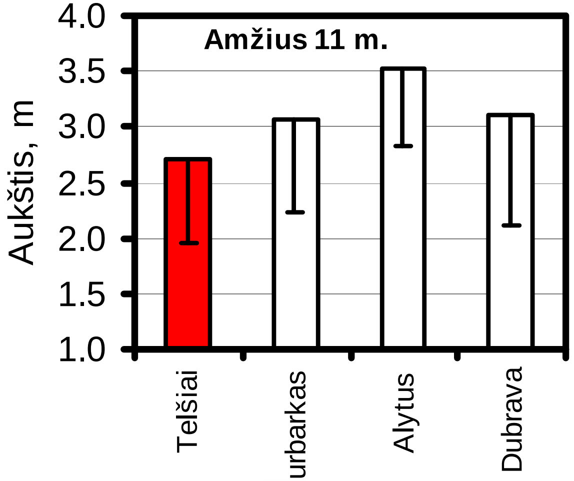


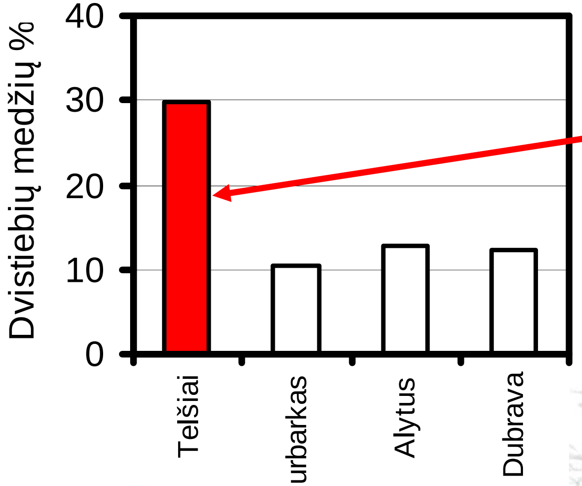


Funded by the European Union

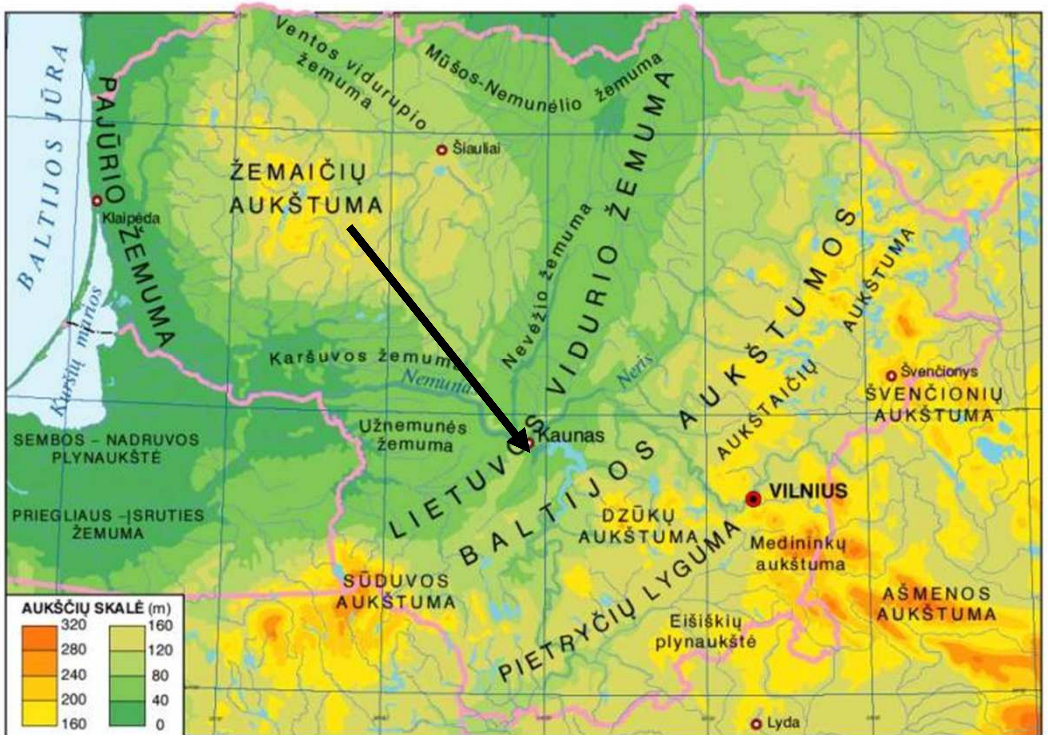
INVESTMENT IN YOUR FUTURE

Transfer effects in LT



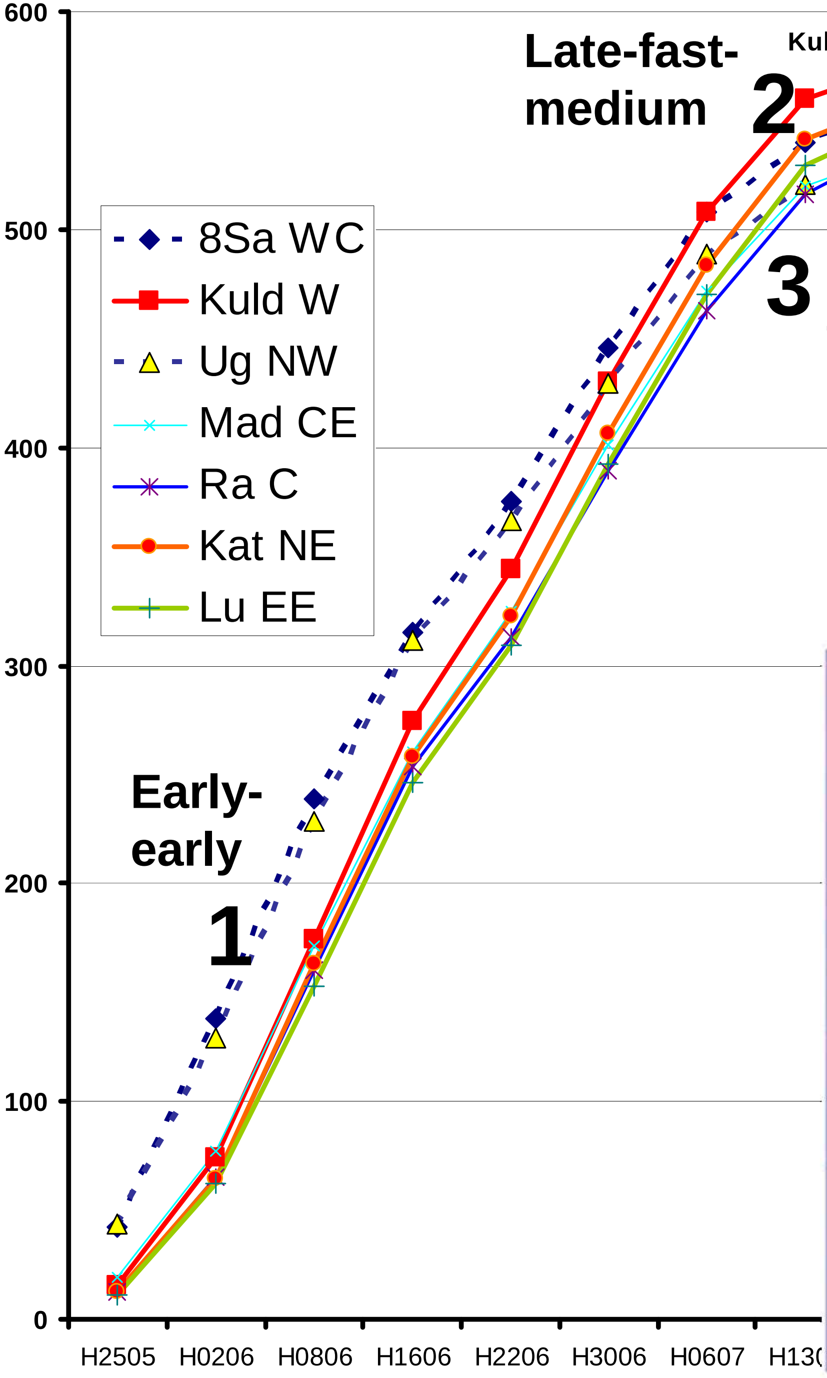


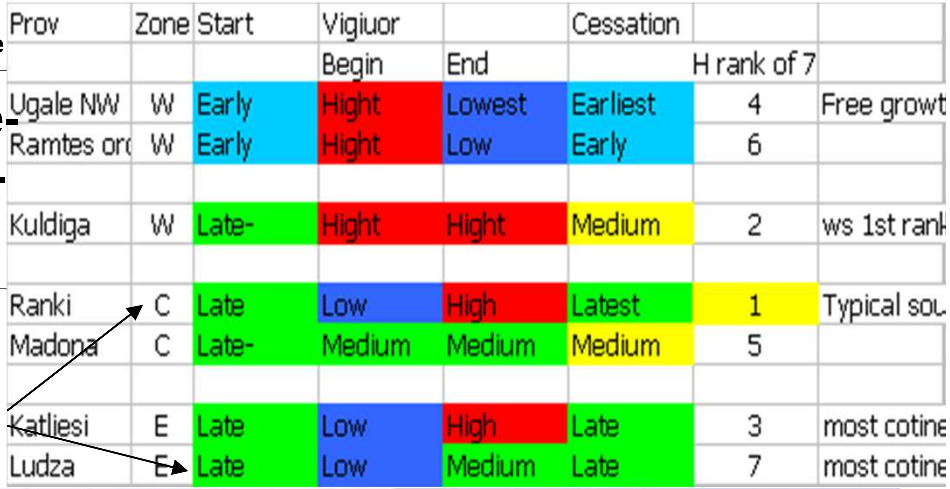
Esminis Lietuvos populiacijų perkėlimo efektas (pvz. iš Telšių į Kauną rajoną)



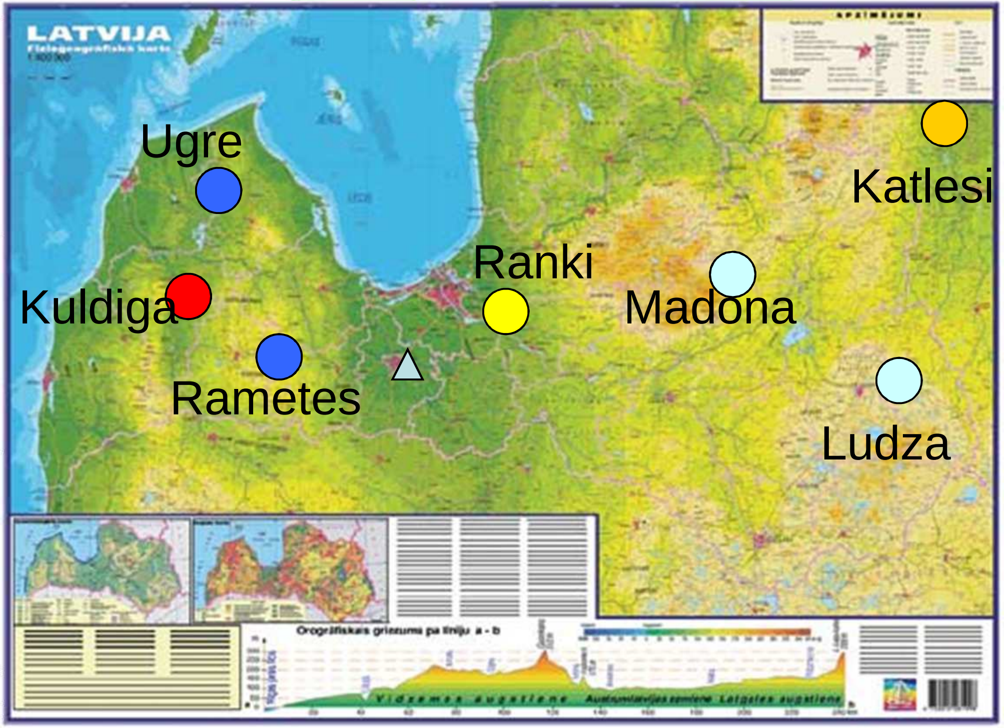
Šalnų pakenktas Telšių kilmės medelis

Growth pattern= 4 groups of populations

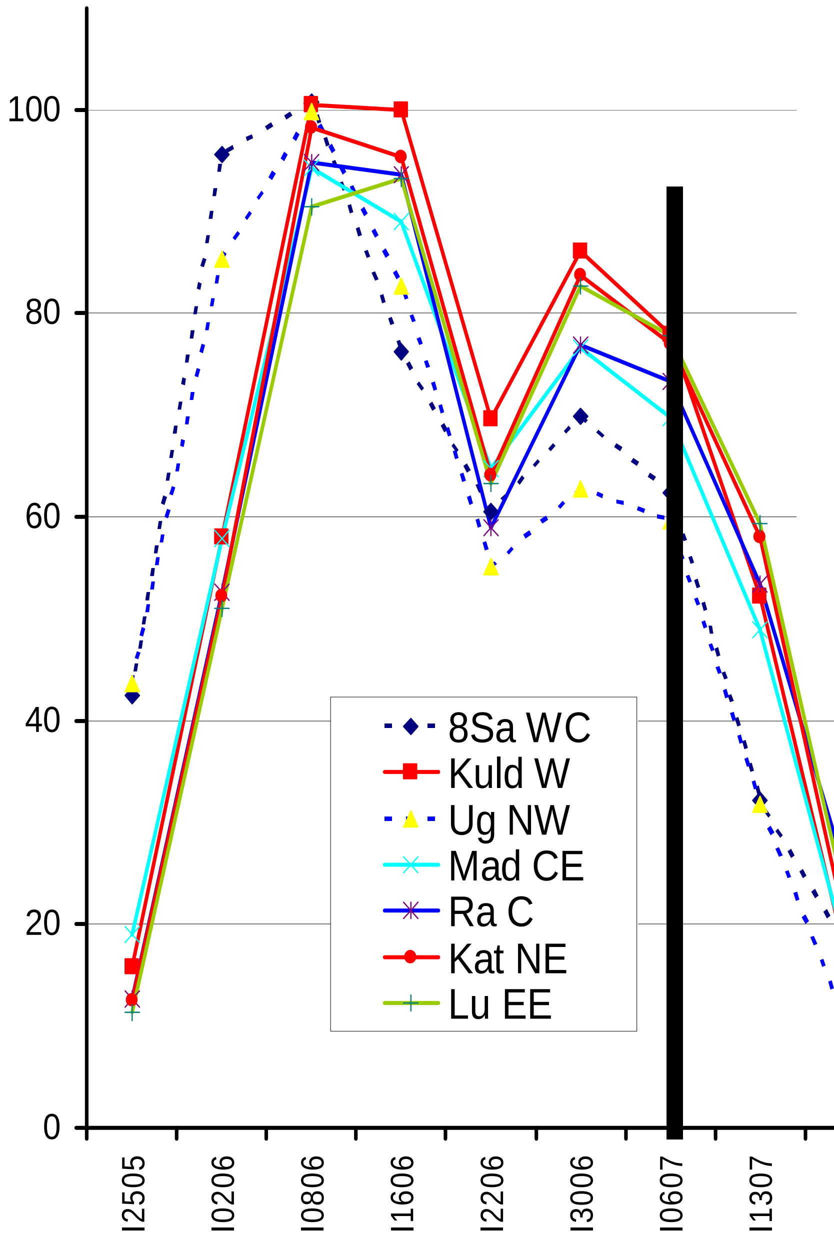


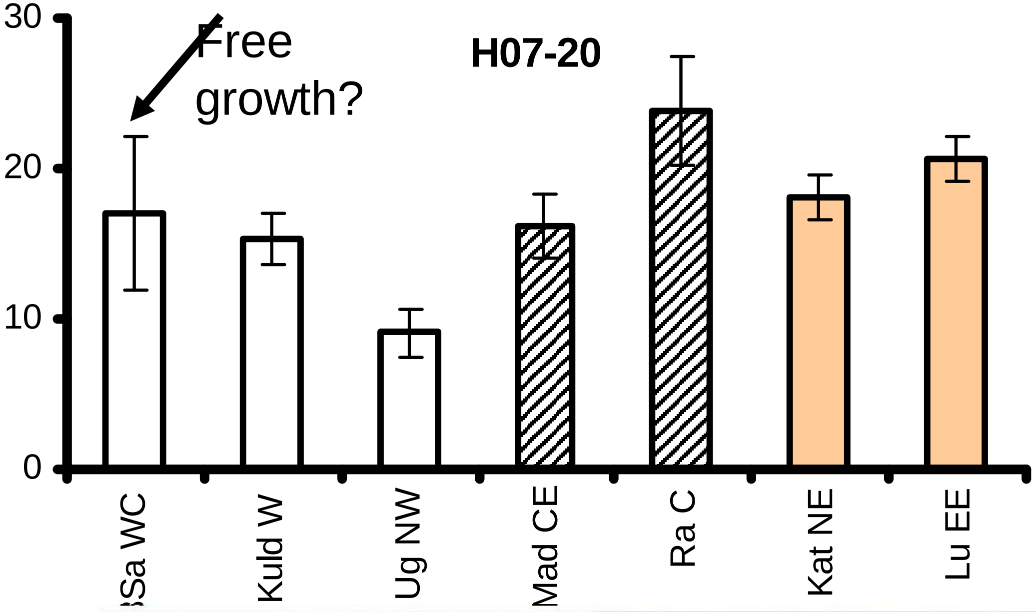


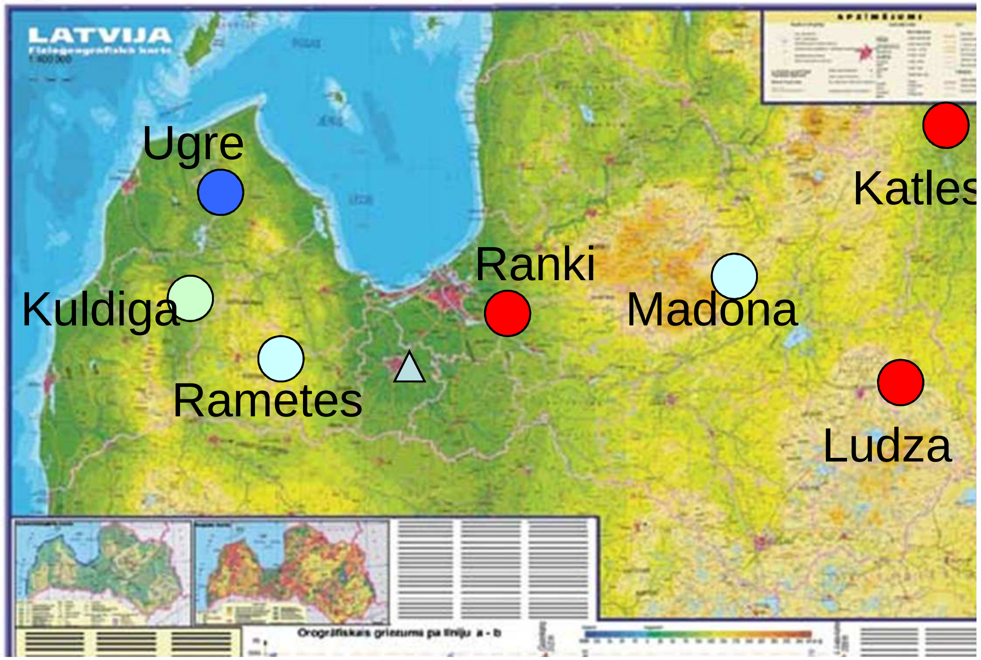
Prov	Zone	Start	Vigiuor		Cessation		
			Begin	End		H rank of 7	
Ugale NW	W	Early	Hight	Lowest	Earliest	4	Free growt
Ramtes or	W	Early	Hight	Low	Early	6	
Kuldiga	W	Late-	Hight	Hight	Medium	2	ws 1st ran
Ranki	C	Late	Low	High	Latest	1	Typical sou
Madona	C	Late-	Medium	Medium	Medium	5	
Katliesi	E	Late	Low	High	Late	3	most cotine
Ludza	E	Late	Low	Medium	Late	7	most cotine



Cessation

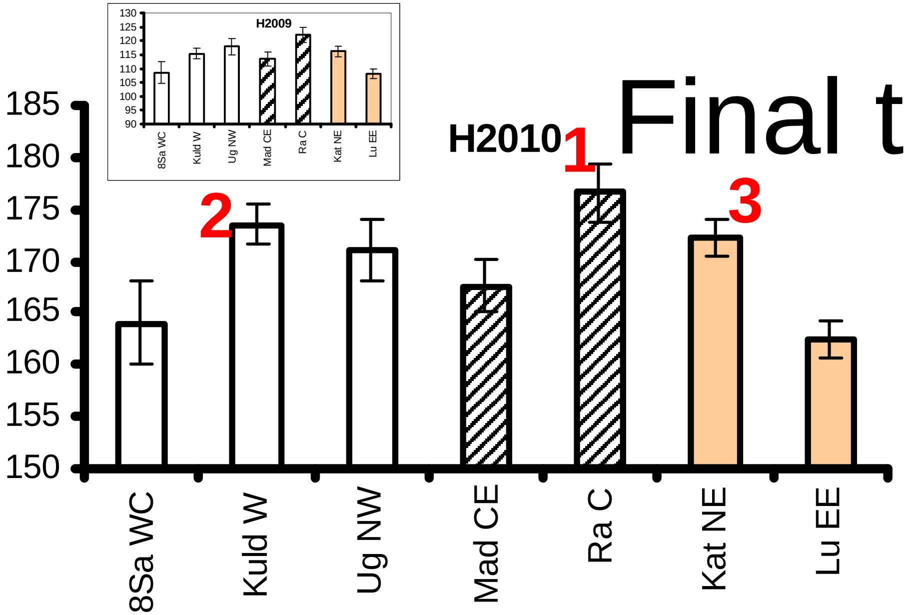

100
80
60
40
20
0
I2505
I0206
I0806
I1606
I2206
I3006
I0607
I1307
I2007
8Sa WC
Kuld W
Ug NW
Mad CE
Ra C
Kat NE
Lu EE

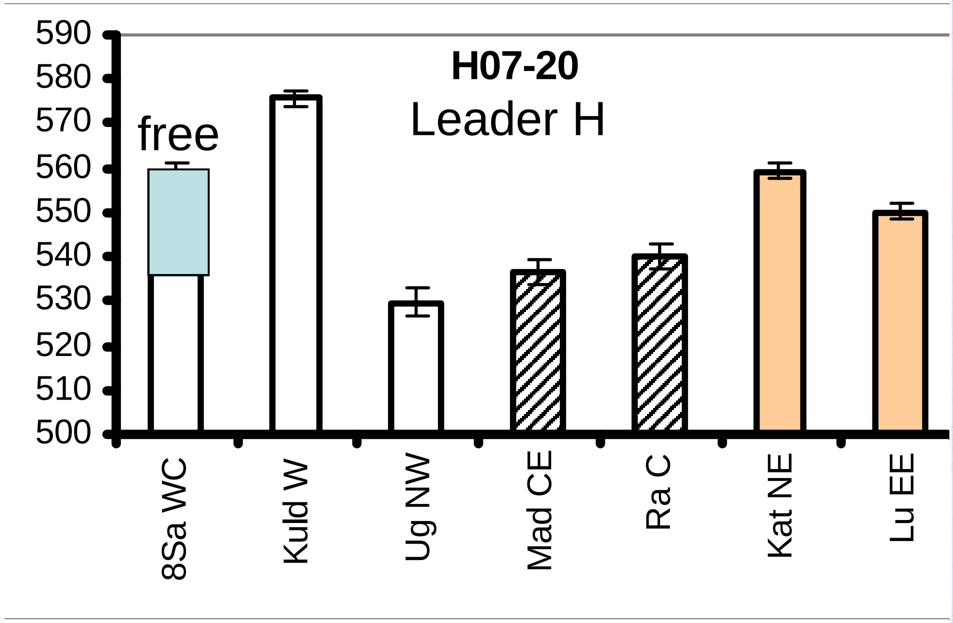

30
20
10
0
Free
growth?
H07-20
8Sa WC
Kuld W
Ug NW
Mad CE
Ra C
Kat NE
Lu EE

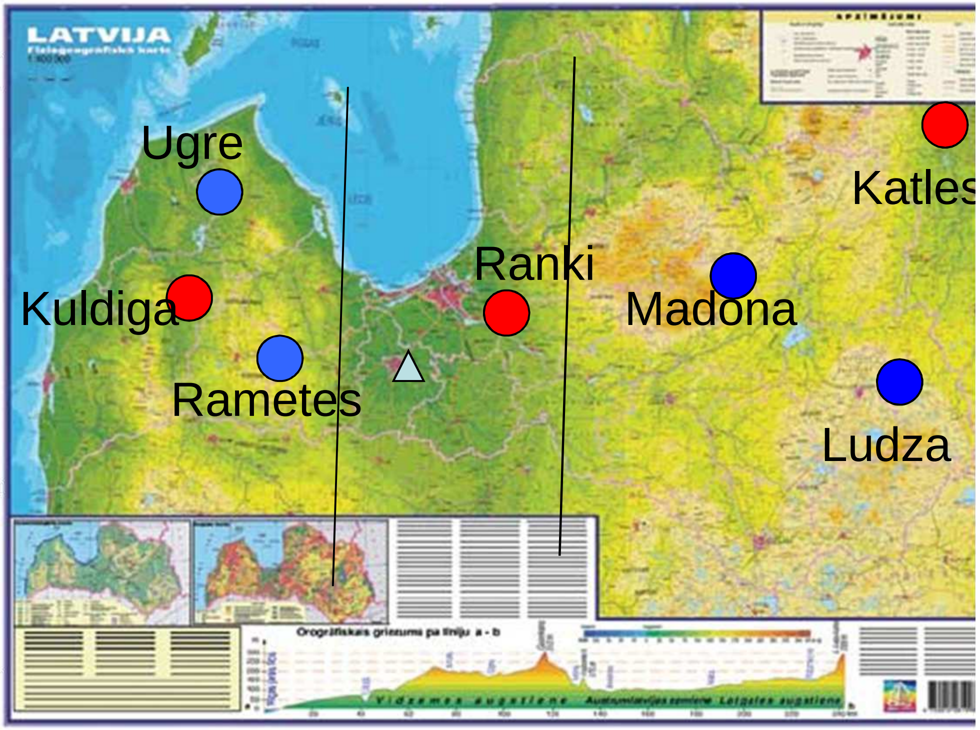

LATVIJA
Ugre
Katles
Ranki
Kuldiga
Madona
Rametes
Ludza

Final tree H

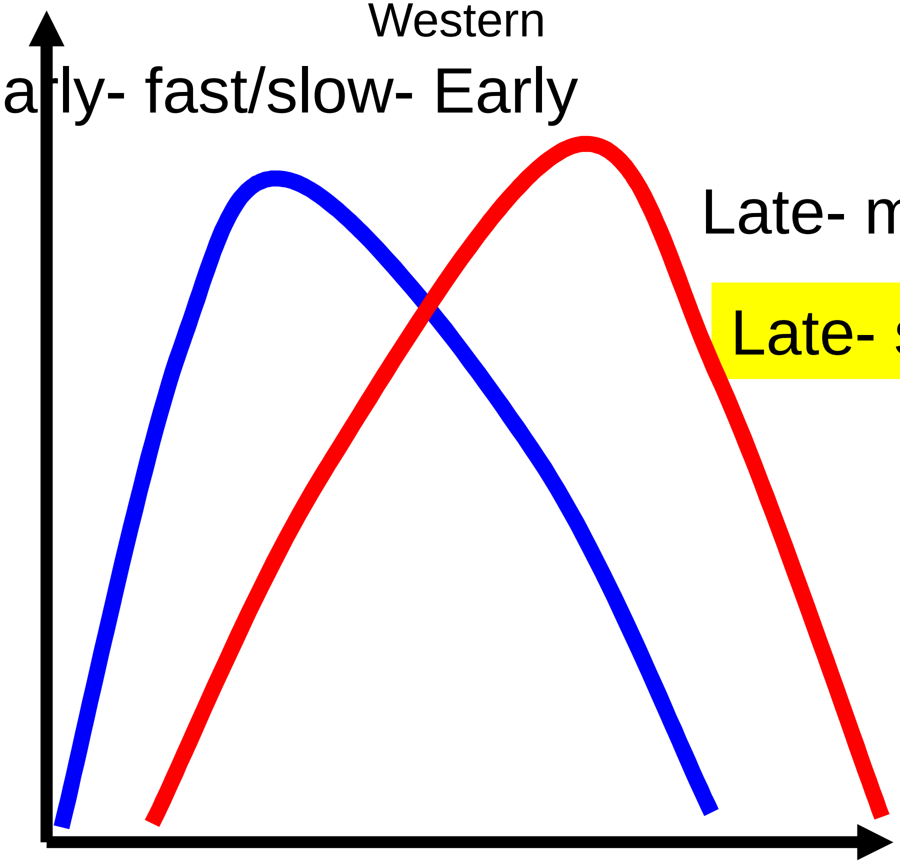
- Leader H = total H
- Effect of altitude after all?







Summary



Western

Early- fast/slow- Early

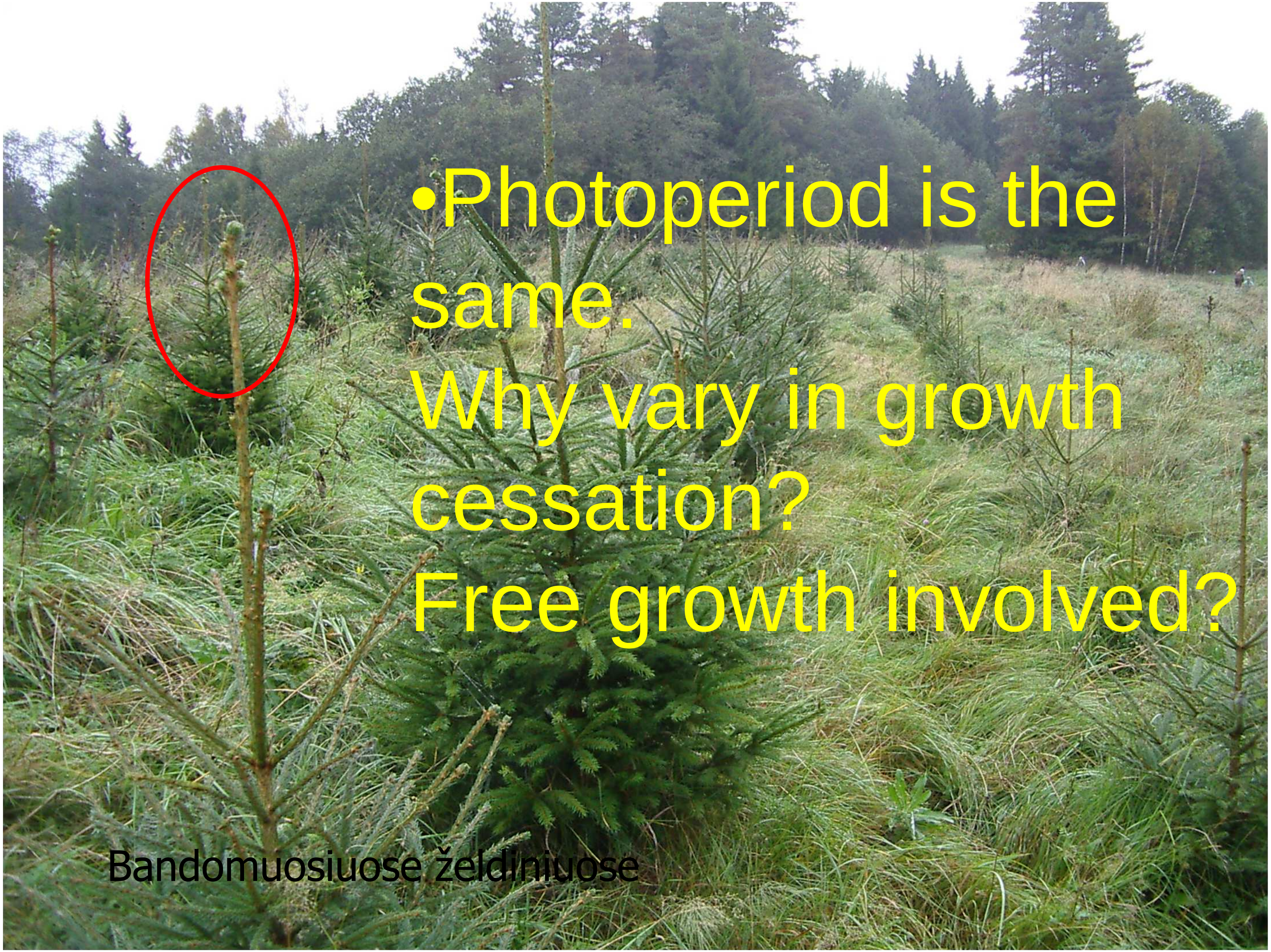
Eastern,
central

Late- medium- medium

Late- slow/fast- Late= tallest

Central,
eastern

Late start and end; together with fast growth at the second half of GP are the features of success (Ranki)



- Photoperiod is the same.

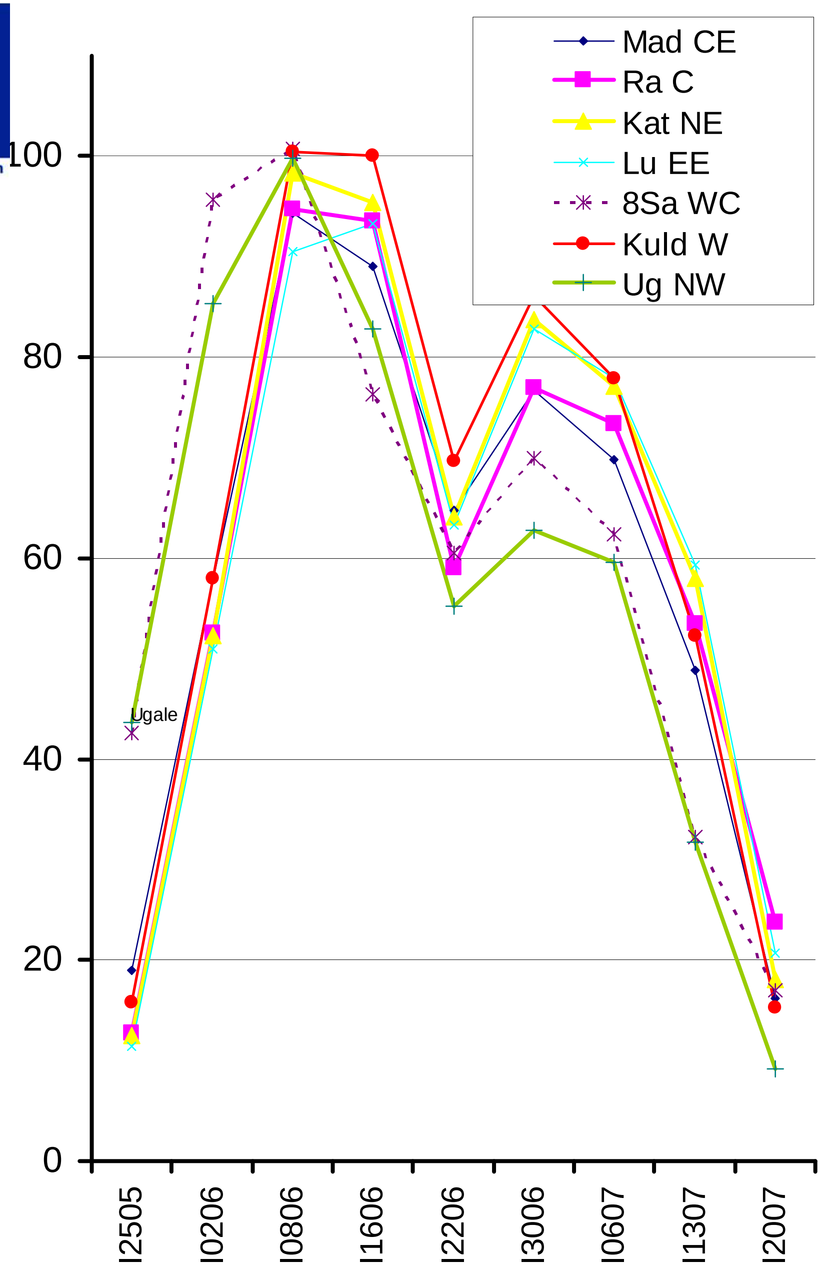
Why vary in growth cessation?

Free growth involved?

Bandomuosiuose želdiniuose

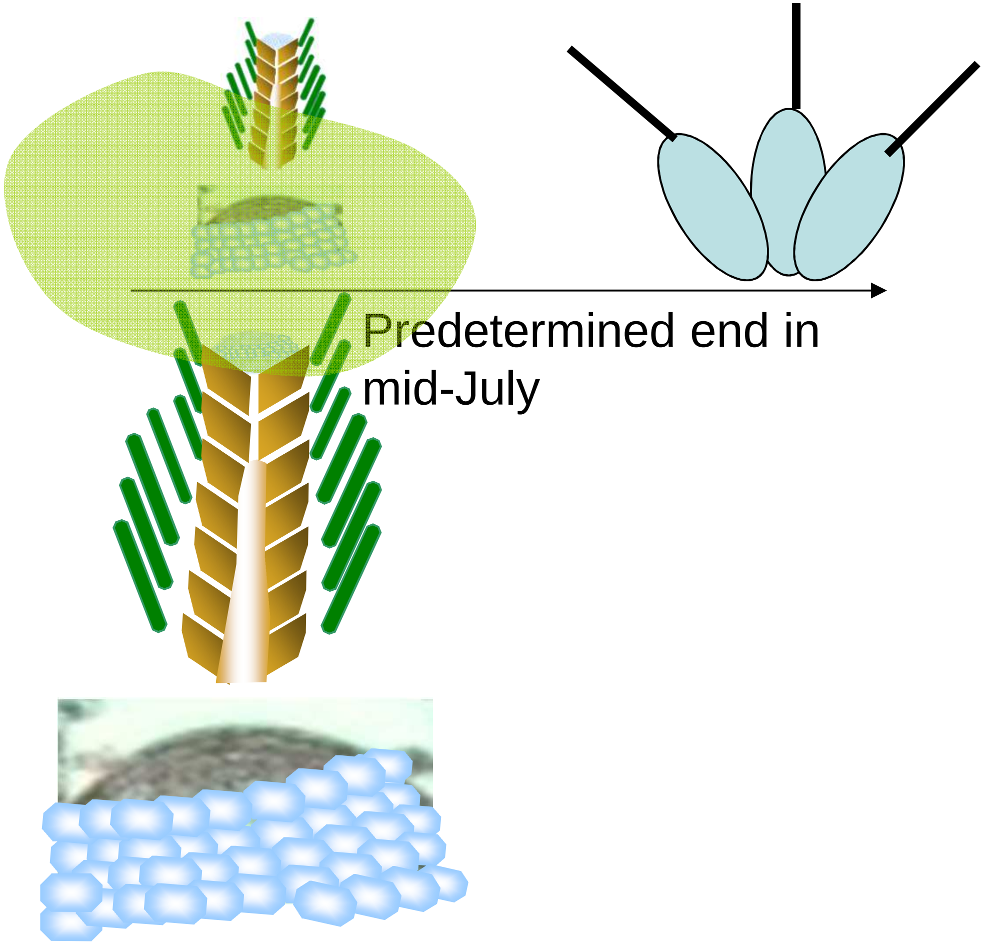
Funded by the European Union

INVESTMENT IN YOUR FUTURE



Early cessation = tendency for free growth

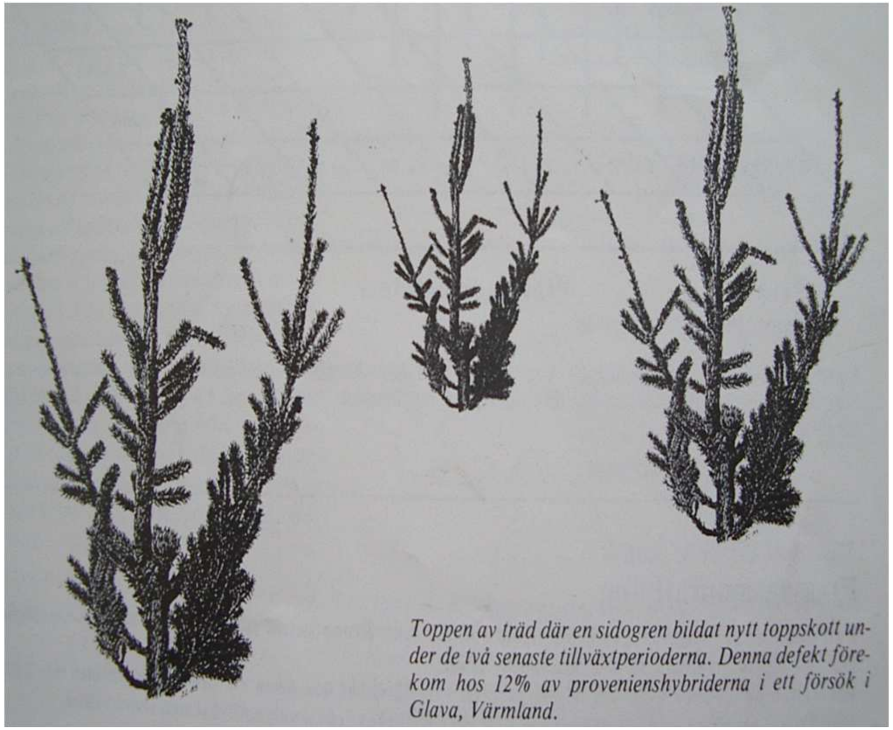
Shoot growth consists od predetermined and free (sylepctic /proleptic) growth



Free syleptic

Free proleptic

Predetermined end in mid-July



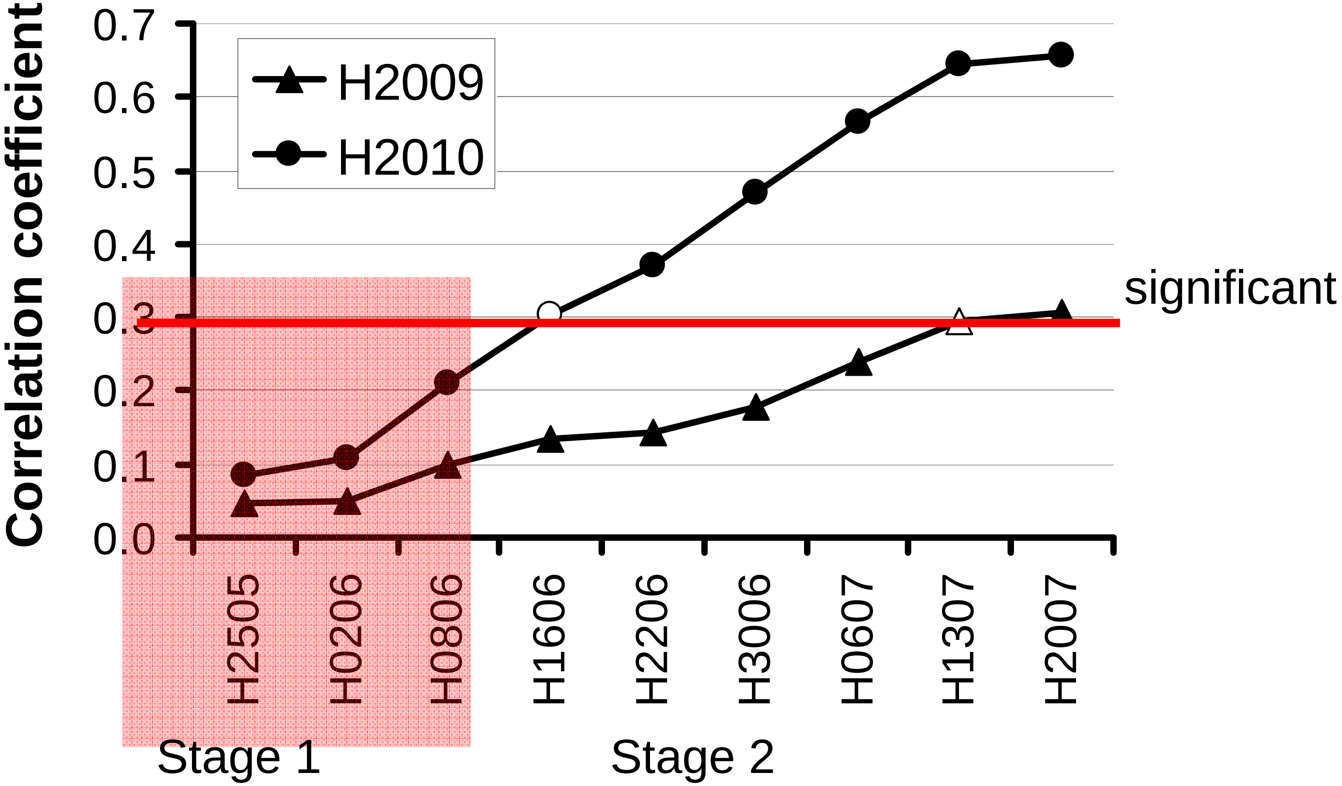
Toppen av träd där en sidogren bildat nytt toppskott under de två senaste tillväxtperioderna. Denna defekt förekom hos 12% av provenienshybriderna i ett försök i Glava, Värmland.

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Correlations

- With what increments the Final H is correlated?
- Length of GP is more important than growth speed , because correlations tend to be significant at 2nd half of GP

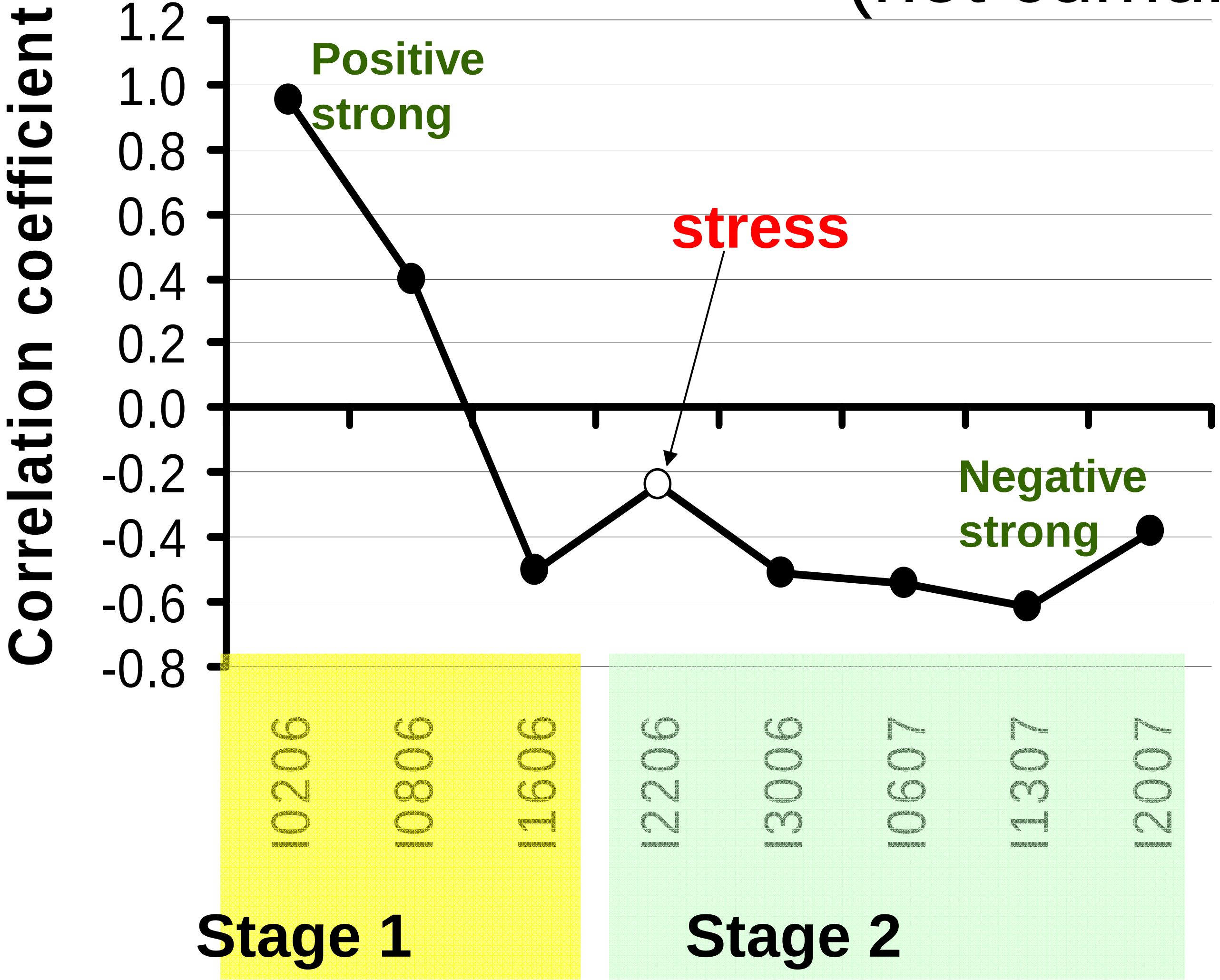


ESF

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Corr between start and subsequent weekly increments (not cumulative)



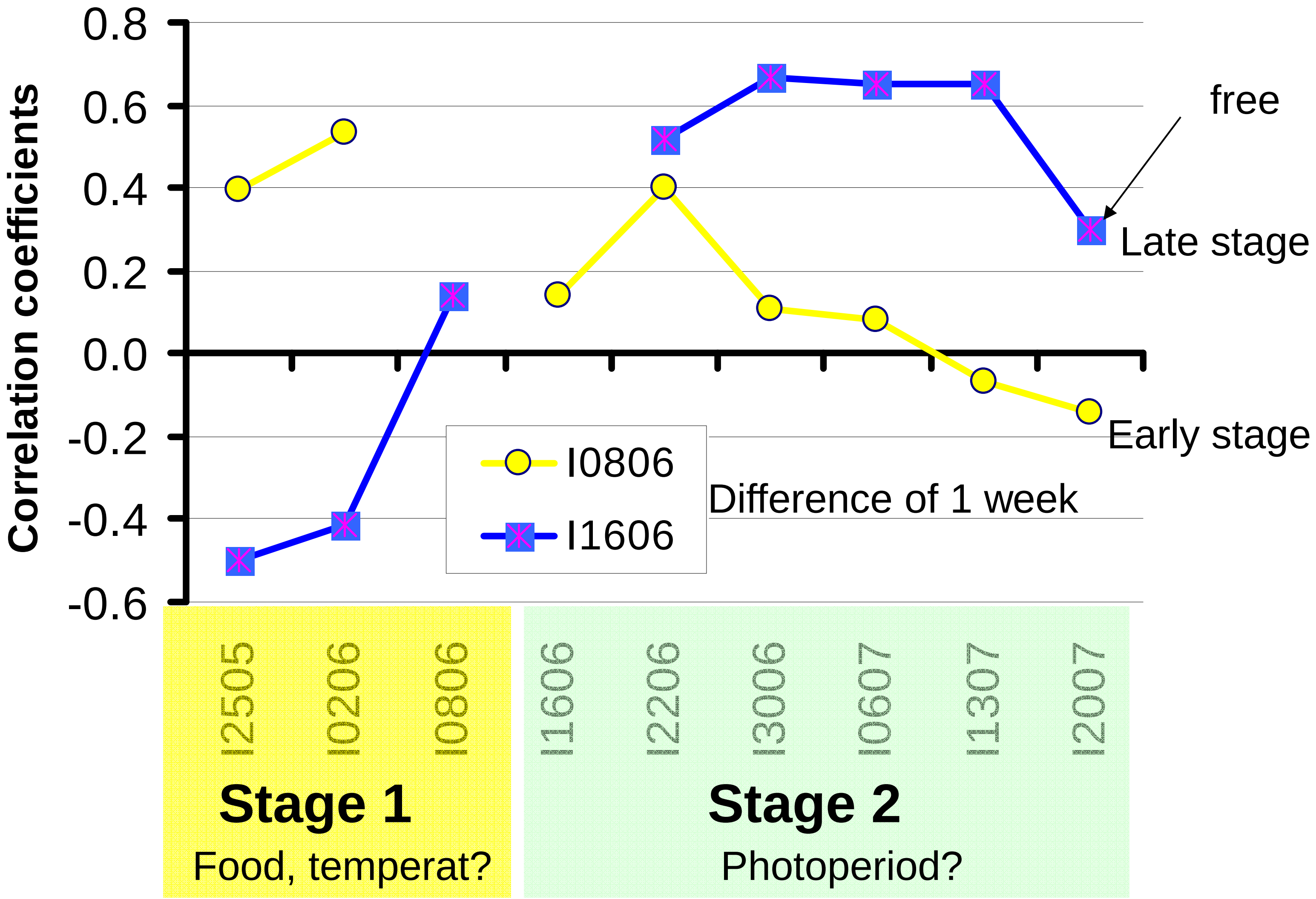
- •Early start means early cessation
- •two uncorrelated growth stages:
- •1 stage of fast initial elongation negatively correlated with later stages of elongation

ESF

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Corrs among weekly increments given for two adjacent dates reflecting different growth stages



free

Late stage

Early stage

Difference of 1 week

Stage 1

Food, temperat?

Stage 2

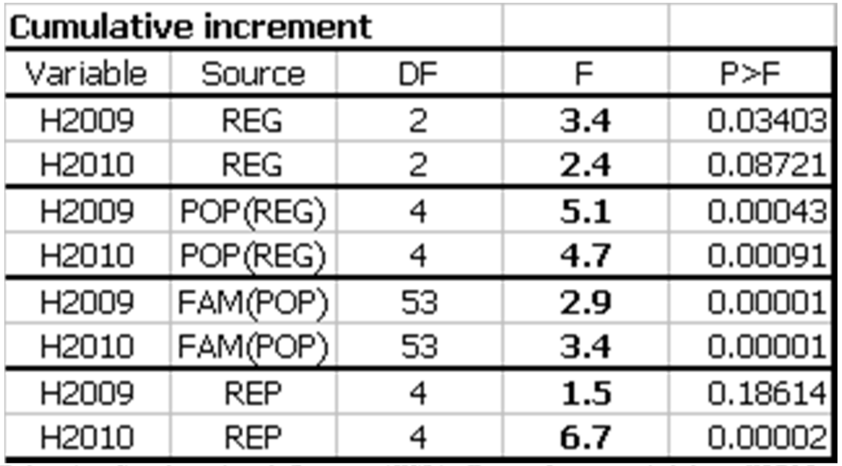
Photoperiod?

Funded by the European Union

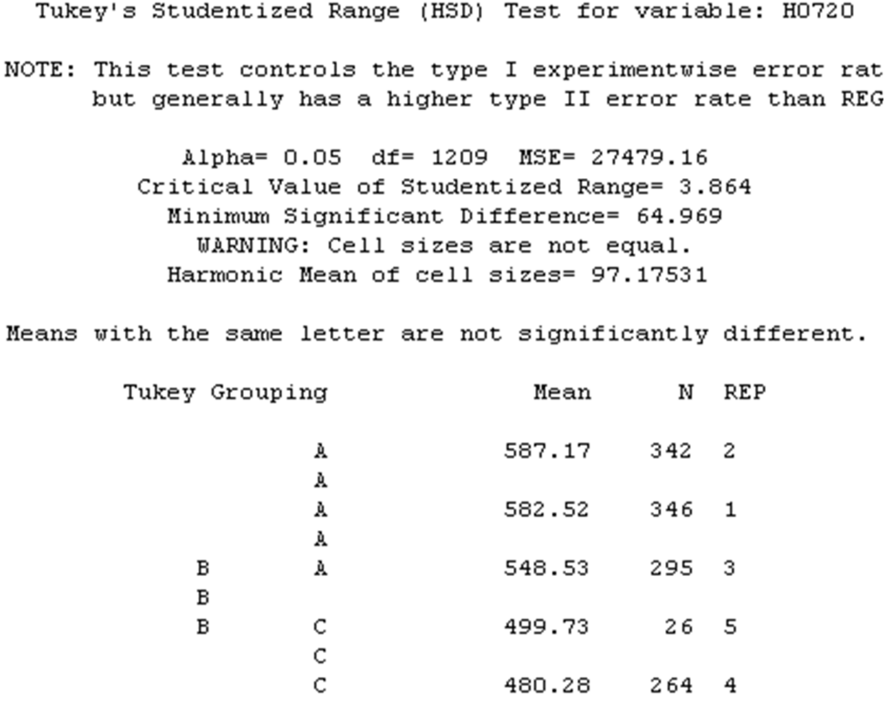
INVESTMENT IN YOUR FUTURE

Genetic parameters

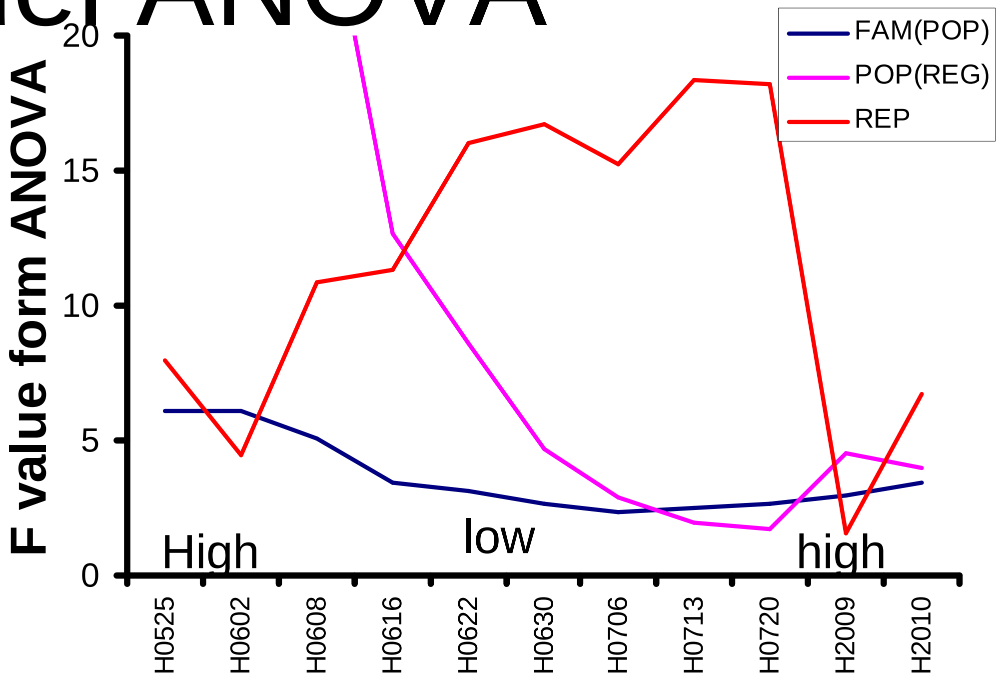
Mixed model ANOVA

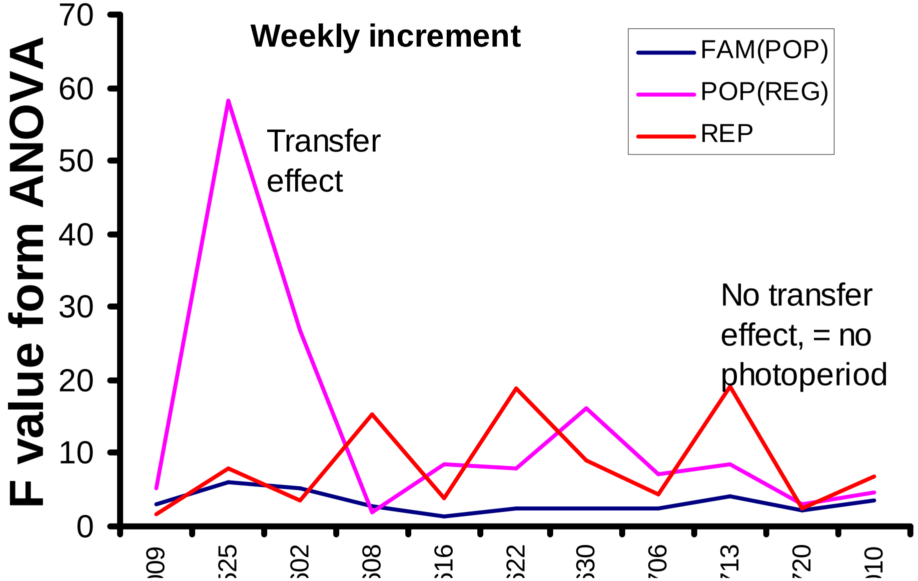


Cumulative increment				
Variable	Source	DF	F	P>F
H2009	REG	2	**3.4**	0.03403
H2010	REG	2	**2.4**	0.08721
H2009	POP(REG)	4	**5.1**	0.00043
H2010	POP(REG)	4	**4.7**	0.00091
H2009	FAM(POP)	53	**2.9**	0.00001
H2010	FAM(POP)	53	**3.4**	0.00001
H2009	REP	4	**1.5**	0.18614
H2010	REP	4	**6.7**	0.00002

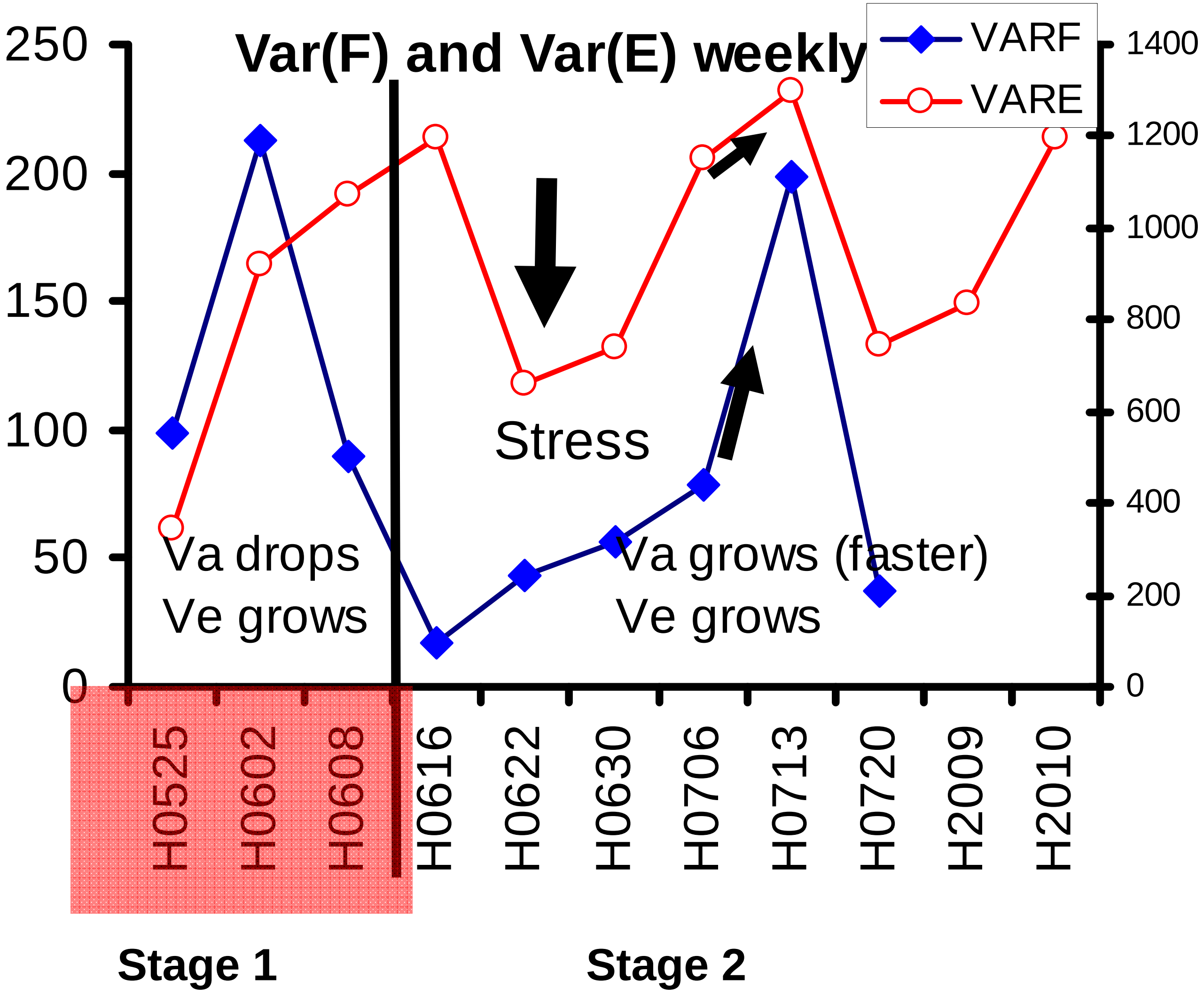


```
Tukey's Studentized Range (HSD) Test for variable: H0720

NOTE: This test controls the type I experimentwise error rat
      but generally has a higher type II error rate than REG

        Alpha= 0.05   df= 1209   MSE= 27479.16
     Critical Value of Studentized Range= 3.864
       Minimum Significant Difference= 64.969
         WARNING: Cell sizes are not equal.
       Harmonic Mean of cell sizes= 97.17531

Means with the same letter are not significantly different.

        Tukey Grouping              Mean       N   REP

                    A             587.17     342   2
                    A
                    A             582.52     346   1
                    A
            B       A             548.53     295   3
            B
            B       C             499.73      26   5
                    C
                    C             480.28     264   4
```



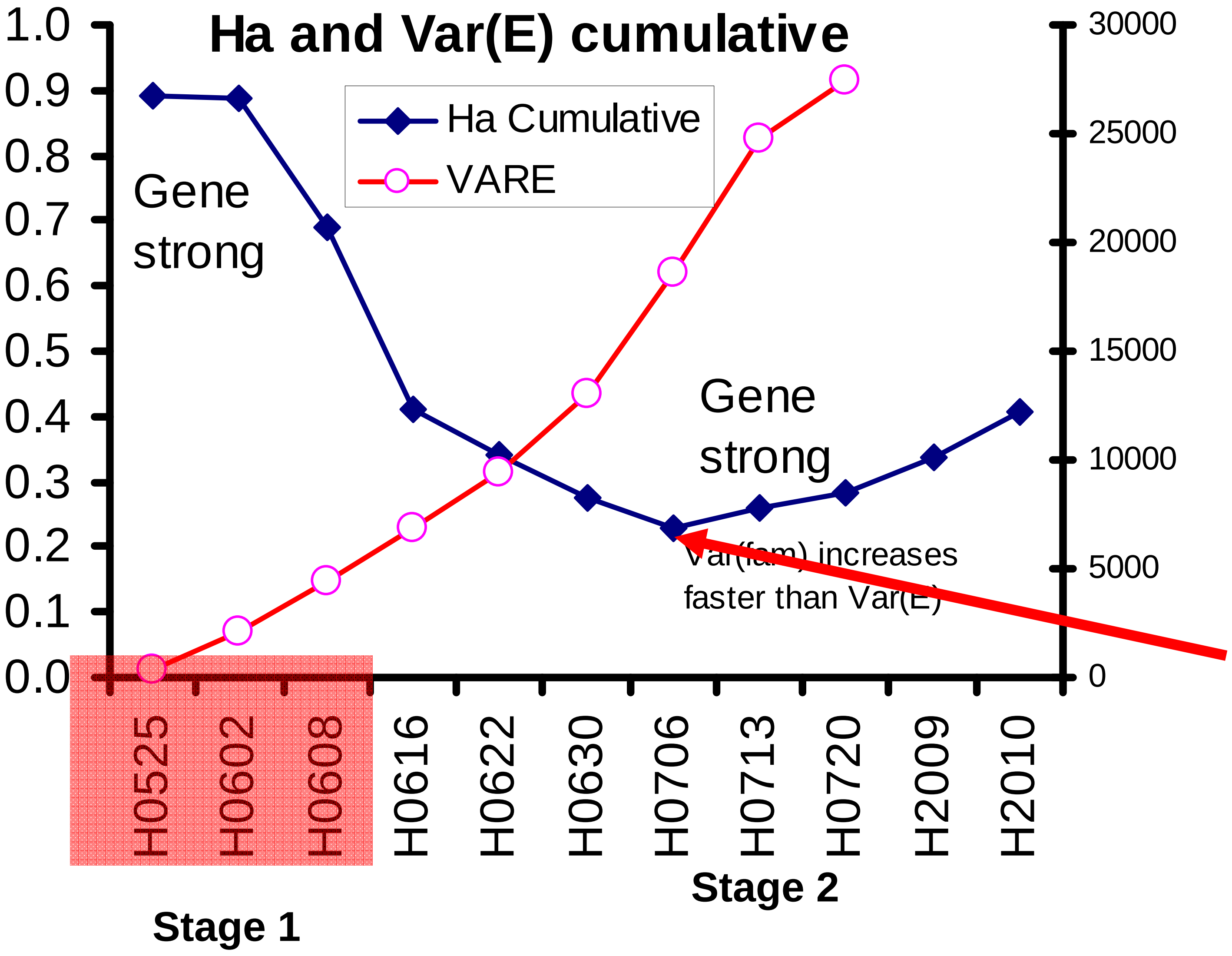


Heritability variation



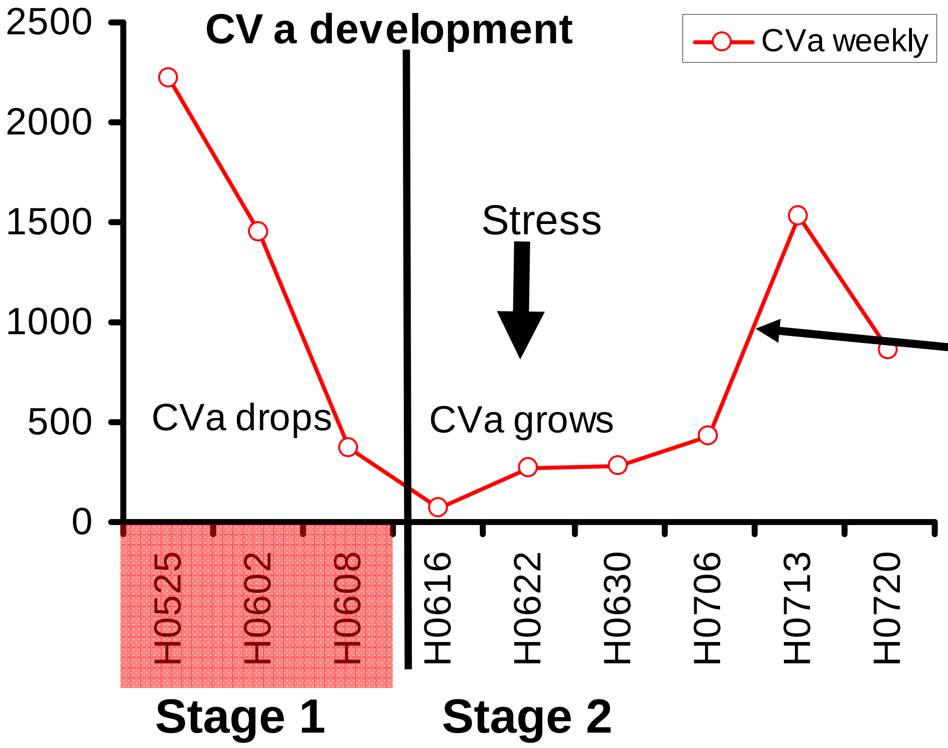
- Strong genetic control at start and end (= growth rhythm)
- Variances increase, but Va increases faster ?
- Stress reduced Ve

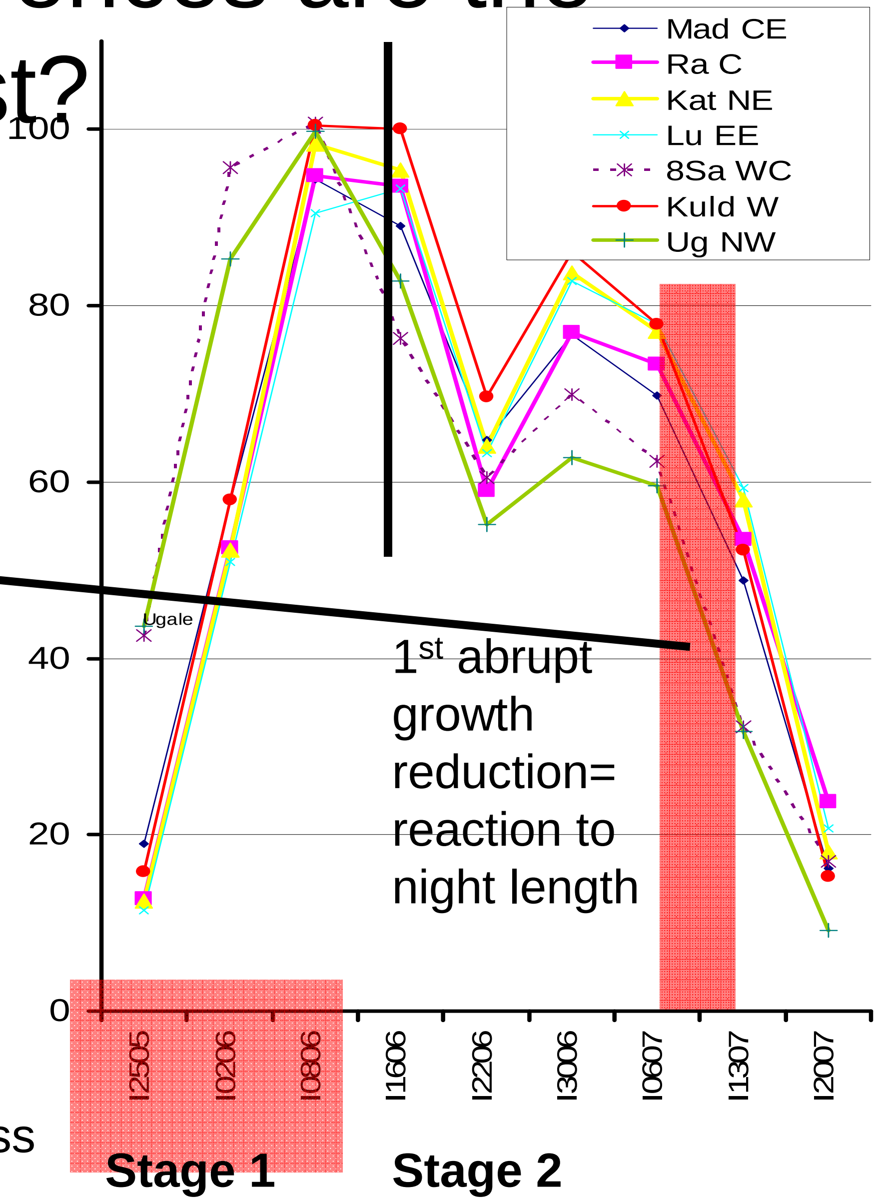
Heritability variation (cumulative)



- Strong photoperiodic response manifested in 6th of July

When genetic differences are the greatest?





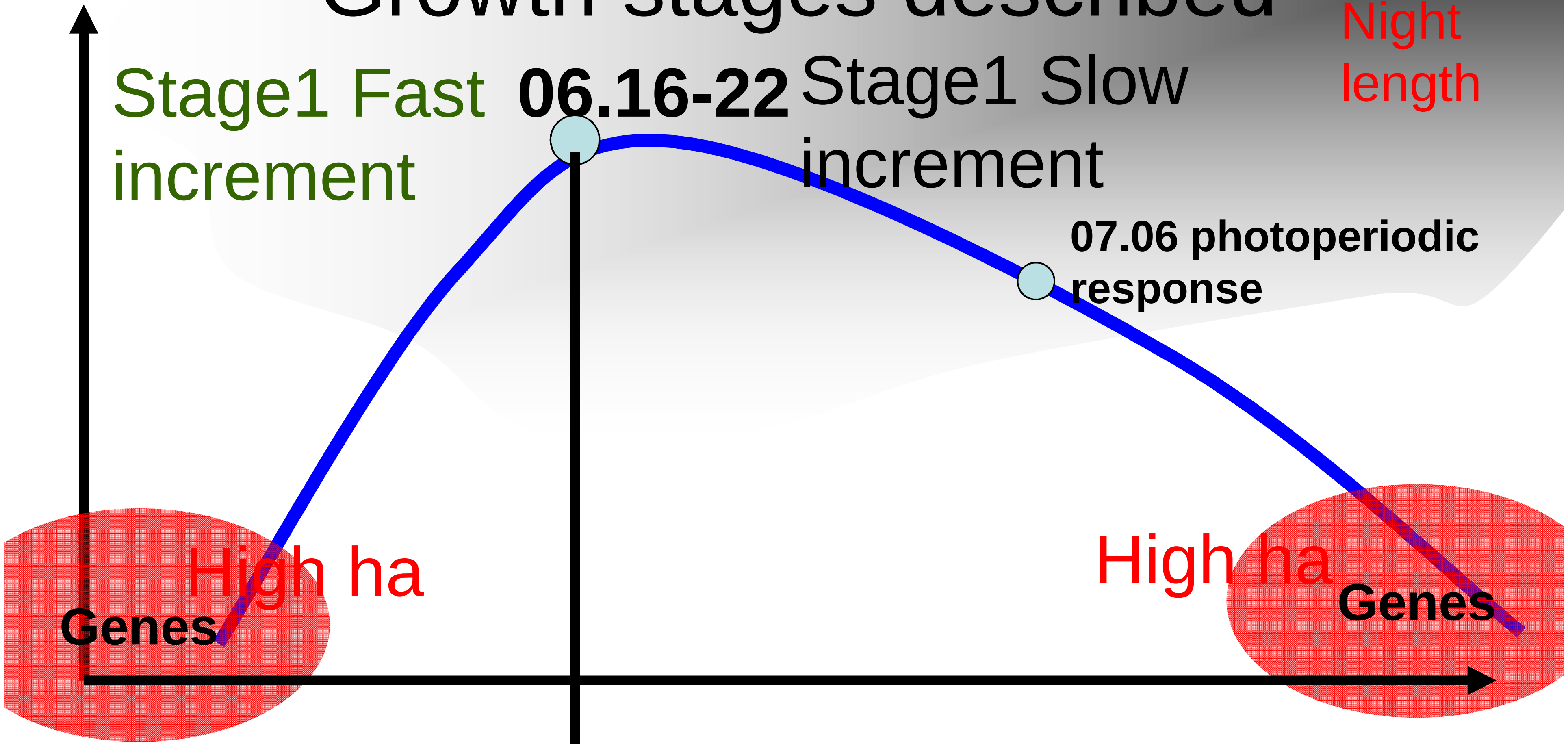
1st abrupt growth reduction= reaction to night length

Gene differentiation increased at stage 2

Gene differentiation slight increased at stress

Gene differentiation sharp increase at 1st slow

Growth stages described



Night length

Stage1 Fast increment

06.16-22

Stage1 Slow increment

07.06 photoperiodic response

High ha

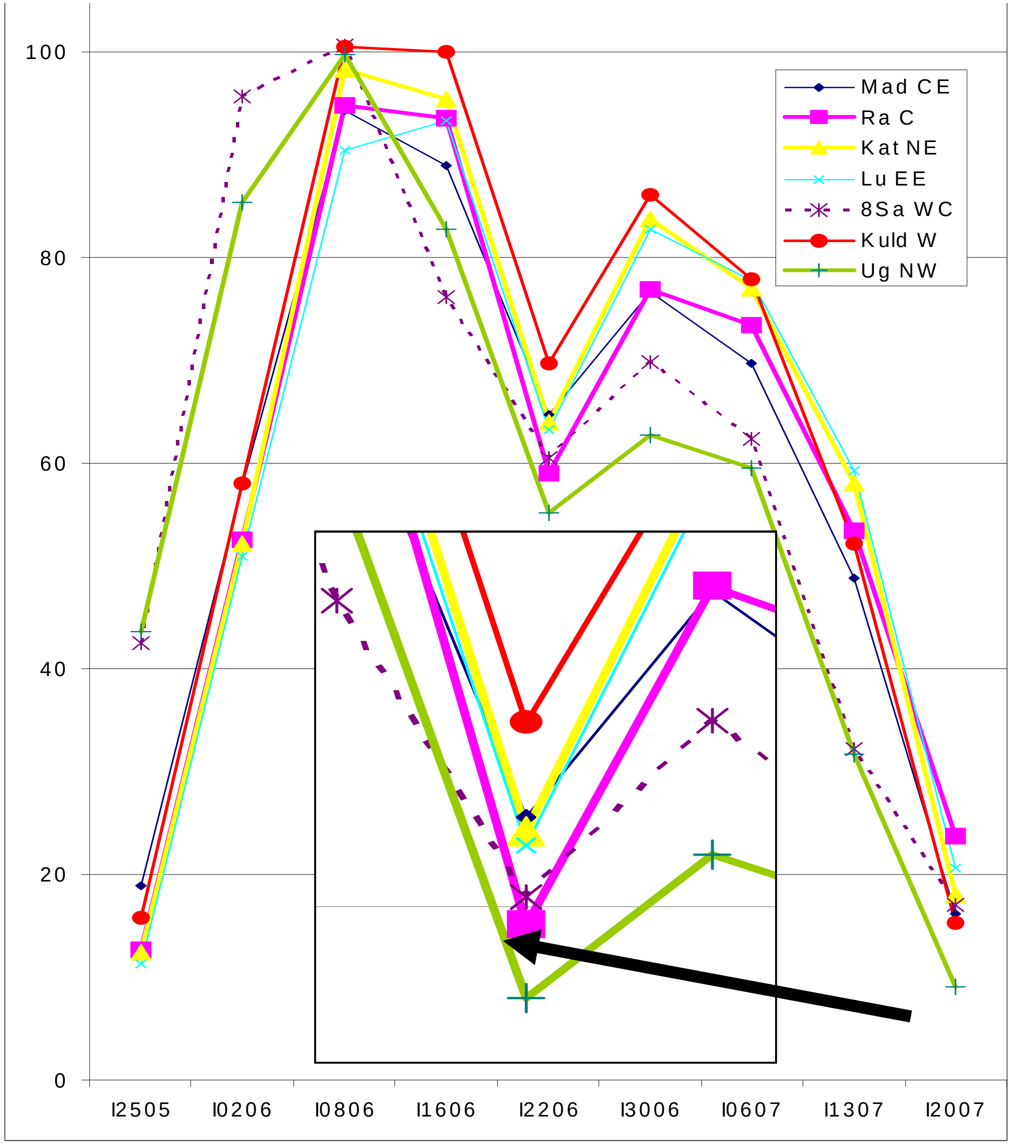
Genes

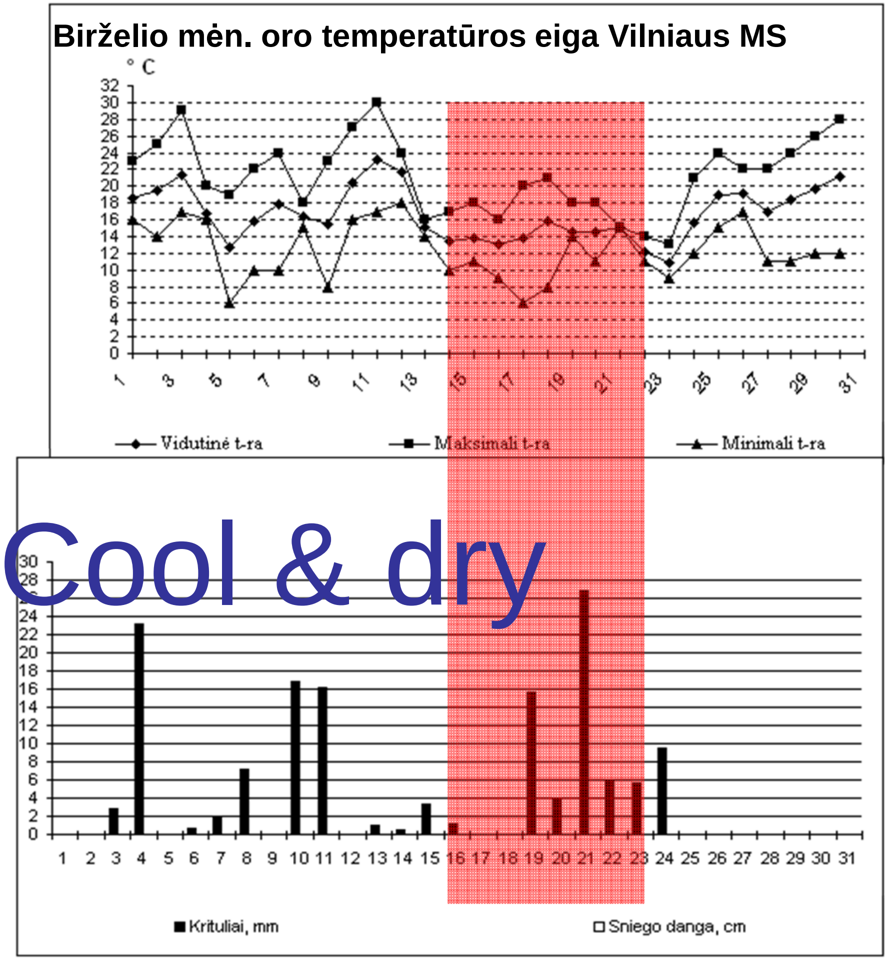
High ha

Genes

CVa	drops	increases
Vf	drops	increases
Ve	increases	increases
Corr with start	(+)	(-)

Stress 16-22 June





Cool & dry

Worst for Ranki= the southern type

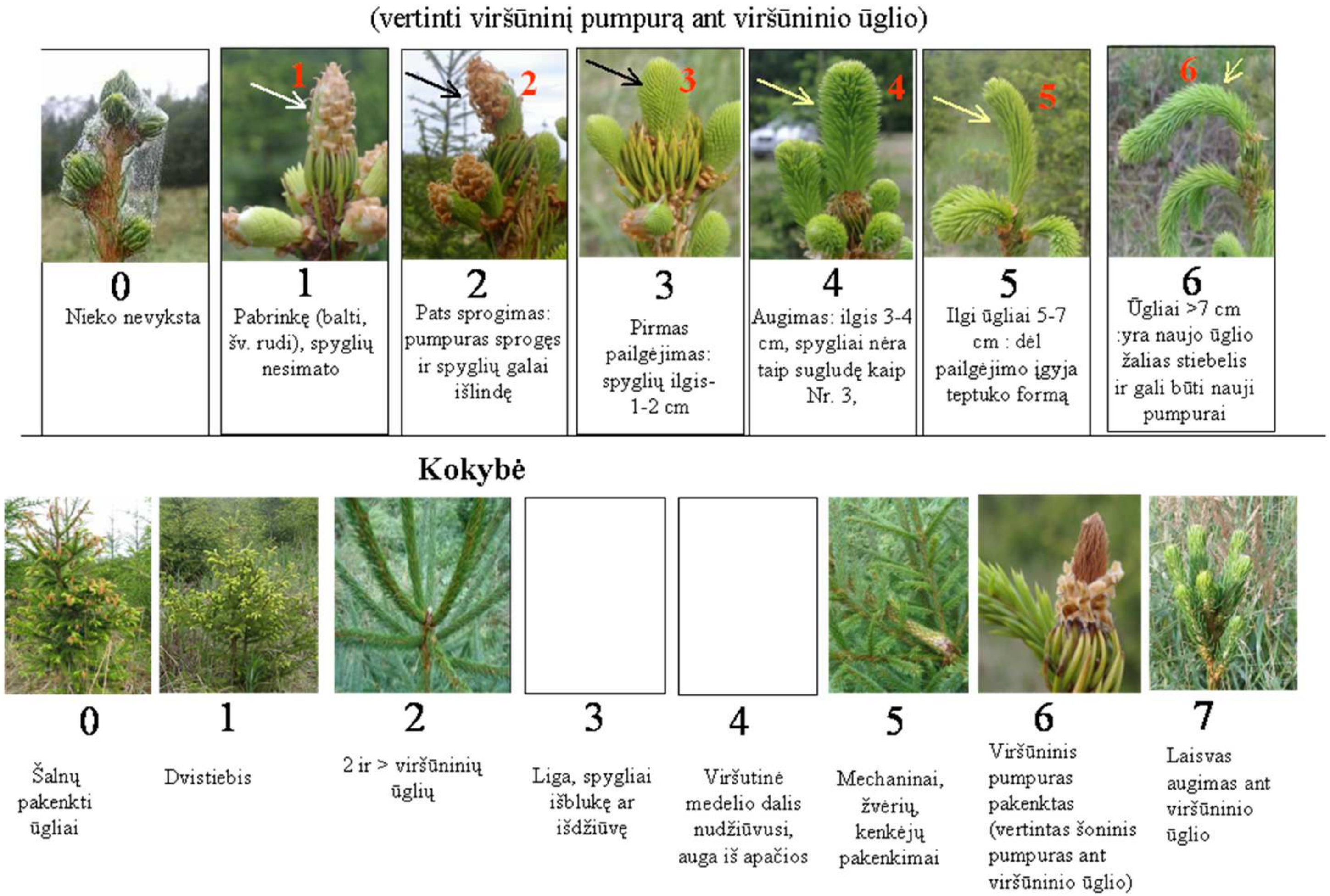
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Conclusions

- Significant effect of altitude (may be 2 sub-zones)
- Population effect strong at start (tsum) but weak at cessation (photoperiod, free growth).
- Correlations: early start means early end.
- Ha and CVa lowest in the middle of GP.
- 2 growth stages:
  - fast growth, Ha, CVa drops, (-) corr with later stages
  - Slow growth: Ha, CVa increases (+) corr with later stages

Funded by the European Union
INVESTMENT IN YOUR FUTURE

The end



(vertinti viršūninį pumpurą ant viršūninio ūglio)

0	Nieko nevyksta
1	Pabrinkę (balti, šv. rudi), spyglių nesimato
2	Pats sprogimas: pumpuras sprogęs ir spyglių galai išlindę
3	Pirmas pailgėjimas: spyglių ilgis- 1-2 cm
4	Augimas: ilgis 3-4 cm, spygliai nėra taip sugludę kaip Nr. 3,
5	Ilgi ūgliai 5-7 cm : dėl pailgėjimo įgyja teptuko formą
6	Ūgliai >7 cm :yra naujo ūglio žalias stiebelis ir gali būti nauji pumpurai

Kokybė

0	Šalnų pakenkti ūgliai
1	Dvistiebis
2	2 ir > viršūninių ūglių
3	Liga, spygliai išblukę ar išdžiūvę
4	Viršutinė medelio dalis nudžiūvusi, auga iš apačios
5	Mechaninai, žvėrių, kenkėjų pakenkimai
6	Viršūninis pumpuras pakenktas (vertintas šoninis pumpuras ant viršūninio ūglio)
7	Laisvas augimas ant viršūninio ūglio

Study carried out in European Social Fund’s Project “Importance of Genetic Factors in Formation of Forest Stands with High Adaptability and Qualitative Wood Properties” (No 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Genome plasticity of Scots pine (*Pinus sylvestris* L.) under different stress conditions

Mag.Biol. Angelika Voronova

Dr.Biol. Dainis Ruņģis (LSFRI Silava, Genetic Resource Centre);

Dr.Silv. Āris Jansons (LSFRI Silava, Forest tree breeding)

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Introduction

Aegilops (wheat wild ancestor), http://www.arcad-project.org

- Short generation time
- Low genetic diversity
- Human selection since 8500 B.C. using phenotypic traits
- High specificity to enviroment
- Molecular markers for selection are broadly used

- Long generation time & Molecular markers
- High genetic diversity
- Natural selection
- high plastisity to enviroment
- Phenotypic traits selection should be used in association with molecular markers

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Retrotransposon variation

- mobile genetic elements
- replicative transposition
- the largest compound of plant genomes (15-90 %)
- claster formation

? rearrangement of genome (instability), - functional mutations,-somaclonal variation,- recombination process,- genome structure upkeep

- transpozitional activation observed in stress conditions

(McClintoc, 1984, Peschke et al.1987, Grandbastien et al. 1998, Hirochika et al. 1993, Poteau et al.1994, Ramallo et al., 2008).

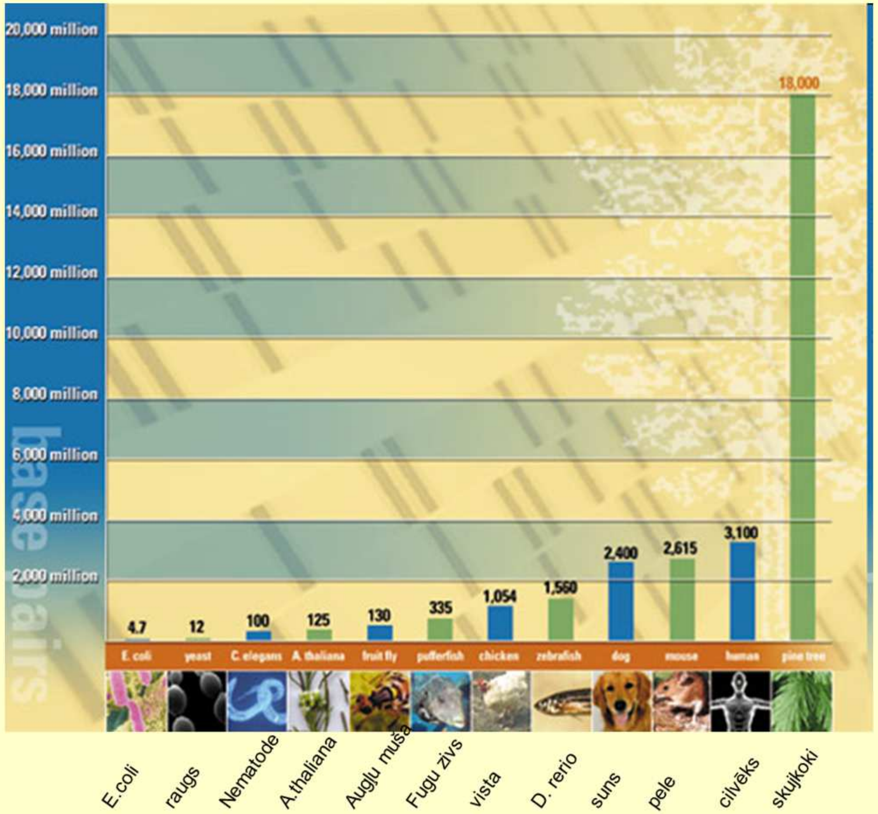
Adaptive selection to larger genomes with higher retrotransposon activity?

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Scots pine genome

- one of the ancient’s plant groups gymnosperms (*Pinophyta*)
- *2n=24* genome size:
  - – 50 pg (Grotkopp et al, 2004);
  - – 42,5 (Bogunic et al., 2003);
  - – 55,6 (Valkonen et al. 1994).

- 70-75 % repetitive sequences
- Pinus nigra population study of variation in genome size (Bogunic et al. 2007) 0,64 pg 2,6%.
- variation is determined by spread of different sequence repeats as satellites and retrotransposons.



http://www.genome.duke.edu/research/highlights/environmental/forestry-genomics.php

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Aims of study

Identify active retrotransposons in Scots pine (*Pinus sylvestris* L.) genome and characterize its structure, distribution and transcriptional rate during different stressors in controlled conditions.

INVESTMENT IN YOUR FUTURE

Brief structure of study

- ✓ Control molecular markes desighn
- ✓ Optimisation of methods;
- ✓ High temperature effects on the transcription of pine mobile genetic elements
    - Confirmation of clonal identity of the ramets;
    - Induction of stress conditions and RNA extraction;
    - Identification of mobile genetic elements;
    - Specific marker desighn;
    - Data collection and analysis.

►Biotic stress effects on transcription of pine mobile genetic elements;

►effects of Salicilic acid and ABA.

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Brief structure of study

► analyses of established molecular markers on the natural pine stands growing in different conditions;

► Full-size retrotransposon isolation and sequencing;

► ► Identification of retrotransposons/ classification/ structural studies / prevalence studies in the pine genome

Funded by the European Union

INVESTMENT IN YOUR FUTURE

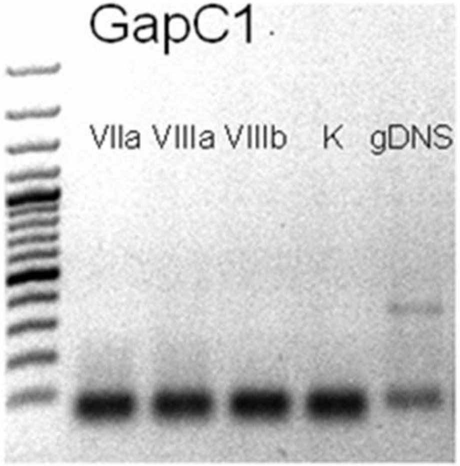
Scots pine ramets and stress initiation

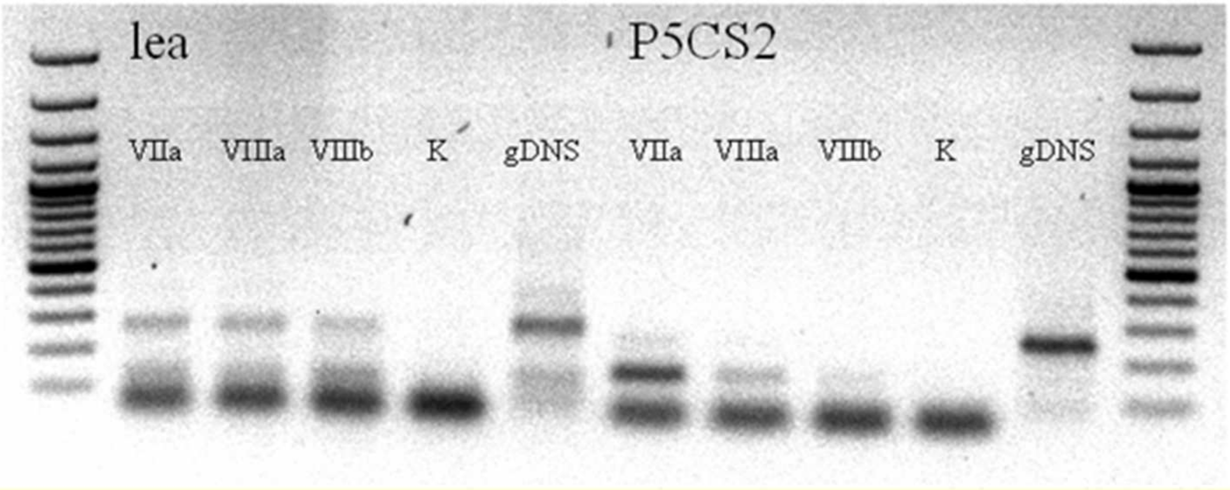
Pine Woolly Aphid
(*Pineus pini*)

Control molecular markes design

- dhn3 (AJ512362.1)
- abaH (FJ201653.1)
- Lea (FJ201577.1)

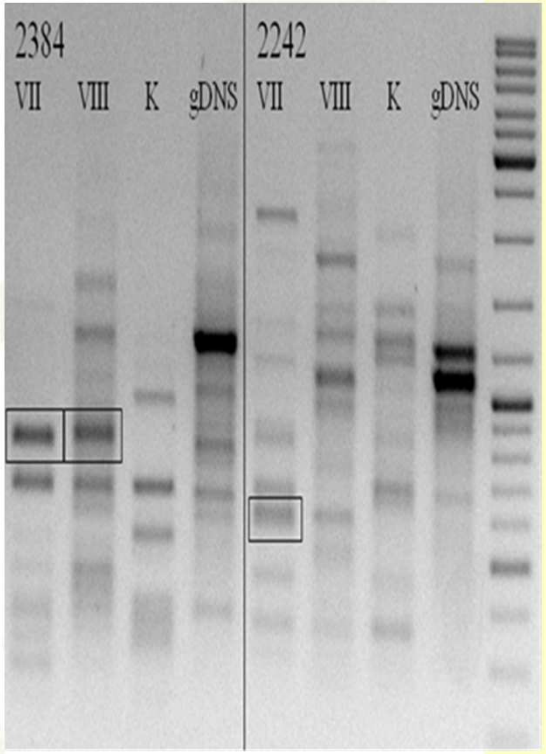
- P5CS2 (NM_115419.4, EF412967.1)
- GapC1 (L07501.1 Jaakola et al. 2004)
- pns (S50350.1)
- lp3 (U67135.1)

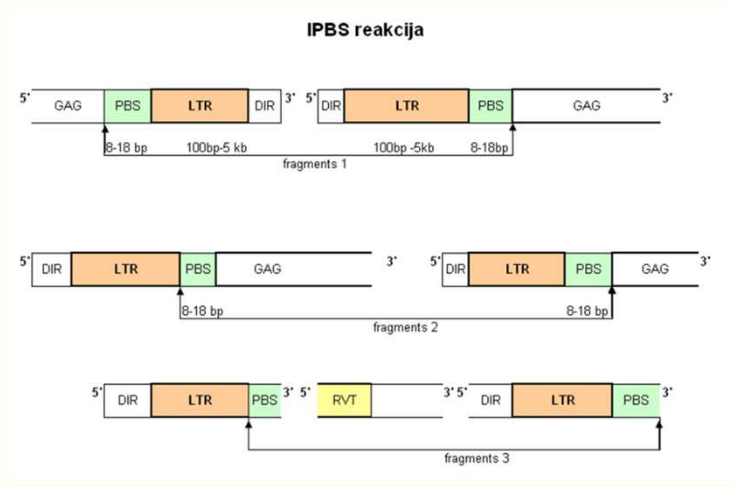




Methods

iPBS reaction (Kalendar et.al., 2010);





Inter PBS amplification. Lanes VII and VIII show fragments amplified from cDNA samples from heat stressed trees, lane K is the cDNA sample from the control tree, lane gDNS shows amplification with genomic DNA of the same ramet, and the last lane is size marker GeneRuler DNA Ladder Mix (Fermentas). Excised fragments are indicated.

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Classification of mobile genetic elements

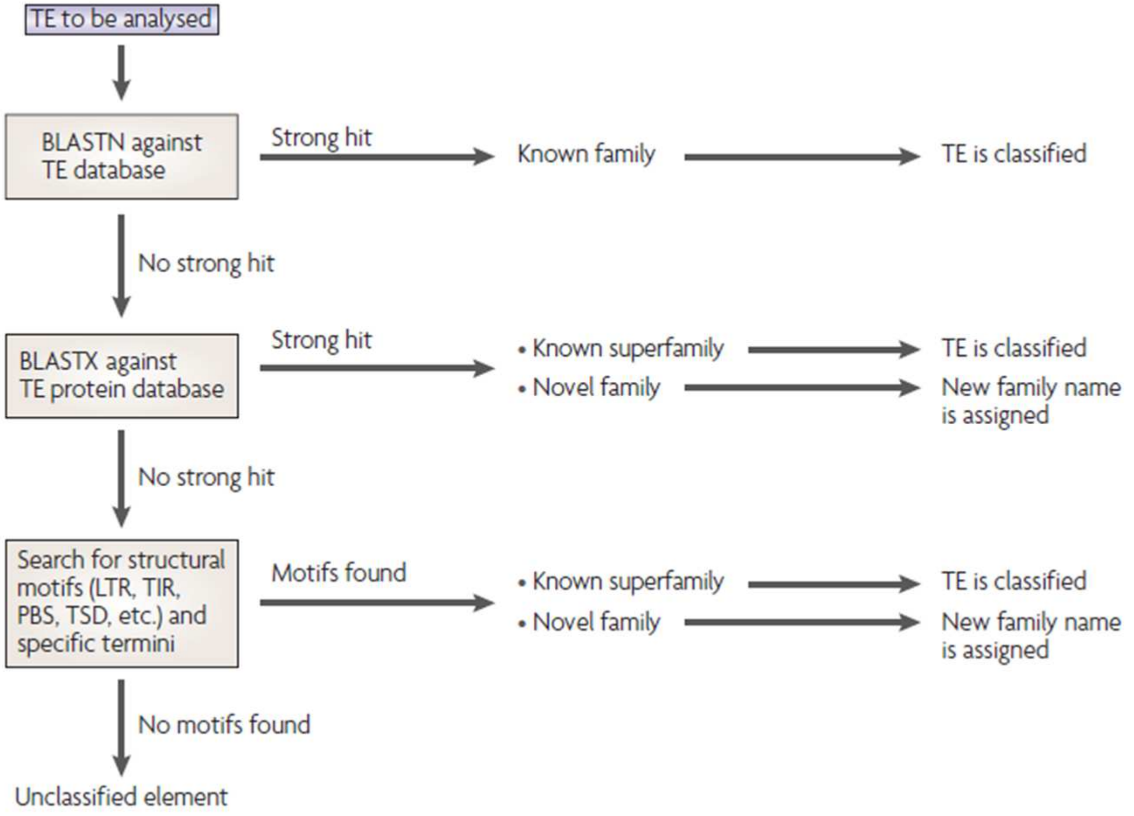
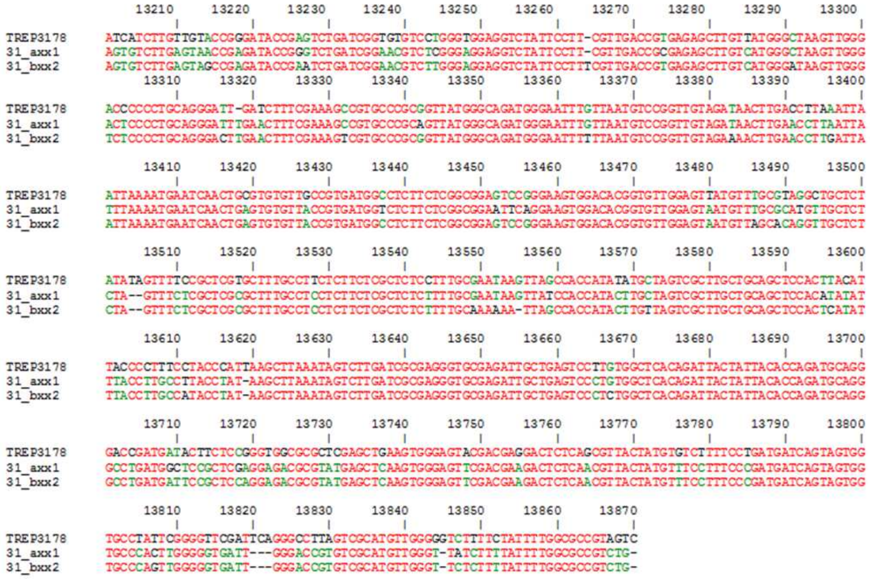


Figure 3 | **Step by step transposable element (TE) classification.** LTR, long terminal repeat; PBS, primer binding site; TIR, terminal inverted repeat; TSD, target site duplication.

Wicker et al., 2007

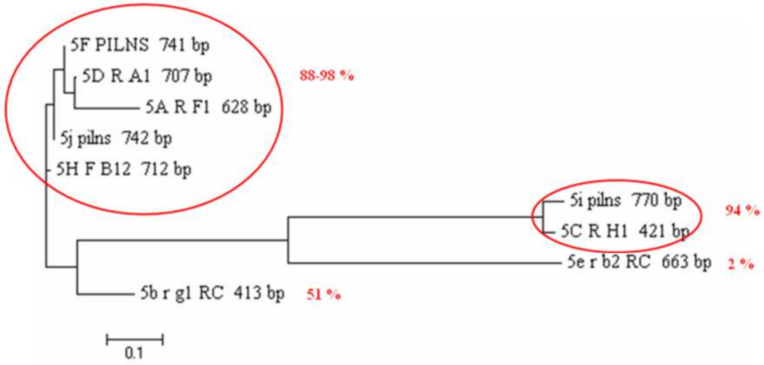
Funded by the European Union
INVESTMENT IN YOUR FUTURE

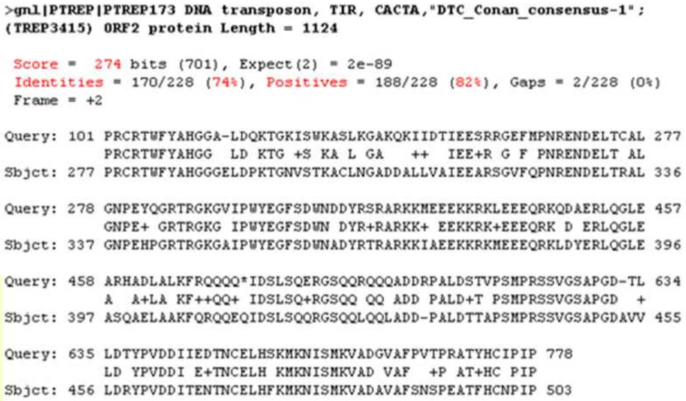
Sequence analyses



```
                   13210     13220     13230     13240     13250     13260     13270     13280     13290     13300
                     |         |         |         |         |         |         |         |         |         |
TREP3178    ATCATCTTGTTGTACCGGGATACCGAGTCTGATCGGTGTGTCCTGGGTGGAGGTCTATTCCTT-CGTTGACCGTGAGAGCTTGTTATGGGCTAAGTTGGG
31_axx1     AGTGTCTTGAGTAACCGAGATACCGGGTCTGATCGGAACGTCTCGGGAGGAGGTCTATTCCTT-CGTTGACCGCGAGAGCTTGTCATGGGCTAAGTTGGG
31_bxx2     AGTGTCTTGAGTAGCCGAGATACCGAATCTGATCGGAACGTCTTGGGAGGAGGTCTATTCCTTTCGTTGACCGTGAGAGCTTGTCATGGGATAAGTTGGG
                   13310     13320     13330     13340     13350     13360     13370     13380     13390     13400
                     |         |         |         |         |         |         |         |         |         |
TREP3178    ACCCCCCTGCAGGGATT-GATCTTTCGAAAGCCGTGCCCGCGGTTATGGGCAGATGGGAATTTGTTAATGTCCGGTTGTAGATAACTTGACCTTAAATTA
31_axx1     ACTCCCCTGCAGGGATTTGAACTTTCGAAAGCCGTGCCCGCAGTTATGGGCAGATGGGAATTTGTTAATGTCCGGTTGTAGATAACTTGAACCTTAATTA
31_bxx2     TCTCCCCTGCAGGGACTTGAACTTTCGAAAGTCGTGCCCGCGGTTATGGGCAGATGGGAATTTTTTAATGTCCGGTTGTAGAAAACTTGAACCTTGATTA

                   13410     13420     13430     13440     13450     13460     13470     13480     13490     13500
                     |         |         |         |         |         |         |         |         |         |
TREP3178    ATTAAAATGAATCAACTGCGTGTGTTGCCGTGATGGCCTCTTCTCGGCGGAGTCCGGGAAGTGGACACGGTGTTGGAGTTATGTTTGCGTAGGCTGCTCT
31_axx1     TTTAAAATGAATCAACTGAGTGTGTTACCGTGATGGTCTCTTCTCGGCGGAATTCAGGAAGTGGACACGGTGTTGGAGTAATGTTTGCGCATGTTGCTCT
31_bxx2     ATTAAAATGAATCAACTGAGTGTGTTACCGTGATGGCCTCTTCTCGGCGGAGTCCGGGAAGTGGACACGGTGTTGGAGTAATGTTAGCACAGGTTGCTCT

                   13510     13520     13530     13540     13550     13560     13570     13580     13590     13600
                     |         |         |         |         |         |         |         |         |         |
TREP3178    ATATAGTTTTCCGCTCGTGCTTTGCCTTCTCTTCTCGCTCTCCTTTGCGAATAAGTTAGCCACCATATATGCTAGTCGCTTGCTGCAGCTCCACTTACAT
31_axx1     CTA--GTTTCTCGCTCGCGCTTTGCCTCCTCTTCTCGCTCTCTTTTGCGAATAAGTTATCCACCATACTTGCTAGTCGCTTGCTGCAGCTCCACATATAT
31_bxx2     CTA--GTTTCTCGCTCGCGCTTTGCCTCCTCTTCTCGCTCTCTTTTGCAAAAAA-TTAGCCACCATACTTGTTAGTCGCTTGCTGCAGCTCCACTCATAT

                   13610     13620     13630     13640     13650     13660     13670     13680     13690     13700
                     |         |         |         |         |         |         |         |         |         |
TREP3178    TACCCCTTTCCTACCCATTAAGCTTAAATAGTCTTGATCGCGAGGGTGCGAGATTGCTGAGTCCTTGTGGCTCACAGATTACTATTACACCAGATGCAGG
31_axx1     TTACCTTGCCTTACCTAT-AAGCTTAAATAGTCTTGATCGCGAGGGTGCGAGATTGCTGAGTCCCTGTGGCTCACAGATTACTATTACACCAGATGCAGG
31_bxx2     TTACCTTGCCATACCTAT-AAGCTTAAATAGTCTTGATCGCGAGGGTGCGAGATTGCTGAGTCCCTCTGGCTCACAGATTACTATTACACCAGATGCAGG

                   13710     13720     13730     13740     13750     13760     13770     13780     13790     13800
                     |         |         |         |         |         |         |         |         |         |
TREP3178    GACCGATGATACTTCTCCGGGTGGCGCGCTCGAGCTGAAGTGGGAGTACGACGAGGACTCTCAGCGTTACTATGTGTCTTTTCCTGATGATCAGTAGTGG
31_axx1     GCCTGATGGCTCCGCTCGAGGAGACGCGTATGAGCTCAAGTGGGAGTTCGACGAAGACTCTCAACGTTACTATGTTTCCTTTCCCGATGATCAGTAGTGG
31_bxx2     GCCTGATGATTCCGCTCCAGGAGACGCGTATGAGCTCAAGTGGGAGTTCGACGAAGACTCTCAACGTTACTATGTTTCCTTTCCCGATGATCAGTAGTGG

                   13810     13820     13830     13840     13850     13860     13870
                     |         |         |         |         |         |         |
TREP3178    TGCCTATTCGGGGTTCGATTCAGGGCCTTAGTCGCATGTTGGGGGTCTTTTCTATTTTGGCGCCGTAGTC
31_axx1     TGCCCACTTGGGGGTGATT---GGGACCGTGTCGCATGTTGGGT-TATCTTTTATTTTGGCGCCGTCTG-
31_bxx2     TGCCCAGTTGGGGGTGATT---GGGACCGTGTCGCATGTTGGGT-TCTCTTTTATTTTGGCGCCGTCTG-
```

Figure 3. Multiple sequence alignment of 3.1 group fragments with LTR *Gypsy*, *Erika* TE (data base number: TREP3178) nucleotide sequences.





```
>gnl|PTREP|PTREP173 DNA transposon, TIR, CACTA,"DTC_Conan_consensus-1";
(TREP3415) ORF2 protein Length = 1124

 Score =  274 bits (701), Expect(2) = 2e-89
 Identities = 170/228 (74%), Positives = 188/228 (82%), Gaps = 2/228 (0%)
 Frame = +2

Query: 101 PRCRTWFYAHGGA-LDQKTGKISWKASLKGAKQKIIDTIEESRRGEFMPNRENDELTCAL 277
           PRCRTWFYAHGG  LD KTG +S KA L GA   ++  IEE+R G F PNRENDELT AL
Sbjct: 277 PRCRTWFYAHGGGELDPKTGNVSTKACLNGADDALLVAIEEARSGVFQPNRENDELTRAL 336

Query: 278 GNPEYQGRTRGKGVIPWYEGFSDWNDDYRSRARKKMEEEKKRKLEEEQRKQDAERLQGLE 457
           GNPE+ GRTRGKG IPWYEGFSDWN DYR+RARKK+ EEKKRK+EEEQRK D ERLQGLE
Sbjct: 337 GNPEHPGRTRGKGAIPWYEGFSDWNADYRTRARKKIAEEKKRKMEEEQRKLDYERLQGLE 396

Query: 458 ARHADLALKFRQQQQ*IDSLSQERGSQQRQQQADDRPALDSTVPSMPRSSVGSAPGD-TL 634
           A  A+LA KF++QQ+ IDSLSQ+RGSQQ QQ ADD PALD+T PSMPRSSVGSAPGD  +
Sbjct: 397 ASQAELAAKFQRQQEQIDSLSQQRGSQQLQQLADD-PALDTTAPSMPRSSVGSAPGDAVV 455

Query: 635 LDTYPVDDIIEDTNCELHSKMKNISMKVADGVAFPVTPRATYHCIPIP 778
           LD YPVDDI E+TNCELH KMKNISMKVAD VAF  +P AT+HC PIP
Sbjct: 456 LDRYPVDDITENTNCELHFKMKNISMKVADAVAFSNSPEATFHCNPIP 503
```

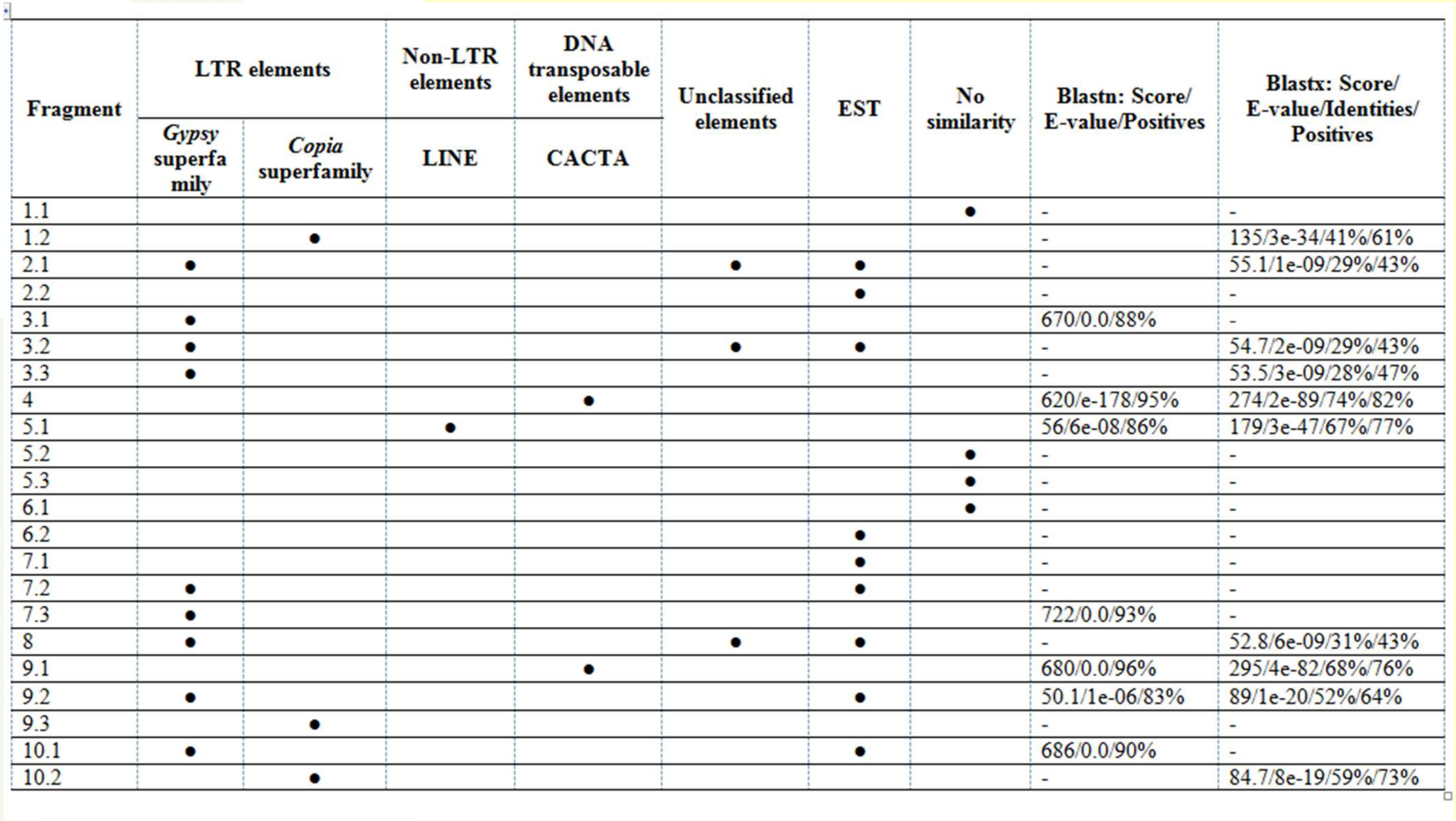
Searches were done in the

- NCBI data base (http://www.ncbi.nlm.nih.gov/BLAST/);
- GrainGenes Triticeae Repeat Sequence Database (http://wheat.pw.usda.gov/ITMI/Repeats/blastrepeats3.html)
- Gypsy Database 2.0 (http://gydb.org/index.php/Blast) (Llorens et al., 2011).

Funded by the European Union

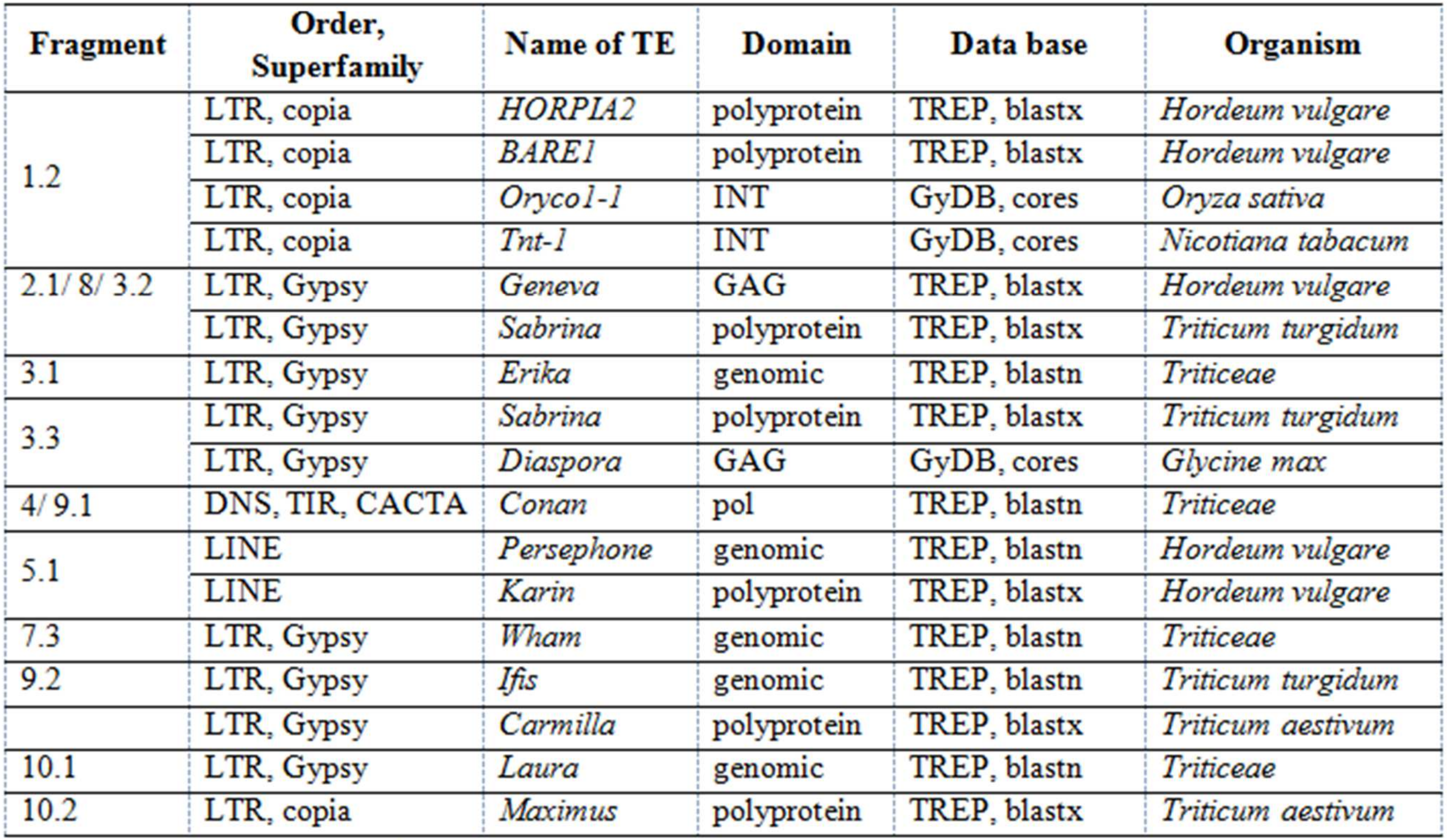
INVESTMENT IN YOUR FUTURE

Results of similarity searches



Fragment	LTR elements		Non-LTR elements	DNA transposable elements	Unclassified elements	EST	No similarity	Blastn: Score/ E-value/Positives	Blastx: Score/ E-value/Identities/ Positives
	Gypsy superfamily	*Copia* superfamily	LINE	CACTA					
1.1							●	-	-
1.2		●						-	135/3e-34/41%/61%
2.1	●				●	●		-	55.1/1e-09/29%/43%
2.2						●		-	-
3.1	●							670/0.0/88%	-
3.2	●				●	●		-	54.7/2e-09/29%/43%
3.3	●							-	53.5/3e-09/28%/47%
4				●				620/e-178/95%	274/2e-89/74%/82%
5.1			●					56/6e-08/86%	179/3e-47/67%/77%
5.2							●	-	-
5.3							●	-	-
6.1							●	-	-
6.2						●		-	-
7.1						●		-	-
7.2	●					●		-	-
7.3	●							722/0.0/93%	-
8	●				●	●		-	52.8/6e-09/31%/43%
9.1				●				680/0.0/96%	295/4e-82/68%/76%
9.2	●					●		50.1/1e-06/83%	89/1e-20/52%/64%
9.3		●						-	-
10.1	●					●		686/0.0/90%	-
10.2		●						-	84.7/8e-19/59%/73%

Classification of analyzed fragment sequences according to transposable elements from the TREP and GyDB databases

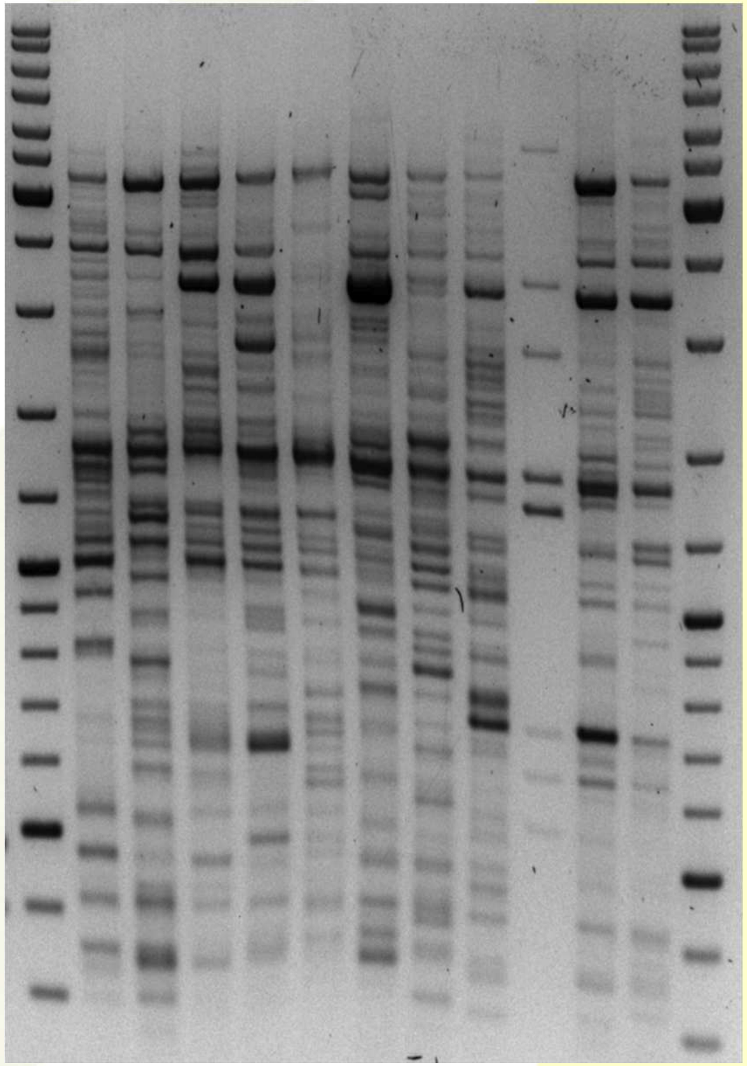


Fragment	Order, Superfamily	Name of TE	Domain	Data base	Organism
1.2	LTR, copia	*HORPIA2*	polyprotein	TREP, blastx	*Hordeum vulgare*
	LTR, copia	*BARE1*	polyprotein	TREP, blastx	*Hordeum vulgare*
	LTR, copia	*Oryco1-1*	INT	GyDB, cores	*Oryza sativa*
	LTR, copia	*Tnt-1*	INT	GyDB, cores	*Nicotiana tabacum*
2.1/ 8/ 3.2	LTR, Gypsy	*Geneva*	GAG	TREP, blastx	*Hordeum vulgare*
	LTR, Gypsy	*Sabrina*	polyprotein	TREP, blastx	*Triticum turgidum*
3.1	LTR, Gypsy	*Erika*	genomic	TREP, blastn	*Triticeae*
3.3	LTR, Gypsy	*Sabrina*	polyprotein	TREP, blastx	*Triticum turgidum*
	LTR, Gypsy	*Diaspora*	GAG	GyDB, cores	*Glycine max*
4/ 9.1	DNS, TIR, CACTA	*Conan*	pol	TREP, blastn	*Triticeae*
5.1	LINE	*Persephone*	genomic	TREP, blastn	*Hordeum vulgare*
	LINE	*Karin*	polyprotein	TREP, blastx	*Hordeum vulgare*
7.3	LTR, Gypsy	*Wham*	genomic	TREP, blastn	*Triticeae*
9.2	LTR, Gypsy	*Ifis*	genomic	TREP, blastn	*Triticum turgidum*
	LTR, Gypsy	*Carmilla*	polyprotein	TREP, blastx	*Triticum aestivum*
10.1	LTR, Gypsy	*Laura*	genomic	TREP, blastn	*Triticeae*
10.2	LTR, copia	*Maximus*	polyprotein	TREP, blastx	*Triticum aestivum*

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Inter Retratransposon amplification



Nine newly developed Retrotransposon Markers

184 fragments were analysed

150 samples from one natural pine stand growing in highland, slope and lowland.

355-279 more fragments were found in the samples from trees growing in highland

Stands	heat stress markers		biotic stress markers		Total
	Sum 40	Average	Sum 38	Average	
pop_highland	2269	56,73	2281	60,03	4550
pop_slope	2173	54,56	2098	55,29	4271
pop_lowland	2135	53,59	2060	54,30	4195

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Conclusions

- Unspecific iPBS amplification reveals significant retrotransposon variation in Scots pine genome;
- Representatives of different families of Retrotransposons are found. Three fragments could be classified to particular TE families with high probability as they showed high similarity at the nucleotide level (LTR, *Gypsy*, *Laura*; LTR, *Gypsy*, *Wham*; DNS, TIR CACTA, *Conan*; LTR, *Gypsy*, *Erica*).
- Analysed sequences are consistently transcribed under various stress conditions as analysed sequences shows similarity with EST database sequences derived from cDNA libraries obtained in various studies of stress responses.
- The presence of sequence variation indicate that the transcripts originate from different copies in the pine genome.

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Conclusions

- One of the analysed sequences showed a similarity to a DNA transposable element *Conan*. Due to the clustering of retrotransposons within genomes, the identified sequences could be fragments or inactive elements within an active element.

- Some of the analysed sequences were similar to several known active retroelement proteins (*BARE-1*, *Tnt-1*) which could indicate that these retroelements possess transposable activity.

- These results indicate that further isolation of complete elements is needed to prove their transcriptional activation and to investigate activation of these elements in differing stress conditions.

- Due to high genetic diversity to acess diferences in natural pine stands affected by retrotransposition more molecular marker needed or we need to choose more homogeneous sample set.

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Presentation of Results

- **Expression of retrotransposon-like sequences in Scots pine (*Pinus sylvestris*. L) in response to heat stress**. 2011. A.Voronova, Ā.Jansons, D.Ruņģis, Enviromental and Experimental Biology, in press.

- 4.2.2010.- 68. Scientific Conference of University of Latvia, Plant biology section.

- 22.-24.04.2009.- 5th International Conference "Research and Conservation of Biological Diversity in Baltic Region", Daugavpils, Latvia (Oral presentation).

- 19.-21.03.2009.– FEBS Workshop „Adaption Potential in Plants", Vienna, Austria (Poster presentation).

- 4.02.2009.– 67. Scientific Conference of University of Latvia, Plant biology section (Oral presentation).

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Acknowledgements

- This study was supported by the European Social Fond project (No. 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146).

EIROPAS SOCIĀLAIS FONDS

- I am thankful to Dr. silv. Imants Baumanis for providing the experimental pine ramets for this study and to Dr. biol. Nils Rostoks for assistance in transformation assay setup and team of Genetic Resorce Centre of LSFRI Silava

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Spruce. Natural durability

Ilze & Co

ESF 146 seminar 30.11.-01.12. 2011

Silava, Kalsnava

‘’Natural durability: the inherent resistance of wood to attack by wood destroying organisms’’ (EN 350)

LVS EN 350-1:2000. Durability of wood and wood-based products - Natural durability of solid wood - Part 1: Guide to the principles of testing and classification of the natural durability of wood

LVS EN 350-2:2000. Durability of wood and wood-based products - Natural durability of solid wood - Part 2: Guide to natural durability and treatability of selected wood species of importance in Europe

LVS EN 113:2000. Wood preservatives - Test method for determining the protective effectiveness against wood destroying basidiomycetes - Determination of the toxic values

Funded by the European Union

INVESTMENT IN YOUR FUTURE

The **AIM**

to determine natural resistance of particular spruce clones regarding fungal degradation

Sapwood/ heartwood

Bromcresol green: heartwood – blue; sapwood - yellow (KUTSCHA and SACHS, 1962).

ESF spruce ~ 25 years

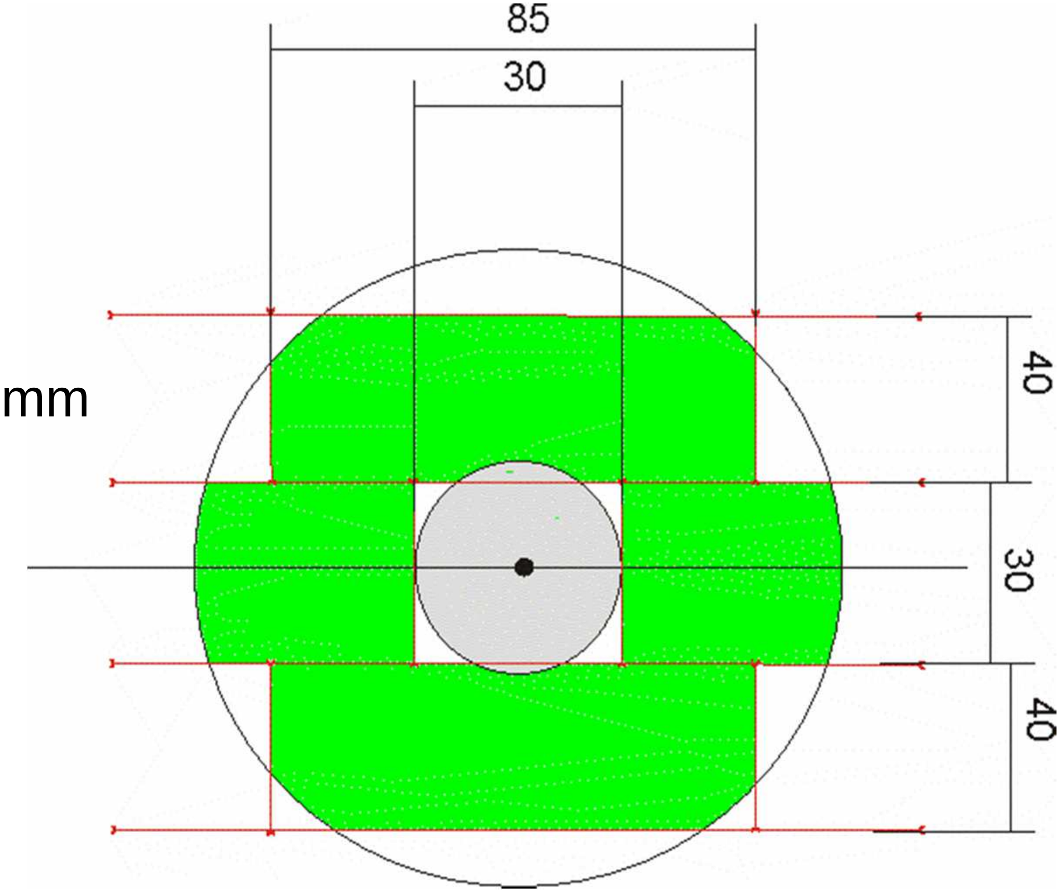
Spruce > 60 years

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Natural durability tests:

- 10 Norway spruce (*Picea abies*) clones: 26, 31, A10, A15, A7, B10, B15, B6, V7, V9
- Control – Scots pine (*P. sylvestris*) sapwood

Tree division in laths, mm



Funded by the European Union

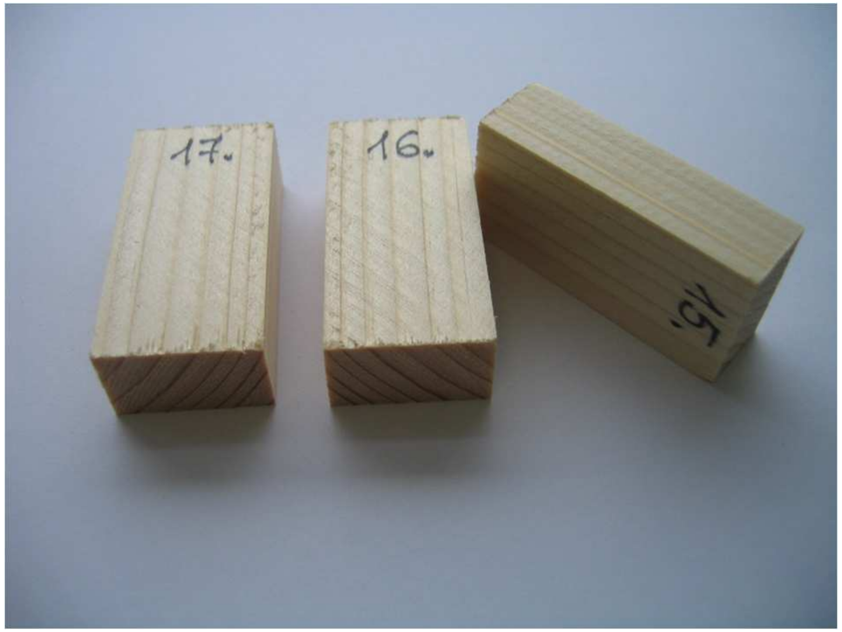
INVESTMENT IN YOUR FUTURE

Drying-kiln, at 60^{o}C

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Specimens at 12% moisture (m/m): 50 x 25 x 15 mm
Theoretical volume: 18,75 cm^3



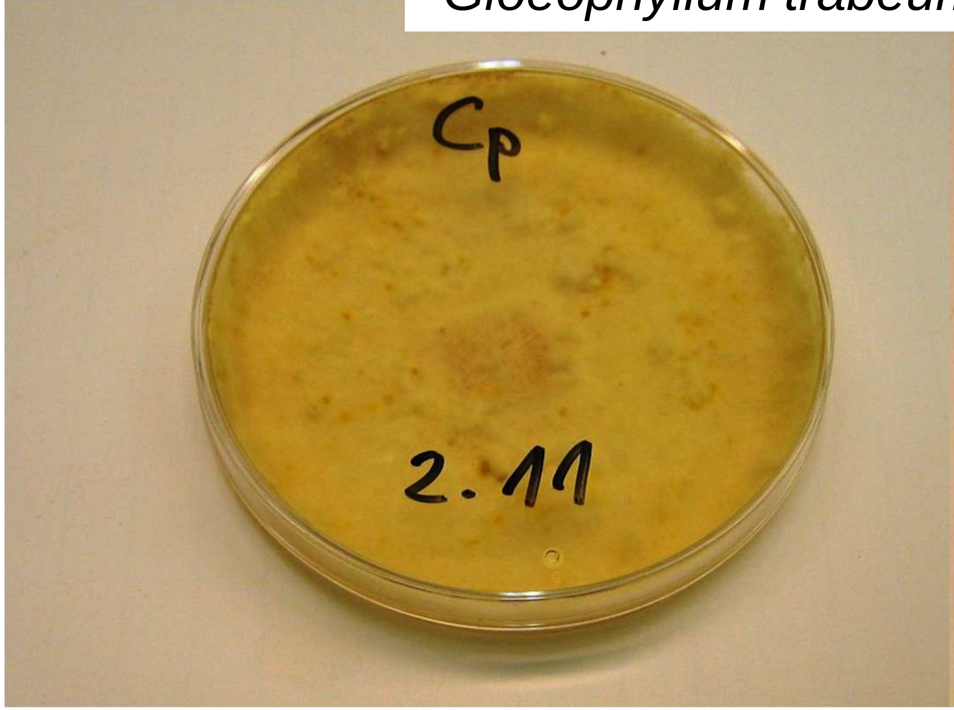
Wood quality:

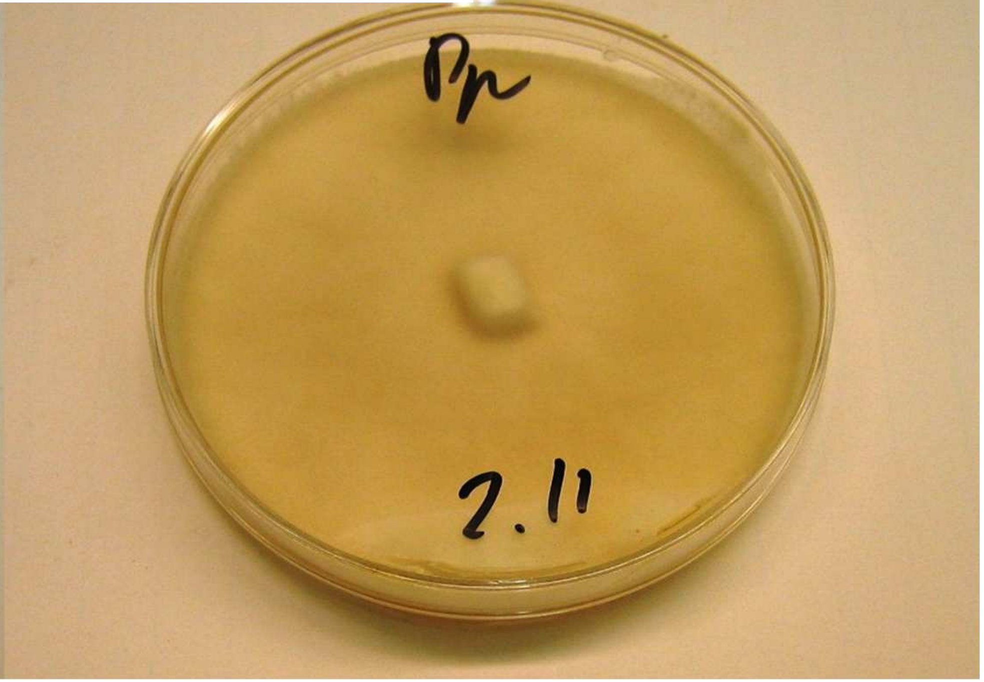
- Free from cracks, stain, decay, insect damage or other defects
- Growth rings in any direction with exception of completely tangential orientation on the broad faces
- Longitudial faces parallel to the direction of grain

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Fungal cultures for conifers:

- *Coniophora puteana* BAM Ebw.15
- *Poria placenta* FPRL 280
- *Gloeophyllum trabeum* BAM Ebw.109





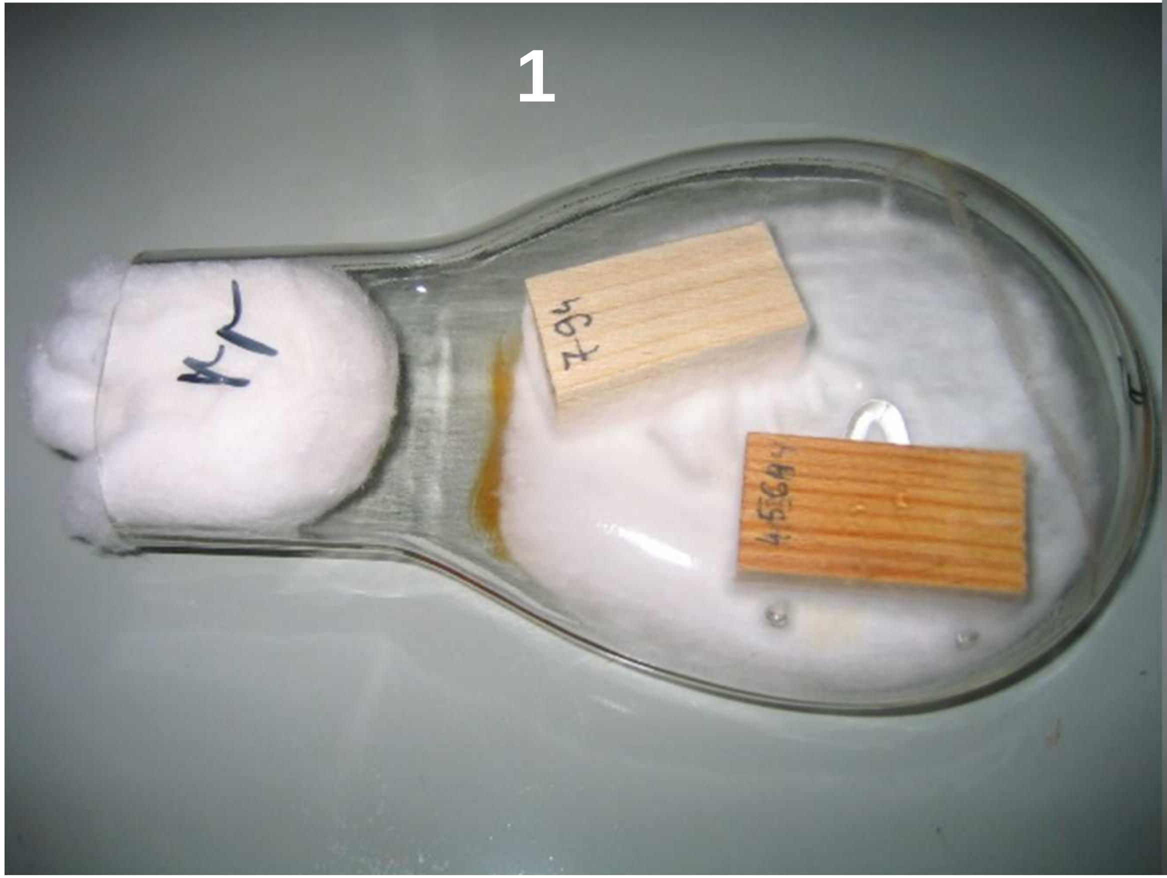
Kolle flasks

Malt-agar medium

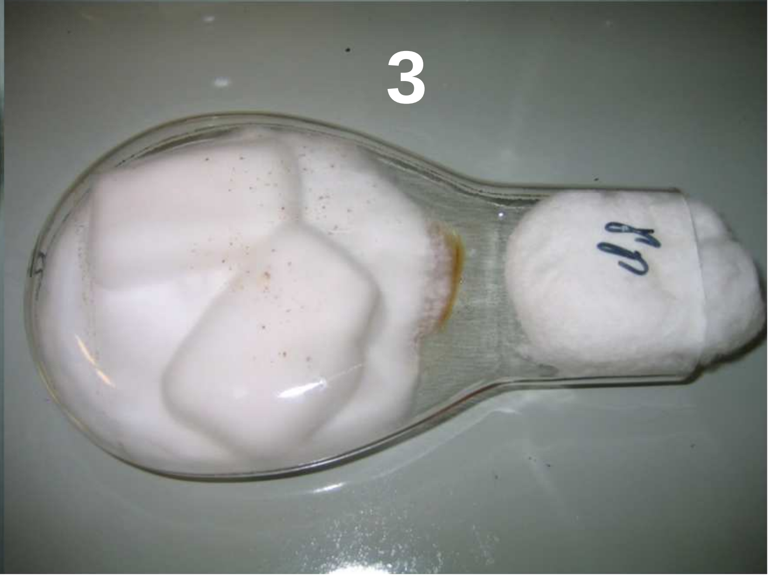
Fungal culture

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Test wood (spruce) + control (pine)


1


2


3

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Test conditions: 22°C/ 70%RH
Duration:16 weeks

Coniophora puteana

Poria placenta

Gloeophyllum trabeum

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Criterion – wood biodegradation i.e. mass loss after the test

Spruce before test

After test (P. placenta)

Funded by the European Union

INVESTMENT IN YOUR FUTURE

EN 350-1. Classification of the natural durability to wood-destroying fungi

Durability class	Description	Lab test results given as X-value*
1	very durable	X ≤ 0.15
2	durable	X > 0.15 but ≤ 0.30
3	moderately durable	X > 0.30 but ≤ 0.60
4	slightly durable	X > 0.60 but ≤ 0.90
5	not durable	X > 0.90
*X = mean mass loss of test wood/ mean mass loss of control		

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Summary results
Spruce durability vs density, extractives, lignin

Spruce clones*	***C. puteana* x – value**	***P. placenta* x – value**	***G. trabeum* x-value**	**Density kg/m^3**	**Extractives %**	**Lignin %**
A 7	0.97	1.06	0.97	405.8	1.15	28.5
A 10	1.01	1.18	0.93	432.6	1.50	27.0
A 15	1.02	0.84	0.88	408.3	1.35	27.5
B 6	1.00	1.23	0.95	399.1	1.63	28.9
B 10	1.04	1.14	0.95	406.3	1.37	28.0
B 15	1.04	1.19	0.9	408.5	1.10	28.3
V 7	0.93	1.09	0.94	388.1	1.23	27.9
V 9	0.92	1.2	0.88	443.1	1.70	27.6
26	0.96	1.12	0.98	394.5	1.30	27.8
31	1.07	1.19	0.96	361.1	1.75	27.9

*** Clone = 2-3 trees (ramets); tree = 4 specimens**

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Discussion

- Acetone extractives **2.22%** in *Picea abies* (Fengel & Wegener, 2003, Wood)
- EN 350-2**:** Density and natural durability of some wood species against fungi

Species	**Origin**	**Density/ range of mean values at 12% (m/m), kg/m^3**	**Durability class**
Picea abies	Europe	440-460-470	4 (slightly durable)
Pinus sylvestris	Europe	500-520-540	3 – 4 (moderately durable-..)
Pinus contorta	N. America	430-460-470	3 - 4
Quercus robur	Europe	670-710-760	2 (durable)

Durability – heartwood only, sapwood – all species class 5 (not durable)

Funded by the European Union

INVESTMENT IN YOUR FUTURE

CONCLUSIONS

- No clear relationship among the wood decay, wood density, content of extractives and lignin.
- Juvenile wood prevailed.
- Wood contained more sapwood with lower density and content of extractives.
- Use for interior structures; for outdoor structures -additional protection neccessary.
- Recommended for manufacturing of wood based products (medium density fiberboards etc.), furniture or pulp and paper.

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Thank you!

Study carried out in European Social Fund’s Project “Importance of Genetic Factors in Formation of Forest Stands with High Adaptability and Qualitative Wood Properties” (No 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Within stand relatedness and genetic diversity

Tiit Maaten

Funded by the European Union

INVESTMENT IN YOUR FUTURE

We have a dream….

to know all sequences by all trees
what we have and their relations
with all traits.

Why to study?

- For determining stand or population structure and diversity
- For evaluating population viability
- For having material for evaluation the influence of breeding on diversity/relatedness
- For determining origin of forest trees
- For any other purpose which could help us understand how trees are behave and use such information by silvicultural or conservation actions

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Such information is very interesting but…

- We are not able to get it
- We must use less sources for getting such information
- It the purpose will be investigaton of single stand (or few stands) then how we could define a term “stand”?
- Do we have enough finances for getting that?

Funded by the European Union

INVESTMENT IN YOUR FUTURE

What is a stand in this case?

- There are many tree species on good site types: number of target individuals per ha could be low
- How old the stand must be? Can we consider two years old stand as a stand?
- Shall we consider some number of trees of the target species as one unit stand? Some average number of effective population size?

ESF

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Background – how to get money? CBD

- **CBD article 2**: **"Biological diversity"** means the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this **includes diversity within species**, between species and of ecosystems.
- **Article 6. General measures:** Each Contracting Party shall, in accordance with its particular conditions and capabilities: (a) Develop national strategies, plans or programmes for the conservation and sustainable use of biological diversity or adapt for this purpose existing strategies, plans or programmes which shall reflect, inter alia, the measures set out in this Convention relevant to the Contracting Party concerned; and (b) **Integrate**, as far as possible and as appropriate, the conservation and sustainable use of **biological diversity into relevant sectoral or cross-sectoral plans, programmes and policies**.
- **CBD article 12**: **Research and Training:** The Contracting Parties, taking into account the special needs of developing countries, shall: b) Promote and encourage research which contributes to the conservation and **sustainable use of biological diversity,** particularly in developing countries, inter alia, in accordance with decisions of the Conference of the Parties taken in consequence of recommendations of the Subsidiary Body on Scientific, Technical and Technological Advice;

Background – how to get money? MCPFE

- **S2**: considering that, above and beyond the conservation of forest species, the essential objective is the conservation of the genetic diversity of these species, which are an essential part of mankind's heritage.
- **S2**: recognizing, also that the use of genetically-improved materials is of great importance for afforestation and restocking, in particular where this is for the purpose of the production of timber.
- **H4**: (Areas for research) Studies on genetic variability of regionally important tree species in response to changes in climate and increased concentration of carbon dioxide, and on the degree and rate of evolutionary processes and adaptation, by means of genetic changes.

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Strasbourg 2 resolution:

- Research for conservation
- Research for breeding (silviculture)

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Conservation of FGR in Europe

- EUFGIS database available www.eufgis.org
- It was compiled on the basis of minimum requirements for gene conservation units

Funded by the European Union
INVESTMENT IN YOUR FUTURE

GCU-s

The units should have a designated status as gene conservation areas of forest trees at national level. The units can be located in forests managed for multiple uses, protected areas or seed stands. The minimum size of a unit depends on tree species and conservation objectives as follows;

1) **500 or more reproducing trees** (when the objective is to **conserve gene diversity** of widely occurring and stand-forming conifers or broadleaf species),
2) **50 reproducing trees** (when the objective is to **conserve adaptive or other traits in marginal or scattered tree populations**) or **50 seed bearing trees** (scattered tree species with sexual dimorphism), and
3) **15 unrelated reproducing trees** (when the objective is to **conserve remaining populations of rare or endangered tree species).**

In light of presented minimum requirements, we are facing the same problem: how define a stand and how many samples do we need for determination the genetic structure and level of relatedness by single stand

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Short overview about literature

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Papers available

- Common fashion by papers: 5-40 samples per stand or per population analysed, different variables calculated
- In some cases all trees analysed, usually in case where stands are very small and/or rare, especially in the Mediterranean region
- One paper where bigger number of forest trees per one stand analysed (Chybicki *et al.*, 2008).

Funded by the European Union

INVESTMENT IN YOUR FUTURE

One problem:

Genome size (bp):	**No of genes,**	**% of coding DNA**
Escherichia coli **- 4,7 x 10^6**	4 000	100
Arabidopsis th. **– 125 x 10^6**	25 500	50
***Picea abies* – 30 000 x 10^6**	25 000 – 50 000	<3
Fritillaria sp. **– 85 000 x 10^6**	25 000	0,02
Homo sapiens **– 3 000 x 10^6**	40 000	<2

ESF
Funded by the European Union
INVESTMENT IN YOUR FUTURE

Spatial Genetic Structure Within Two Contrasting Stands of Scots Pine (*Pinus sylvestris L.)*

The spatial genetic structure of two contrasting stands of Scots pine located within one continuous population investigated: (i) the even aged qualified seed-tree stand utilized for commercial seed collections (321 trees) and (ii) the naturally established unevenaged and unmanaged stand (173 trees). Genetic variation at 14 allozyme loci (*Fest, Gdh, Aat-1, Aat-2, Aat-3, Mdh-1, Mdh-3, Mdh-4, 6Pgdh-1, 6Pgdh-2, Pgi-2, Pgm-1 and Shdh-1)* studied

Two stands differed substantially in the levels of inbreeding. The estimated *FST coefficients also showed that the* two studied stands genetically are not very differentiated at the single locus level (although at the multilocus genotypic level they are)

In spite of such strong differences there were only slight differences either in genetic diversity and spatial genetic structure.

Funded by the European Union
INVESTMENT IN YOUR FUTURE

Common conclusion by investigations of Scots pine populations

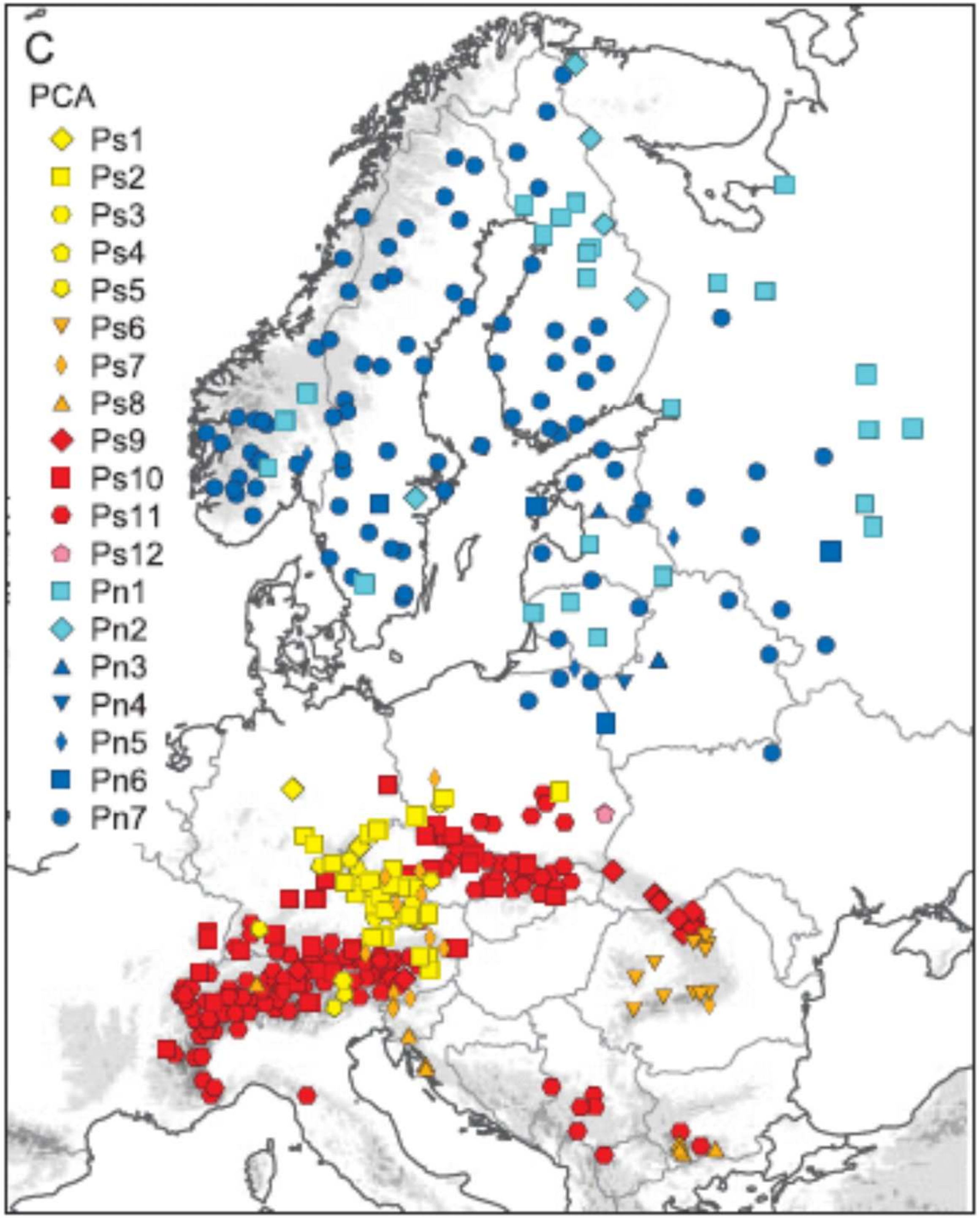
Despite periodic interstadial fragmentation episodes, Scots pine biology provides for the long –term maintenance of high within-population and low among-population genetic diversity at neutral genetic markers (Robledo-Arnuncio *et al.*, 2005)

This conclusion was made on the basis of cpSSR analyses

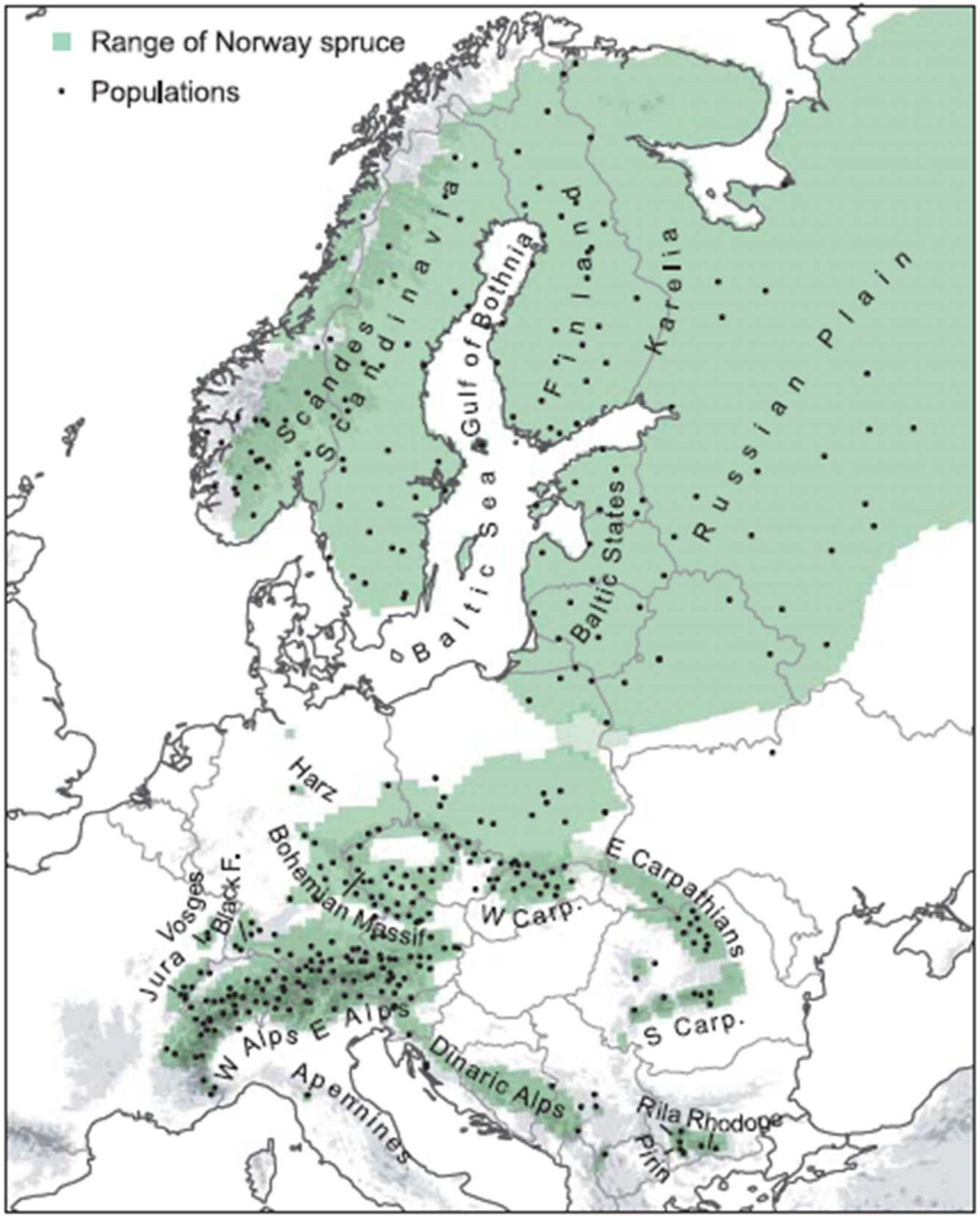
ESF

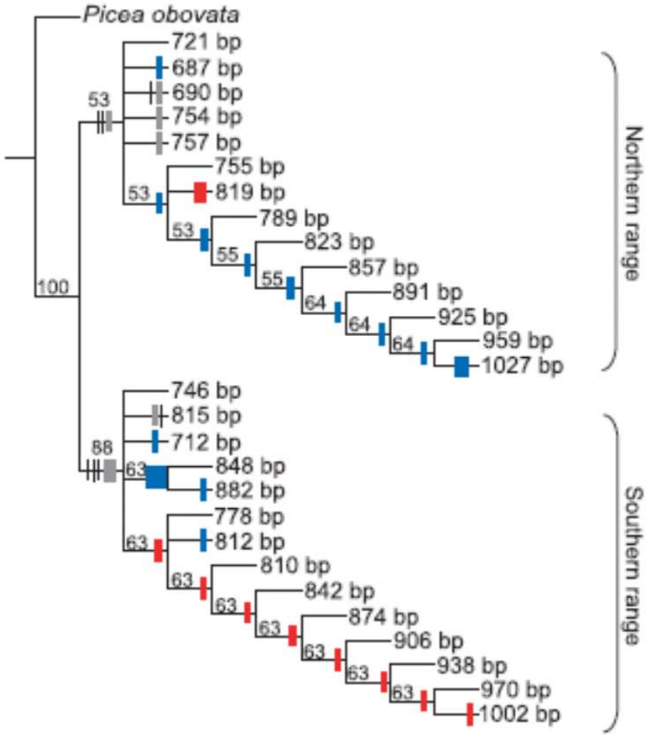
Funded by the European Union

INVESTMENT IN YOUR FUTURE

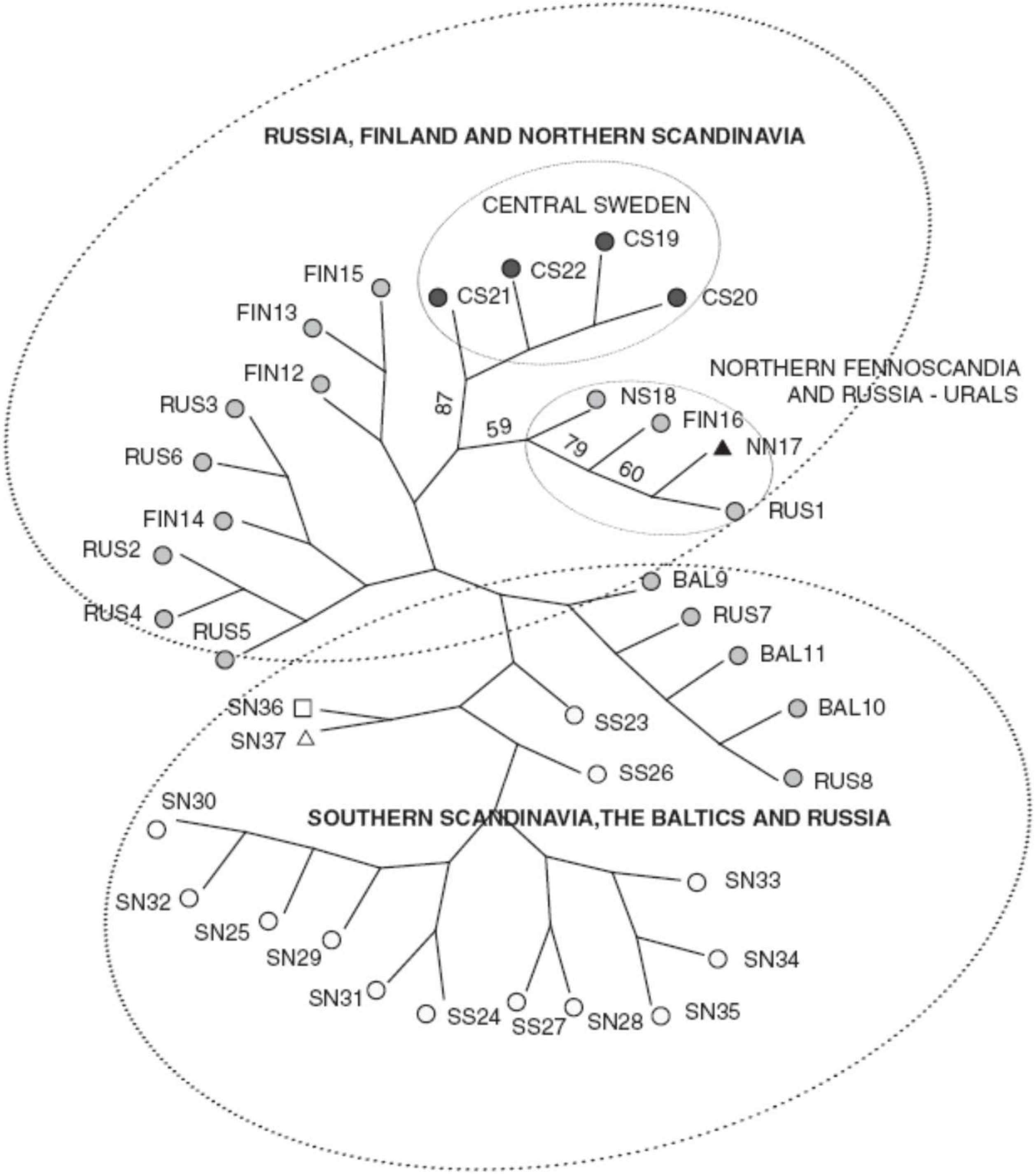


Tollefsrud *et al*., 2008. Genetic consequences of glacial survival and postglacial colonization in Norway spruce: combined analysis of mitochondrial DNA and fossil pollen – Molecular Ecology, 17, 4134 - 4150





Tollefsrud *et al.*, 2008. Genetic consequences of glacial survival and postglacial colonization in Norway spruce: combined analysis of mitochondrial DNA and fossil pollen – Molecular Ecology, 17, 4134 - 4150



Combined analysis of nuclear and mitochondrial markers provide new insight into the genetic structure of North European Picea abies (*Tollefsrud* et al. *2009 (Heredity)*)

Thanks!

European Social Fond project (No.
2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)

ESF

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Wood trait differences of hybrid aspen clones

Mārtiņš Zeps

Uldis Grīnfelds

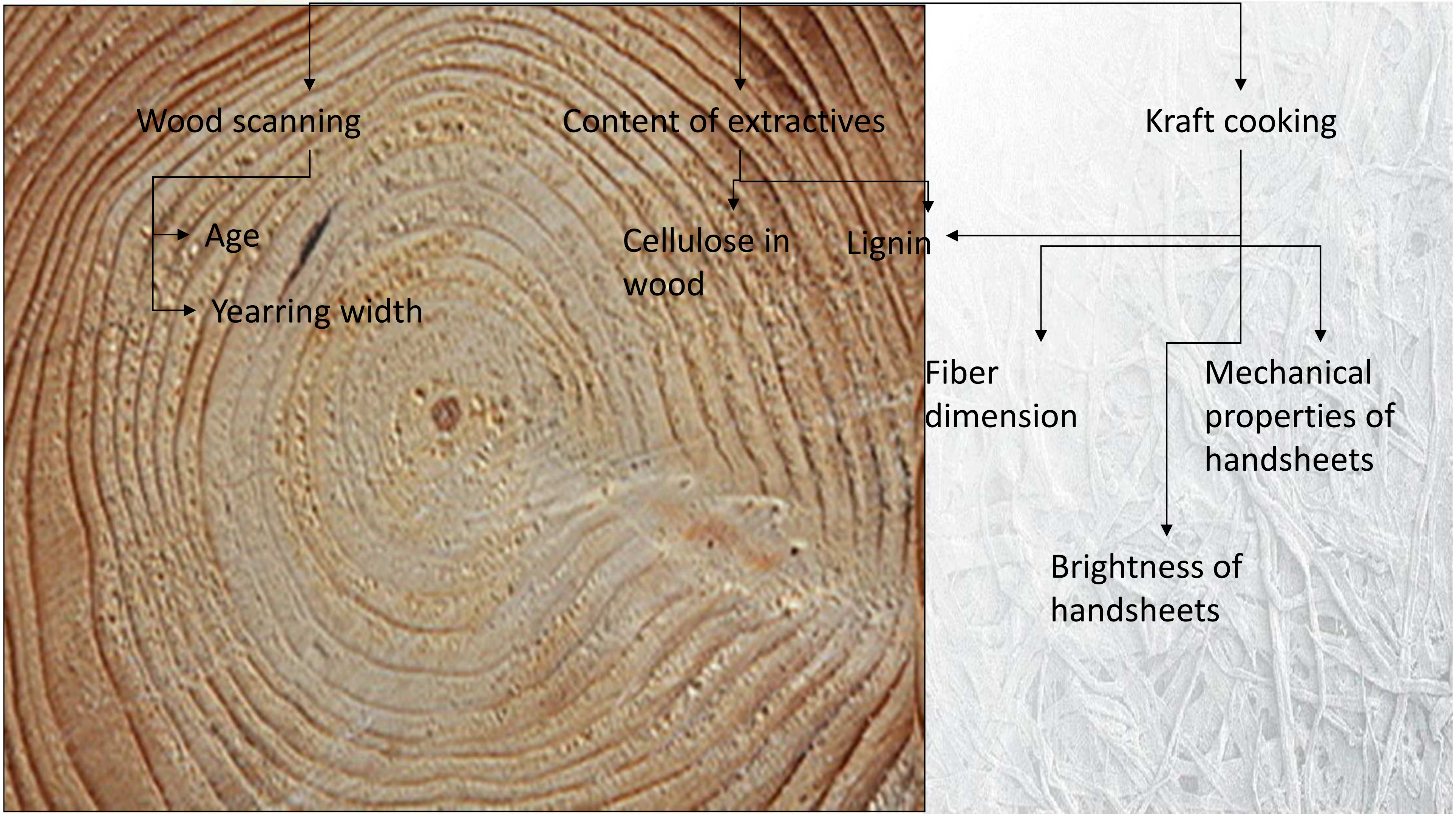
martins.zeps@silava.lv

Materials and method

Sample trees cut at age 12, in 2 hybrid aspen clones experimental trial, and addition sample trees cut in another 2 experiments.

Wood used for analysis of the trunk from 0.5 to 1.3 meters in height from the ground.

Materials and method



Wood scanning

- Age
- Yearring width

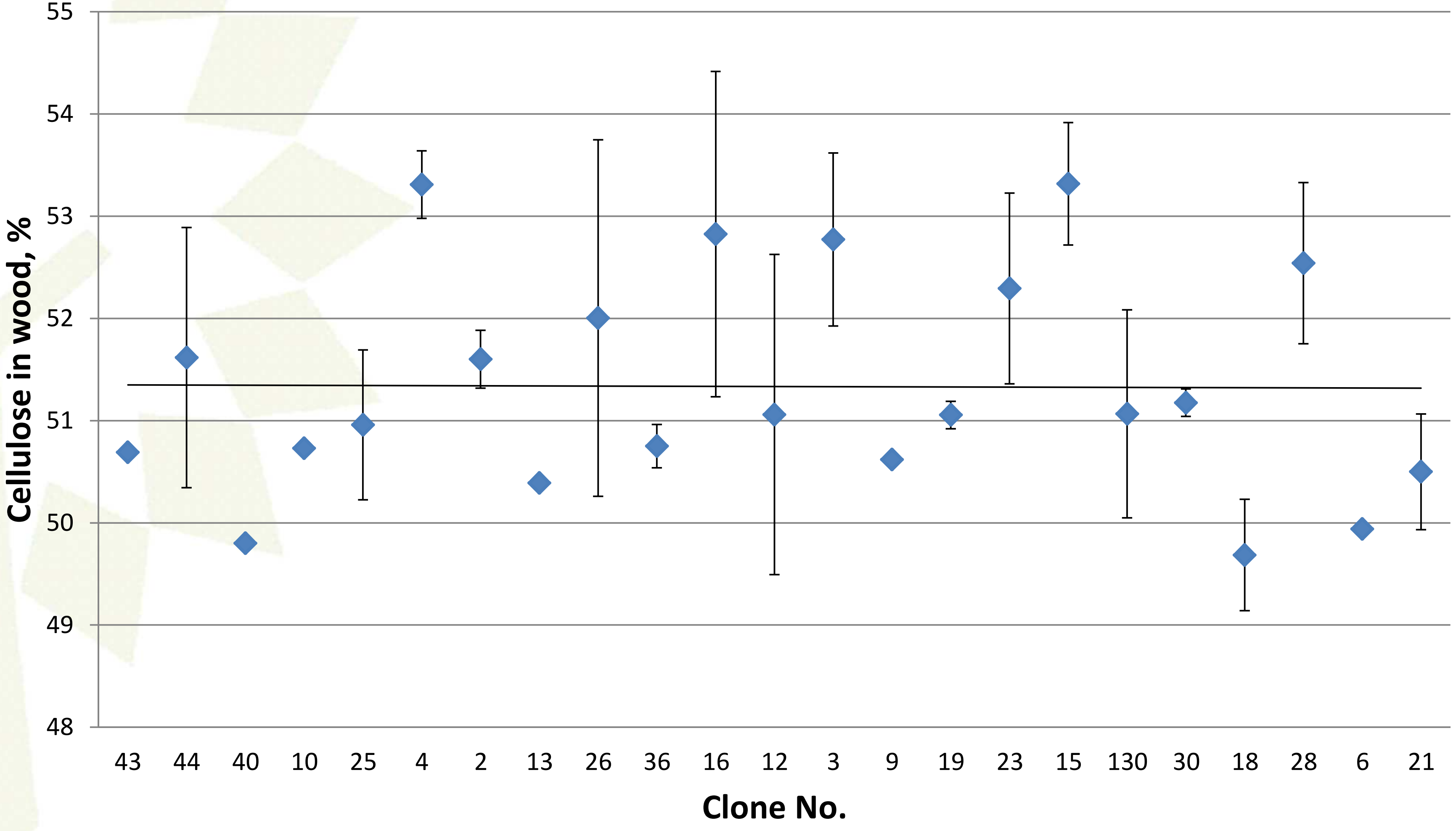
Content of extractives

- Cellulose in wood
- Lignin

Kraft cooking

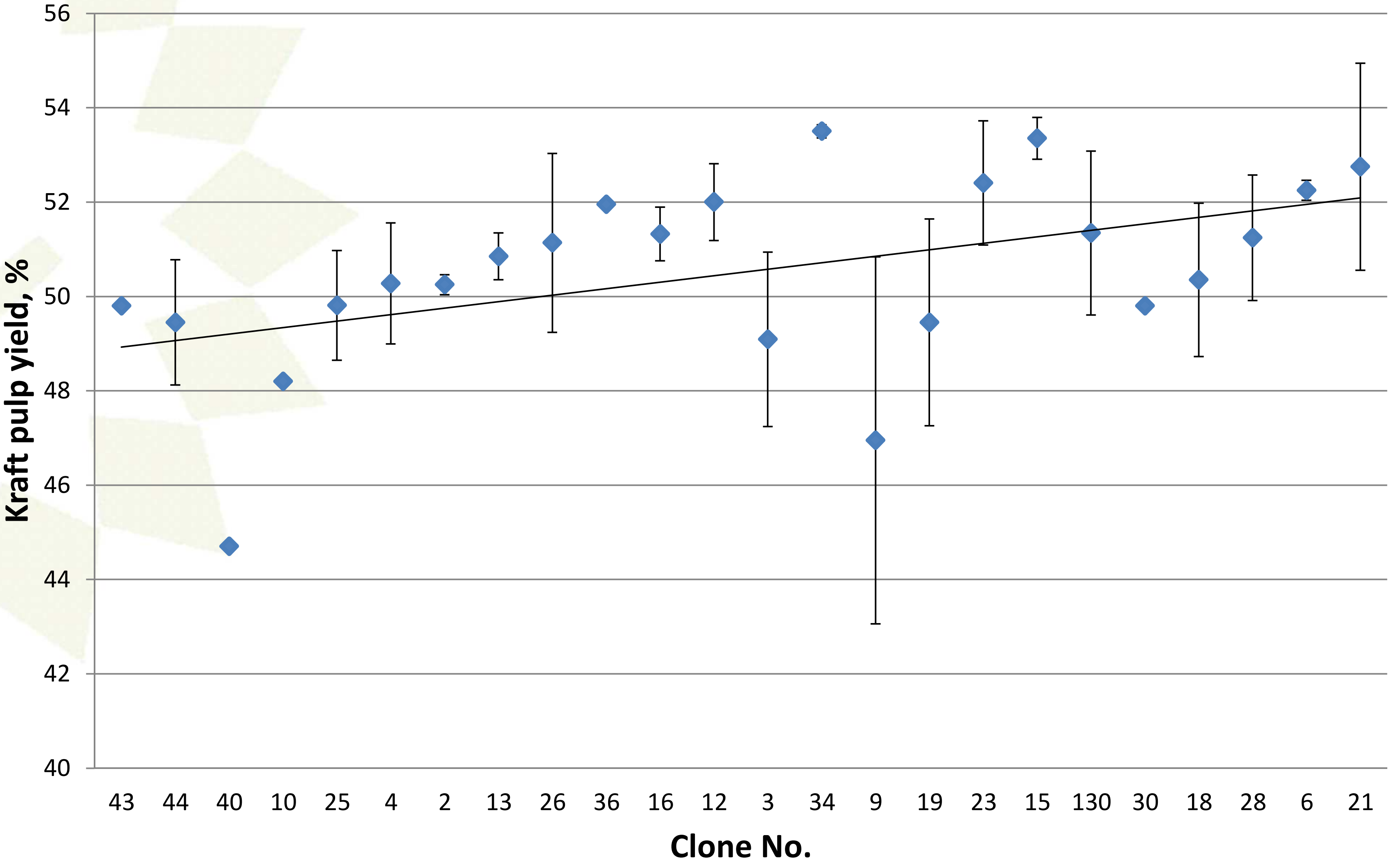
- Lignin
- Fiber dimension
- Mechanical properties of handsheets
- Brightness of handsheets

Results of Cellulose in wood, %

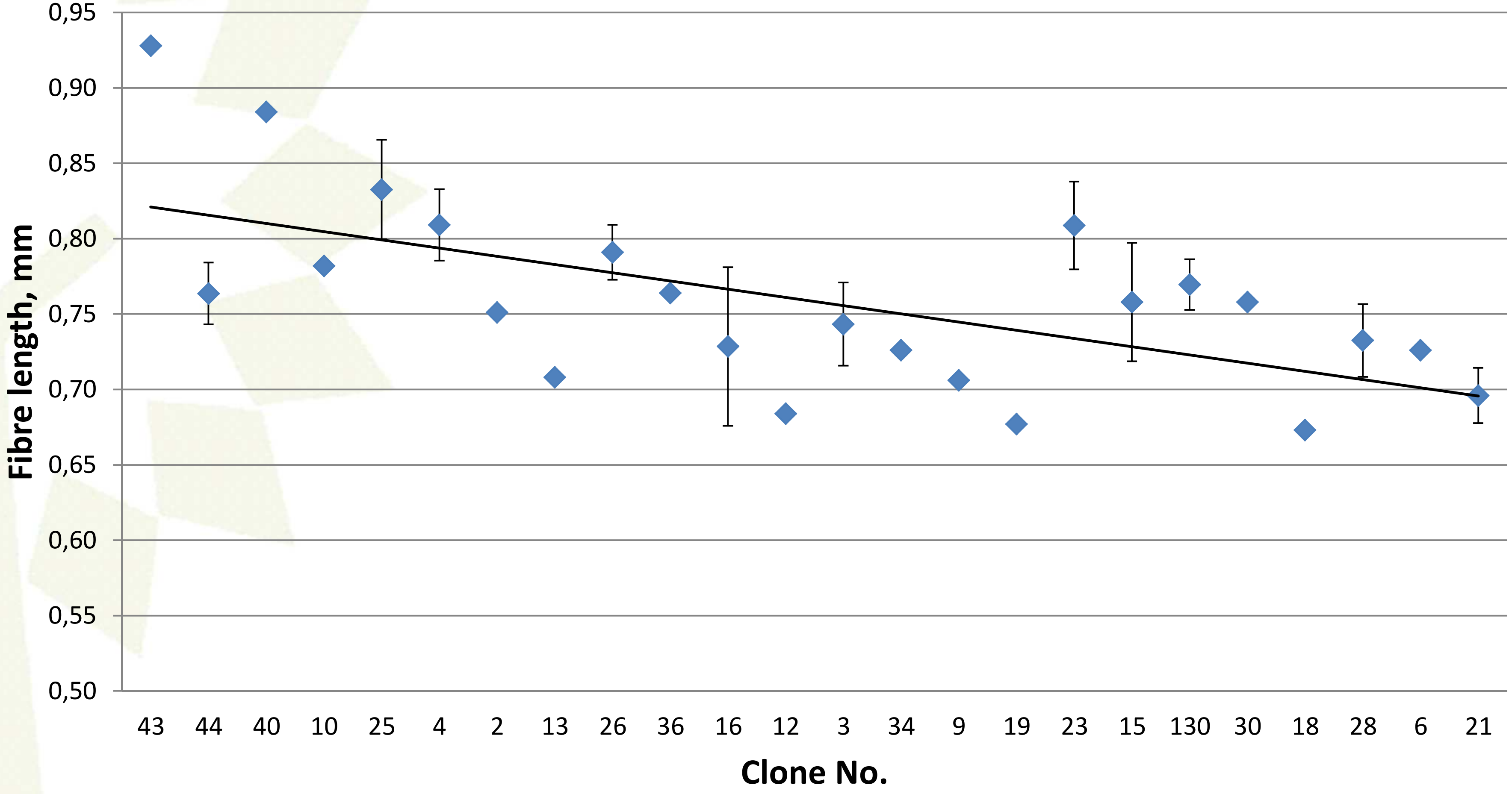


Funded by the European Union
INVESTMENT IN YOUR FUTURE

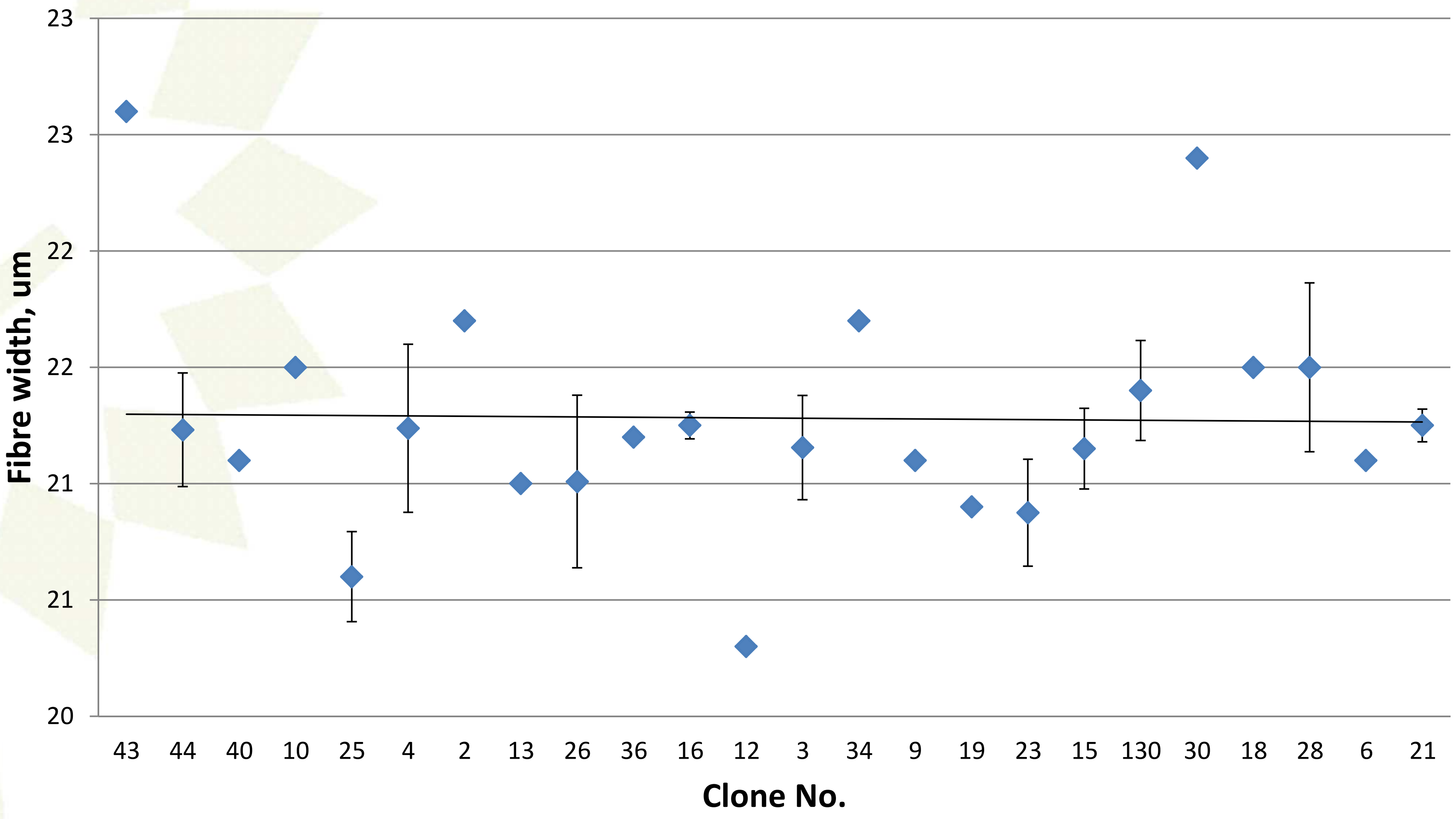
Results of Kraft pulp Yield %



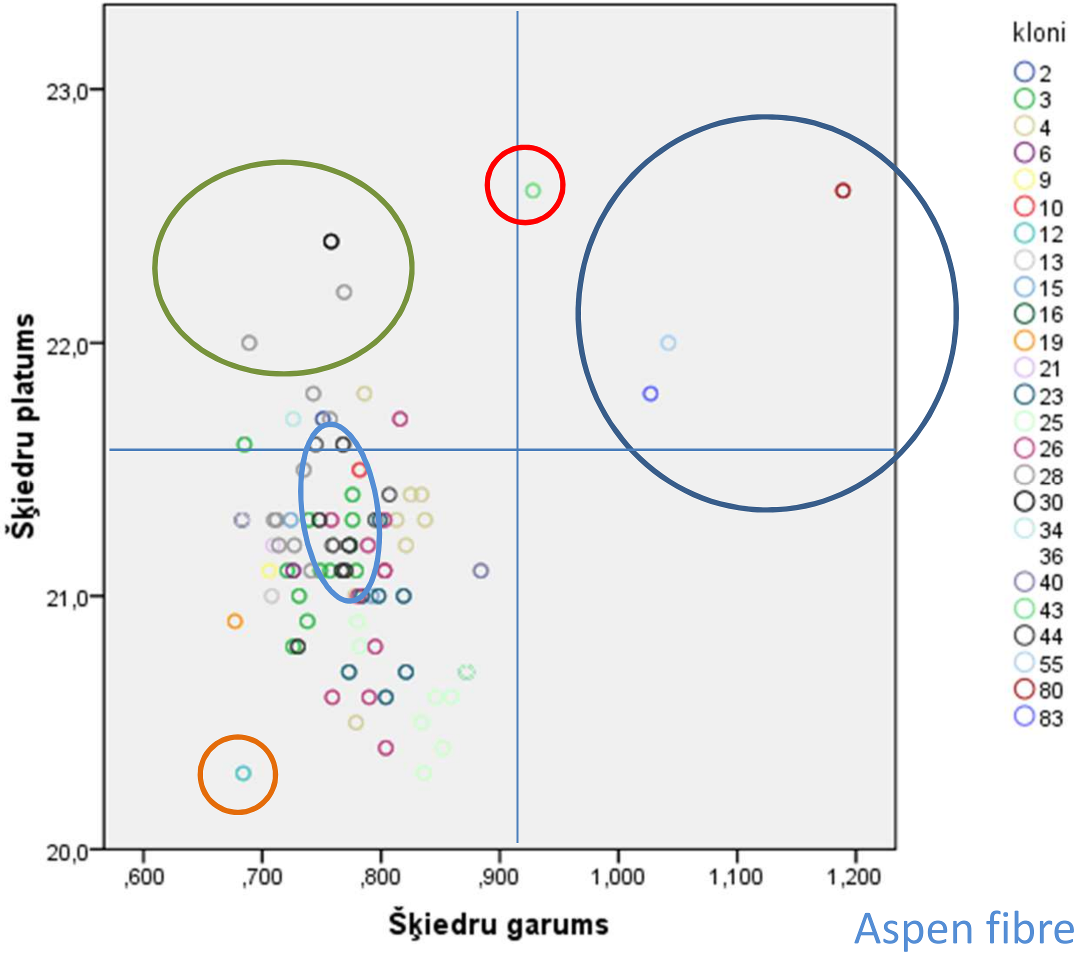
Results of Fibre length, mm



Results of Fibre width, um



Results of Fibre length and width



Aspen fibres region

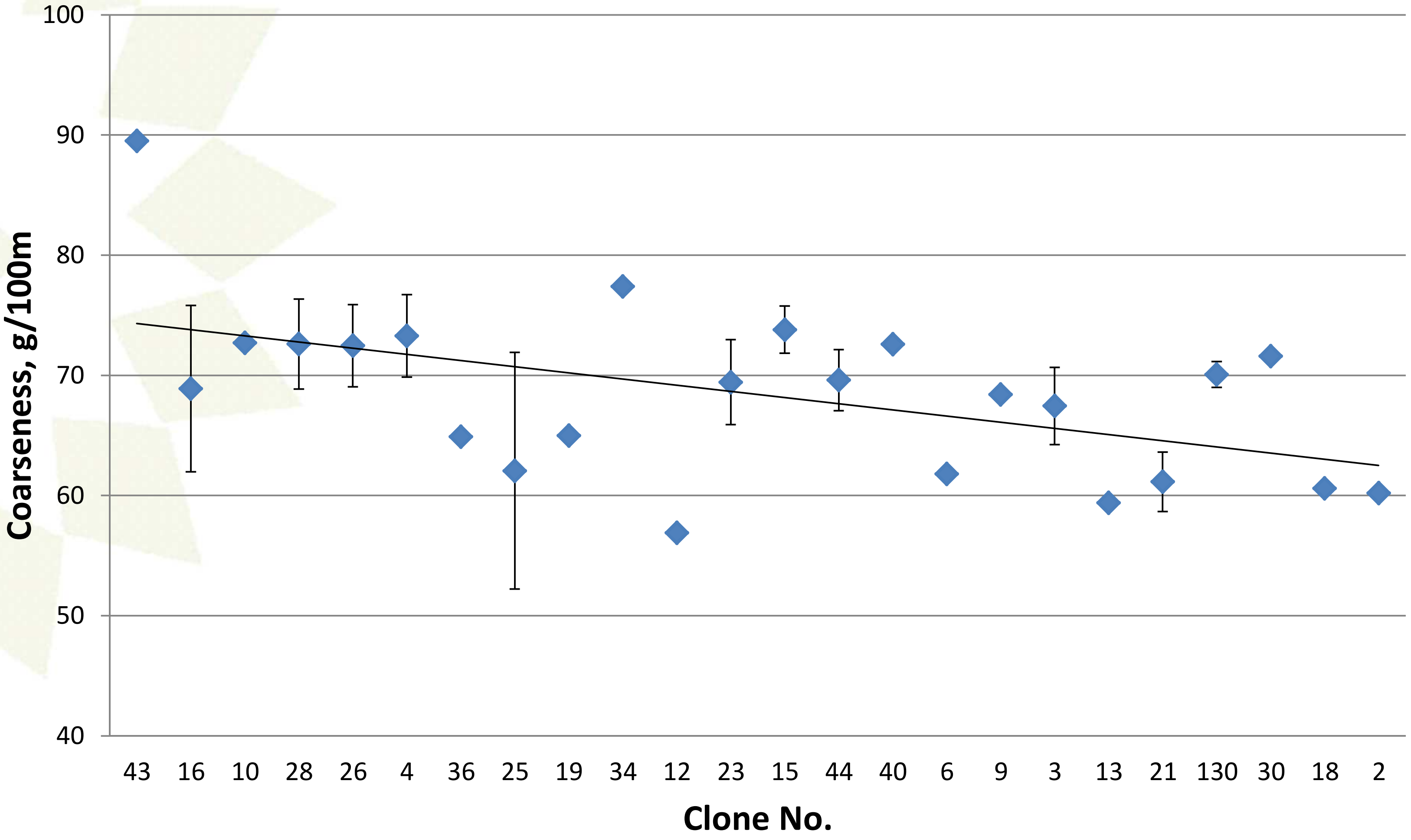
Old aspen hybrids (~40y)

43 to present higest length and width

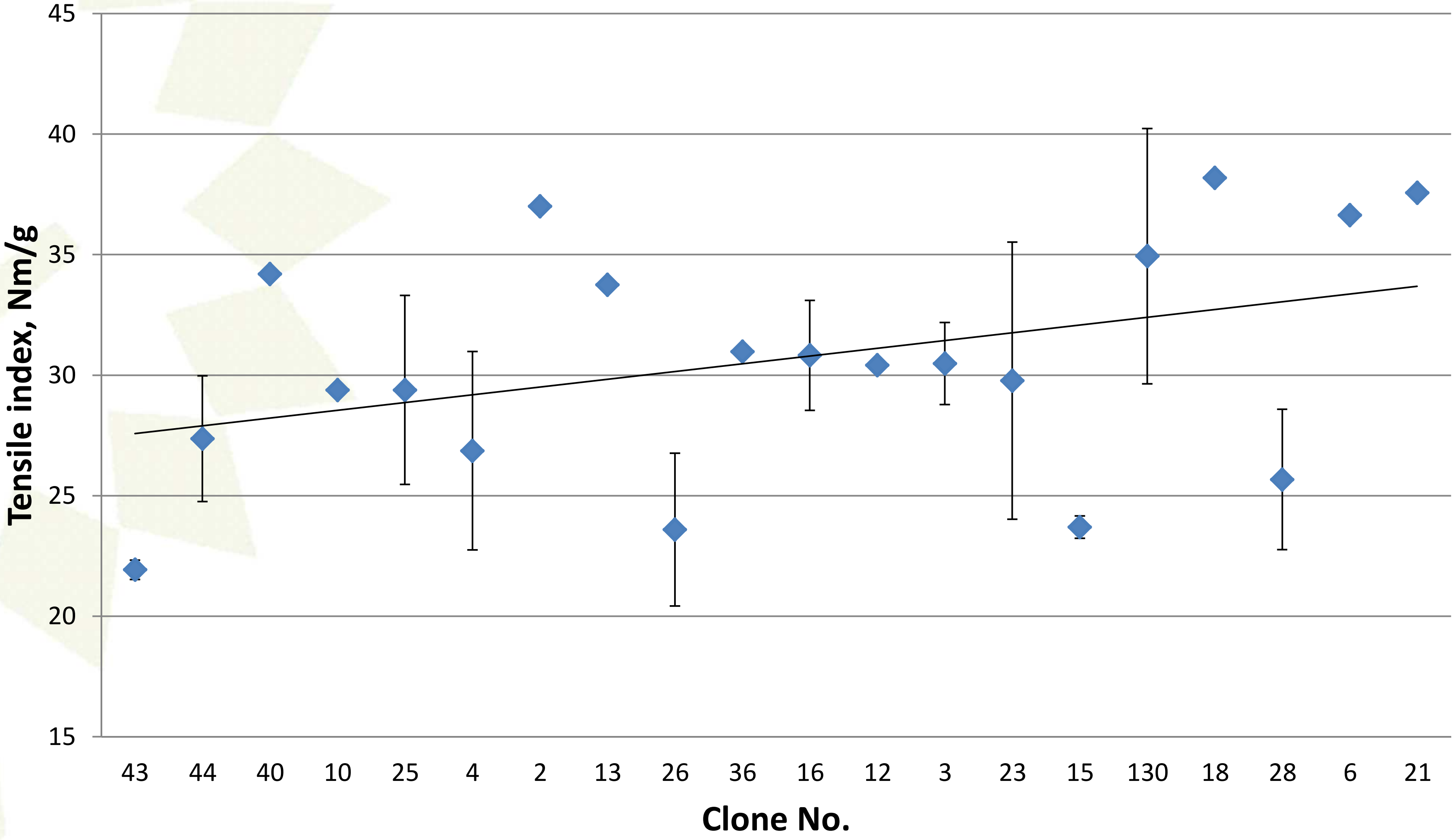
12 presents shorter and more arrow fibres

28, 30 are presented by “shorter” and more wider fibres

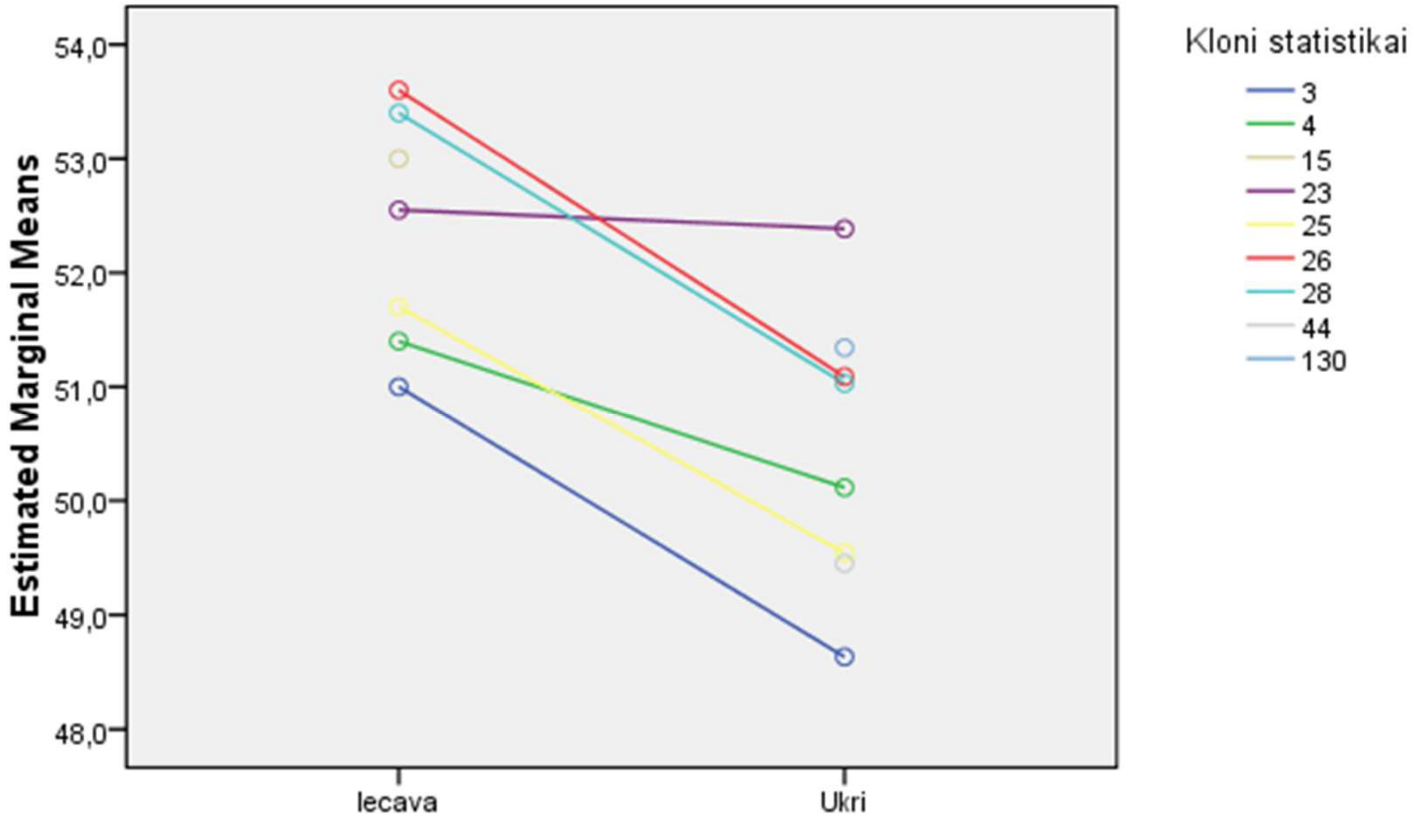
Results of Coarseness, g/100m

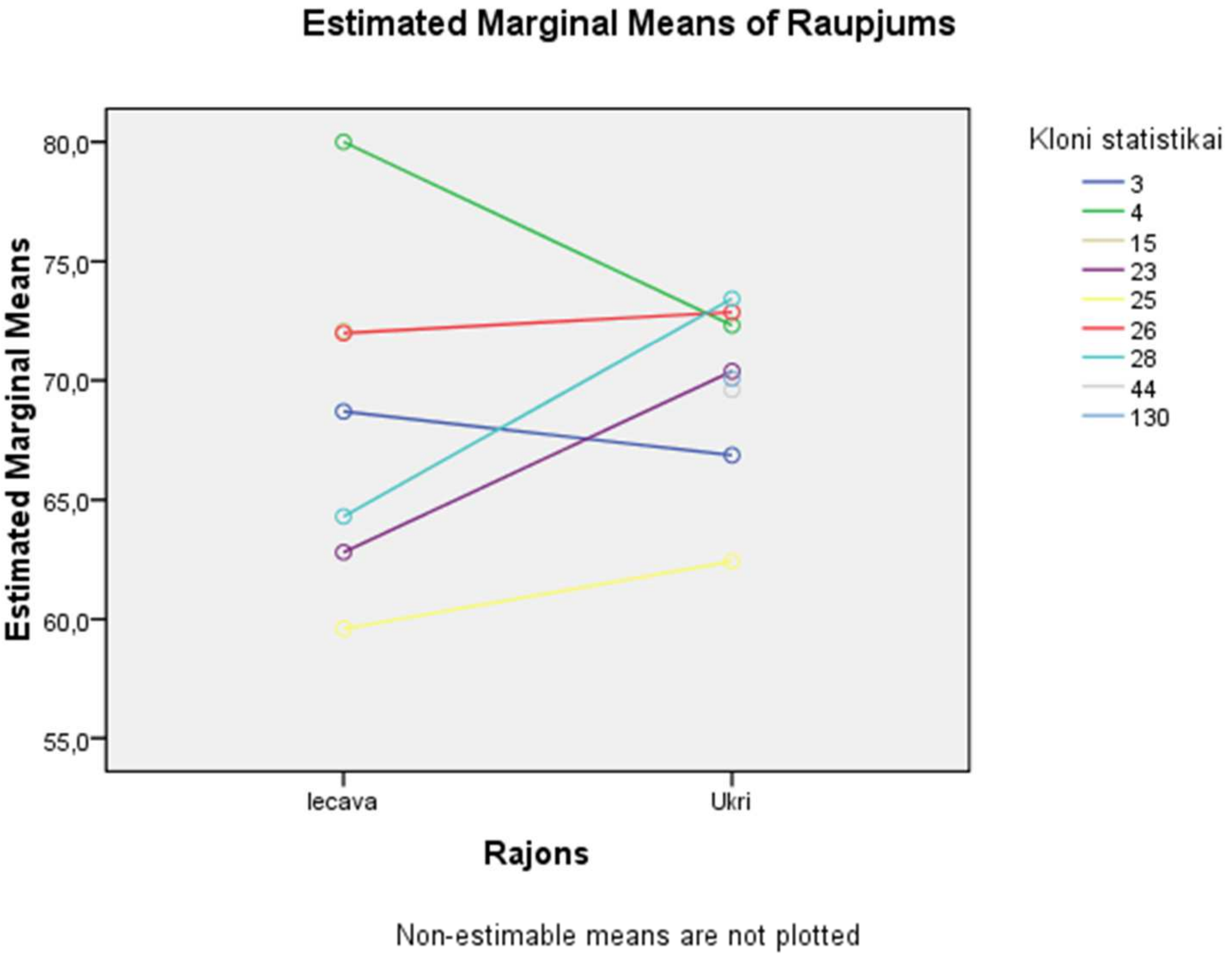


Results of Tensile index, Nm/g



Best clones for pulp un paper plantations is 23
Plantation region makes effect on Kraft pulp yield of Aspen (130); 25, 26 and 28 hybrid aspen clones, but no so much effect on hybrid clone No.4.




Estimated Marginal Means of Raupjums
Estimated Marginal Means
80,0
75,0
70,0
65,0
60,0
55,0
Iecava
Ukri
Rajons
Kloni statistikai
3
4
15
23
25
26
28
44
130
Non-estimable means are not plotted

Results

1. It is possibilities to select hybrid aspen clons for polp and paper production. Perspective clones for pulp and peper industry is 23, 43, 4 , 28, 40.
2. Hybrid aspen clone 23 is stable in different plantations.
3. Hybrid aspen clones have more cellulose content in wood comparison this common aspen. For industrial purposes is it essentially.

Funded by the European Union

INVESTMENT IN YOUR FUTURE

Thank You for attention!

Study has been partly funded by:
ESF project "Importance of Genetic Factors in Formation of Forest Stands with High Adaptability and Qualitative Wood Properties" (No 2009/0200/1DP/1.1.1.2.0/09/APIA/VIAA/146)