



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

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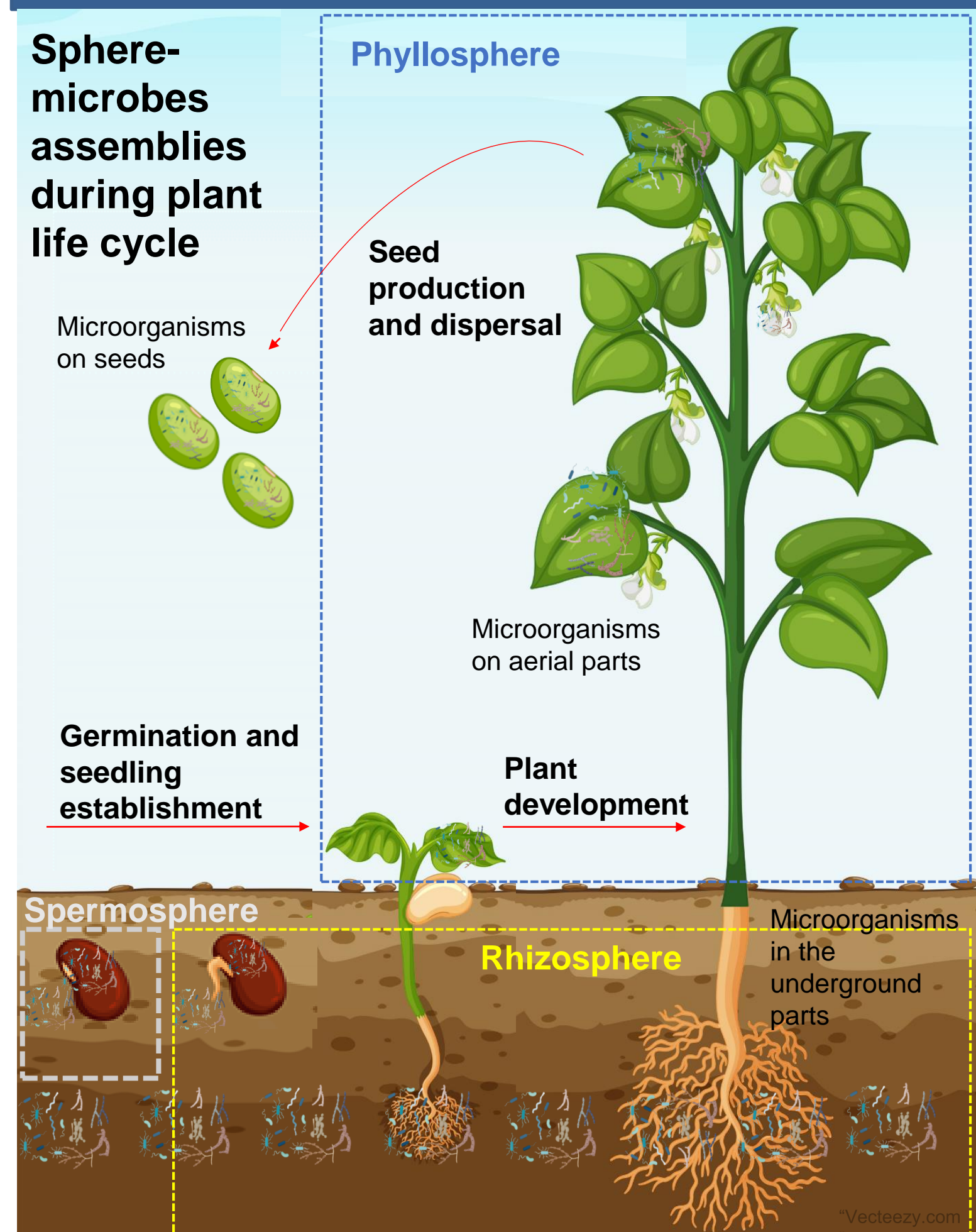
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Characterisation of the spermosphere of the common bean seed (*Phaseolus vulgaris*)

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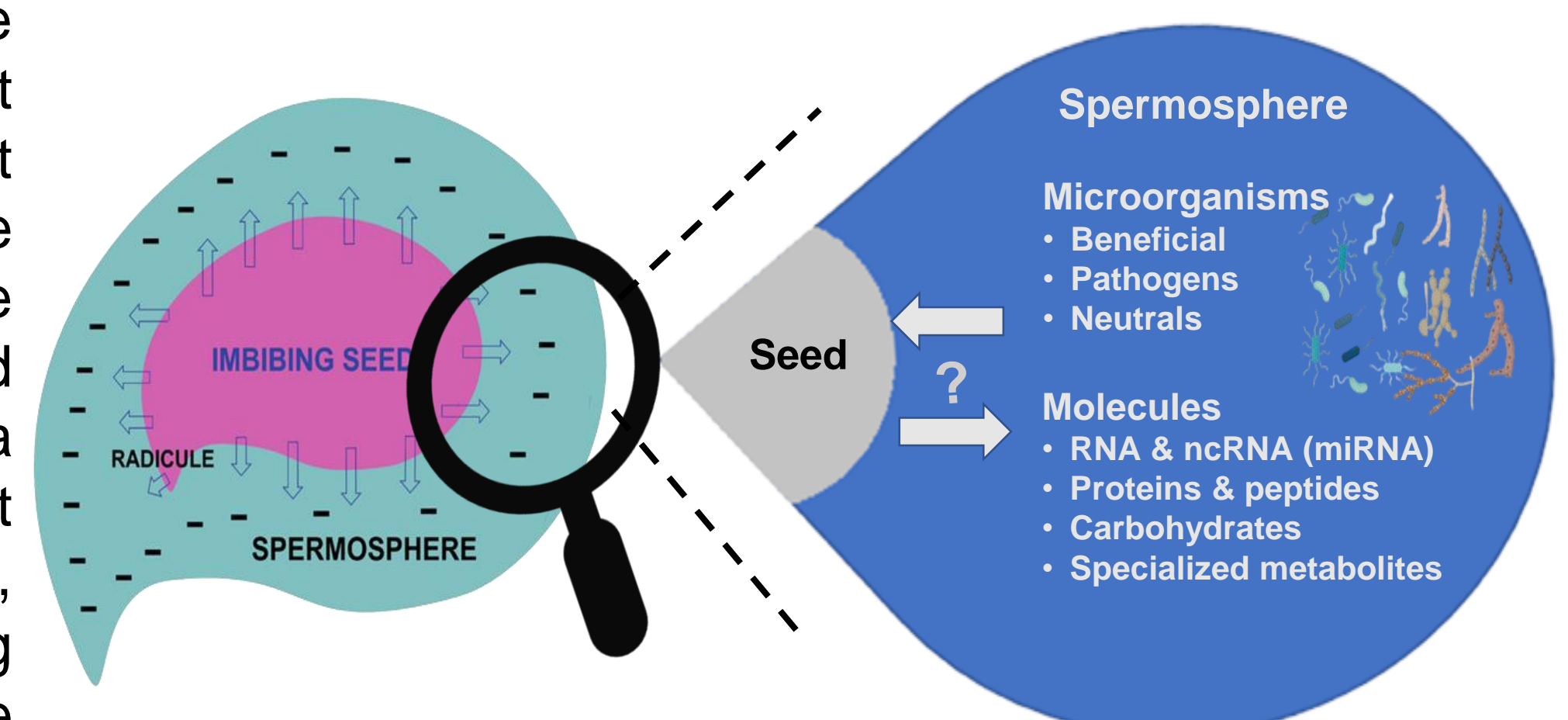
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Introduction



Seed plants have co-evolved with microorganisms by forming beneficial relationships in order to facilitate their adaptation to terrestrial lifestyle^[1]. 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^[2]. 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^[3].

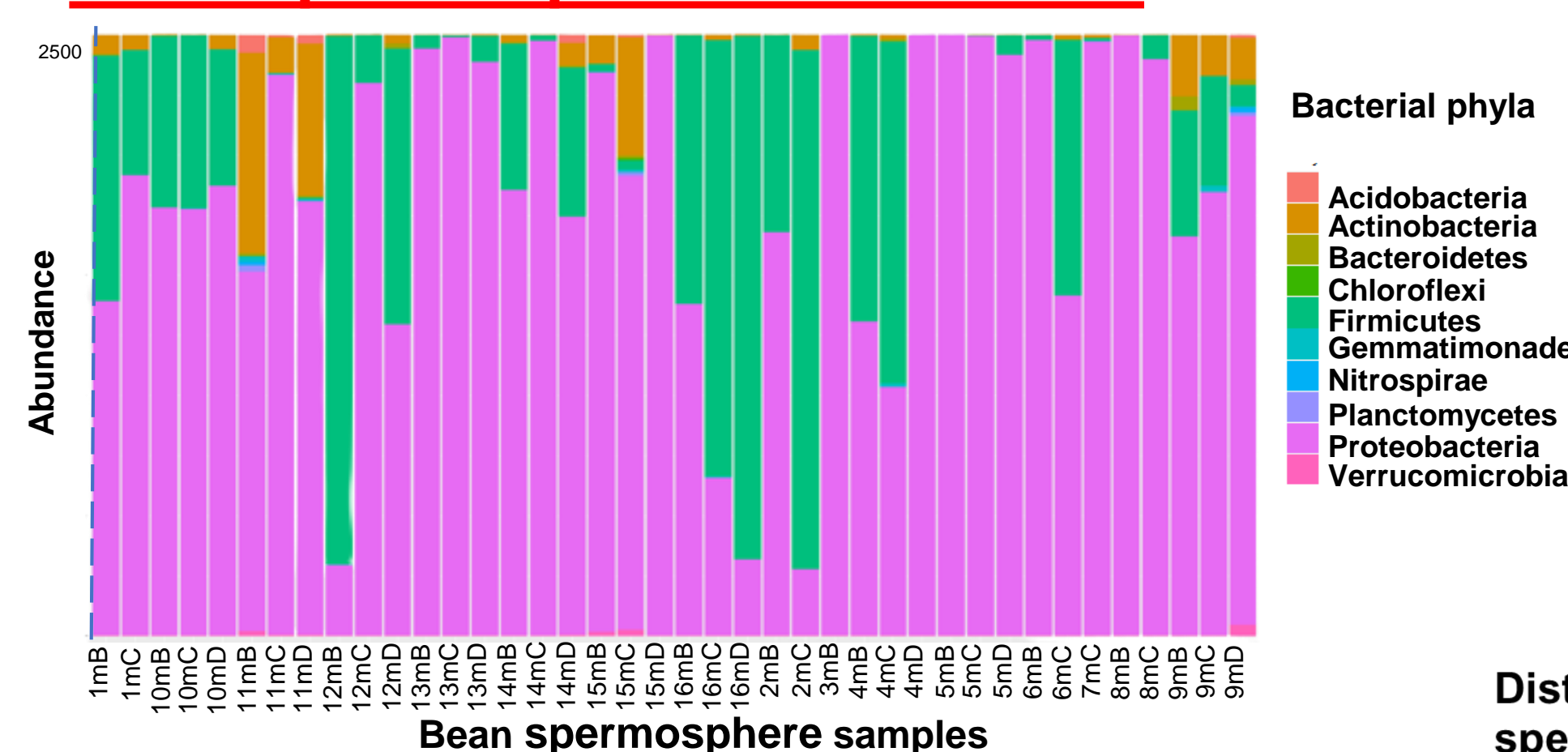
While plant microbiome in the phyllosphere and rhizosphere has been well studied, seed spermosphere and microbiome have remain relatively unnoticed^[4]. Yet, seeds have an important distinctive function in the inheritance process by connecting plant generations and serving as a critical point in the continuity of the plant microbiome^[4]. 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^[5]. 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

Bean spermosphere microbiome

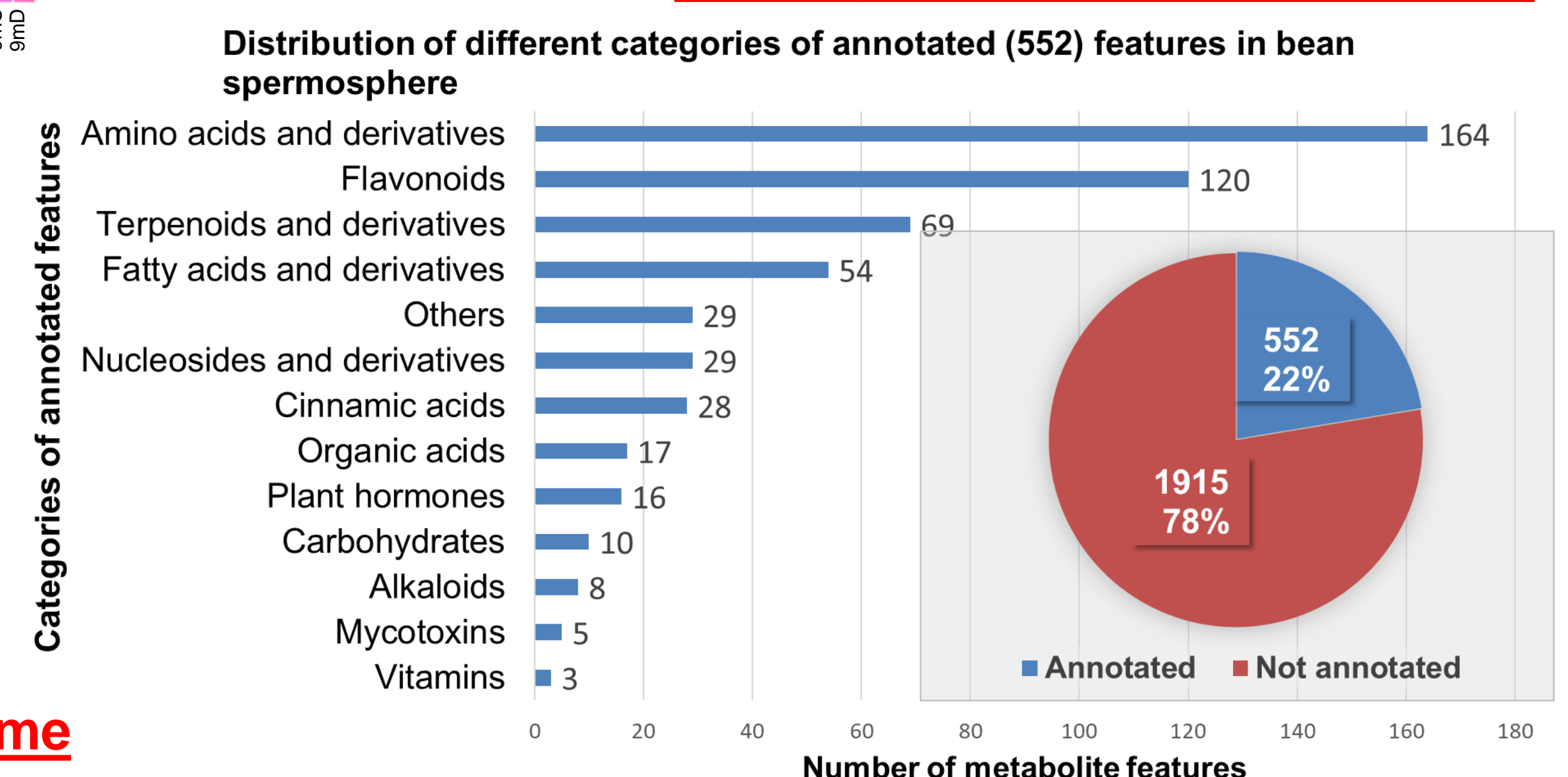


- 2467 metabolite features
- Metabolite annotation using metabolomic libraries and bio-informatic tool MetGEM based on clustering methods using spectral fragmentation
- Genotype is the major effect driving metabolite accumulation (results not shown)

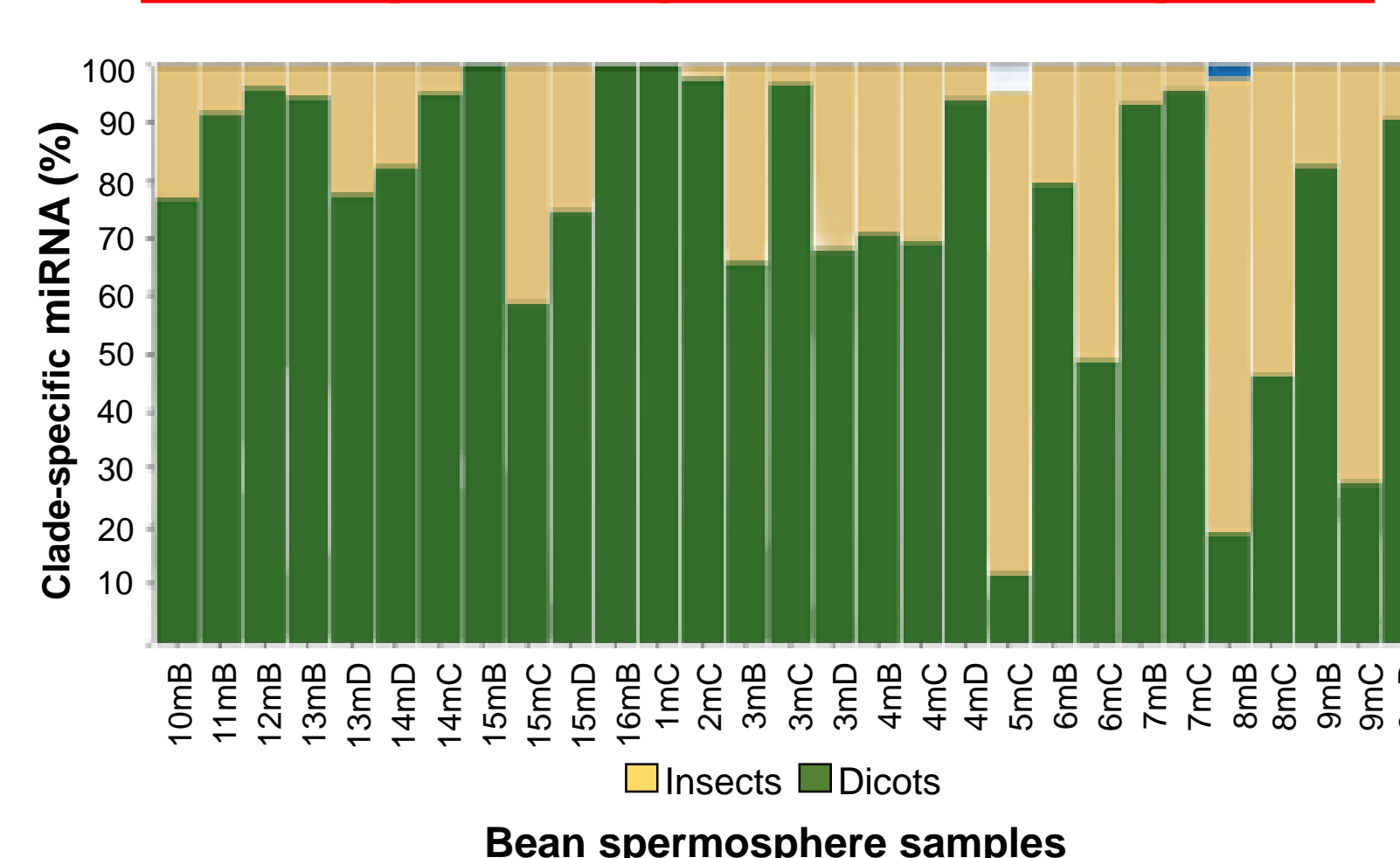
Results

- 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

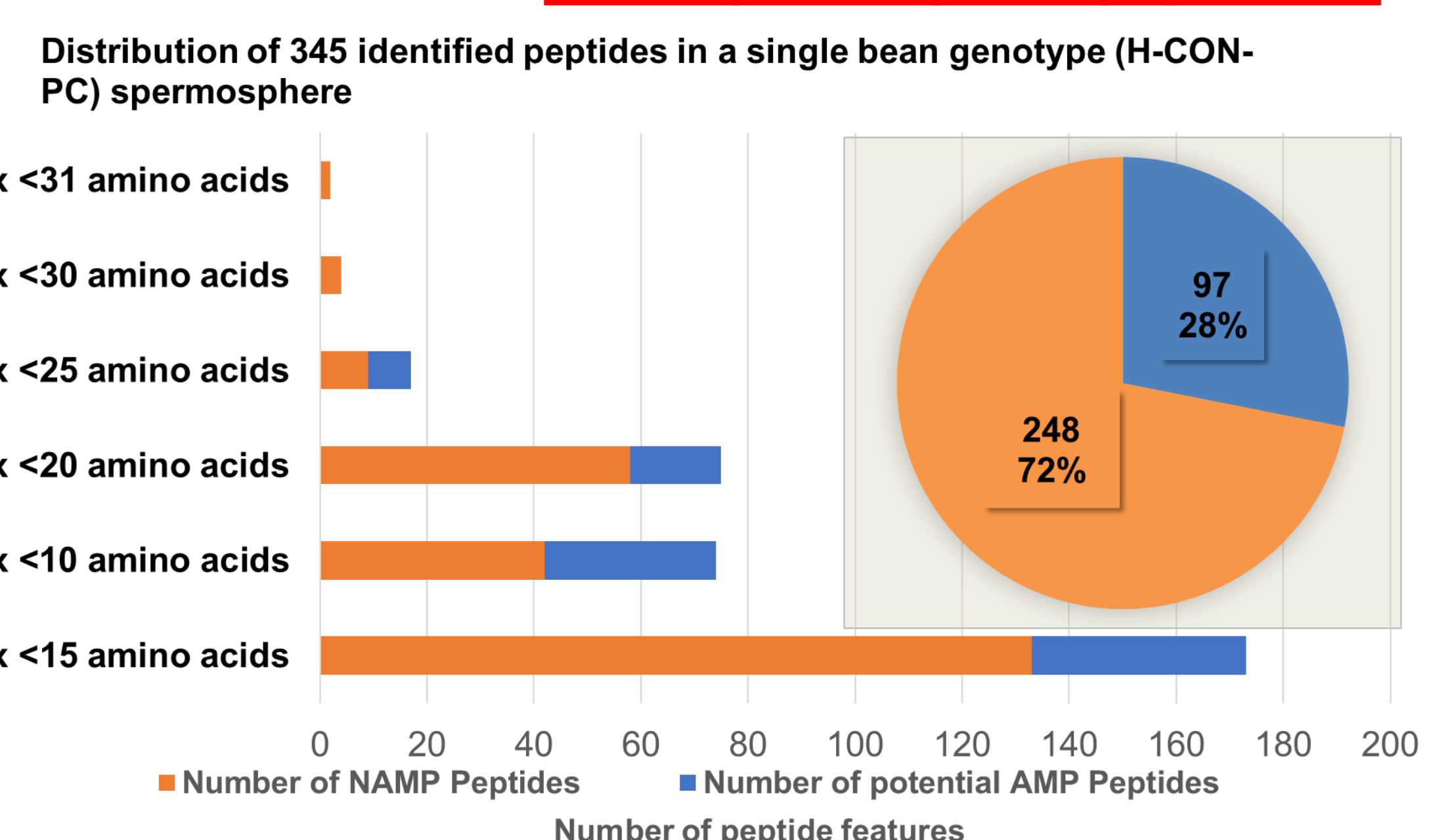


Bean spermosphere transcriptome



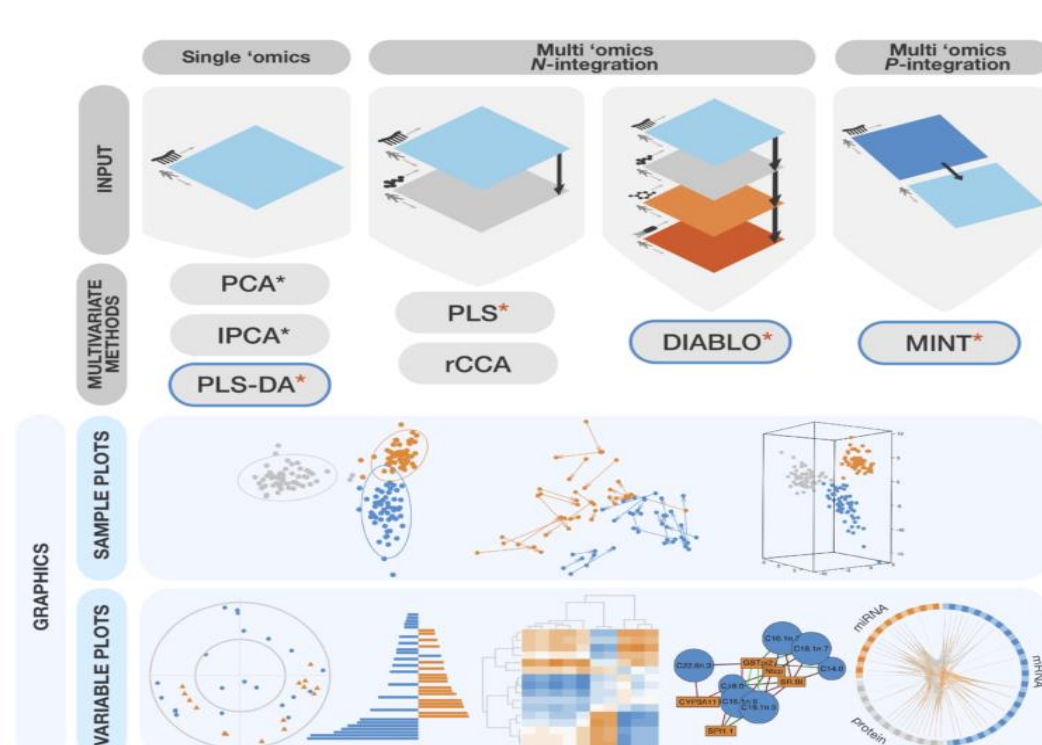
- Small Non Coding RNAs: Ribosomal RNAs (rRNA), Transfer RNAs (tRNAs) and Micro RNAs (miRNAs)
- 15 to 25 nucleotides long (results not shown)
- rRNAs most abundant (>80%) while miRNAs least abundant (<5%)
 - 14 miRNA families from common bean
 - 8 miRNA families from insects

Bean spermosphere peptidome



Future perspectives

- Integration of multi-omics^[7] 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

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