



**HAL**  
open science

## Characterisation of the spermosphere of the common bean seed (*Phaseolus vulgaris*)

Chandrodhay Saccaram, Marie Simonin, Stéphanie Boutet, Céline Brosse, Tracy François, Boris Collet, José Caius, Etienne Delannoy, Benoit Bernay, Massimiliano Corso, et al.

### ► To cite this version:

Chandrodhay Saccaram, Marie Simonin, Stéphanie Boutet, Céline Brosse, Tracy François, et al.. Characterisation of the spermosphere of the common bean seed (*Phaseolus vulgaris*). Journée annuelle des Jeunes Chercheuses et Chercheurs (JJC) 2023, Apr 2023, Clermont-Ferrand, France. hal-04528599

**HAL Id: hal-04528599**

**<https://hal.science/hal-04528599>**

Submitted on 1 Apr 2024

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

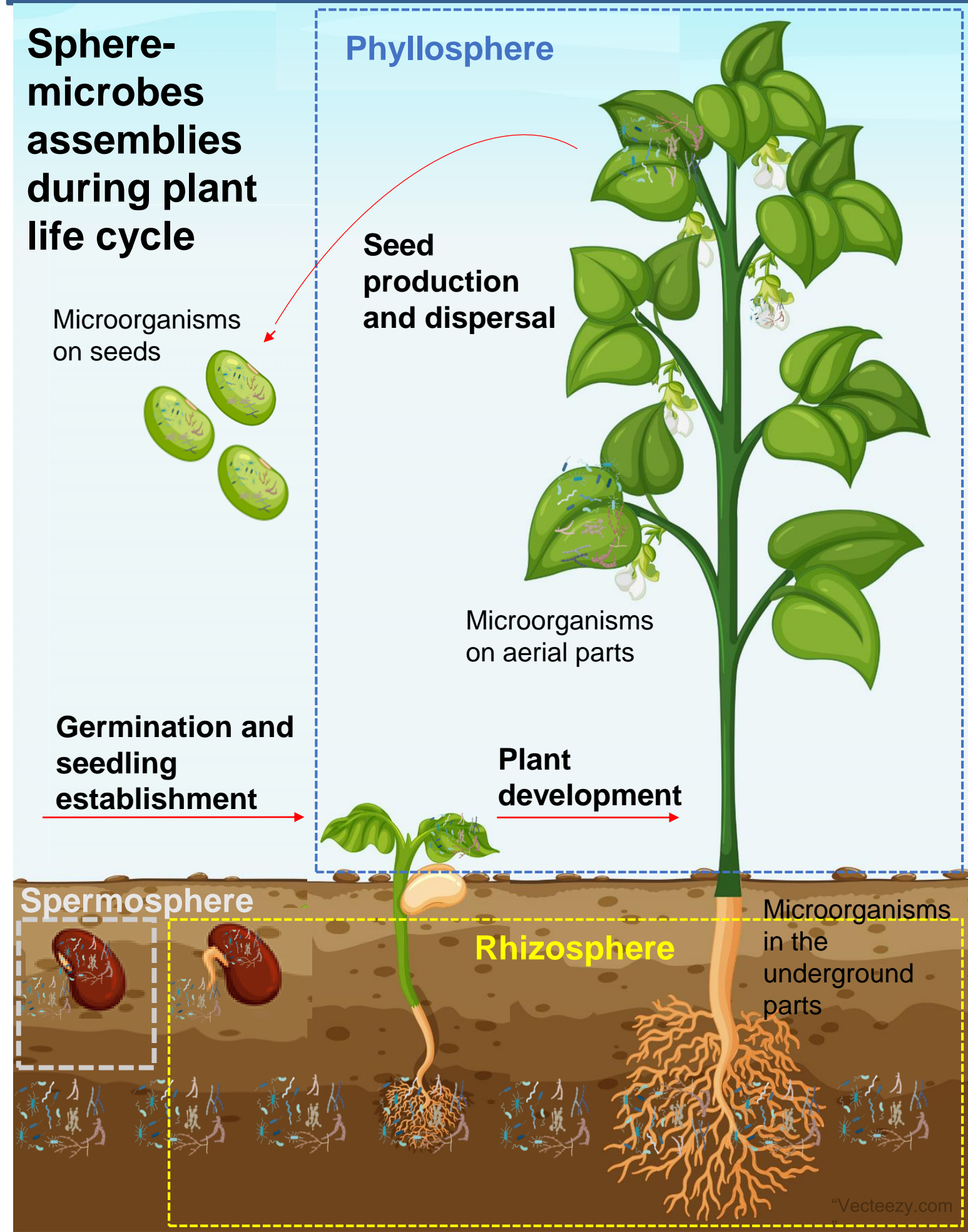
Public Domain

# Characterisation of the spermosphere of the common bean seed (*Phaseolus vulgaris*)

C.Saccaram<sup>1</sup>, M.Simonin<sup>2</sup>, S.Boutet<sup>1</sup>, C.Brosse<sup>1</sup>, T.Fran ois<sup>1</sup>, B.Collet<sup>1</sup>, J.Caius<sup>3</sup>, E.Delannoy<sup>3</sup>, B.Bernay<sup>4</sup>, M.Corso<sup>1</sup>, L.Rajjou<sup>1</sup>

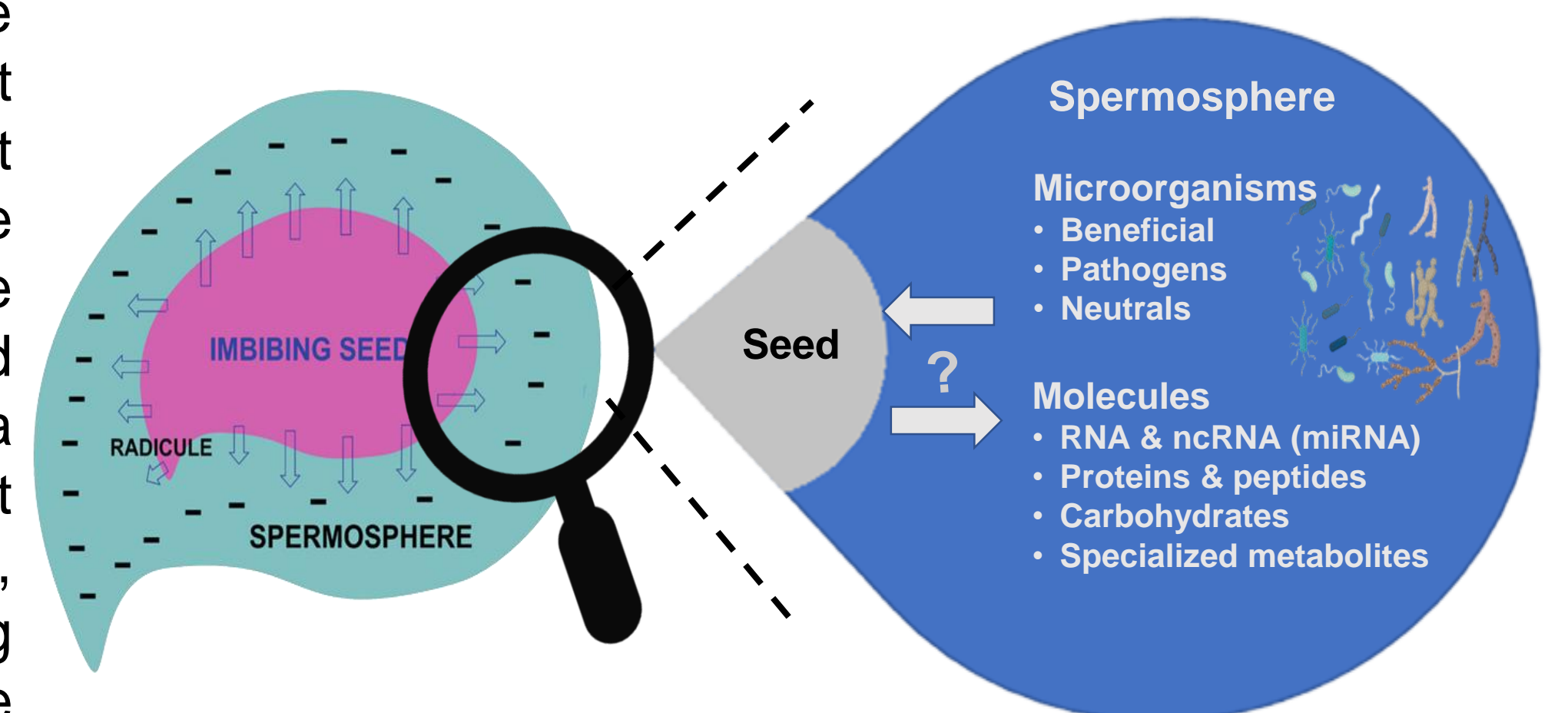
<sup>1</sup> Universit  Paris-Saclay, INRAE, AgroParisTech, Institut Jean-Pierre Bourgin (IJPB), 78000, Versailles, France  
<sup>2</sup> Institut de Recherche en Horticulture et Semences (IRHS), Universit  d'Angers, INRAE, Institut Agro, 49071 Beaucouz , France  
<sup>3</sup> Universit  Paris-Saclay, CNRS, INRAE, Univ Evry, Institute of Plant Sciences Paris-Saclay (IPS2), 91405, Orsay, France  
<sup>4</sup> PROTEOGEN Core Facility SF 4206 ICORE, UNICAEN, Esplanade de la Paix, 14032 Caen, France

## Introduction



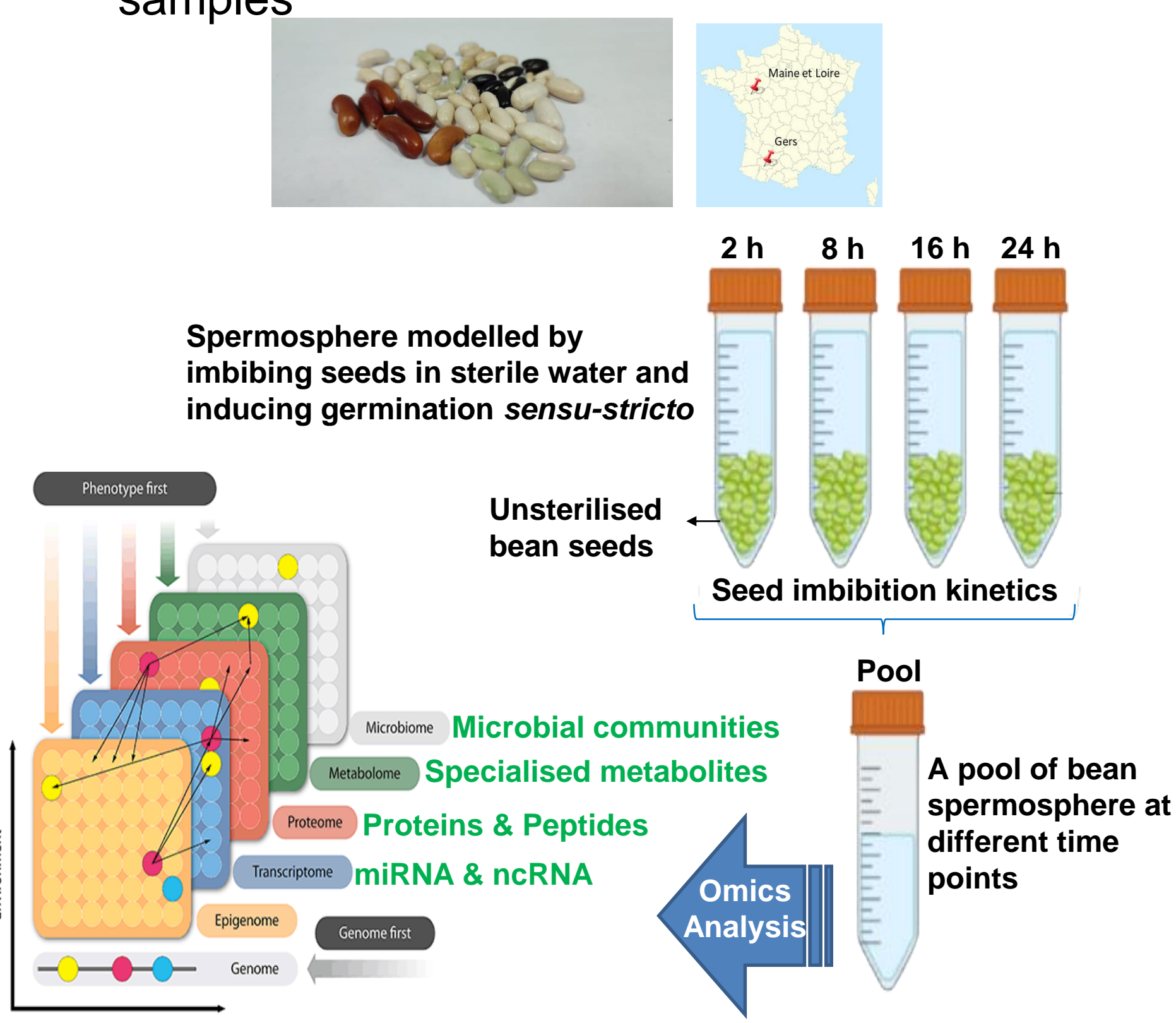
Seed plants have co-evolved with microorganisms by forming beneficial relationships in order to facilitate their adaptation to terrestrial lifestyle<sup>[1]</sup>. Indeed, more and more studies are demonstrating the inter-relationships of the microbiome and their hosts and the resulting impacts of such relationships in terms of the host's fitness, environmental response, adaptation and evolution<sup>[2]</sup>. These studies have given rise to a relatively new concept of the holobiont which views the host organism and its associated microbiota as a single functional unit, where evolutionary selection occurs between both the host and its microbiota, as well as among different microbial species within the microbiota<sup>[3]</sup>.

While plant microbiome in the phyllosphere and rhizosphere has been well studied, seed spermosphere and microbiome have remain relatively unnoticed<sup>[4]</sup>. Yet, seeds have an important distinctive function in the inheritance process by connecting plant generations and serving as a critical point in the continuity of the plant microbiome<sup>[4]</sup>. However, the fate of seed-borne microorganisms after germination is relatively unexplored. Seed germination, a transient process giving rise to a microenvironment known as the spermosphere, is a critical point for the establishment of the future plant microbiome. Indeed, seed exudation after imbibition is hypothesized to be the driving force for microbial selection, growth and interaction in the spermosphere<sup>[5]</sup>. The aim of this study is to characterize the germinating bean spermosphere with multi-omics technologies to understand the complex interactions between seed borne microorganisms and seed exudates.



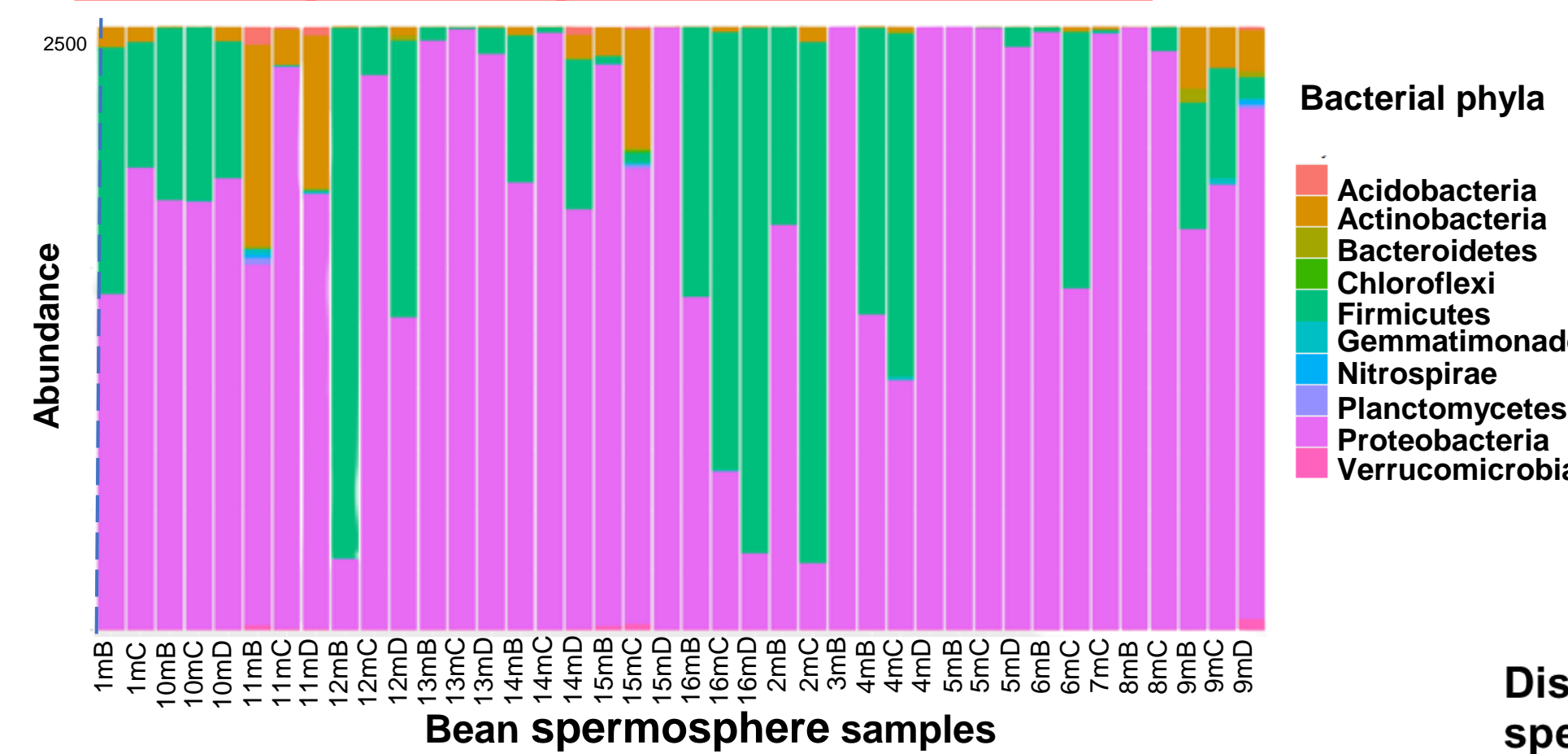
## Experimental design

- 8 different common bean (*Phaseolus vulgaris*) genotypes, cultivated in France, produced in 2 different locations were used in the experiment
- Bean genotypes were selected based on their contrasting phenotypes (germination vigor, size, colour, weight)
- Metabarcoding, untargeted metabolomics (LC-MS/MS), peptidomics and transcriptomics (smallRNAs) were carried out on spermosphere samples



## Results

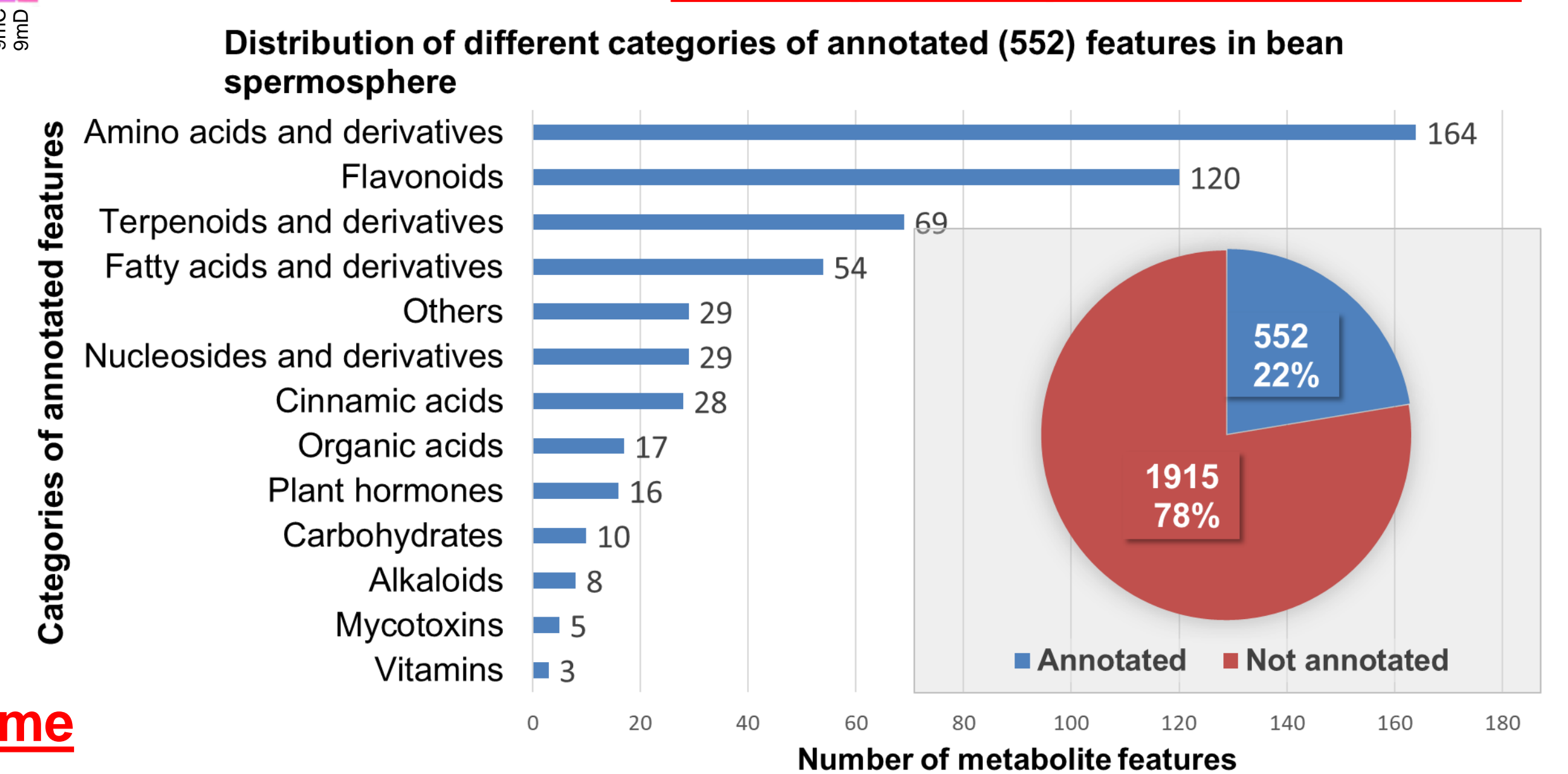
### Bean spermosphere microbiome



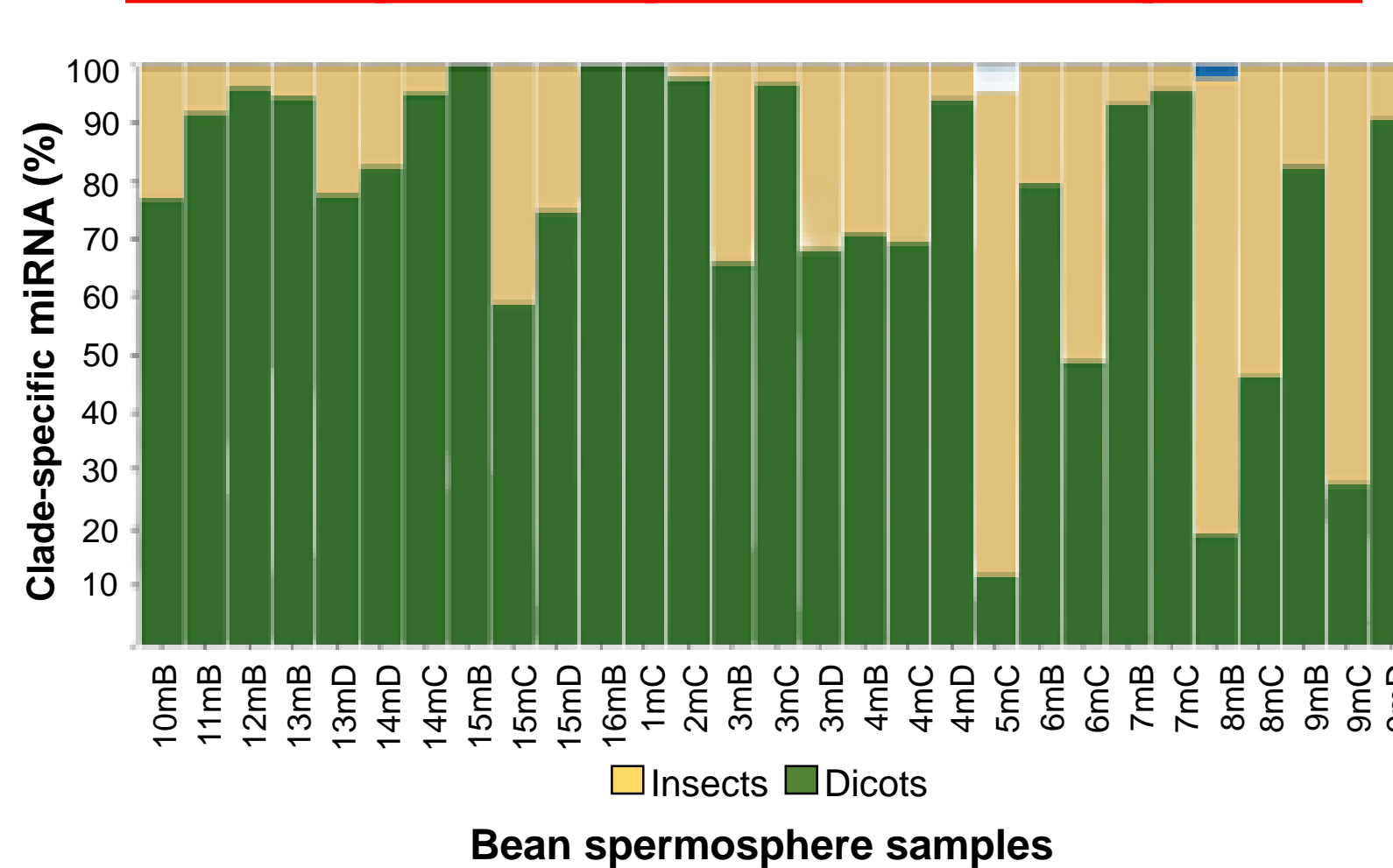
- 2467 metabolite features
- Metabolite annotation using metabolomic libraries and bio-informatic tool MetGEM based on clustering methods using spectral fragmentation
- Genotype is the major effect driving metabolite accumulation (results not shown)

- 10 identified bacterial phyla
- Ascomycota & Basidiomycota (not shown) only identified fungal phyla
- Genotype is the major effect driving bacterial communities
- Environment of seed production is the major effect driving fungal communities (results not shown)

### Bean spermosphere metabolome



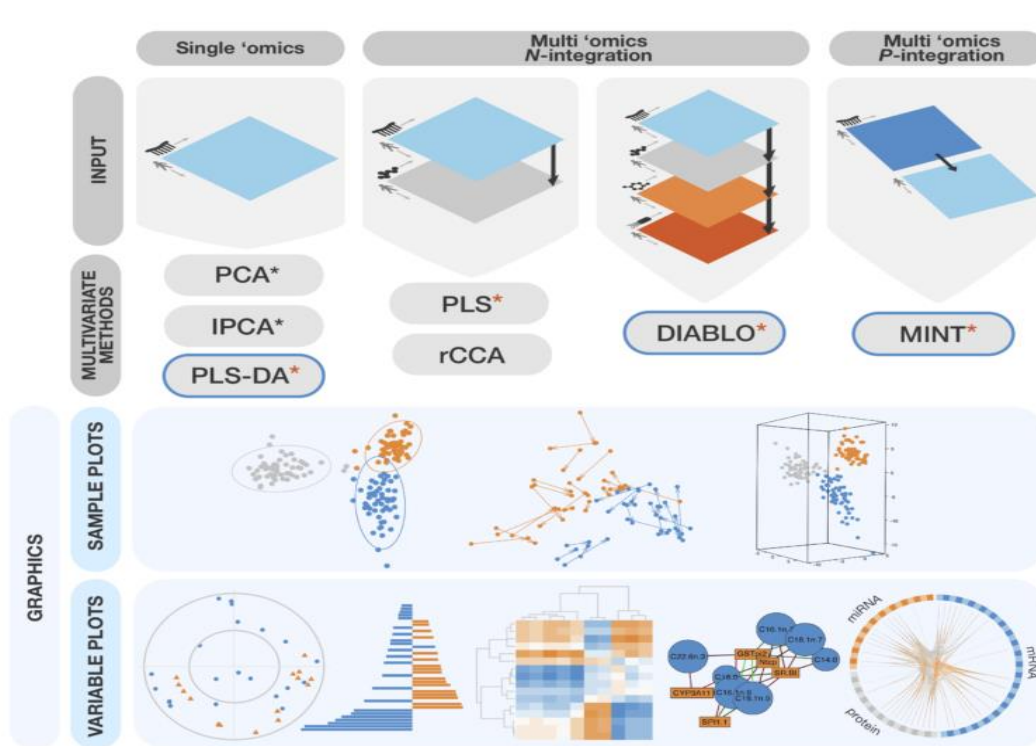
### Bean spermosphere transcriptome



- Small Non Coding RNAs: Ribosomal RNAs (rRNA), Transfer RNAs (tRNAs) and Micro RNAs (miRNAs)
- 15 to 25 nucleotides long (results not shown)
- rRNAs most abundant (>80%) while miRNAs least abundant (<5%)
  - 14 miRNA families from common bean
  - 8 miRNA families from insects

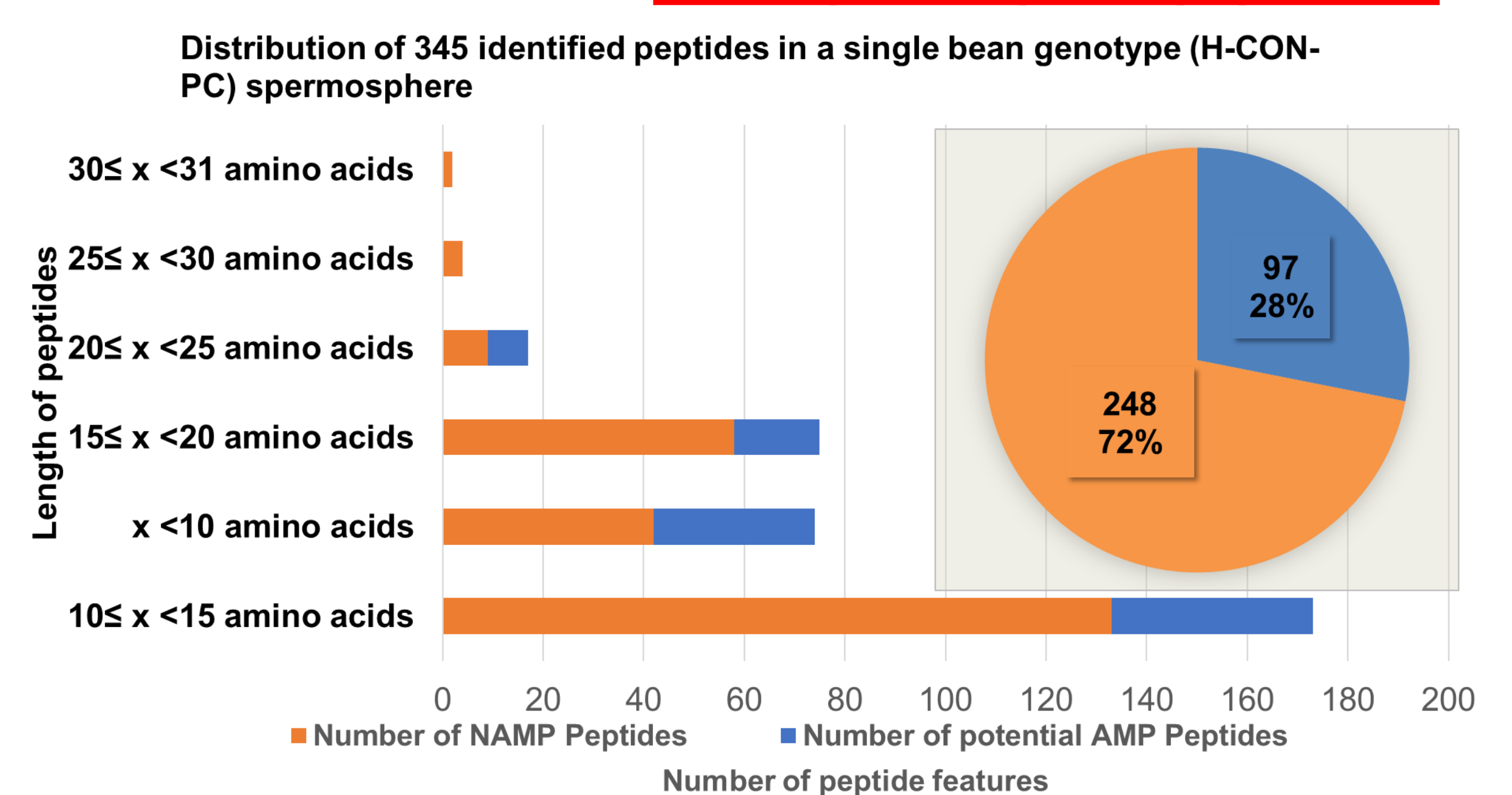
## Future perspectives

- Integration of multi-omics<sup>[7]</sup> data to identify correlations between spermosphere molecules and macromolecules and microbiome



- Development of biobased alternatives to synthetic pesticides to protect and stimulate seeds in a context of agro-ecological transition

### Bean spermosphere peptidome



- 345 peptides from 1 bean genotype (H-CON-PC)
- Peptide lengths: 7 to 32 amino acids
- Most abundant: categories of 10 to 20 amino acids
- Anti-microbial peptides (AMPs) predicted using 4 different prediction models.
  - 3 AMPs were identified by all 4 models

## Contact

Chandrodhay Saccaram  
 Institut Jean Pierre Bourgin (IJPB)  
 INRAE  
 Email: chandrodhay.saccaram@inrae.fr



## References

1. Delaux PM, Schornack S. Plant evolution driven by interactions with symbiotic and pathogenic microbes. *Science*. 2021
2. Singh BK, Trivedi P, Egidi E, Macdonald CA, Delgado-Baquerizo M. Crop microbiome and sustainable agriculture. *Nat Rev Microbiol*. 2020
3. Rosenberg E, Zilber-Rosenberg I. Microbes Drive Evolution of Animals and Plants: the Hologenome Concept. *mBio*. 2016
4. Abdelfattah A, Tack AJM, Lobato C, Wassermann B, Berg G. From seed to seed: the role of microbial inheritance in the assembly of the plant microbiome. *Trends Microbiol*. 2022
5. Nelson, E.B. The seed microbiome: Origins, interactions, and impacts. *Plant Soil* 422, 7–34 (2018).
6. Hasin Y, Seldin M, Lusi A. Multi-omics approaches to disease. *Genome Biol*. 2017
7. Rohart F, Gautier B, Singh A, L  Cao KA. mixOmics: An R package for 'omics feature selection and multiple data integration. *PLoS Comput Biol*. 2017