Impact of high throughput phenotyping on estimation of genetic parameters

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Impact of high throughput phenotyping on estimation of genetic parameters

- High throughput phenotyping?
- Why?
- What?
- How?
- When?

High throughput phenotyping?

Forest Research:
phenology,
Sex reproduction,
Frost and drought **resistance**
Pest resistance
Annual radial growth
Root characteristics
Stem architecture
Wood properties
(some examples from bolded ones)

WHY?

Aim:

- Tree breeding
- Assessing optimal deployment of forest regeneration material
- Assessing evolution of tree populations

⟶ Estimation of genetic parameters

⟶ Estimation of genetic basis of phenotypes

Estimation of genetic parameters

Phenotypic variance,

$V_P = V_A + V_D + V_I + V_E$

Additive value (V_A)

Environmental deviation (V_E)

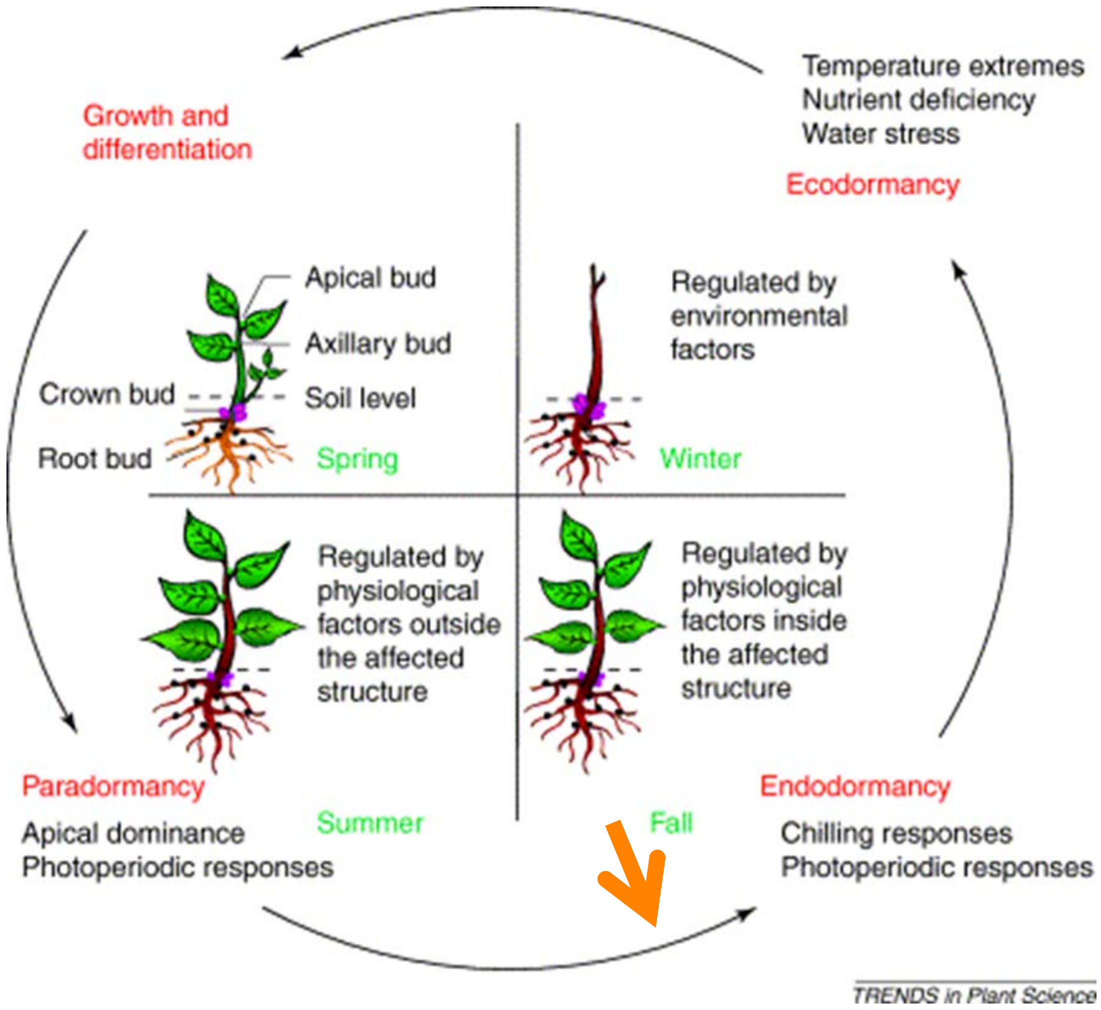
”true” environmental variation

+ measurement errors

$h^2 = V_A/V_P$

WHAT? Aim: How to identify the most suitable trait?

Case 1: Phenology – selection on growth rhythm



Horvath et al. 2003. Trends Plant Sci

Aim: How to identify the most suitable trait?

Case 1: Phenology – selection on growth rhythm: Cessation of growth (95% of final height) vs. bud-set, greenhouse study

Cessation of growth (when 95% of final height reached) and timing of budset

Variance components and genetic parameters for cessation of growth

			Variance components			Genetic parameters					
Population	Seedlings	Mean	$\widehat{\sigma_f^2}$	$\widehat{\sigma_i^2}$	$\widehat{\sigma_e^2}$	V_A	CV_A	V_P	CV_P	h^2	SD h^2
Punkaharju	11919/12000	96.04	2.71	0.00	66.27	10.83	0.03	68.98	0.09	0.16	0.02

Variance components and genetic parameters for budset

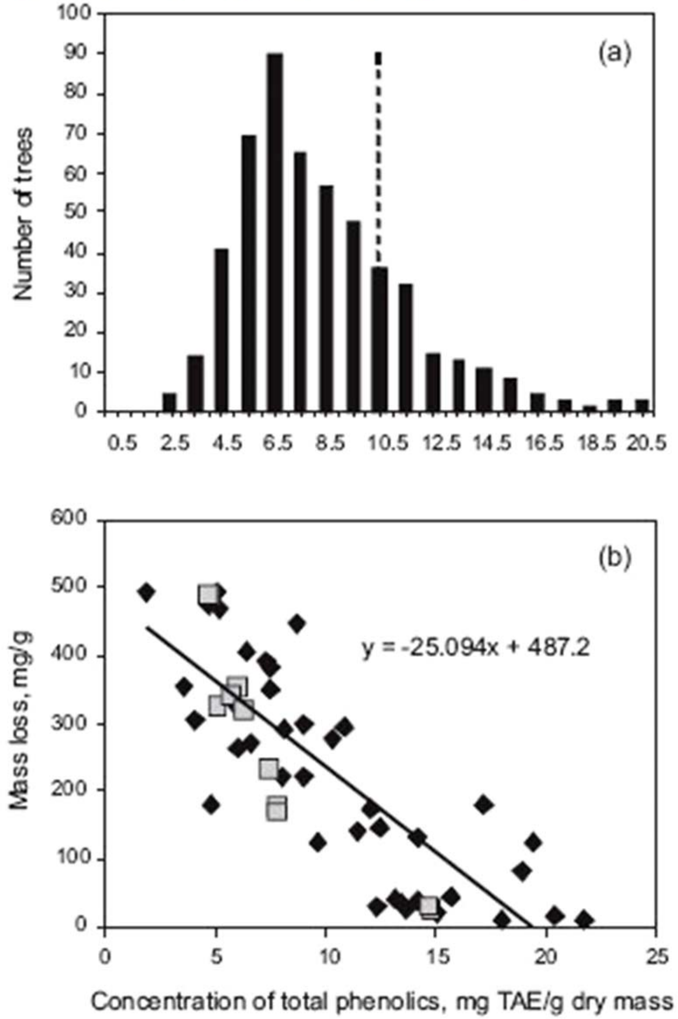
			Variance components			Genetic parameters					
Population	Seedlings	Mean	$\widehat{\sigma_f^2}$	$\widehat{\sigma_i^2}$	$\widehat{\sigma_e^2}$	V_A	CV_A	V_P	CV_P	h^2	SD h^2
Punkaharju	11884/12000	102.99	10.00	0.71	73.33	39.99	0.06	84.03	0.09	0.48	0.04

Avia, Kärkkäinen & Savolainen, MS

WHAT? Aim: How to identify the most suitable trait?

Case 2: Decay resistance of timber

Decay tests: correlation between decay resistance and concentration of phenolics



Total phenolics

Conclusions:

Decay tests necessary,
but phenotyping may be more efficient
using chemical traits

Harju & Venäläinen 2006. Can J. For Res.

How?

Aim: High-throughput phenotyping

→ Non-destructive
→ Low cost, fast
→ Optical analyses

How? Aim: High-throughput phenotyping

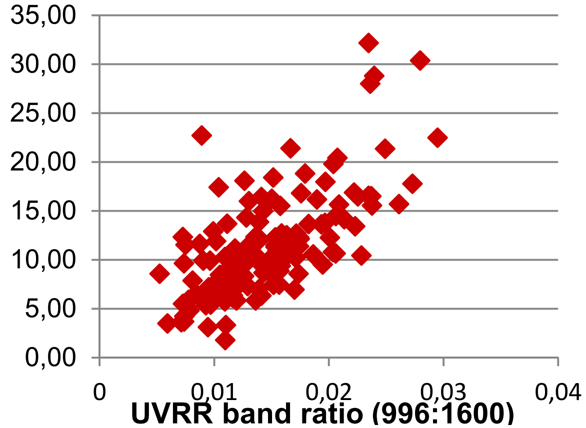
Case 1: Heartwood extractives in Scots pine: wet chemistry vs. two optical methods

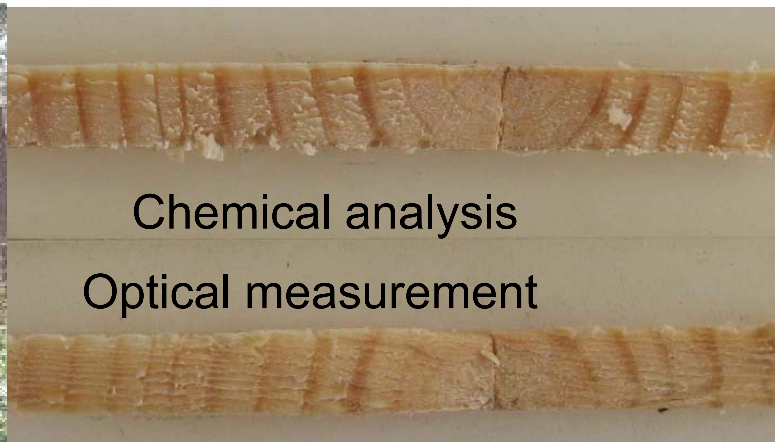
Parallel samples for

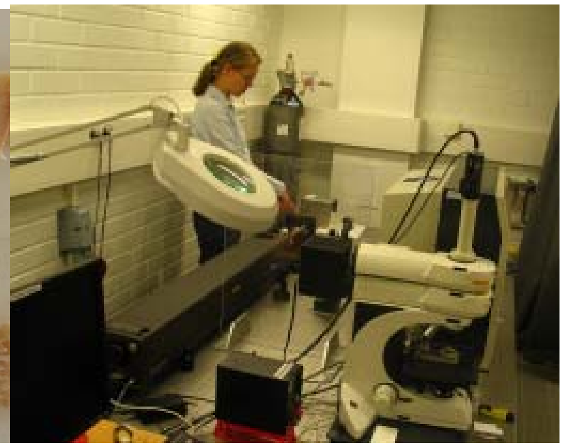
GC-MS (wet chemistry; Luke)

UVRRaman (Aalto Univ)

NIRS (INRA, Innventia)







Aim: High-throughput phenotyping

Case 1: Heartwood extractives in Scots pine: wet chemistry vs. two optical methods

Method	Va	h2	Mean	CVa	SD(h2)
GC	14,15	0,85	11,30	0,33	0,30
UVRaman	6,94	0,33	10,14	0,26	0,21
NIRS	12,93	0,84	11,39	0,32	0,29

Aim: High-throughput phenotyping

Case 2: Heartwood extractives in larch:

Objective:

Evaluate variability of extractives content in relation to natural durability

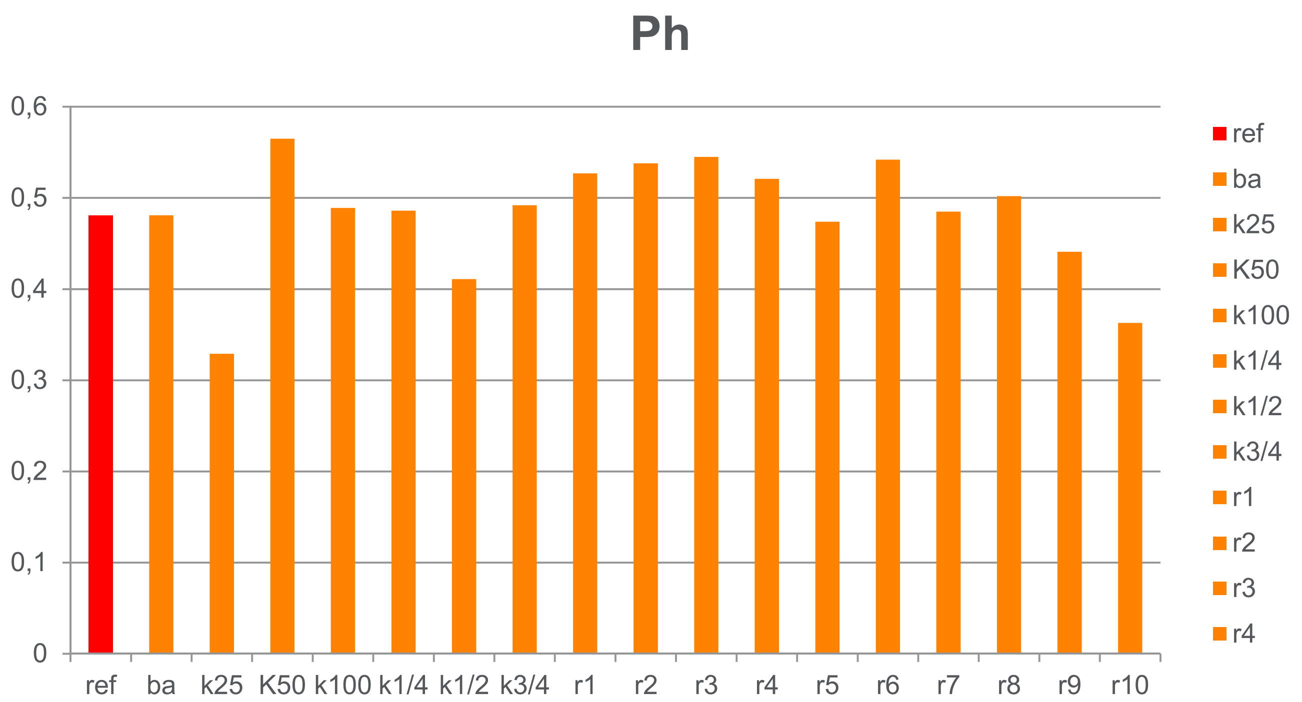
Develop a NIRS calibration model for both extractives and natural durability

Material: 42 FS progenies from 12 EL x 8 JL

355 individuals (out 1302 increment cores collected), +/- 8.4 sibs/family

NIRS spectra and calibration models

Family heritability variation: wet chemistry (red) vs. optical analyses: impact of different calibration models



Ref: Reference HPLC (wet chemistry)
1) batch: ¼ used to build up the model, prediction of the next ¾.
2-7) sets of calibration made of 25, 50, 100, ¼, ½ and ¾ of individuals
8-17) 10 random samples of 100 individuals in the training set

How? Aim: High-throughput phenotyping

Case 3: Physical wood characteristics in larch: towards high-throughput phenotyping

Material:
- 25 FS hybrid larch progenies (~10 trees/family)

Measurements:
- Pilodyn: 2 directions; in 1993 (age 11); mm
- Density (from microdensitometry): ring 1989-1995 (age 13); kg/m3
- MOE (from rigidimeter on standing trees): in 1998 (age 16); MPa

Case 3: Physical wood characteristics in larch: towards high-throughput phenotyping

Level of throughput (trees around 20-25 yrs)

Technique	Operation	Timing	Throughput Nber of samples per M/D	'efficiency' towards MOE
MOE (rigidimeter)	Pruning & measure	20-25 trees/D Need 2 persons	12	1
Pilodyn	Measure	250 trees/M/D	250	21
Infradensity (cores)	Collect Measure	100 cores/M/D 200 cores/M/D	70	6
Microdensitometry	Collect Sawing RX Windendro	100 core/M/D 50 cores/M/D 150 /M/D 50/M/D	18	1.5

M = person
D = day

Estimation of heritability (family level) and of direct and indirect genetic gains from family selection

Heritability, absolute and relative gains for direct FS family selection (i=1)

	Mean	σpFS	H^2FS	ΔG abs	ΔG rel (%)
MOE (MPa)	7169.827	819.378	0.706 (0.500-0.851)	578.48	8.1
Density (Kg/m3)	411.764	19.658	0.726 (0.534-0.861)	14.27	3.5
Pilodyn (mm)	14.312	1.325	0.678 (0.452-0.837)	0.898	6.3

Case 3: Physical wood characteristics in larch: towards high-throughput phenotyping

Correlated response

Target trait: MOE

	Correlated gain with MOE (MPa) (i=1)	Selection efficiency	i Due to throughput level	Correlated gain with MOE (MPa)	Selection efficiency
Pilodyn	394.612	0.682	2.459	970.351	1.677
Infradensity	375.786*		1.96	736.541	1.273
Density	375.786	0.650	1.271	477.624	0.826

* Supposed gain equal to that from microdensity

WHEN?

→ Phenotypic variation in different life stages



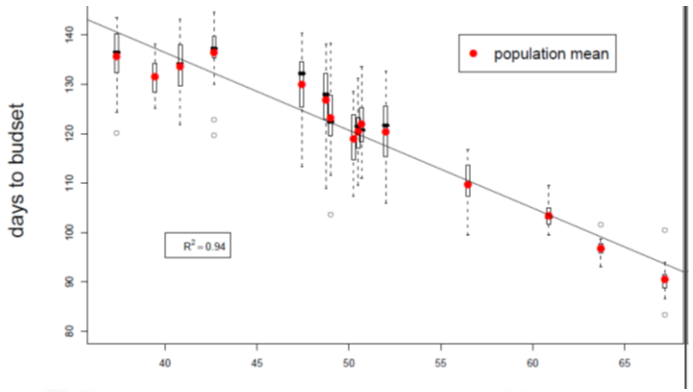


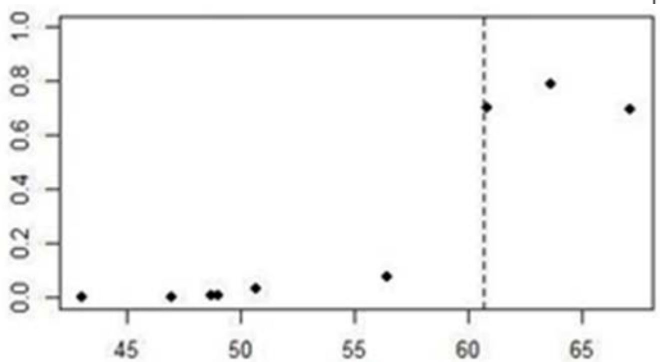
→ Phenotyping when it matters

When? Correlation between phenotypic variation in different life stages

Case1: Growth rhythm in different life stages

Bud-set in greenhouse of 1st yr seedlings v. survival (10 yrs) in field





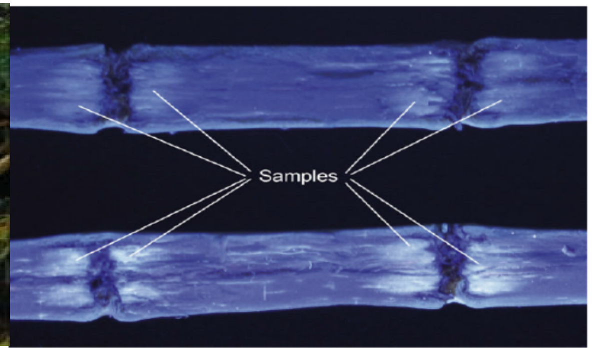
Apuli et al, MS

When? Correlation between phenotypic variation in different life stages

Case 2: Can induced defense of seedlings used to assess constitutive heartwood extractives?

Extractive (mg g^{-1} d.w.)	h^2_{OP}
PS	0.31
PSM	0.09
Sum of stilbenes	0.20
Sum of RAC	0.13

Harju et al 2008. Tree Physiol.



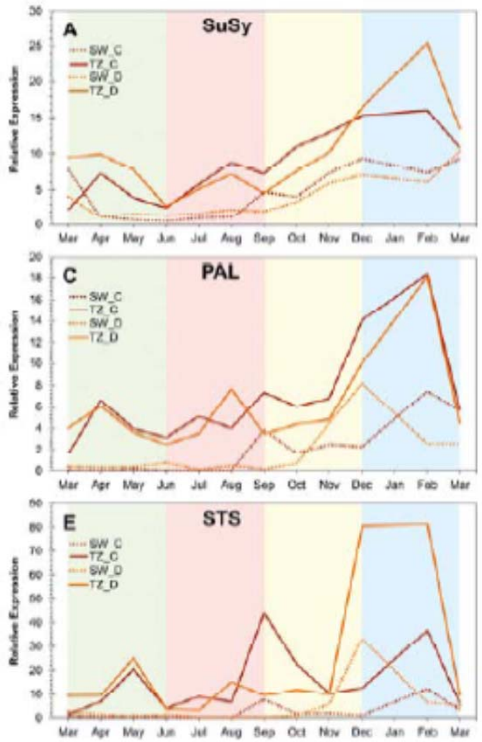
Conclusions

High-throughput phenotyping

- Why?
- What?
- How?
- When?

Important to plan well beforehand

Future demands: more detailed phenotypes for genomic selection




Thank you