Phenomic Selection Workshop

Tuesday September 20th 2022

Renaud Rincent & Vincent Segura

Genomic Selection

Phenotype

DNA polymorphisms
(SNP)

$$\mathbf{y} = \mathbf{X}\beta + \epsilon$$

Training Population → Genotyping & Phenotyping → Train GS Model

Breeding Material → Genotyping → Calculate GEBV → Make Selections
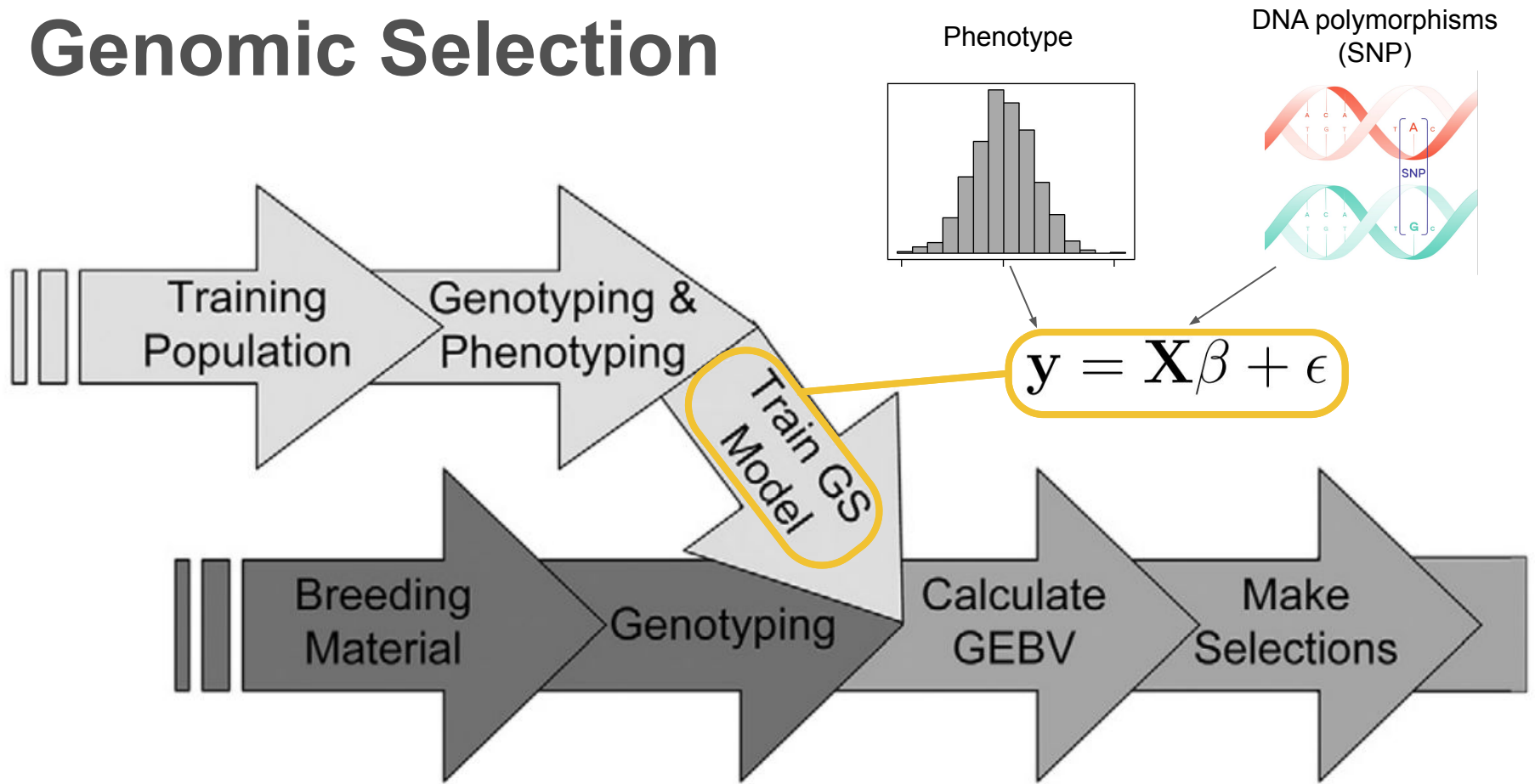
(Heffner *et al.*, 2009)

Genomic BLUP (Van Raden, 2008)
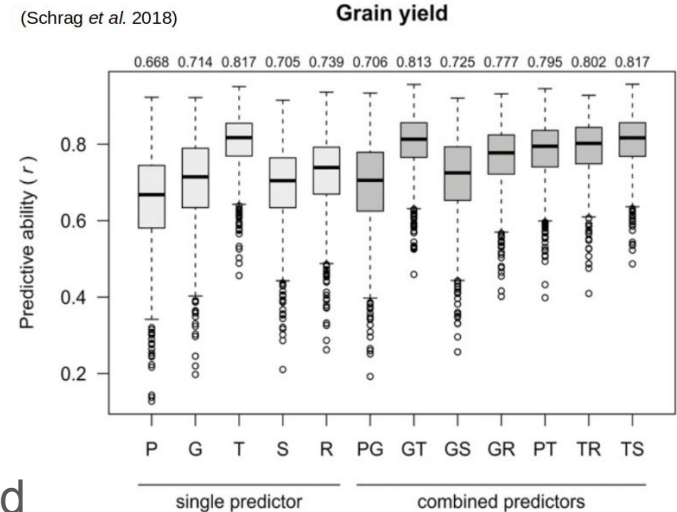
$$\mathbf{y} = \mu + \mathbf{Z}\mathbf{g} + \epsilon$$

$$\mathbf{g} \sim \mathcal{N}(0, \sigma_g^2 \mathbf{K})$$

$$\mathbf{K} = \mathbf{X_c}\mathbf{X_c^T}/(2\sum_i p_i(1 - p_i))$$

Estimating kinship with other molecular variants

- Other kind of **omic data** (metabolites, sRNA, mRNA…) have been proposed to capture genetic variability / estimate relatedness (Fu et al. 2012, Schrag et al. 2018)

- **Molecular (endo) phenotypes** are expressed phenotypes

- These variants capture **non additive effects** (G×G,G×E), which can be an **advantage** (fixed material) or a **drawback** (parental selection)

- Has the same limit as classic GS: it is **expensive**

  ⇒ **Can we find a low-cost alternative ?**

(Schrag *et al.* 2018)

Grain yield

0.668 0.714 0.817 0.705 0.739 0.706 0.813 0.725 0.777 0.795 0.802 0.817

Predictive ability (r)

P G T S R PG GT GS GR PT TR TS

single predictor   combined predictors

NIRS

- Characterize the **molecular composition** of a sample (Beer-Lambert law)

- **High-throughput** / **Low-cost** / (**Non destructive**)

- Often **routinely collected** in (plant) breeding programs

- Has been proposed for **barcoding** like a (DNA) **marker**

It's barcoding Jim, but not as we know it

ROBERT H. CRUICKSHANK[1] & LARS MUNCK[2]

Barcoding without DNA? Species identification using near infrared spectroscopy

JAIME I. RODRÍGUEZ-FERNÁNDEZ[1,2] , CLAUDIO J. B. DE CARVALHO[1], CELIO PASQUINI[3], KÁSSIO MICHELL GOMES DE LIMA[4] , MAURICIO O. MOURA[1] & GREGORIO G. CARBAJAL ARÍZAGA[5]

# Phenomic Selection Is a Low-Cost and High-Throughput Method Based on Indirect Predictions: Proof of Concept on Wheat and Poplar

Renaud Rincent,* Jean-Paul Charpentier,[†,‡] Patricia Faivre-Rampant,[§] Etienne Paux,*
Jacques Le Gouis,* Catherine Bastien,[†] and Vincent Segura[†,1]

(Heffner et al. 2009)
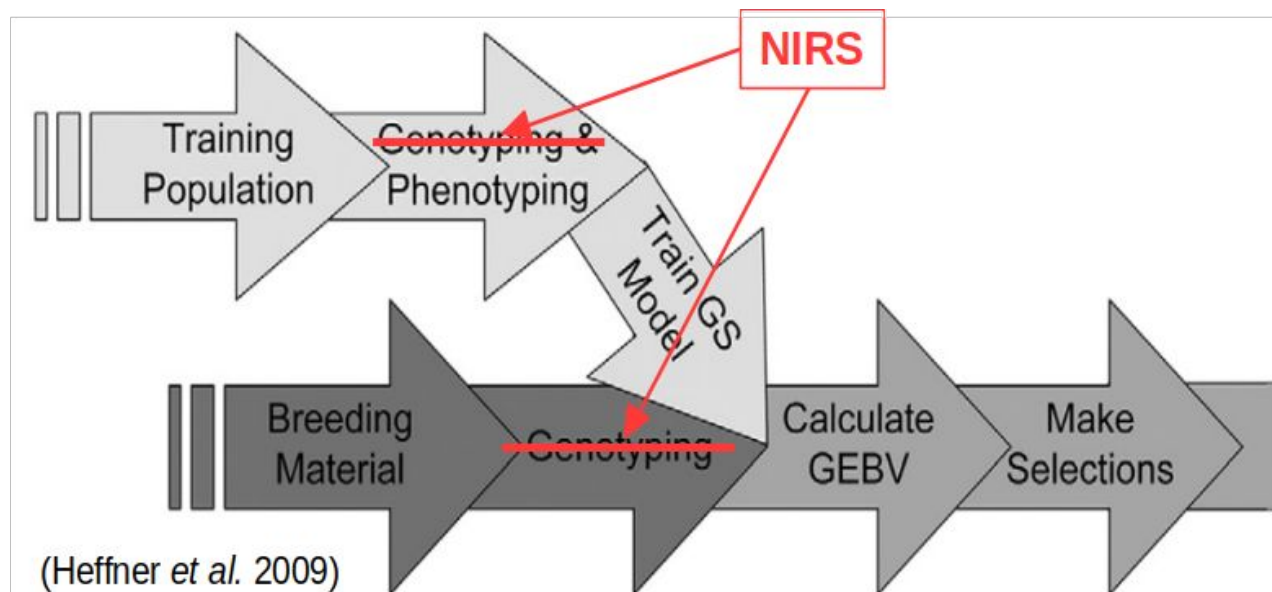
Proof of concept - material

- **<u>Wheat:</u>** A panel of 228 French elite varieties of winter wheat evaluated in Clermont-Ferrand under two hydric treatments and a subset of 161 varieties in 6 independent trials (other years/locations/treatments)
  - *Genotyping*: TaBW280K genotyping array → 84,259 SNPs (Rimbert et al. 2018)
  - *NIRS*: Grain & Leaves; FOSS spectrometers (visible and NIR)
  - *Phenotyping*: Yield and Heading date

- **<u>Poplar:</u>** An association population of 1,160 cloned genotypes evaluated in two common garden experiments at two locations (Orléans and Savigliano)
  - *Genotyping*: Illumina Infinium BeadChip array → 7,918 SNPs for 858 genotypes (Faivre-Rampant et al. 2016)
  - *NIRS*: Wood; PerkinElmer Spectrum400 (FT-IR NIR) (Gebreselassie et al. 2017)
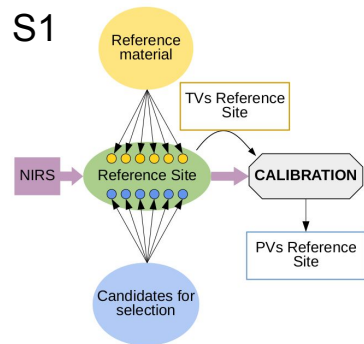 - *Phenotyping*: Growth, Phenology, Rust resistance

Variance partition along spectra
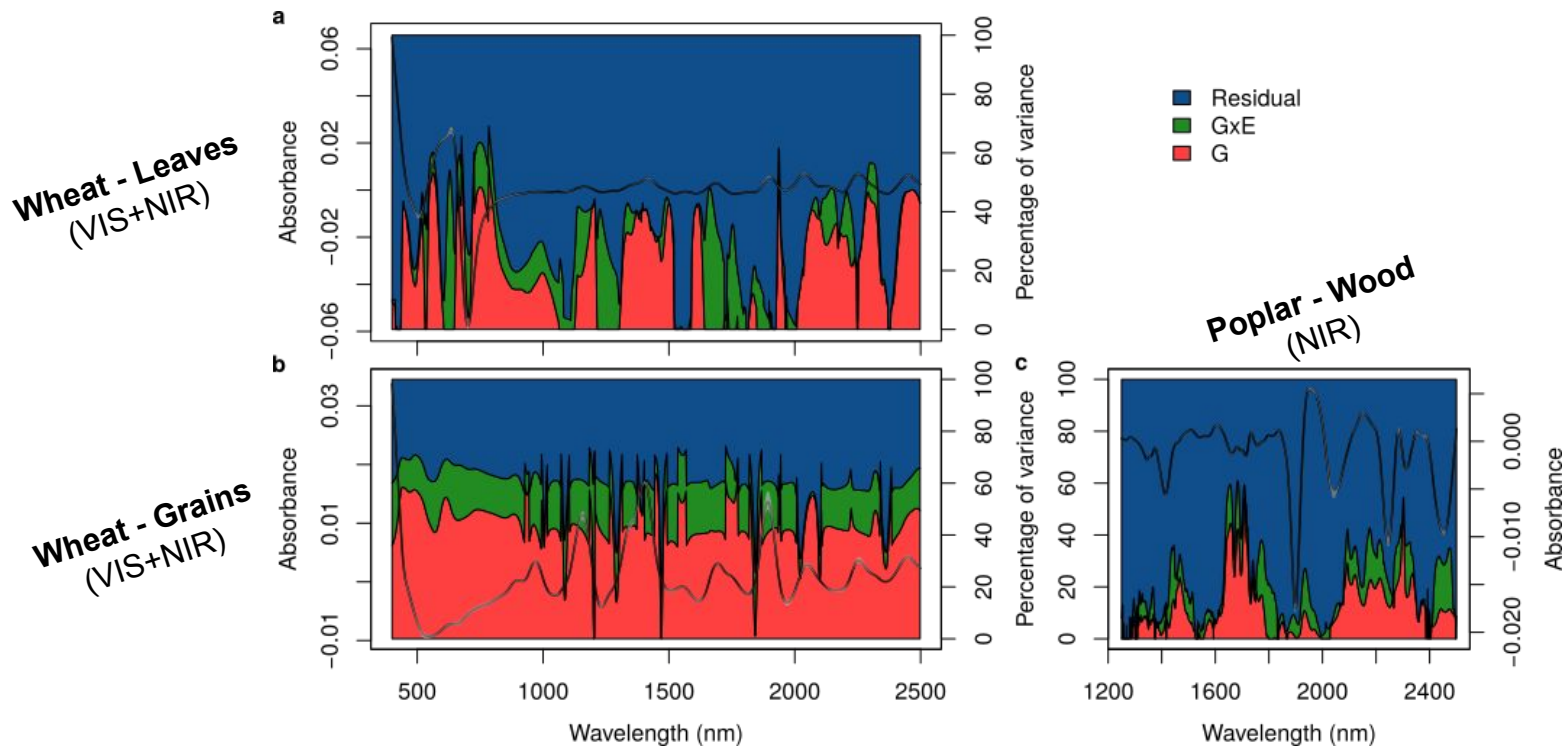
$$\mathbf{y} = \begin{bmatrix} \mathbf{y_1} \\ \mathbf{y_2} \end{bmatrix} = \mathbf{X}\beta + \mathbf{Zu} + \mathbf{e} \qquad var(\mathbf{u}) = \begin{bmatrix} \sigma_{u_1}^2 & \sigma_{u_{12}} \\ \sigma_{u_{21}} & \sigma_{u_2}^2 \end{bmatrix} \otimes \mathbf{K} \qquad var(\mathbf{e}) = \begin{bmatrix} \sigma_{e_1}^2 & 0 \\ 0 & \sigma_{e_2}^2 \end{bmatrix} \otimes \mathbf{I}$$
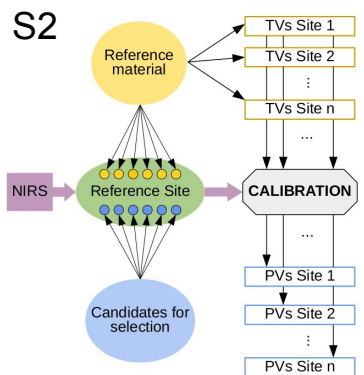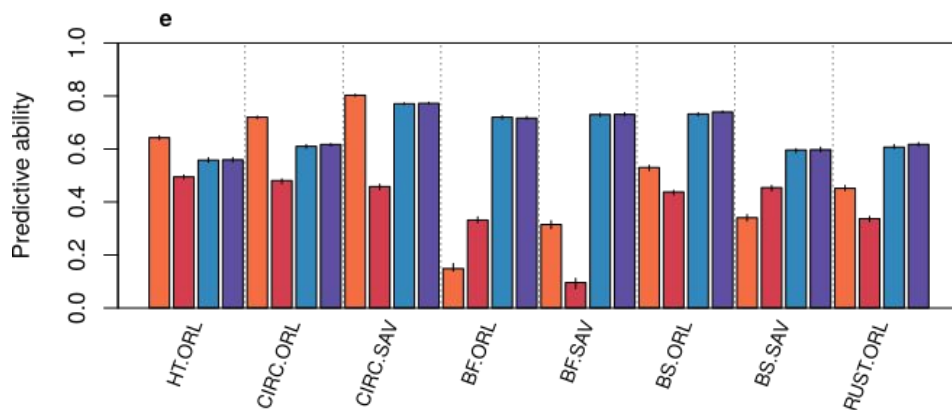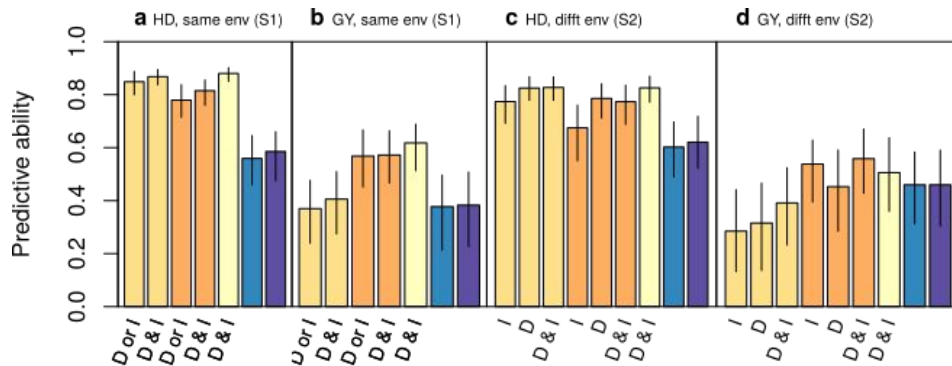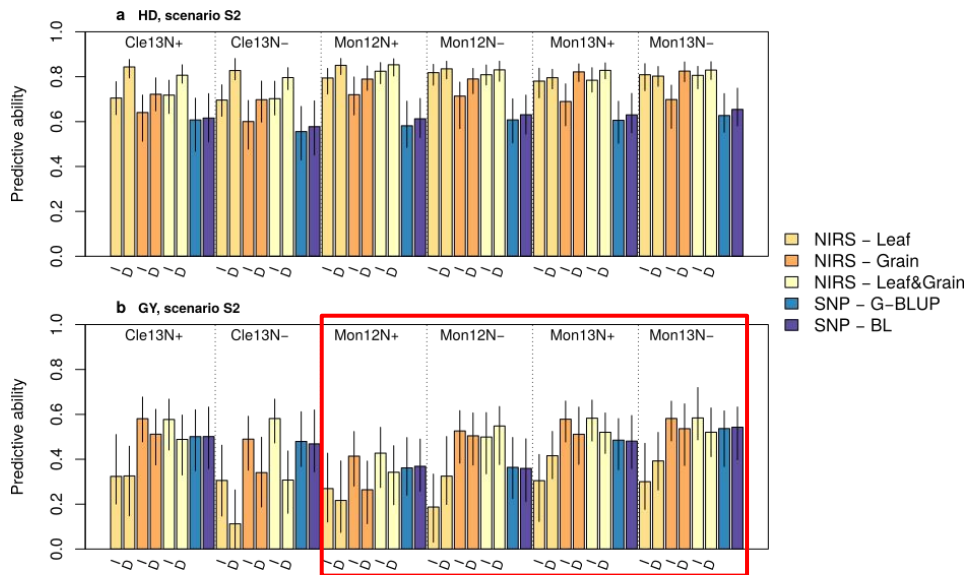
Phenomic & Genomic prediction accuracies

Phenomic & Genomic prediction accuracies

Theoretical increase in genetic gain (%) when using PS instead of GS

Given a total budget of 200 k€ for genotyping or NIRS acquisition, but varying GS and PS reliabilities, and genotyping and NIRS costs.
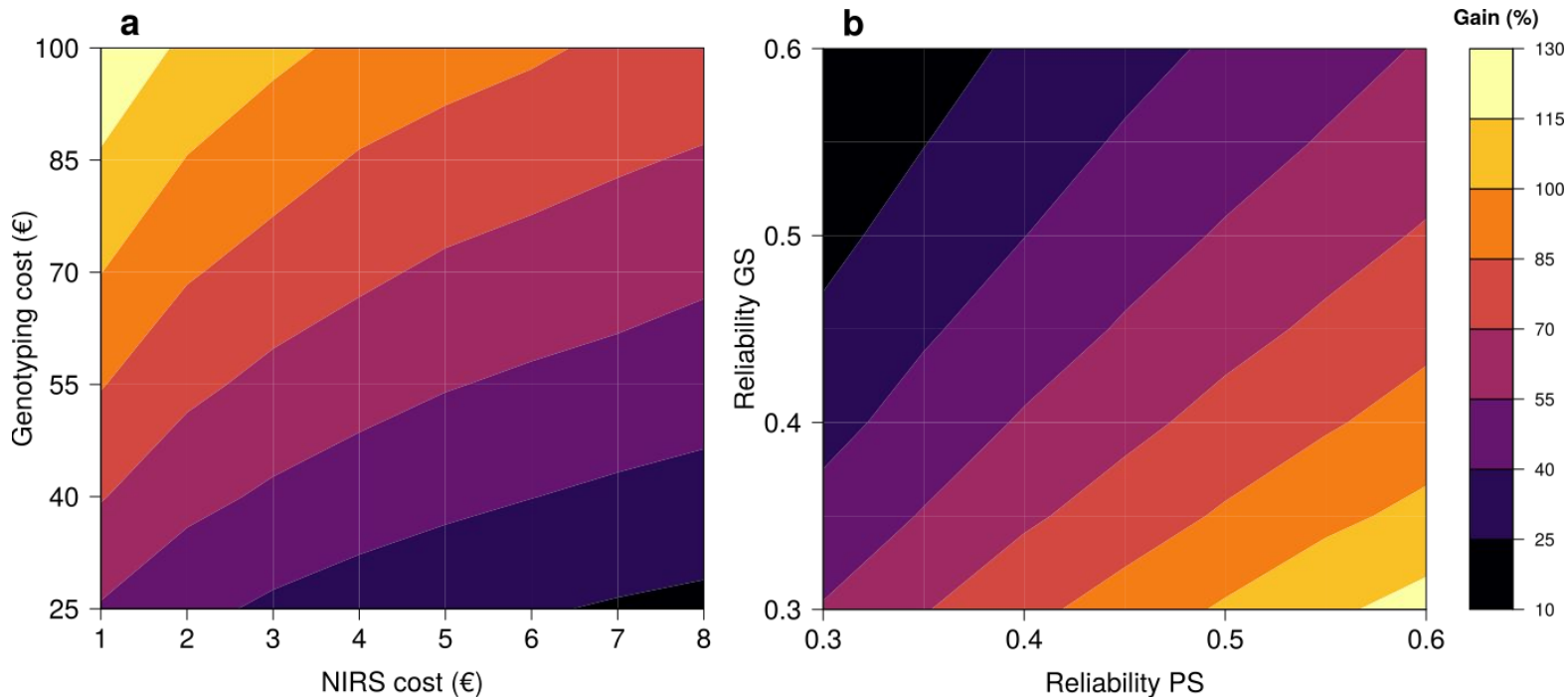
PS definition / use of NIRS in breeding (other than chemistry)

Phenomic selection: a new and efficient alternative to genomic selection

Running title: Phenomic Selection

Authors: Pauline Robert[1,2,*], Charlotte Brault[3,4,5,*], Renaud Rincent[1,2,#], Vincent Segura[3,5,#]

- NIRS is a proxy of yield

- NIRS is a secondary trait

- Phenomic Selection **(S1)**

- GLOB (Genomic-Like Omics Based) prediction **(S2)**

Individual / plot level

Variety / genotype level

Recent literature (PS & GLOB)

Interest of phenomic prediction as an alternative to genomic prediction in grapevine

Charlotte Brault[1,2,3] · Juliette Lazerges[1,2] · Agnès Doligez[1,2] · Miguel Thomas[1,2] · Martin Ecarnot[1] · Pierre Roumet[1] · Yves Bertrand[1,2] · Gilles Berger[1,2] · Thierry Pons[1,2] · Pierre François[1,2] · Loïc Le Cunff[1,2,3] · Patrice This[1,2] and Vincent Segura[1,2*]

Theoretical and Applied Genetics (2022) 135:895–914
https://doi.org/10.1007/s00122-021-04005-8

ORIGINAL ARTICLE

Phenomic selection in wheat breeding: identification and optimisation of factors influencing prediction accuracy and comparison to genomic selection

Pauline Robert[1,2,3,4] · Jérôme Auzanneau[3] · Ellen Goudemand[4] · François-Xavier Oury[2] · Bernard Rolland[5] · Emmanuel Heumez[6] · Sophie Bouchet[2] · Jacques Le Gouis[2] · Renaud Rincent[1,2]

Received: 23 July 2021   Accepted: 3 November 2021

DOI: 10.1002/ppj2.20027

The Plant Phenome Journal

ORIGINAL RESEARCH

Phenomic selection is competitive with genomic selection for breeding of complex traits

Xintian Zhu[1,2] | Willmar L. Leiser[2] | Volker Hahn[2] | Tobias Würschum[1]

Theoretical and Applied Genetics (2022) 135:653–665
https://doi.org/10.1007/s00122-021-03997-7

ORIGINAL ARTICLE

The performance of phenomic selection depends on the genetic architecture of the target trait

Xintian Zhu[1,2] · Hans Peter Maurer[2] · Mario Jenz[2,3] · Volker Hahn[2] · Arno Ruckelshausen[3] · Willmar L. Leiser[2] ·

Phenomic selection in wheat breeding: prediction of the genotype-by-environment interaction in multi-environment breeding trials

Pauline Robert[1,2,3,4] · Ellen Goudemand[4] · Jérôme Auzanneau[3] · François-Xavier Oury[2] · Bernard Rolland[5] · Emmanuel Heumez[6] · Sophie Bouchet[2] · Antoine Caillebotte[1] · Tristan Mary-Huard[1,3] · Jacques Le Gouis[2] · Renaud Rincent[1,2]

Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat

Margaret R. Krause,* Lorena González-Pérez,[†] José Crossa,[†] Paulino Pérez-Rodríguez,[‡] Osval Montesinos-López,[§] Ravi P. Singh,[†] Susanne Dreisigacker,[†] Jesse Poland,** Jessica Rutkoski,[††] Mark Sorrells,* Michael A. Gore,* and Suchismita Mondal[†,1]

Theoretical and Applied Genetics (2021) 134:1409–1422
https://doi.org/10.1007/s00122-021-03779-1

ORIGINAL ARTICLE

Early prediction of biomass in hybrid rye based on hyperspectral data surpasses genomic predictability in less-related breeding material

Rodrigo José Galán[1] · Angela-Maria Bernal-Vasquez[2] · Christian Jebsen[2] · Hans-P Patrick Thorwarth[1,2] · Philipp Steffan[2] · Andres Gordillo[4] · Thomas Miedaner[1]

Received: 4 July 2019   Accepted: 21 January 2020

DOI: 10.1002/ppj2.20002

Plant Phenome Journal

ORIGINAL RESEARCH

Phenomic selection and prediction of maize grain yield from near-infrared reflectance spectroscopy of kernels

Holly M. Lane[1] | Seth C. Murray[1] | Osval A. Montesinos–López[2] | Abelardo Montesinos–López[3] | José Crossa[4] | David K. Rooney[1] | Ivan D. Barrero-Farfan[1] | Gerald N. De La Fuente[1] | Cristine L. S. Morgan[1,5]

Phenomic Selection: A New and Efficient Alternative to Genomic Selection

Pauline Robert, Charlotte Brault, Renaud Rincent, and Vincent Segura

Conclusion

- NIRS capture some *G* & *G×E* variance

- **PS** works for different **tissues** and **traits**, and it can be **as accurate as GS**

- NIRS is much **cheaper** than genotyping → PS can yield a **higher genetic gain** than GS even when **less accurate**

- **Limits**:

  - PS do not predict BVs, but phenotypic values → advantage & drawback !

  - GxE → advantage & drawback ! How to combine NIRS collected in different environments on different varieties?