

# XVIIIth Eucarpia Biometrics in Plant Breeding Conference

21-23 September 2022

Gif-sur-Yvette

## Welcome book



## Welcome

We welcome you to the 18th meeting of the EUCARPIA Section Biometrics in Plant Breeding on 21-23 September 2022 in Paris-Saclay University Campus, France. This meeting is organised by the GQE-Le Moulon research unit (INRAE, Paris-Saclay University, CNRS and AgroParisTech).

Follow us on Twitter @EucarpiaBiom22 for up-to-the-minute information on the conference and regular updates.

## Scientific committee

Dietrich Borchardt, KWS

Alain Charcosset, INRAE, Le Moulon

Pawel Krajewski, Polish Academy of Science

Ian J Mackay, SRUC, Edinburgh

Chris Maliepaard, WUR Univ.

Tristan Mary-Huard, INRAE, Le Moulon

Laurence Moreau, INRAE, Le Moulon

Hans-Peter Piepho, Univ. Hohenheim

Fred van Eeuwijk, WUR Univ.

Maria Carlota VazPatto, Instituto de Tecnologia Química e Biológica

## Organisation committee

Laurence Moreau

Tristan Mary-Huard

Julie Fiévet

Hans-Peter Piepho

Sarah Ben Sadoun

Aurélien Beugnot

Annaïg De Walsche

Maud Fagny

Alizarine Lorenzi

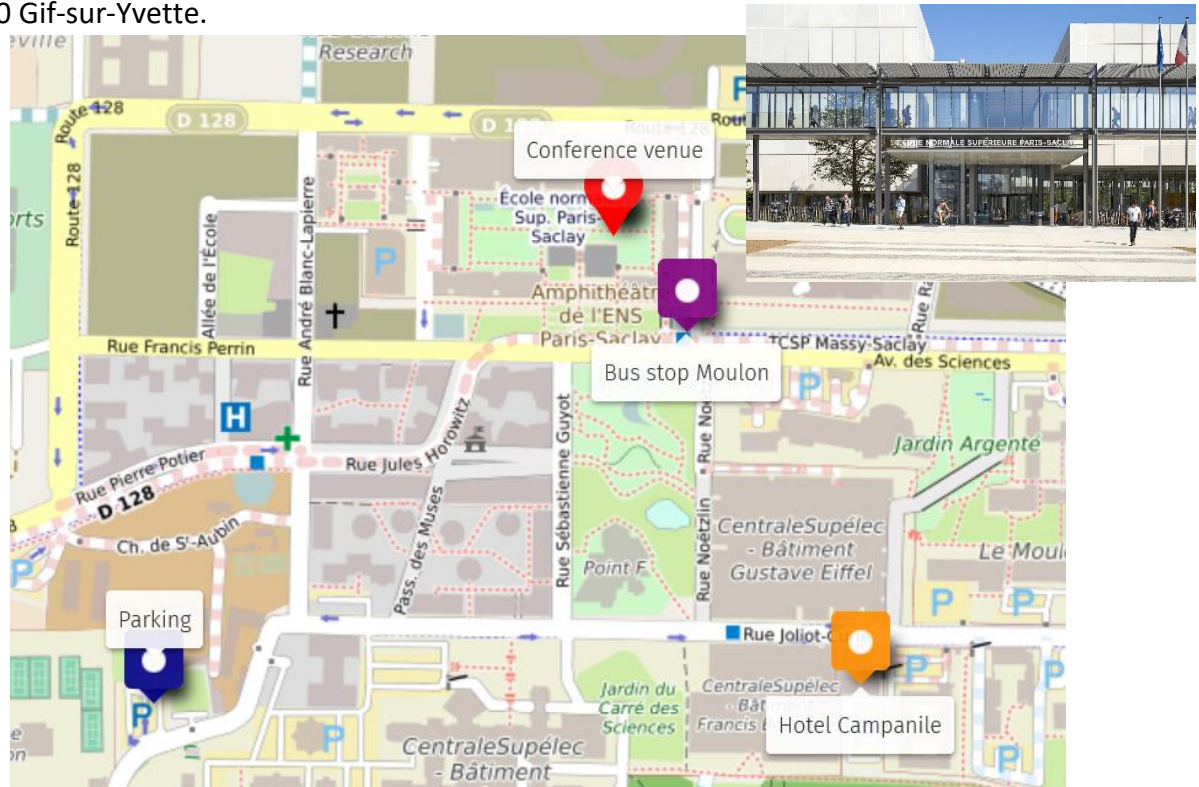
Stéphane Nicolas

Renaud Rincent

Dimitri Sanchez

## How to come to the conference?

The conference will take place at École Normale Supérieure Paris-Saclay, 4 Av. des Sciences, 91190 Gif-sur-Yvette.



### By public transport

**Important: You will need to take a bus to come to the conference venue. It is recommended to buy tickets (the basic metro ticket: ticket t+) in advance at any metro or RER station.**

#### From Palaiseau (Adagio Hotel)

At bus stop "Place Marguerite Perey"

Take one of the following buses:

- Bus 91.06 (Christ de Saclay)
- Bus 91.10 (Saint-Quentin-en-Yvelines)

Stop at « Moulon »

#### From Gif-sur-Yvette (Le Village Hotel)

At bus stop "Croix de Fer", Take the Bus 11 (Parc Orsay Université), Stop at « Joliot Curie »

#### From Orsay (Hotel d'Orsay)

At bus stop "Gare du Guichet", take the Bus 9 (Campus HEC, Saclay), Stop at "Moulon"

#### From Massy

At bus stop "Gare de Massy-Palaiseau"

Take one of the following buses:

- Bus 91.06 (Christ de Saclay)/Bus 91.10 (Saint-Quentin-en-Yvelines), Stop at « Moulon »

## From Paris

Take the RER B (Saint-Rémy-les-Chevreuse), Stop at « Le Guichet »  
Then take the Bus 9 (Christ de Saclay), Stop at « Moulon »

## By car from Paris

- By the N118: Pont de Sèvres, follow "Nantes-Bordeaux". Exit 9: "Centre Universitaire". At the round-about, take the second exit.

- By the A6: Take the A6 then the A10 towards "Nantes-Bordeaux". Follow the direction "Cité Scientifique" then "Saclay". Continue on the D36. Turn left onto the D128 towards "Centre Universitaire". Pass 2 round-abouts. At the 3rd round-about take the 2nd exit.

GPS coordinates

Enter in your GPS : Rue Yvette Cauchois

Latitude North : 48° 42' 47.318

Longitude East : 2° 9' 43.715

Latitude : 48.713144

Longitude : 2.162143

## Parking near the conference:

“Parking Plaine des Sports” - 15 Chemin de Moulon, 91190 Gif-sur-Yvette

Other possibilities at <https://www.parkinsaclay.fr/>

## Where to eat?

### Near the conference venue

Yu Cai sushi: 33 Mail Pierre Potier, 91190 Gif-sur-Yvette

FO Pizza: 49 Mail Pierre Potier, 91190 Gif-sur-Yvette

Brass and Co: 24 - 26 Mail Pierre Potier, 91190 Gif-sur-Yvette (only for lunch, snacks and drinks in the evening)

### Near Adagio Hotel – Palaiseau

19: 19 Cours Gilbert Simondon, 91120 Palaiseau

Living room: 10 Bd Gaspard Monge, 91120 Palaiseau

### Near Le Village Hotel – Gif-sur-Yvette

L'île o crêpes: 1 Rue Neuve, 91190 Gif-sur-Yvette

Le canapé: 1 Rue Gustave Vatonne, 91190 Gif-sur-Yvette

### Near Hotel d'Orsay – Orsay

Tan An: 37 Rue Charles de Gaulle, 91400 Orsay

Mon Liban: 8bis Rue Charles de Gaulle, 91400 Orsay

## At Massy

You will find near the RER Train station several restaurants from fast-food restaurants to more traditional ones.

Wednesday, September 21<sup>st</sup>, 2022

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<b>08:00 - 09:00</b>	<b>Registration</b>
<b>09:00 - 09:15</b>	<b>Welcome and opening address</b>
<b>09:15 - 11:00</b>	<b>Session: Multi-omics data integration</b> <i>Chairman: Pawel Krajewski</i>
<b>09:15 - 10:00</b>	<b>Invited speaker : Julio Isidro y Sánchez</b> Enabling comparative research through multi-omics data harmonization
10:00 - 10:15	› eQTLs are key players in the integration of genomic and transcriptomic data for phenotype prediction <i>Vincent Segura, Biologie intégrée pour la valorisation de la diversité des Arbres et de la Forêt</i>
10:15 - 10:30	› Integration of DNA methylation and transcriptome data improves complex trait prediction in <i>Hordeum vulgare</i> <i>Pernille Bjarup Hansen, Center for Quantitative Genetics and Genomics, Aarhus University, 4200 Slagelse</i>
10:30 - 10:45	› Phenomic Selection in a structured hybrid rapeseed population using near-infrared reflectance spectroscopy <i>Lennard Ehrig, Department of Plant Breeding, Justus Liebig University Giessen</i>
10:45 - 11:00	› Beyond QTL effects in quantitative genetics: comparative genomics and machine learning techniques for prediction across populations - <i>Guillaume Ramstein, Aarhus University</i>
<b>11:00 - 11:30</b>	Coffee break
<b>11:30 - 12:15</b>	<b>Invited speaker: Miguel Pérez-Enciso</b> Loving and hating deep learning
<b>12:15 - 13:30</b>	Lunch

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<b>13:30 - 15:15</b>	<b>Session: High Throughput Phenotyping</b> <i>Chairman: Fred van Eeuwijk</i>
<b>13:30 - 14:15</b>	<b>Invited Speaker : Andreas Hund</b> Phenotyping of crop development to dissect GxE into small-effect responses to environmental covariates
14:15 - 14:30	› Genomic selection using information on multiple phenotypic traits and multiple growing environments <i>Jon Bancic, The Roslin Institute</i>
14:30 - 14:45	› Analysis of longitudinal, image-based canopy cover estimates as a quality indicator in wheat variety trials <i>Jip Ramakers, Wageningen University and Research</i>
14:45 - 15:00	› Illuminating and enhancing wheat breeders' eyes based decisions with drone-based phenomic predictions <i>Lukas Roth, ETH Zurich, Institute of Agricultural Sciences</i>
15:00 - 15:15	› Genetic Factor-Analytic BLUP for Improved Genomic Prediction with High-Dimensional Secondary Traits <i>Jonathan Kunst, Biometris, Wageningen University and Research</i>
<b>15:15 - 17:30</b>	<b>Session: Diversity Management</b> <i>Chairman: Alain Charcosset</i>
<b>15:15 - 16:00</b>	<b>Invited speaker: John Hickey, TBA</b>
<b>16:00 - 16:30</b>	<b>Coffee break</b>
16:30 - 16:45	› Quantifying the Drivers of Genetic Change in Plant Breeding <i>Thiago Oliveira, The University of Edinburgh</i>
16:45 - 17:00	› Comparison of genomic enabled cross selection criteria for the improvement of inbred line populations <i>Alice Danguy des Déserts, Syngenta</i>
17:00 - 17:15	› Improving the use of plant genetic resources to sustain breeding programs efficiency <i>Dimitri Sanchez, Génétique Quantitative et Evolution - Le Moulon, LIDEA</i>
17:15 - 17:30	› Artificial intelligence guided allele stacking to develop high yielding, highly resistant varieties <i>Kai Voss-Fels, Geisenheim University, University of Queensland</i>
<b>18:00 - 20:00</b>	<b>Happy poster session (Posters + drinks and snacks)</b>

Thursday, September 22<sup>nd</sup>, 2022

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<b>08:30 - 10:15</b>	<b>Session: Non-Additive Genetic Effects</b> <i>Chairman: Ian Mackay</i>
<b>08:30 - 09:15</b>	<b>Invited speaker: Zulma Vitezica</b> Genomic prediction with dominance and epistasis
09:15 - 09:30	› IBD-based mixed model approaches for genetic studies in multi-parent populations (MPPs): additive, epistatic, and QTL-by-environment effects <i>Wenhao Li, Wageningen University &amp; Research</i>
09:30 - 09:45	› Defining the causes and consequences of phantom epistasis in heterotic hybrids <i>Chin Jian Yang, Scotland's Rural College (SRUC)</i>
09:45 - 10:00	› Genome-Based prediction of sub-genome genetic interaction effects in wheat populations <i>David González-Diéguez - International Maize and Wheat Improvement Center (CIMMYT)</i>
10:00 - 10:15	› Uncovering directional epistasis in bi-parental populations using genomic data <i>Simon Rio, CIRAD - UMR, AGAP, Université de Montpellier, INRAE, Institut Agro</i>
<b>10:15 - 10:45</b>	<b>Coffee break</b>
<b>10:45 - 11:45</b>	<b>Session: Others</b> <i>Chairman: Rex Bernardo</i>
10:45 - 11:00	› Effects of systematic data reduction on trend estimation from German registration trials <i>Jens Hartung, University of Hohenheim</i>
11:00 - 11:15	› A comprehensive review of fast algorithms for large-scale genome-wide association studies based on linear mixed models <i>Yong Jiang, Leibniz Institute of Plant Genetics and Crop Plant Research [Gatersleben]</i>
11:15 - 11:30	› Empirical comparison of times series models and tensor product penalised splines for modelling spatial dependence in plant breeding field trials. <i>Bev Gogel, University of Wollongong</i>
11:30 - 11:45	› Understanding the recombination landscape of breeding lines in wheat and barley <i>Rajiv Sharma, Scotland's Rural College (SRUC)</i>
<b>11:45 - 12:00</b>	<b>Information - Social Event &amp; Gala organized</b>
<b>12:00 - 13:15</b>	<b>Lunch</b>
<b>13:15 - 23:55</b>	<b>Social Events &amp; Gala - In Paris!</b>

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## Social events: 13:15 – 18:45

### Excursion to the Jardin des Plantes de Paris

A shuttle service will take you to the Jardin des Plantes from the conference venue at 13:15. Each participant was assigned to a group according to their choice of activity between the Great Gallery, of Evolution, the Great Greenhouse, or the National Herbarium.

The timetable of the different activities according to the groups is displayed below:

Group A	Greenhouses (14:40)	Great Gallery of Evolution (15:50)
Group B	Greenhouses (15:00)	Great Gallery of Evolution (16:00)
Group C	Greenhouses (15:10)	Great Gallery of Evolution (16:10)
Group D	Great Gallery of Evolution (14:50)	Greenhouses (16:00)
Group E	Great Gallery of Evolution (15:00)	Greenhouses (16:10)
Group F	Herbarium (14:40)	Greenhouses (16:00)
Group G	Great Gallery of Evolution (15:20)	Herbarium (16:30)

A member of the organisation will be waiting for you at the entrance of each building to give you a ticket. Please respect your group and the timetable.



## Gala: 19:45 – 02:00

Get on board a “Bateau Mouche” for the conference Gala evening!

A shuttle service will take you to the boat landing from the Jardin des Plantes at 18:45. The boat is leaving at 19:45, please be on time. The boat will land at 23:00, after which people will have the opportunity to stay on board for a late drink until 02:00. Several shuttles will bring you back to the conference venue, stopping in Massy at 23:00, 00:00, 01:00 and 02:00.



Friday, September 23<sup>rd</sup>, 2022

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<b>09:00 - 10:30</b>	<b>Session: Gene-by-Environment interaction and Crop Growth Modeling</b> <i>Chairman: Carlota Vaz Patto</i>
<b>09:00 - 09:45</b>	<b>Invited speaker: Mark Cooper</b> Revisiting the Breeder's Equation: Implications of our advancing understanding of trait genome-to-phenome relationships
09:45 - 10:00	› A framework based on differential equations for the dynamic modelling of crop growth for sets of genotypes <i>George Van Voorn, Wageningen University &amp; Research</i>
10:00 - 10:15	› Functional–Structural Plant Modeling Highlights How Diversity in Leaf Dimensions and Tillering Capability Could Promote the Efficiency of Wheat Cultivar Mixtures <i>Jérôme Enjalbert, UMR 0320 Génétique Quantitative et Évolution - Le Moulon</i>
<b>10:30 - 11:00</b>	<b>Coffee break</b>
<b>11:00 - 12:30</b>	<b>Session: Gene-by-Environment interaction and Crop Growth Modeling</b> <i>Chairman: Dietrich Borchardt</i>
<b>11:00 - 11:45</b>	<b>Invited speaker: Emilie Millet</b> TBA
11:45 - 12:00	› Quantifying genetic drivers of yield variability of UK cereal crops - <i>Joanna Raymond, University of East Anglia</i>
12:00 - 12:15	› Resource allocation optimization for multi-environment trials in cereals breeding <i>Lucia Gutierrez, University of Wisconsin Madison</i>
12:15 - 12:30	› Design of a CIMMYT Australian ICARDA Germplasm Evaluation (CAIGE) experiment using an Incomplete multi-environment trial (IMET) design approach incorporating genetic relatedness <i>Lu Wang, Centre for Biometrics and Data Science for Sustainable Primary Industries</i>
<b>12:30 - 13:45</b>	<b>Lunch</b>

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**13:45 - 14:00** Information

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**14:00 - 15:00** **Session: Gene-by-Environment interaction and Crop Growth Modeling**  
- *Chairman: Hans-Peter Piepho*

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14:00 - 14:15 › Meta-analysis of GWAS for studying GxE interactions  
*Annaïg De Walsche, INRAE GQE - Le Moulon, MIA Paris*

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14:15 - 14:30 › Genomic selection using random regressions on known and latent environmental covariates  
*Daniel Tolhurst, The Roslin Institute*

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14:30 - 14:45 › learnMET: an R package to apply nonlinear algorithms for genomic prediction using multi-environment trial data  
*Cathy Westhues, Division of Plant Breeding Methodology, Center for Integrated Breeding Research (CiBreed), University of Göttingen, Computomics*

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14:45 - 15:00 › Revisiting superiority and stability measures in multi-environment trials using genomic data  
*Humberto Fanelli Carvalho, Centro de Biotecnología y Genómica de Plantas (CBGP-INIA), Universidad Politécnica de Madrid (UPM) – Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA) Campus Montegancedo-UPM*

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**15:00 - 16:30** Closing and Farewell - Closing and Farewell

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	Wednesday 21	Thursday 22	Friday 23		
08:00	Registration				
		Zulma Vitezica			
09:00	Welcome		Mark Cooper		
	Julio Isidro y Sánchez	Non Additive Genetic Effects	Gene-by-Environment interaction and Crop Growth Modeling		
10:00	Multi-omics data integration	Coffee break	Coffee break		
11:00	Coffee break	Others	Emilie Millet		
	Miguel Pérez-Enciso	Information	Gene-by-Environment interaction and Crop Growth Modeling		
12:00	Lunch	Lunch	Lunch		
13:00					
	Andreas Hund	Social events	Information		
14:00	High Throughput Phenotyping		Gene-by-Environment interaction and Crop Growth Modeling		
15:00	John Hickey		Closing and Farewell		
16:00	Coffee break				
	Diversity Management				
17:00					
18:00	Happy poster session				
19:00					
20:00		Gala evening (19:45 – 02:00)			



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