



**Violeta Andjelkovic**  
**Chair Maize Working Group**  
**MRIZP - SERBIA**



**Maize diversity**  
 (Photos by V. Babic, Maize Research Institute, Serbia)

[www.ecgpr.cgiar/working-groups/maize](http://www.ecgpr.cgiar/working-groups/maize)



**Carlotta Balconi**  
**Vice Chair Maize Working Group**  
**CREA Research Centre for Cereal and Industrial Crops –ITALY**  
 carlotta.balconi@crea.gov.it



**ECPGR Activity Grant Scheme**  
**Proposal Form**  
**First Call – Phase XI (2024–2028)**



**Aranjuez, 04.03.2026**

**“MAize LAndraces traits phenomic prediction using Near InfraRed Spectra” (MALANIRs) 2025-2027**

**Coordinator - Stéphane Nicolas**  
**GQE- Le Moulon, INRAE - FRANCE**



# **MA**ize **LA**ndraces traits phenomic prediction using **N**ear **I**nfra**R**ed **S**pectra

## **? MALANIRs main scientific questions ?**

- How to use **genomic** and **phenomic prediction** based on **NIRs** to **characterize** agronomic traits including seed composition of **maize landraces** from **European Genebanks**?
- Could be **NIRs** a **low cost alternative** to **genotyping** for predicting agronomic and quality traits in **Genebanks**?



# MAize LAndraces traits phenomic prediction using Near InfraRed Spectra

## Background



### ECPGR Maize Working Group

ECPGR Homepage / ECPGR Working Groups / ECPGR Maize Working Group

## EVA

European Evaluation Network



**MineLandDiv**  
Mining allelic diversity of maize landraces for tolerance to abiotic and biotic stresses



2022 Joint FACCE-JPI SusCrop Call on Agrobiodiversity



Chair **Violeta Andjelkovic**

Coordinator **Sandra Goritschning**

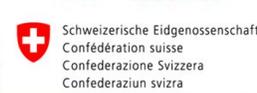
Coordinator **Stéphane Nicolas**



### EVA Maize Network



- 18 partners from 9 countries
- 10 genebanks and/or research institutes
- 8 breeding companies



**Mine - Mining**  
**Land - Landraces**  
**Div - Diversity**  
under abiotic and biotic stresses



14 avr. 2023 16:02:55

# Background

# EVA

European Evaluation Network

## TAKE HOME MESSAGE

Public-private partnerships exploring maize genetic diversity available in European genebanks

### Genotyping

**EVA**  
European Evaluation Network



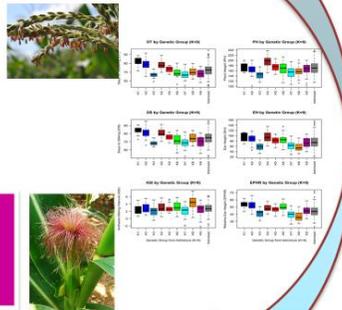
### Field phenotyping

Genetic Groups from Admixture (K=9)

- K1 (Popcom)
- K2 (SE-Spanish)
- K3 (SC-Italian)
- K4 (Corn Belt Dent)
- K5 (N-Italian)
- K6 (Portuguese)
- K7 (Galicia)
- K8 (Northern Flint)
- K9 (Pyrenean)



**18 EVA Maize partners  
9 Countries  
9 Genebanks  
626 maize landraces**



**EVA Maize Collection provides valuable pre-breeding sources of diversity for facing climate change due to the varieties local adaptation**

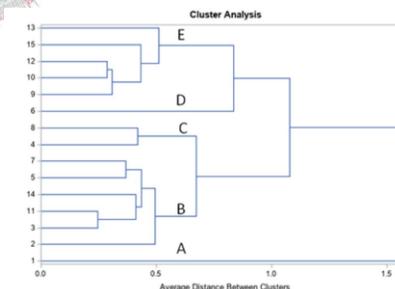
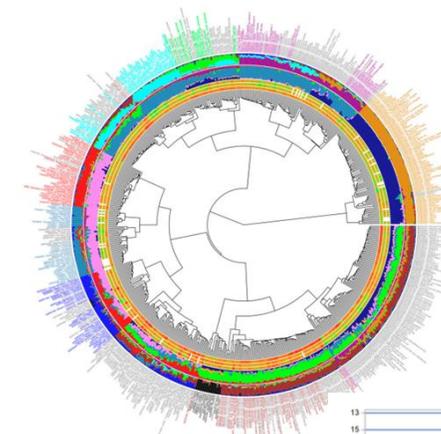
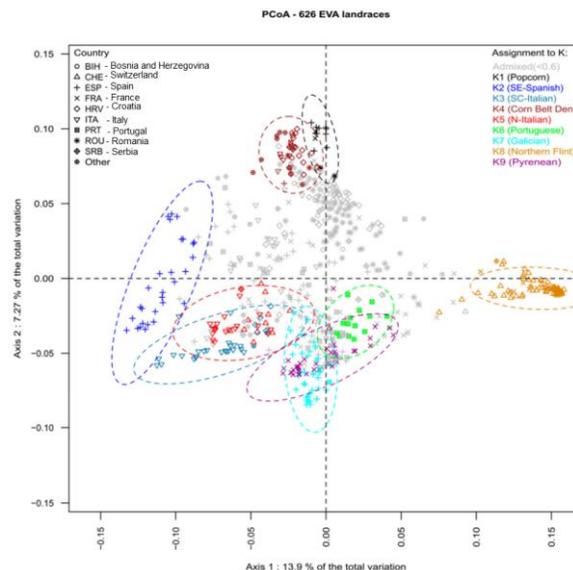


Biology 2024, 13, 454. <https://doi.org/10.3390/biology13060454>

Article

## Genetic and Phenotypic Evaluation of European Maize Landraces as a Tool for Conservation and Valorization of Agrobiodiversity

Carlotta Balconi <sup>1,\*</sup>, Agustin Galaretto <sup>2,t</sup>, Rosa Ana Malvar <sup>3</sup>, Stéphane D. Nicolas <sup>2</sup>, Rita Redaelli <sup>1</sup>, Violeta Andjelkovic <sup>4</sup>, Pedro Revilla <sup>3</sup>, Cyril Bauland <sup>2</sup>, Brigitte Gouesnard <sup>5</sup>, Ana Butron <sup>3</sup>, Alessio Torri <sup>1</sup>, Ana Maria Barata <sup>6</sup>, Natalija Kravic <sup>4</sup>, Valérie Combes <sup>2</sup>, Pedro Mendes-Moreira <sup>7,8</sup>, Danela Murariu <sup>9</sup>, Hrvoje Šarčević <sup>10</sup>, Beate Schierscher-Viret <sup>11</sup>, Morgane Vincent <sup>5</sup>, Anne Zanetto <sup>5</sup>, Bettina Kessel <sup>12</sup>, Delphine Madur <sup>2</sup>, Tristan Mary-Huard <sup>2,13</sup>, André Pereira <sup>7,8</sup>, Domnica Daniela Placinta <sup>9</sup>, Alexandre Strigens <sup>14</sup>, Alain Charcosset <sup>2</sup> and Sandra Goritschnig <sup>15,\*</sup>



## Connection of **MALANIRs** with projects MineLandDiv and ECPGR EVA maize

2023-2027

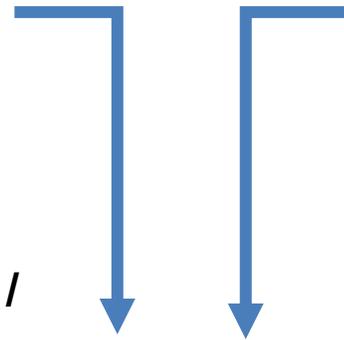
Coordinator: S. Nicolas



**MineLandDiv**

Mining allelic diversity of maize landraces for tolerance to abiotic and biotic stresses

- Design **Targeting sequencing**
- Pipeline for calling SNP from targeted sequencing
- **Field trial network** for training **genomic / phenomic prediction model**
- Development of **genomic / phenomic prediction methods**



**EVA**

European Evaluation Network

2020-2025

Coordinator: S. Goritschnig

- **Field trial data** for training **genomic / phenomic prediction model**
- European **Genebank Network**



**MALANIRs** (2024-2027)

**Proof-of-concept for phenomic to predict traits using grain from Genebanks seed stocks**

- **Extending targeting sequencing genotyping** to 500 new landraces
- **Extending Field trial network** for evaluating landraces from MineLandDiv panel and local landraces in new environments
- **NIRs characterization** of 1440 samples from **Field trial**
- **NIRs characterization** of 2105 samples from **Genebank** for phenomic prediction and prediction of biochemical composition
- **Standardization of NIRs** devices across network
- **Common meetings of MALANIRs, MineLandDiv & ECPGR**



**A network of 15 partners including 10 national European genebanks** Chair Maize Working group: **Violeta Andjelkovic (MRIZP)** & **ECPGR representant: Sandra Goritshchning**

Partner ID	Responsible	Institute	Country
1	Stéphane NICOLAS Coordinator	Institut National de la Recherche pour l'Agriculture, l'Alimentation et l'Environnement (INRAE)	France 
2	Natalija KRAVIC	Maize Research Institute Zelmun Polje (MRIZP)	Serbia 
3	Domagoj SIMIC	Agricultural Institute Osijek	Croatia
4	Hrvoje ŠARČEVIĆ	University of Zagreb	Croatia 
5	Danela MURARIU	Suceava Genebank (SVG)	Romania 
6	Rosa Ana MALVAR	Misión Biológica de Galicia - CSIC	Spain 
7	Carlotta BALCONI	Council for Agricultural Research and Economics (CREA) - Bergamo	Italy 
8	Ana Maria BARATA	Banco Português de Germoplasma Vegetal - (BPGV-INIAV)	Portugal 
9	Beate SCHIERSCHER VIRET	Agroscope	Switzerland 
10	Zoran JOVOVIĆ	University of Montenegro	Montenegro
11	Najada KADIASI	Agricultural University of Tirana	Albania 
12	Pedro MENDES MOREIRA	Politécnico de Coimbra – Escola Superior Agrária de Coimbra (ESAC-IPC)	Portugal
13	Gönül CÖMERTPAY	Eastern Mediterranean Agricultural Research Institute (DATAEM)	Turkey 
14	Sylvia VOGL	Austrian Agency for Health and Food Safety (AGES)	Austria
15	Elisabetta FRASCAROLI	University of Bologna	Italy

**MA**ize **LA**ndraces traits phenomic prediction using **N**ear **I**nfra**R**ed **S**pectra

## Objectives and context:



1. **Extending genomic characterization of 500 new landraces from European using DNA bulk targeted sequencing approach designed in MineLandDiv project (Task 1)**
2. **Predicting traits in contrasted environments of these 500 landraces using a genomic prediction models trained on genotyping and trait measured on landraces in Maize EVA Network and MineLandDiv and MALANIRs field trials (Task 1)**
3. **Evaluating use of NIRs in place of genomic data to predict agronomic traits in contrasted environment using a phenomic prediction models trained on NIRs of kernel lots harvested and agronomic traits measured in MineLandDiv and MALANIRs field trials (Task 2)**
4. **Evaluating the proof-of-concept of using individual near infrared spectra (NIRs) on grains from genebank seed stocks to predict agronomic traits and grain composition of maize landraces (Task 3)**





# MAize LAndraces traits phenomic prediction using Near InfraRed Spectra

## Action plan:



➤ **Task 1 – Targeting sequencing of landraces for genomic prediction**

➤ **Task 2 – NIRs of kernels harvested in field trials**



➤ **Task 3 – Phenomic prediction of traits and grain composition based on individual NIRs of kernels from genebank seed stocks**



➤ **Task 4 – Feeding EURISCO Database**



➤ **Task 5 – Face Meetings and training**



➤ **Task 1 – Targeting sequencing of landraces for genomic prediction**

**FOCUS** - Predict traits of landraces in Genebank with genomic selection using DNA bulk (MineLandDiv and EVA)

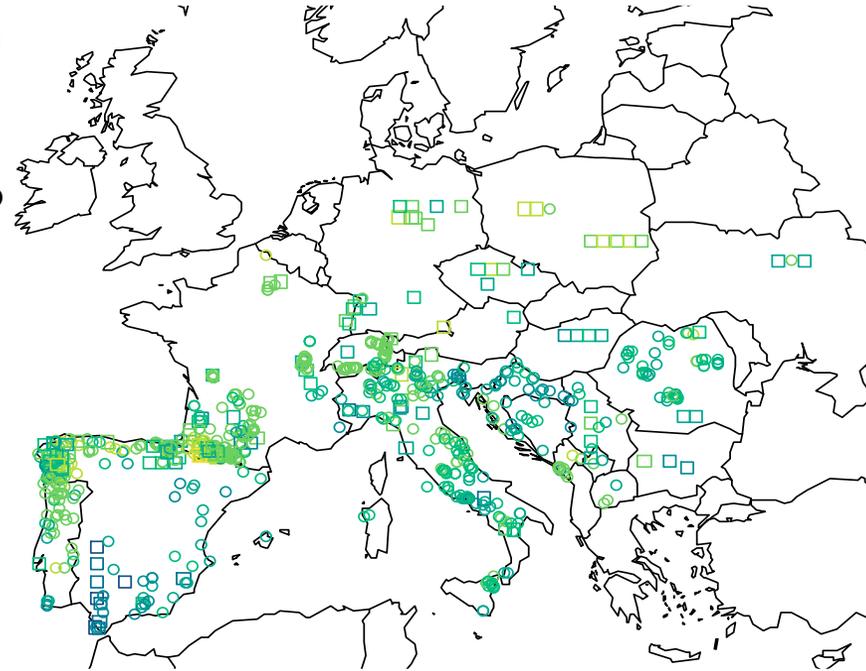
**Combine landraces phenotypic with genotypic data to predict traits in landraces**

=> **Development of a genomic approach to predict traits in landraces**



**Map variation of male flowering time range across Europe**

**Genomic prediction on 1047 temperate landraces genotyped with 50K using GBPLUP**



Days to Male Flowering	
□	Observed
○	Predicted
•	55-60
•	60-65
•	65-70
•	70-75
•	75-80
•	80-85
•	85-90
•	90-95
•	95-100
•	100-105



(A.O. Galaretto)

The training set of the GBLUP model

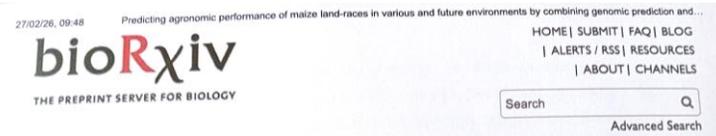
171 landraces from Europe (129) and America (42) evaluated in 1998 at two locations for flowering time (Moulon, Mauguio) with 2 replicates  
**Genotyped with 50K**



(S. Ben Sadoun)



$$y = Xb + Za + \epsilon$$



**Predicting agronomic performance of maize land-races in various and future environments by combining genomic prediction and ecogenetics**

- Agustin O. Galaretto, Marie Pégard, Rosana Malvar, Laurence Moreau, Ana Butrón,
- Pedro Revilla, Delphine Madur, Valérie Combes, Carlotta Balconi, Cyril Bauland,
- Pedro Mendes-Moreira, Hrvoje Šarčević, Ana M. Barata, Danela Murariu, Beate Schierscher-Viret,
- Alex Stringens, Violeta Andjelkovic, Sandra Goritschnig, Brigitte Gouesnard, Alain Charcosset,
- Stéphane D. Nicolas

➤ **Task 1 - Targeting sequencing of 500 new landraces from different Genebanks for diversity analysis and genomic prediction** 

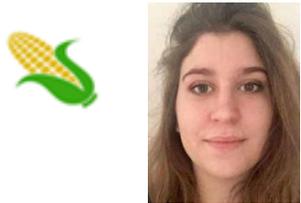
**Selection of 500 MALANIRs among 643 proposed by 11 partners for targeted sequencing**

Seed reception of 643 candidate landraces from 10 partners including new accessions

+ **EVA** accessions for **NIRs analysis** (Agroscope + University of Zagreb)

European Evaluation Network

Seed reception of 643 new landraces in GQE



(L. Nunes)

DNA extraction of 543 new landraces extracted by GQE



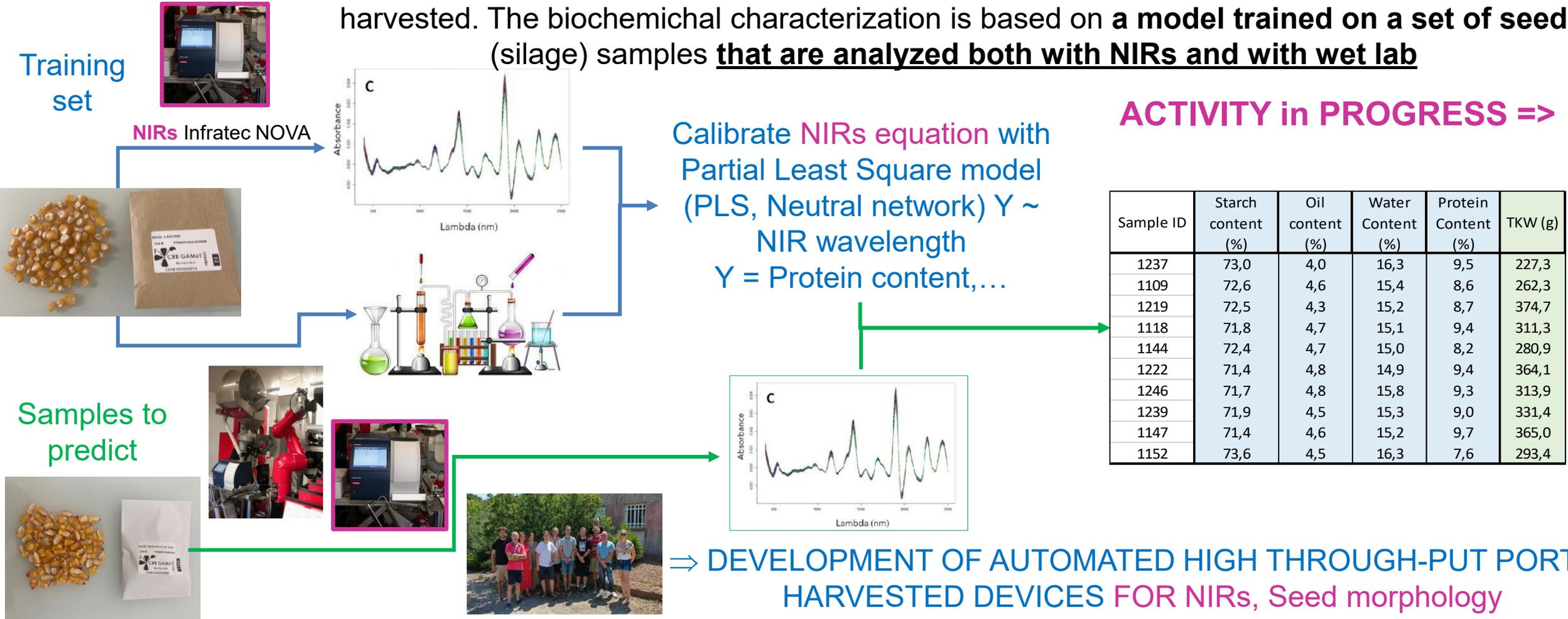
(D. Madur, V. Combes, W. Cornette)

Country	Institute Name	Institute Code	Accessions received (seeds)	DNA extracted in MRS	Accessions retained for tGBS
Austria	AGES	AUT001	44	44	44
Croatia	AIO	HRV021	21	21	21
Albanie	PGRC	ALB026	45	45	45
Italy	CREA	ITA386	83	53	61
Montenegro	University of Montenegro	MNE001	55	55	55
Switzerland	Agroscope	CHE001	119	50	40
Portugal	BPGV - INIAV	PRT001	40	40	40
Portugal	IPC	PRT053	28	28	25
Serbia	MRIZP	SRB001	150	149	51
Croatia	University of Zagreb	HRV041	58	58	58
France	INRAE (CRB GAMèt)	FRA014	0	0	60
<b>TOTAL</b>			<b>643</b>	<b>543</b>	<b>500</b>

➤ **Task 2 - NIRs of kernels harvested in field trials and from Genebank stocks**

**FOCUS - Predict seed composition of landraces by NIRs**

**NIRs** a **low cost** and **non destructive approach** used in breeding programs to evaluate seed biochemical composition (or digestibility) using **NIRs on seeds** (or silage) harvested. The biochemical characterization is based on a **model trained on a set of seed (silage) samples that are analyzed both with NIRs and with wet lab**



Experimental station DiaScope

⇒ **DEVELOPMENT OF AUTOMATED HIGH THROUGH-PUT PORT HARVESTED DEVICES FOR NIRs, Seed morphology (UE DIASCOPE, F. Meunier) / AGAP Institute (M. Ecartot)**

# ? MALANIRs main scientific questions ?

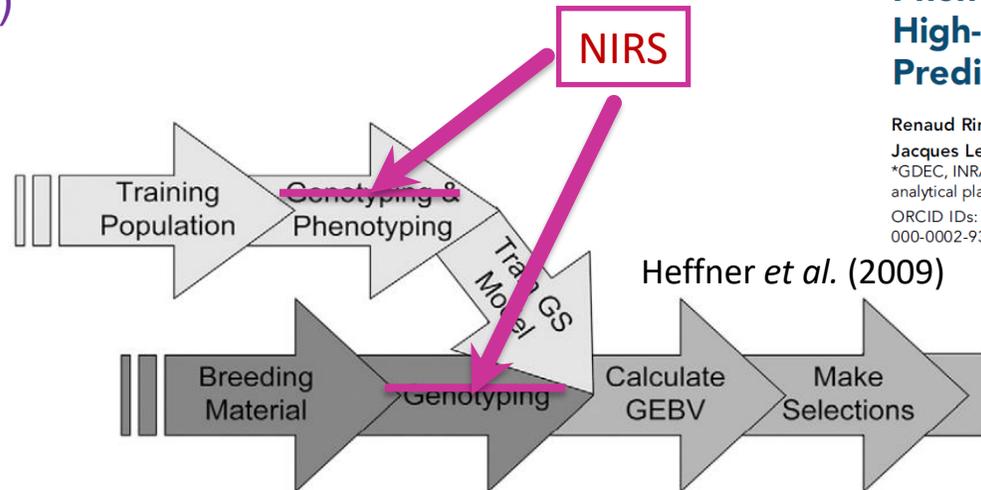
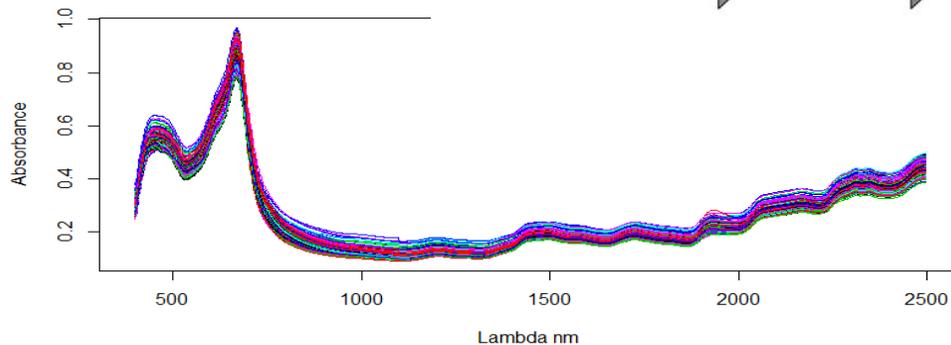
- Could be NIRs a low cost alternative to genotyping for predicting agronomic and quality traits in Genebanks?



**MAIN FOCUS:** Principle of phenomic selection, a low-cost and efficient alternative to genomic selection (Rincent, Segura et al., 2018)



(R. Rincent)



## 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,<sup>1,†</sup> Patricia Faivre-Rampant,<sup>§</sup> Etienne Paux,\* Jacques Le Gouis,\* Catherine Bastien,<sup>†</sup> and Vincent Segura<sup>1,†</sup>  
 \*GDEC, INRA, UCA, 63000 Clermont-Ferrand, France, <sup>†</sup>BioForA, INRA, ONF, 45075 Orléans, France, <sup>‡</sup>GenoBois analytical platform, INRA, 45075 Orléans, France, and <sup>§</sup>EPGV, INRA, CEA-IG/CNG, 91057 Evry, France  
 ORCID IDs: 0000-0003-0885-0969 (R.R.); 0000-0002-6029-0498 (J.-P.C.); 0000-0002-3094-7129 (E.P.); 0000-0001-5726-4900-0002-9391-6637 (C.B.); 0000-0003-1860-2256 (V.S.)

Estimation of a similarity matrix based on **NIRs spectra instead of genomic data** to calibrate model and predict trait using HBLUP

$$H(i, j) = \frac{\sum_{k=1}^{n_p} [S(i, k) \times S(j, k)]}{n_p}$$

**ACTIVITY in PROGRESS =>**

# ➤ Task 3 - Proof-of-concept of phenomic prediction of traits and grain composition of landraces based on individual NIRs of kernels from Genebank seed stocks

**Objective:** Evaluate feasibility of combining NIRs of seed lots from field trials and from Genebanks to predict agronomic traits and grain composition (oil, starch, protein)



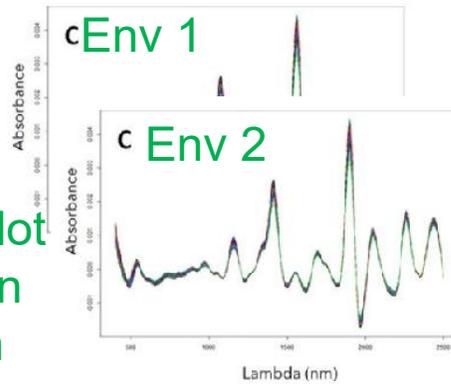
Traits (including biochemical composition of grain)



UE Diascope



NIRs from grain harvested in each plot for 300 landraces in different trials with automated devices



Estimation of similarity between NIR spectra

$$H(i, j) = \frac{\sum_{k=1}^{n_p} [S(i, k) \times S(j, k)]}{n_p}$$

(R. Rincent)



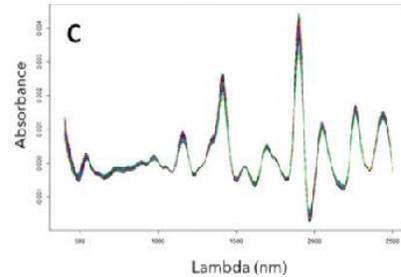
Train a HBLUP model using phenotyping data from trial to predict trait

Genebanks (ECPGR MALANIRs, AGAP Institute)



NIRs of new landraces maintained in Genebank

NIRs of seeds from genebank



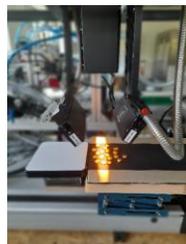
Estimation of NIR spectra similarity of grain with NIR spectra from field trial

$$y = Xb + Za + \epsilon$$

Predict traits (including biochemical composition of grain) of landraces maintained in genebank based on their NIR spectra



(M. Ecartot)



Aranjuez, 04.03.2026

ACTIVITY in PROGRESS =>

➤ **Task 4 - Feeding EURISCO database**



**FOCUS** Sharing data using ThaliaDB for genotyping and for phenotyping

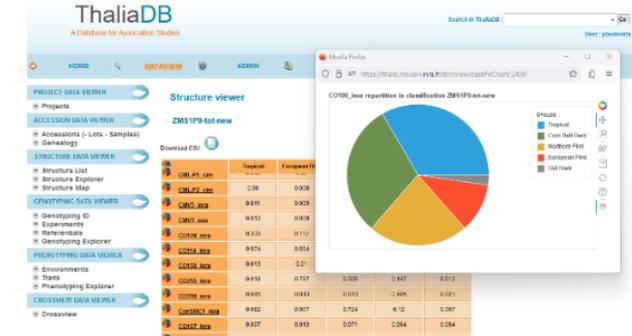
➤ **Establish a good traceability of landraces analyzed in MALANIRs + Sharing genotyping data in a secured way**

❑ Use of official Accession code from each genebank + seed-lot (year of multiplication...)

❑ Minimal description dataset - Accession code and name, passport data, Genebank seed-lot, multiplication year, collection site with geolocation, collection date...

❑ If possible / available: human uses, human practices

❑ Using ThaliaDB (<https://thalia.moulon.inra.fr>) for genotyping and phenotyping data



	SR_108245	SR_104697	SR_104627	SR_104633	SR_104666	SR_104674	SR_104674A	SR_1046770	SR_1046790	SR_1046801	SR_1046815	SR_1046906	SR_1046909
Genome Version	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z
Chromosome	8	8	8	8	8	8	8	8	8	8	8	8	8
Position	1 028 268	1 046 507	1 046 627	1 046 633	1 046 666	1 046 714	1 046 744	1 046 770	1 046 790	1 046 801	1 046 815	1 046 906	1 046 909
SR_LMa_C2T06ACXX:2:29235878	GO	G/G	NA	NA	NA	C/C	G/G	NA	NA	NA	C/C	NA	NA
SR_LMa_C2T06ACXX:2:29235878	NA	NA	NA	NA	NA	NA	NA						
19_332_3M1_F03_041213	N/N	N/N	N/N	N/N	N/N	N/N	N/N						
SR_C_Fa_C2T06ACXX:2:29235913	GO	G/G	C/C	G/G	C/C	C/C	G/G	C/C	C/C	G/G	C/C	G/G	T/T
SR_C_Fa_C2T06ACXX:2:29235913	NA	G/NA	G/NA	NA	NA	C/NA	G/C	G/C	G/C	G/C	G/C	C/NA	NA
SR_LMa_C2T06ACXX:2:29235966	NA	G/G	C/C	G/G	C/C	C/C	G/G	C/C	C/C	G/G	C/C	G/G	T/T
SR_LMa_C2T06ACXX:2:29235966	NA	NA	NA	NA	NA	C/NA	G/G	G/NA	NA	NA	NA	NA	NA
SR_C_Fa_C2T06ACXX:2:29235966	NA	G/G	C/C	G/G	C/C	C/C	G/G	C/C	C/C	G/G	C/C	G/G	T/T
SR_C_Fa_C2T06ACXX:2:29235966	NA	NA	NA	NA	NA	NA	NA						
19_19_C-Fa_C03_041213	N/N	N/N	N/N	N/N	N/N	N/N	N/N						
SR_C_Fa_C2T06ACXX:2:29235918	GO	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	T/T
SR_C_Fa_C2T06ACXX:2:29235918	GO	NA	NA	NA	NA	C/C	NA						
SR_C_Fa_C2T06ACXX:2:29235971	NA	G/G	C/C	G/G	C/C	C/C	G/G	C/C	C/C	G/G	C/C	G/G	T/T
SR_C_Fa_C2T06ACXX:2:29235971	NA	C/C	C/C	NA	C/C	NA	NA						
22_332_3M1_F03_041213	N/N	N/N	N/N	N/N	N/N	N/N	N/N						
SR_C_Fa_C2T06ACXX:2:29236436	GO	G/G	C/C	G/G	C/C	C/C	G/G	C/C	C/C	G/G	C/C	G/G	T/T
SR_C_Fa_C2T06ACXX:2:29236436	GO	NA	G/C	G/G	G/C	C/C	G/G	C/C	C/C	NA	G/C	NA	NA

**ACTIVITY in PROGRESS => Each MALANIRs Partner => Fill information in Thalia DB account**

## ECPGR Activity Grant Scheme: **MALANIRs**

### ➤ **Task 5 – Face Meetings and training**



**Joint EVA MAIZE Network and MALANIRs  
Annual Meeting - Bergamo – ITALY - 26-27 February 2025**

## ECPGR Activity Grant Scheme: MALANIRs

**EVA**

European Evaluation Network

### ➤ Task 5 – Face Meetings and training



**Joint ECPGR Maize WP, EVA Maize Network and MALANIRs  
Meeting - Belgrade – SERBIA - 2 October 2025**

# Gantt Chart – Where we are?

Task Description		2024	2025				2026				2027		
		Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3
<b>Task 1</b> 	Targeting sequencing of 500 landraces		█	█									
	Genomic prediction for 500 landraces				█	█	█			█			
<b>Task 2</b>  	Field trials			█	█			█	█				
	NIRs of kernels harvested in field trial	█	█			█							
	Phenomic prediction in fields						█	█	█	█			
<b>Task 3</b>  	NIRs of kernels from seed stock in genebank		█	█	█								
	Phenomic prediction in genebank						█	█	█	█			
<b>Task 4</b>	Feeding and sharing data 					█	█					█	█
<b>Task 5</b>	Meeting in person / <b>videoconference</b> 			█		█		█				█	





**Stéphane Nicolas**  
**Charcosset A.**

Moreau L.



**Madur D.**

Bauland C.



**Combes V.**

**Ben Sadoun S.**



**Arca M.**

Mary-Huard T.



**Roux A.**

Fievet J.



**Galaretto A.O.**

**Rincent R.**

De Oliviera. Y



**M. Tenailon**



**Gouesnard B.**

Zanetto A.

Teres P.

Vincent M.

Diaw Y.

**Ecarnot M.**



**Faivre-Rampant P.**

Hissinger D.

Bérard A.

Chevreau A.

UE SMH

Palaffre C.

UE Diascope

**R. Chapuis**

F. Meunier

P. Sartre



A. Butron

P. Revilla

R.A Malvar



**Gianfranco Mazzinelli**

**Rita Redaelli**



ECPGR

**S. Goritschnig**



**Violeta Andelkovic** MRIZP  
ECPGR Maize WG Chair

**Funding**

- Amaizing
- Diversity Zea
- ECPGR EVA maize
- Dromamed
- MineLandDiv



**MineLandDiv**  
Mining allelic diversity of maize landraces for tolerance to abiotic and biotic stresses



**AND all people who collected, maintained landraces and inbred lines collection in different European Genebanks and in France Center of genetic resources CRB Gamèt at Montpellier and lines collection at Experimental unit Saint Martin de Hinx**



**Aranjuez, 04.03.2026**