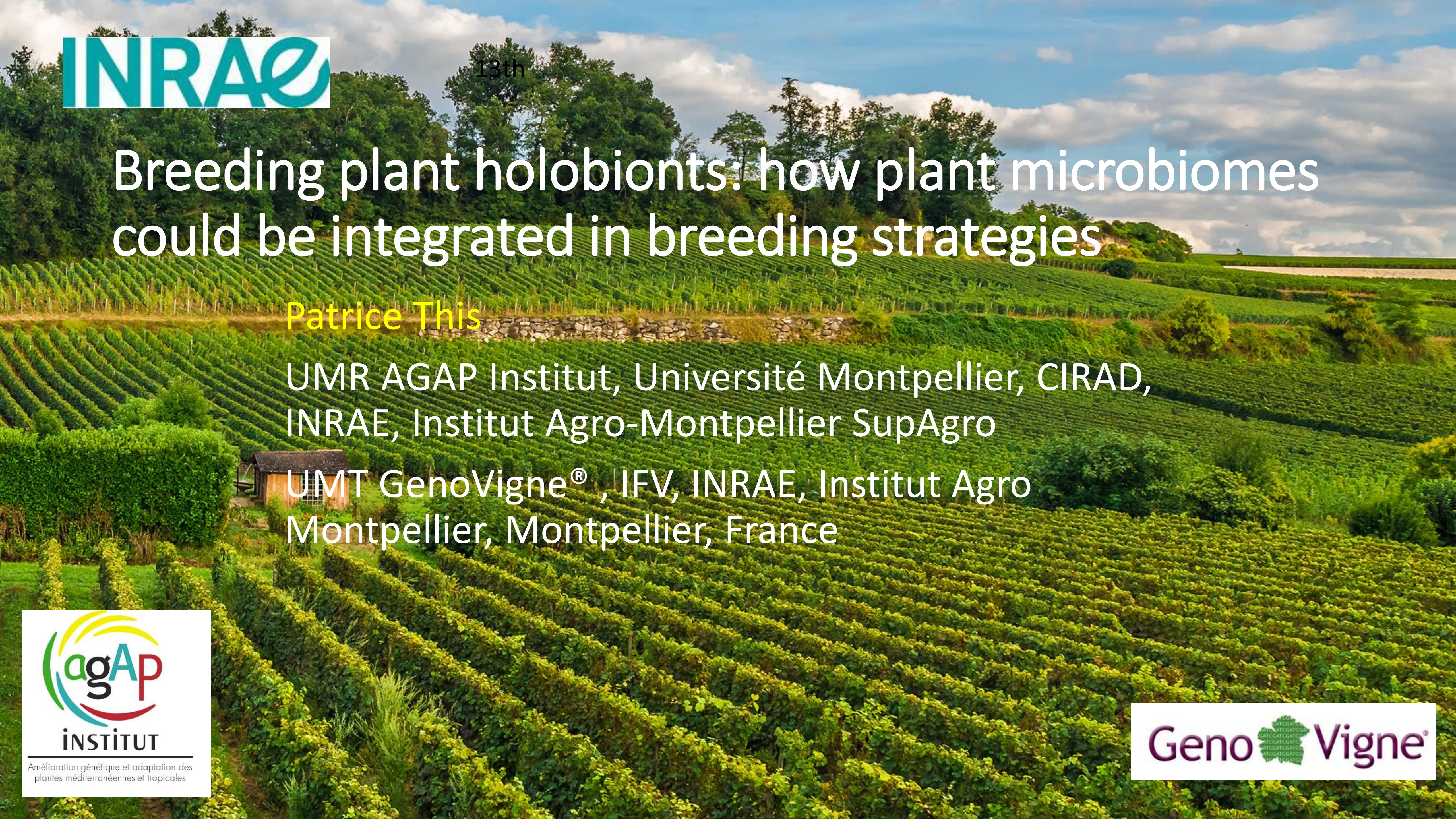


13th

Breeding plant holobionts: how plant microbiomes could be integrated in breeding strategies

Patrice This

UMR AGAP Institut, Université Montpellier, CIRAD, INRAE, Institut Agro-Montpellier SupAgro

UMT GenoVigne® , IFV, INRAE, Institut Agro Montpellier, Montpellier, France

INSTITUT
Amélioration génétique et adaptation des plantes méditerranéennes et tropicales

The Holobionte and the microbiome

- **Animals and plants** are no longer viewed as autonomous entities, but rather **as "holobionts"** composed of the **host plus all of its symbiotic microbes**
- As such, their **collective genomes forge a "hologenome,"** and models of animal and plant biology that do not account for these intergenomic associations are incomplete

(Bordenstein & Theis 2015)

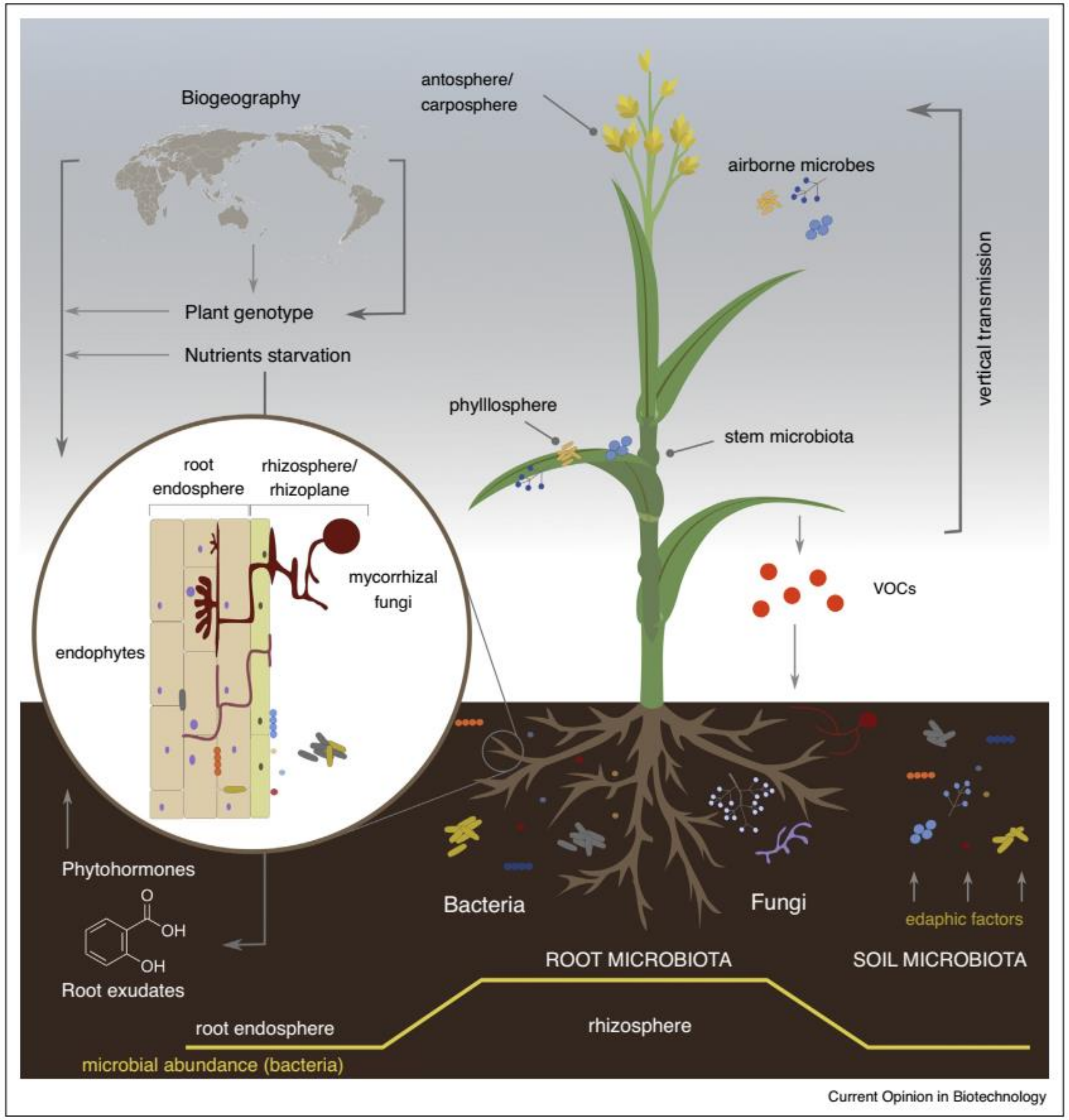
The Holobionte and the microbiome

- **microbiome** is the collective name for the **ecological communities** that **live on, in or near an organism**, including pathogenic, commensal and symbiotic partners

The microbiome

Plants are hosts to different microbiotas on various tissues (roots, leaves, seeds, stems, flowers), which represent
specific niches characterized by distinct chemical and physical properties

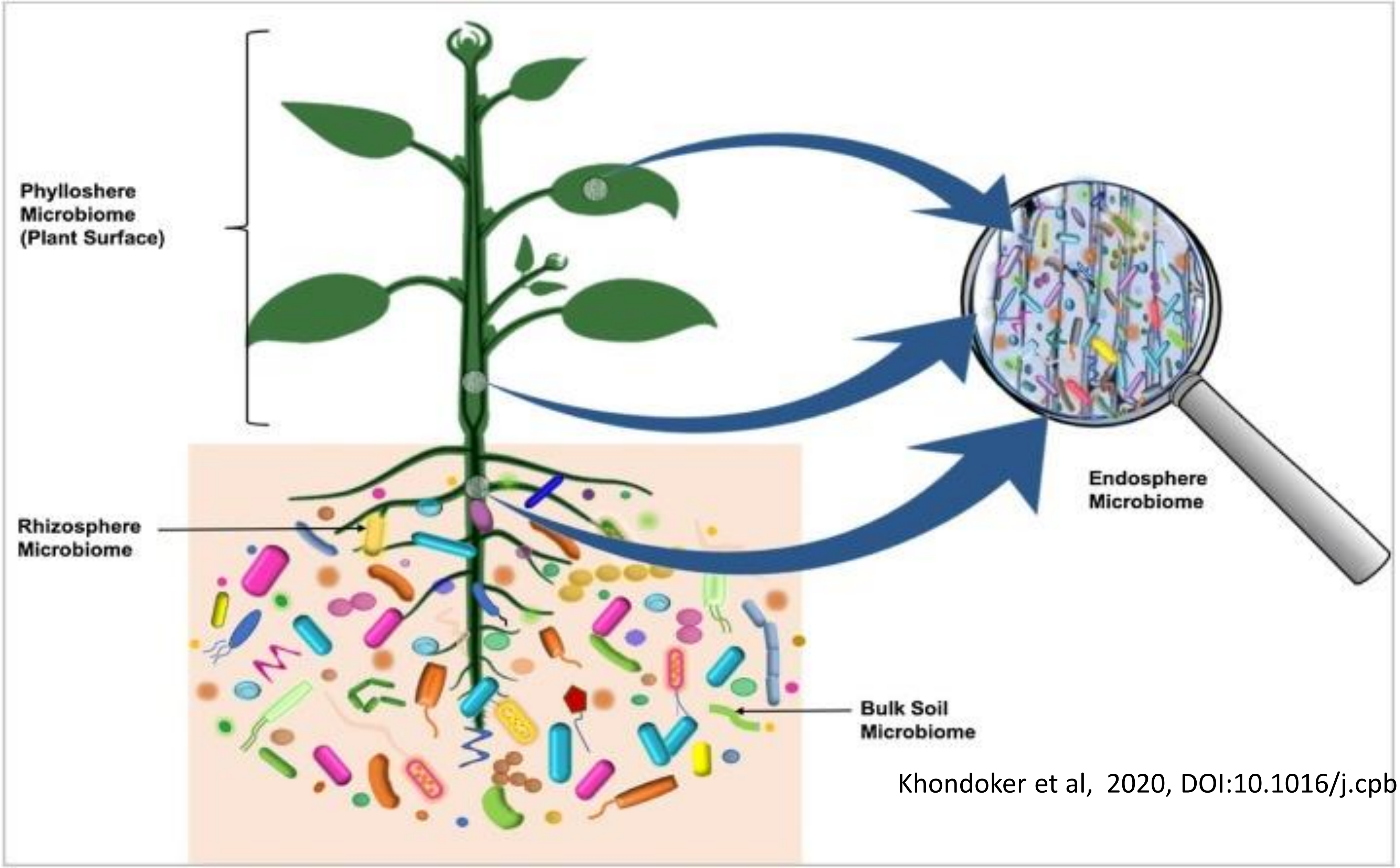
Figure 1 From Chiala et al, 2022



Scheme summarizing the main factors shaping plant-associated microbiota along the different host compartments. Plant-associated microbes are mainly recruited from the soil, by vertical transmission through seeds and by airborne microbes. VOCs. Volatile Organic Compounds.

Current Opinion in Biotechnology 2022, **73**:135–142 www.sciencedirect.com

The different components of the microbiome



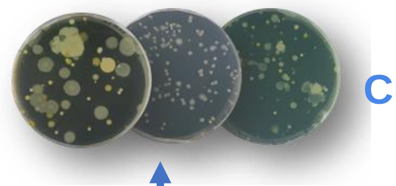
Khondoker et al, 2020, DOI:10.1016/j.cpb.2020.100161

How to analyse the microbiome ?

How do we analyse the microbiome ?

- **The Culture dependent approach**

Soil washing, organ extract, solution of washing

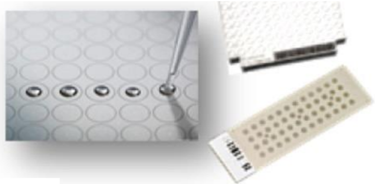


Culturing

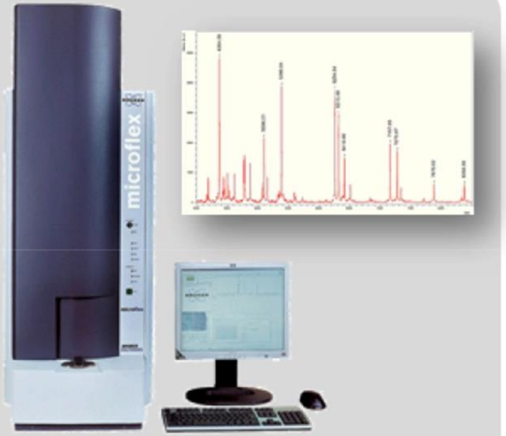
Subculturing

Colony for bacteria identification

Direct smear on target



MALDI target

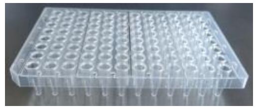


Spectra acquisition and microorganism identification

Microorganism NOT identified

Microorganism identified

DNA extraction + PCR (ITS for fungi, 26S for yeast, 16S for bacteria)



Sanger sequencing

Adapted from Hou et al, 2019 & Fournier et al, 202

How do we analyse the microbiome ?

- **The Culture independent approaches : Metabarcoding**

DNA Extraction → PCR Amplification → Sequencing

Soil → **Soil microbiota**

complete organ (Seed, wood, leave, root, …) → **Epiphytic microbiota**

washing → **Endophytic microbiota**

→ PCR on ITS (for fungi) / PCR on 16S (for bacteria) → NextSeq 2000 sequencing → Bioinformatics

Adapted from Fournier et al, 2022

How do we analyse the microbiome ?

- **The Culture independent approaches : Metabarcoding**

Bioinformatics → Data analysis

NextSeq 2000 sequencing → abundance tables of microbial Operational Taxonomic Units (OTUs) or Amplicon Sequence Variants (ASVs) in samples

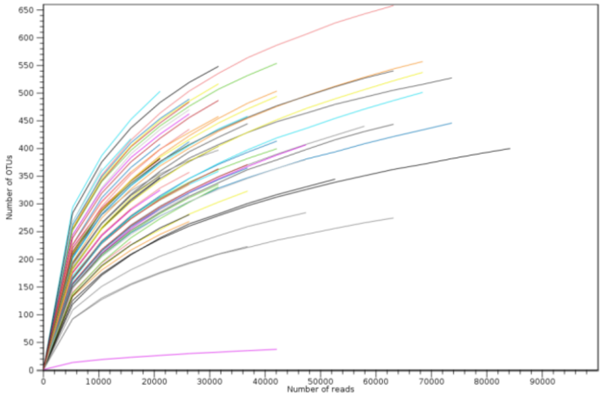


Figure (5) Rarefaction curves.

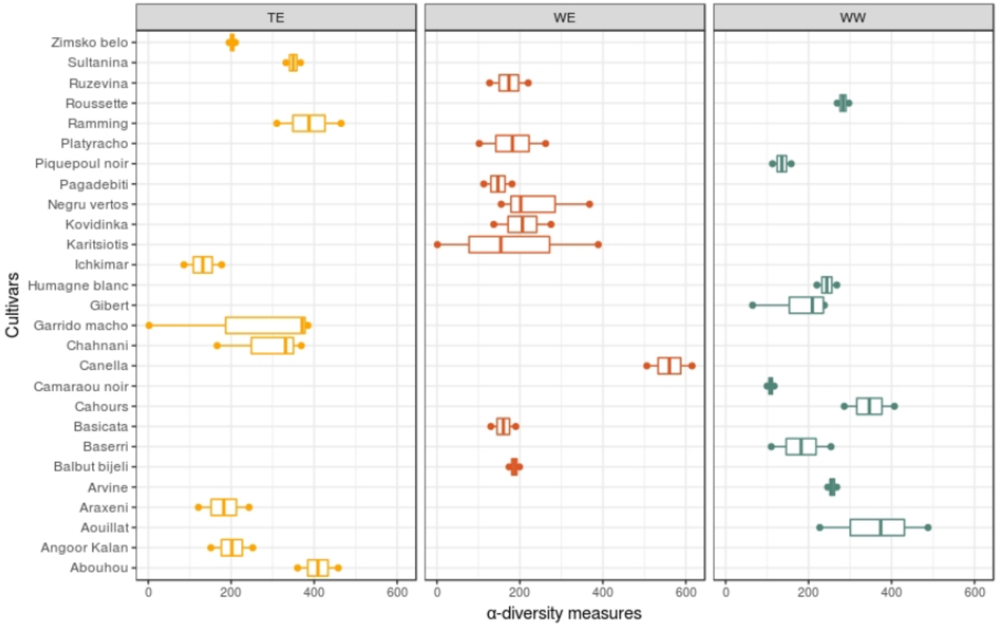


Figure (10) estimates of alpha diversity, **Genetic Pool**: at F = 0.623, P = 0.5; **Cultivar**: at F = 2.1, P = 0.02*

How do we analyse the microbiome ?

- **The Culture independent approaches : Metabarcoding**

Bioinformatics

Data analysis

NextSeq 2000 sequencing → abundance tables of microbial Operational Taxonomic Units (OTUs) or Amplicon Sequence Variants (ASVs) in samples

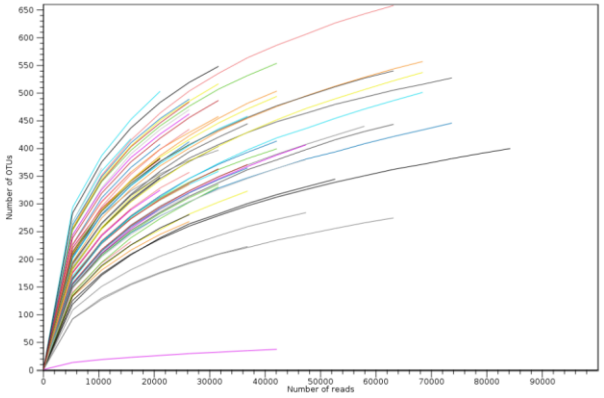


Figure (5) Rarefaction curves.

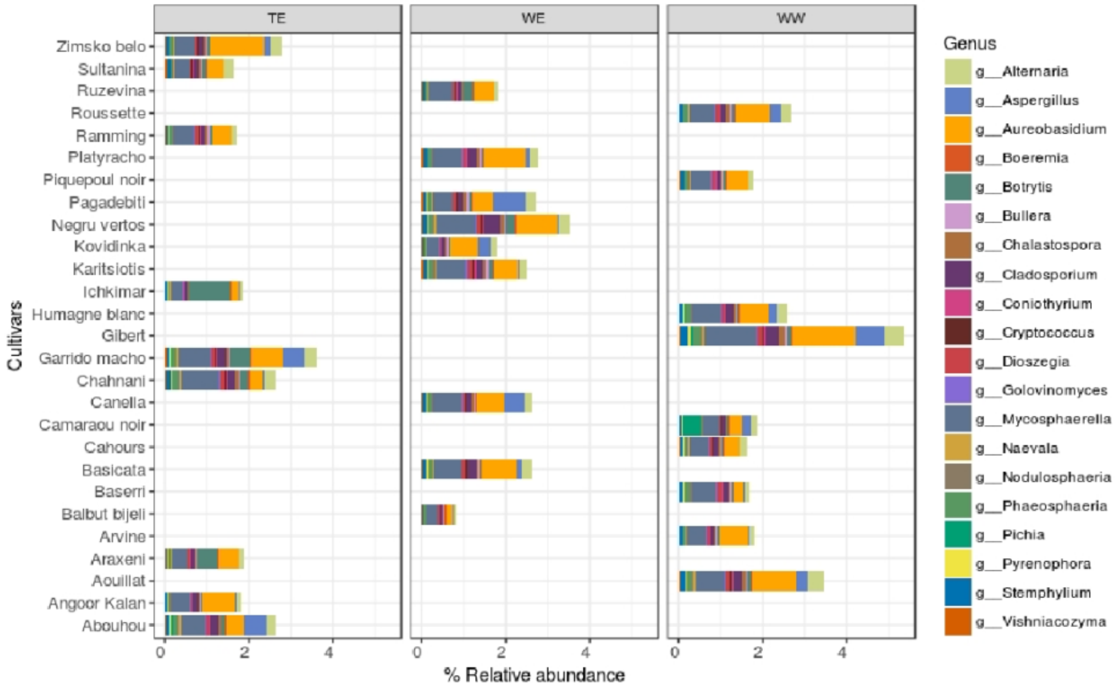


Figure (12) Fungal relative abundances(top 20 taxa)

How do we analyse the microbiome ?

- **The Culture independent approaches : Shotgun Metagomics**

DNA Extraction → Sequencing → Bioinformatics

Soil → **Soil microbiota**

complete organ (Seed, wood, leave, root, …) → **Epiphytic microbiota**

washing → **Endophytic microbiota**

→ Pacbio, Nonopore sequencing → Alignment to reference genomes

=> Contigs and metagenome assembled genomes

Adapted from Fournier et al, 2022

How do we analyse the microbiome ?

- **Other studies :**
  - **qPCR for more accurate quantification**
  - **Metatranscriptomics**
  - **Metabolomics**

How do we analyse the microbiome ?

- **Comparing the different methods**

- **Culture independent methods,** revea
  methods since a large part of the mic

=> development of new media culture t

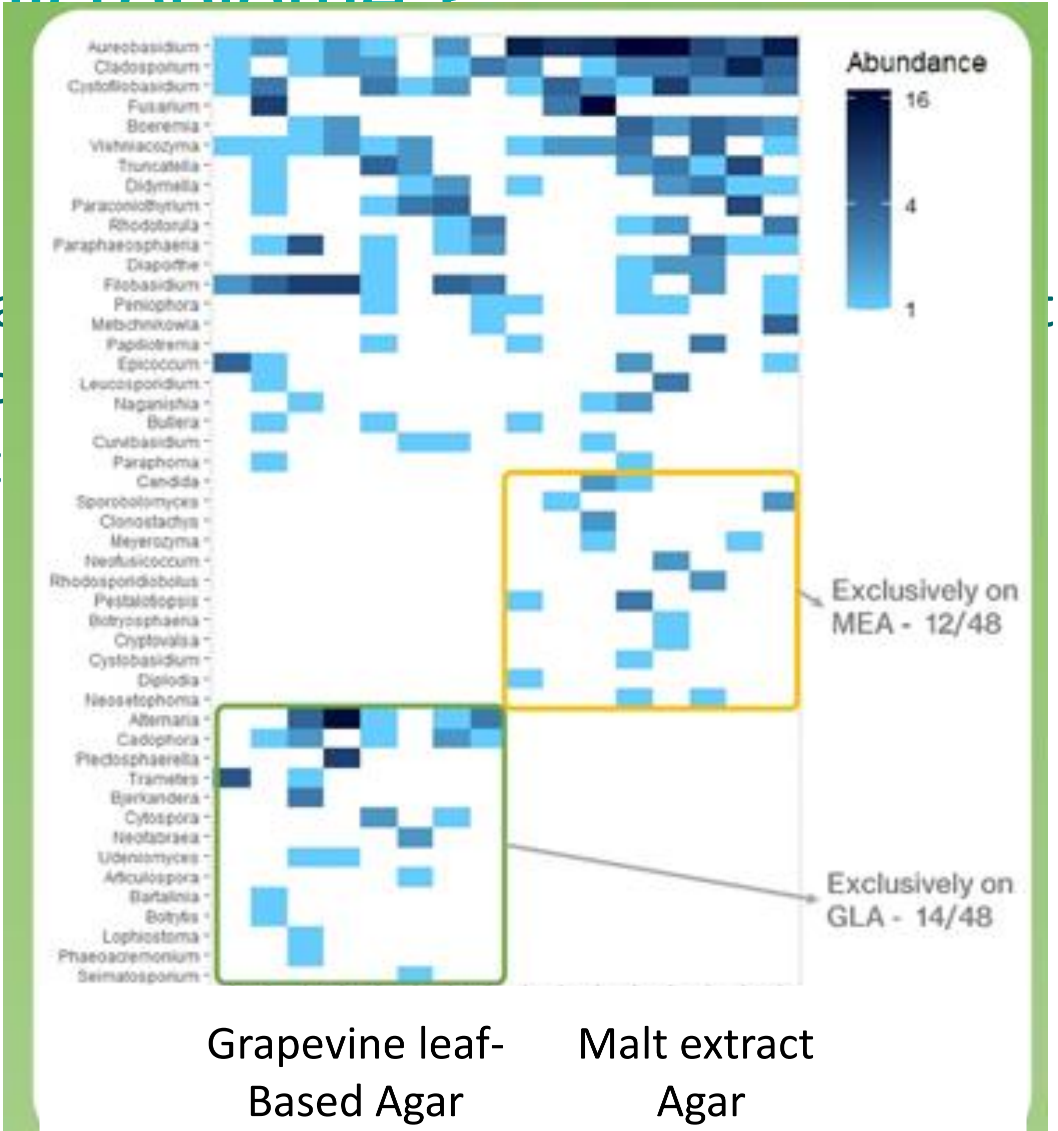


Fig.2: Filamentous fungi and yeast genera (n = 48) identified by Sanger sequencing on 2 media (GLA and MEA)

Adapted from Jaswa et al, 2023

How do we analyse the microbiome ?

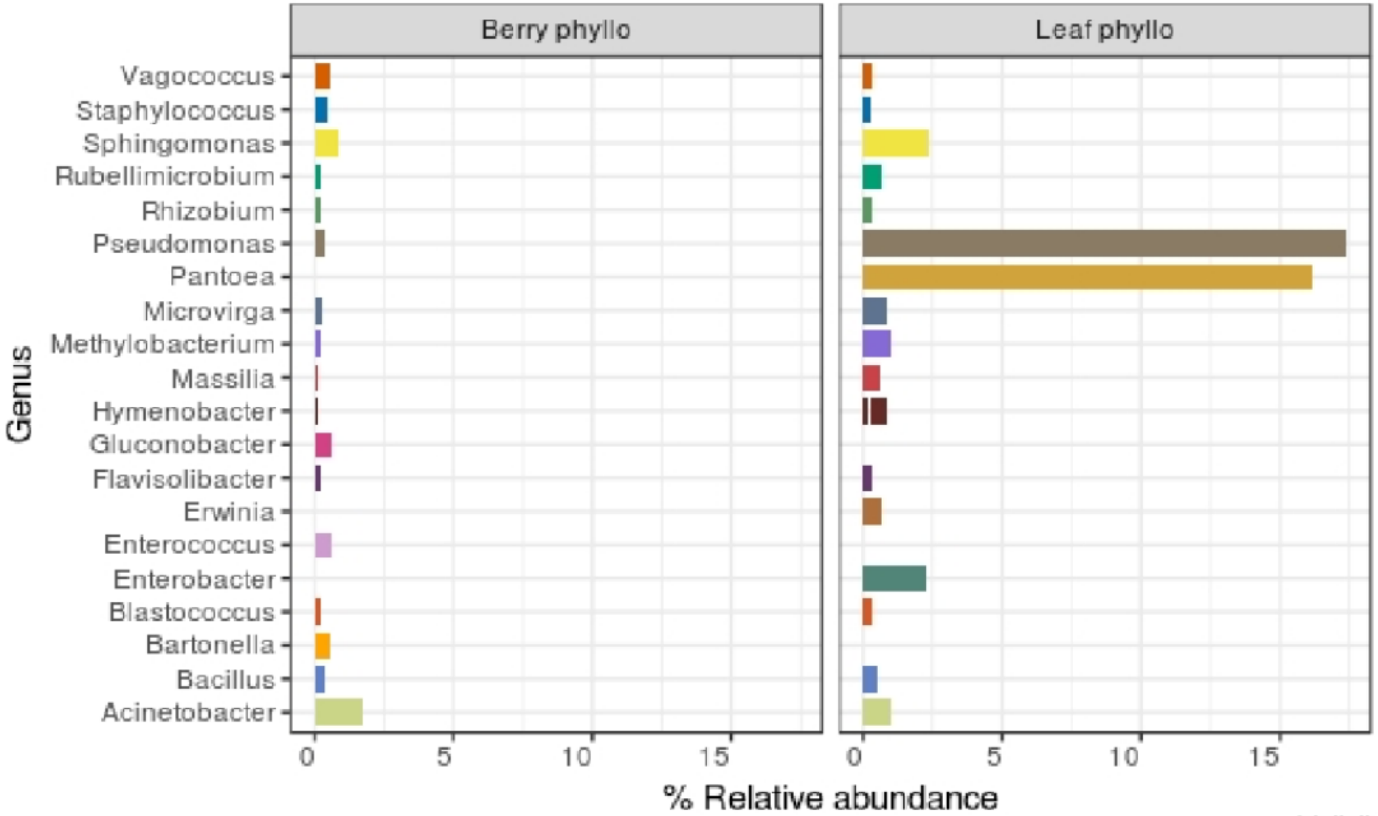
- **Comparing the different methods**

- **Culture independent methods,** reveal more diversity than culture dependent methods since a large part of the microbia cannot be cultivated

⇒development of new media culture to cultivate more micro-organisms

- Microbiota revealed by **Culture independent methods** will not always be further analyzed to confirm their action.

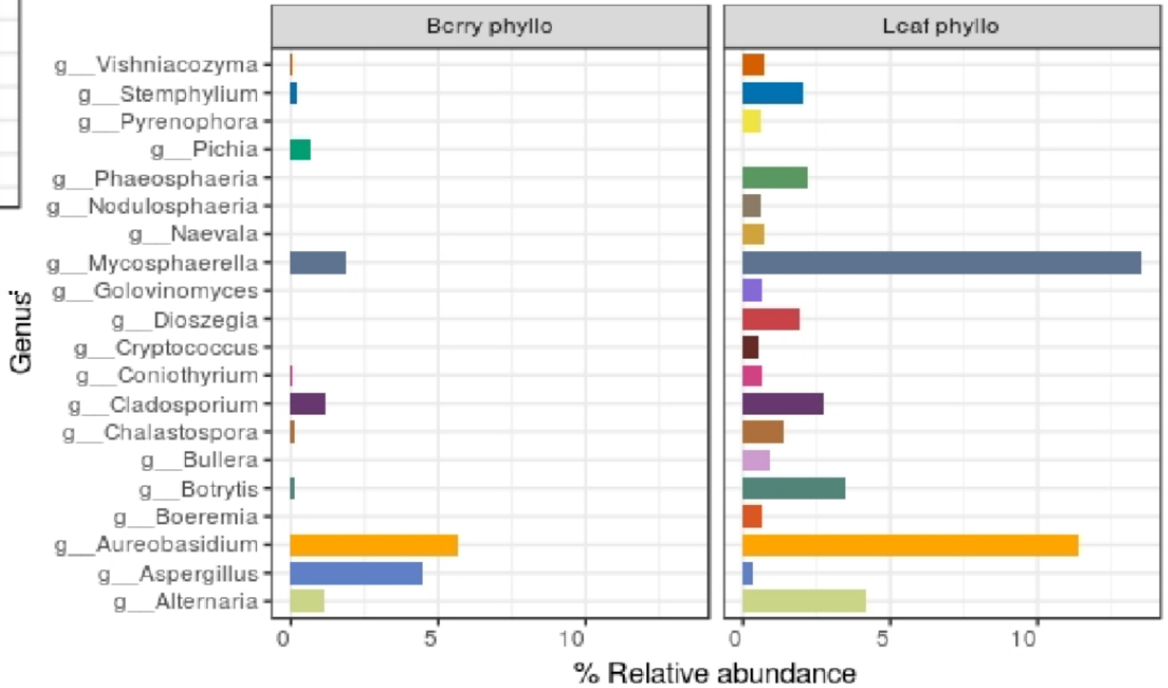
The microbiome diversity : Example, the phyllosphere



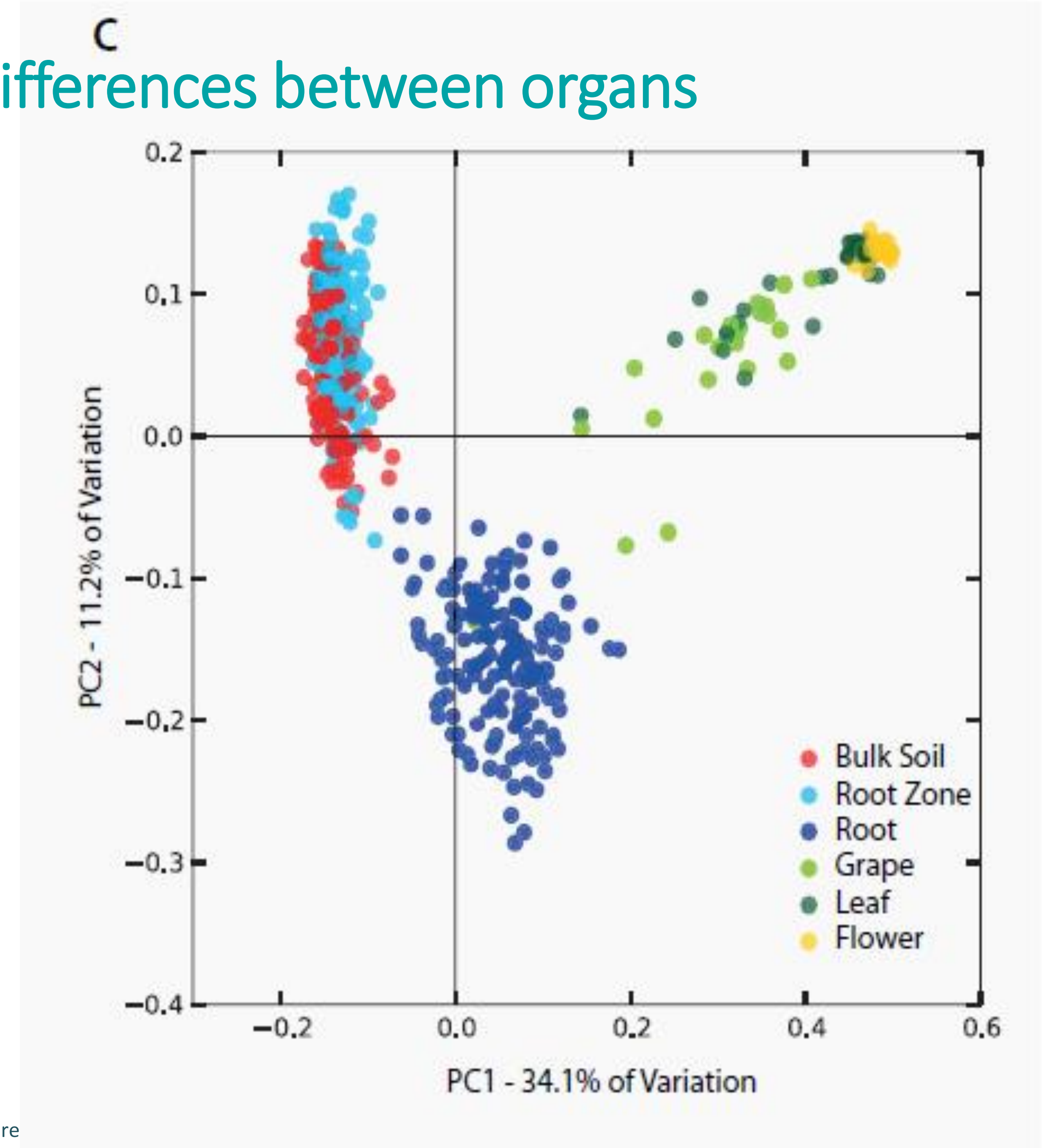
Bacterial relative abondance

From Prashant Singh PHD

Fungal relative abondance



The microbiome diversity : Differences between organs



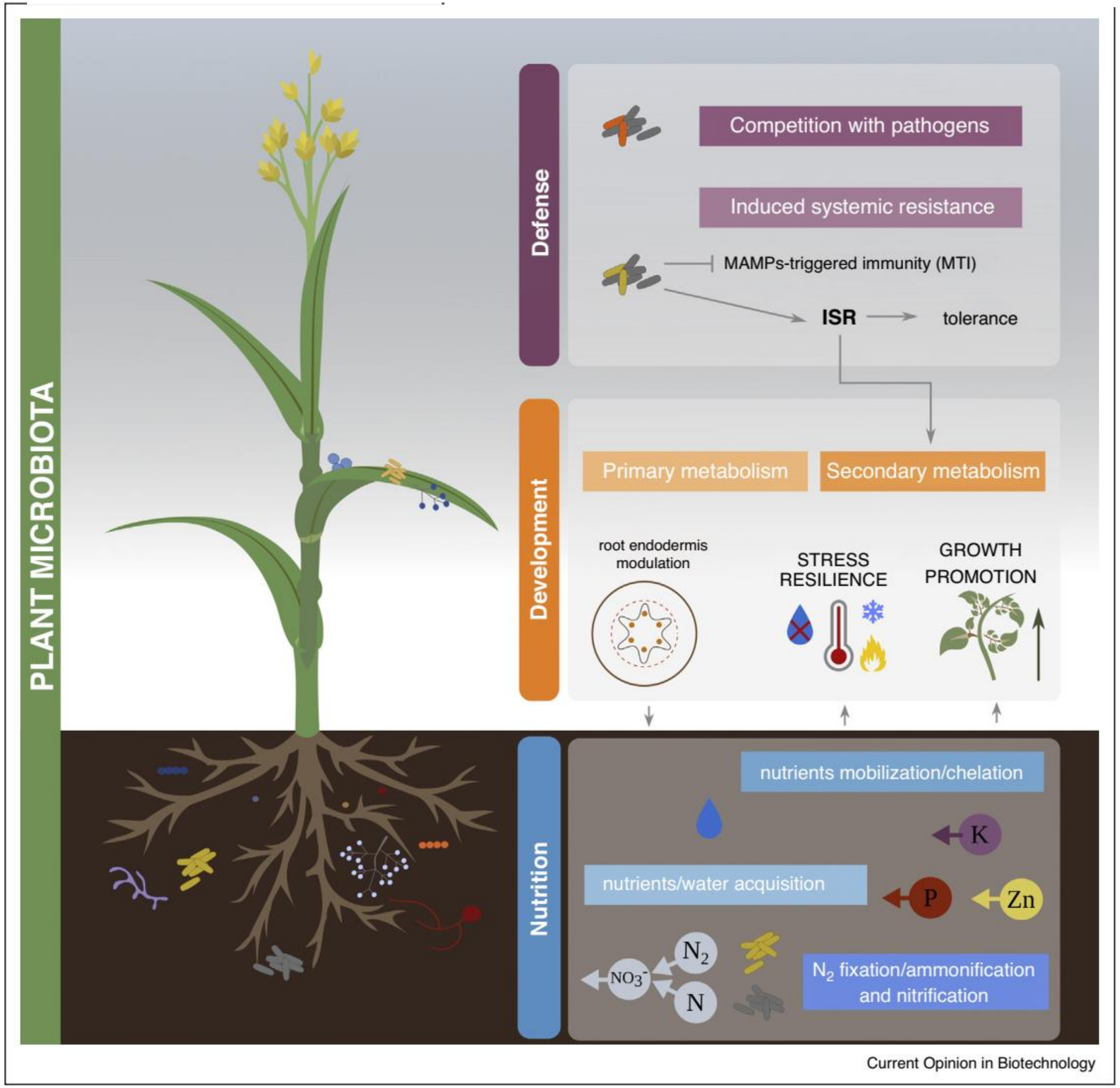
Analysis of microbiomes from the soil, rhizosphere and endophytes/epiphytes from different organs by metagenomics

(from Zarraonaindia et al, 2015)

From diversity to function: leads to an extended plant

The microbiota modulates regulatory networks involved in nutrient acquisition, plant development, and immune responses.

Figure 2 From Chiala et al, 2022 **Current Opinion in Biotechnology** 2022, **73**:135–142

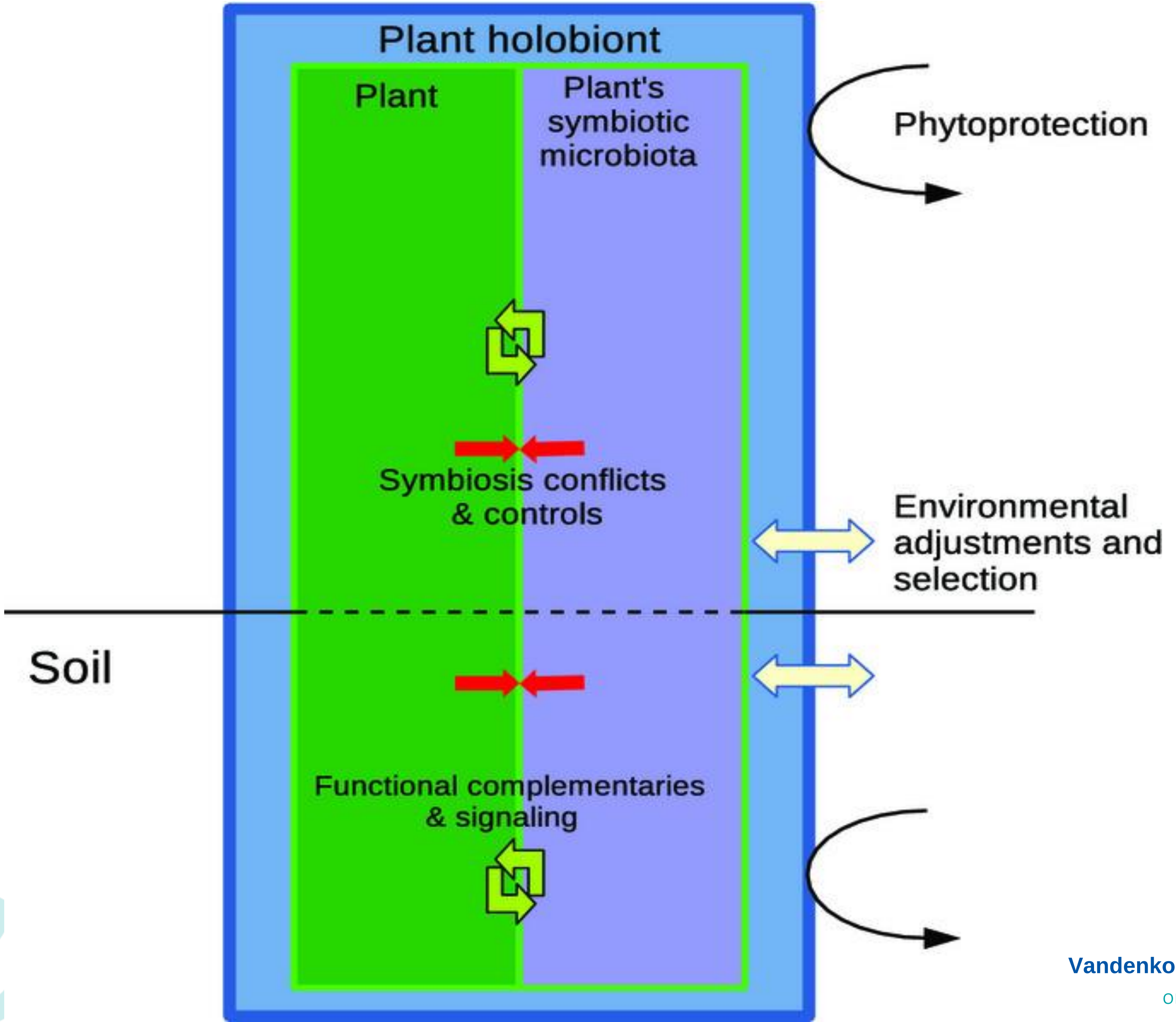


Current Opinion in Biotechnology

Beneficial effects of microbiota on plant nutrition, development and defense. ISR, Induced Systemic Resistance.

The function of plant microbiome

The importance of the microbiome of the plant holobiont



Vandenkoornhuysee et al, 2015

- **Therefore, Plant microbiome,** which mostly belong to Bacteria and Fungi, are involved in **major functions** such as **plant nutrition and plant resistance to biotic and abiotic stresses** (Vandenkoornhuyse et al 2015), but also diseases. In grape, microbiome on berries may also have an impact on wine fermentation (Bokulich et al 2016).

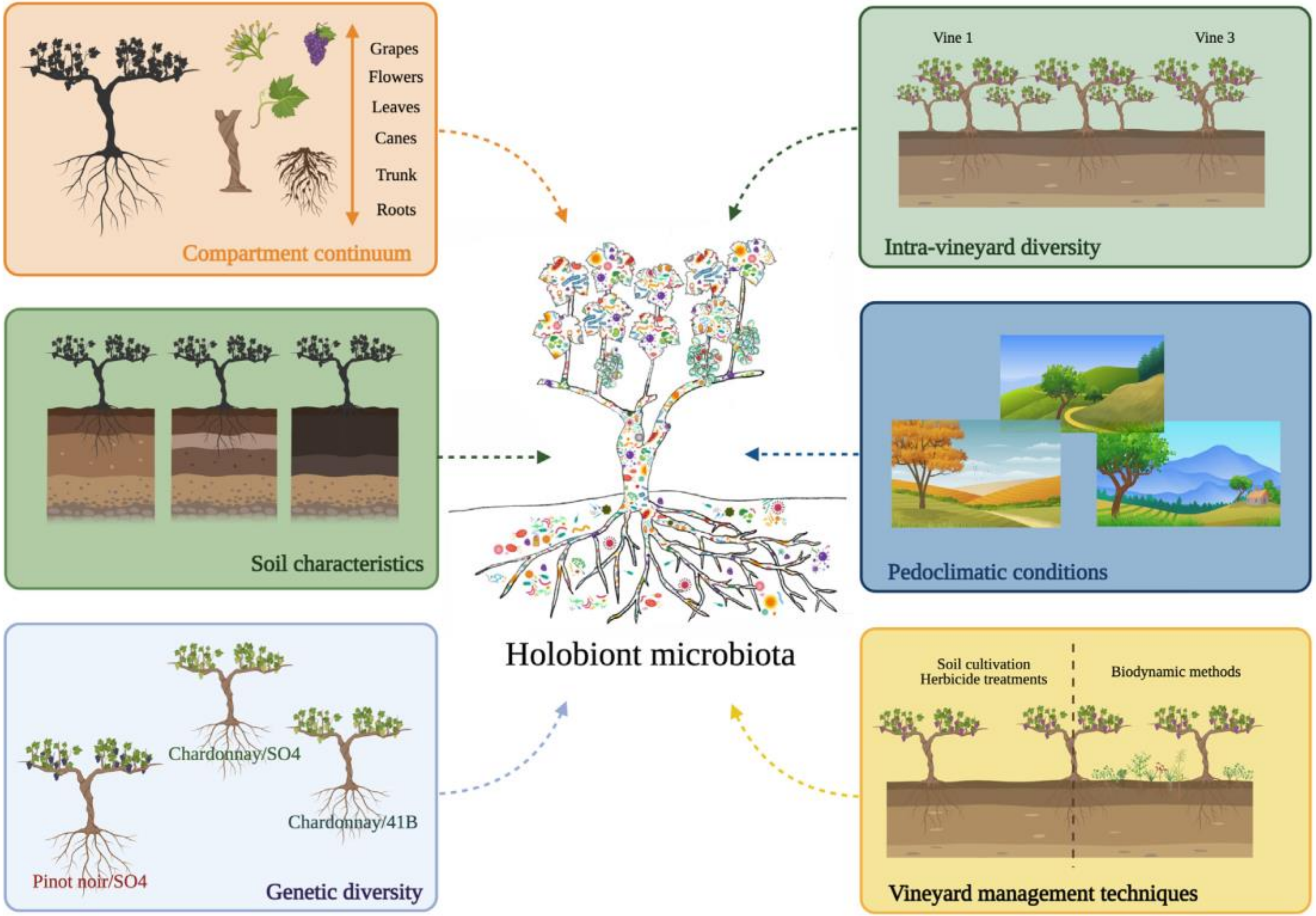


Fig. 1. Factors known to affect the composition and the structure of grapevine microbiota.

P. Bettenfeld, J. Cadena i Canals, L. Jacquens et al. Journal of Advanced Research 40 (2022) 1–15

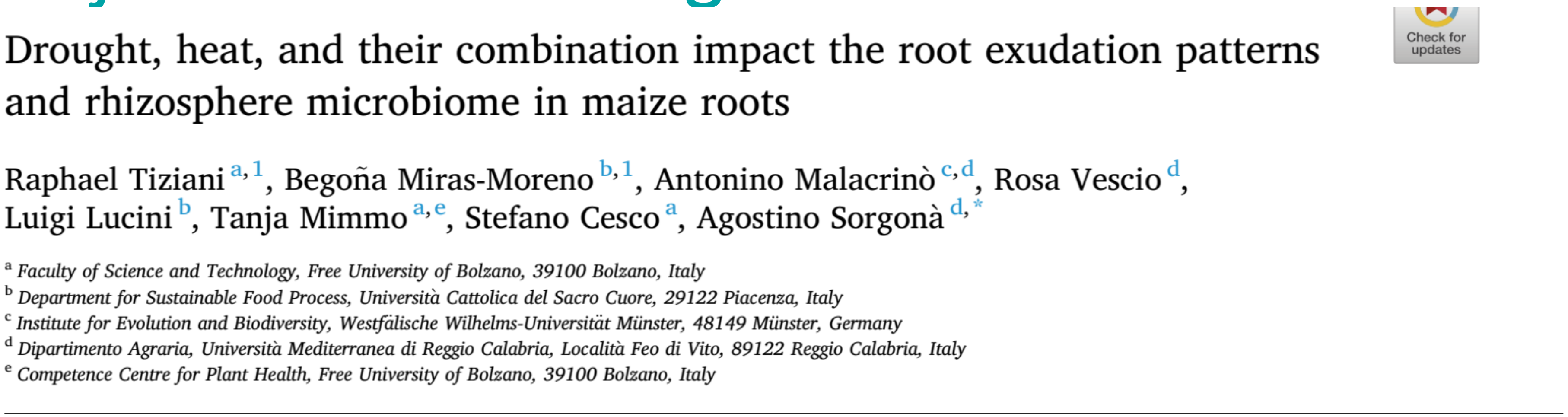
Major factors affecting microbiome

- <u>Environment</u>
    - Location (Bokulich et al, 2014, Gao et al 2019)
    - Time of the year/seasonal (Guzon et al, 2021; Marzano et al, 2016)
    - Soil composition (Ph, carbon, moisture, ..) (Zarraonaindia et al 2015)
    - Drougth (Carbone et al 2021)

- <u>cultural practices</u>
    - Farming system (Castrillo et al, 2019; Vega-Avila et al, 2016) and more specifically coper treatments (Martins et al, 2012, depend on the formulation)
    - Soil management, cover crop presence and cover crop mix, tillage (Burns et al 2016; Cordero-Bueso et al, 2011), effect on soil microbiome but not fruit (Chou et al, 2018)
    - Watering and Tillage (Vink et al 2021, mild effect)

- <u>Plants</u>
    - Age of the plant (Berlanas et al, 2019; Ji et al, 2018)
    - Health of the plant
    - Organ age (developmental stage; Martins et al, 2012
    - Post-harvest treatments (Salvetti et al, 2016)

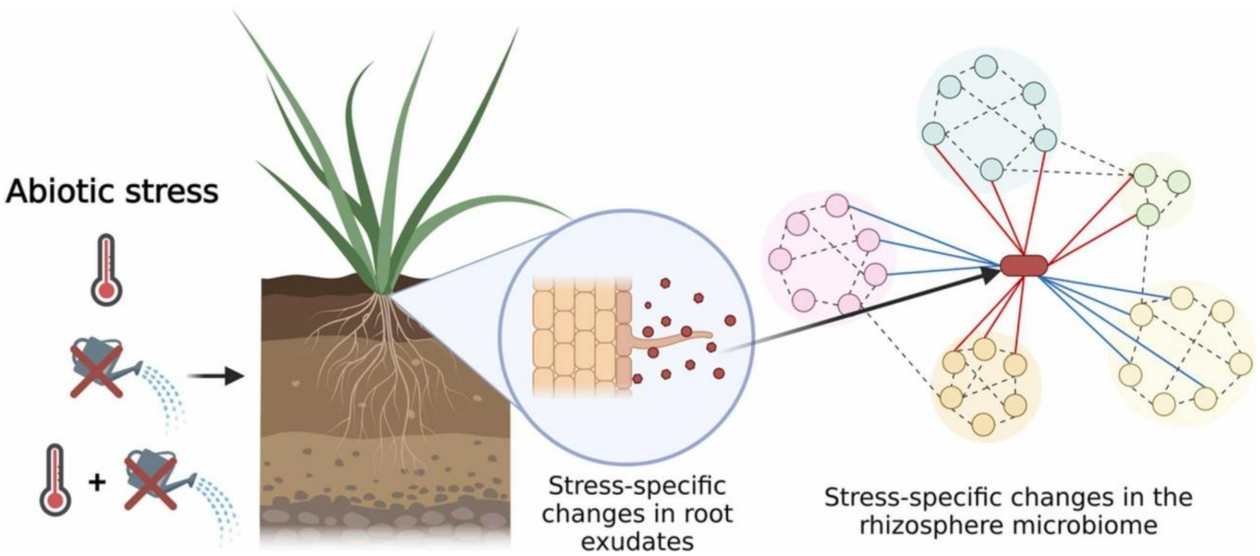
Major factors affecting microbiome



Drought, heat, and their combination impact the root exudation patterns and rhizosphere microbiome in maize roots

Raphael Tiziani [a,1], Begoña Miras-Moreno [b,1], Antonino Malacrinò [c,d], Rosa Vescio [d], Luigi Lucini [b], Tanja Mimmo [a,e], Stefano Cesco [a], Agostino Sorgonà [d,*]

[a] *Faculty of Science and Technology, Free University of Bolzano, 39100 Bolzano, Italy*
[b] *Department for Sustainable Food Process, Università Cattolica del Sacro Cuore, 29122 Piacenza, Italy*
[c] *Institute for Evolution and Biodiversity, Westfälische Wilhelms-Universität Münster, 48149 Münster, Germany*
[d] *Dipartimento Agraria, Università Mediterranea di Reggio Calabria, Località Feo di Vito, 89122 Reggio Calabria, Italy*
[e] *Competence Centre for Plant Health, Free University of Bolzano, 39100 Bolzano, Italy*



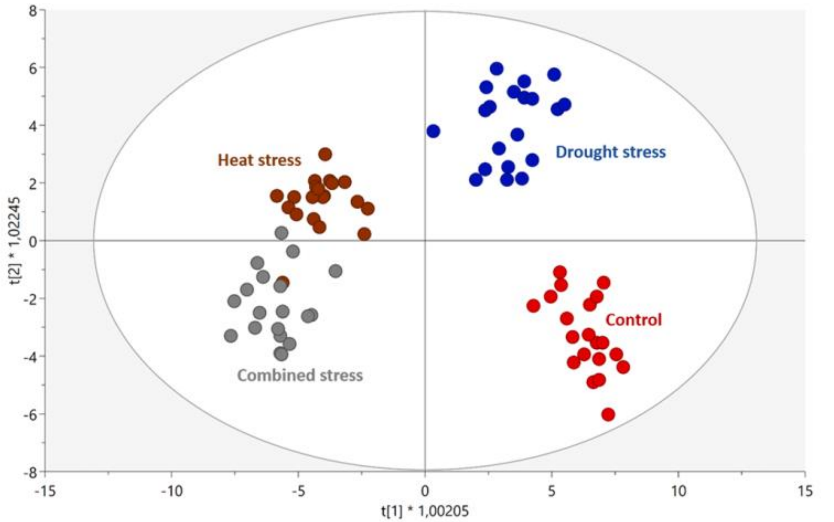


Fig. 4. Score plot of orthogonal projection to latent structures discriminant analysis (OPLS-DA) supervised modelling carried out from untargeted metabolomics profiles of root exudates (correlation $R^2Y = 0.83$, prediction ability $Q^2Y = 0.48$).

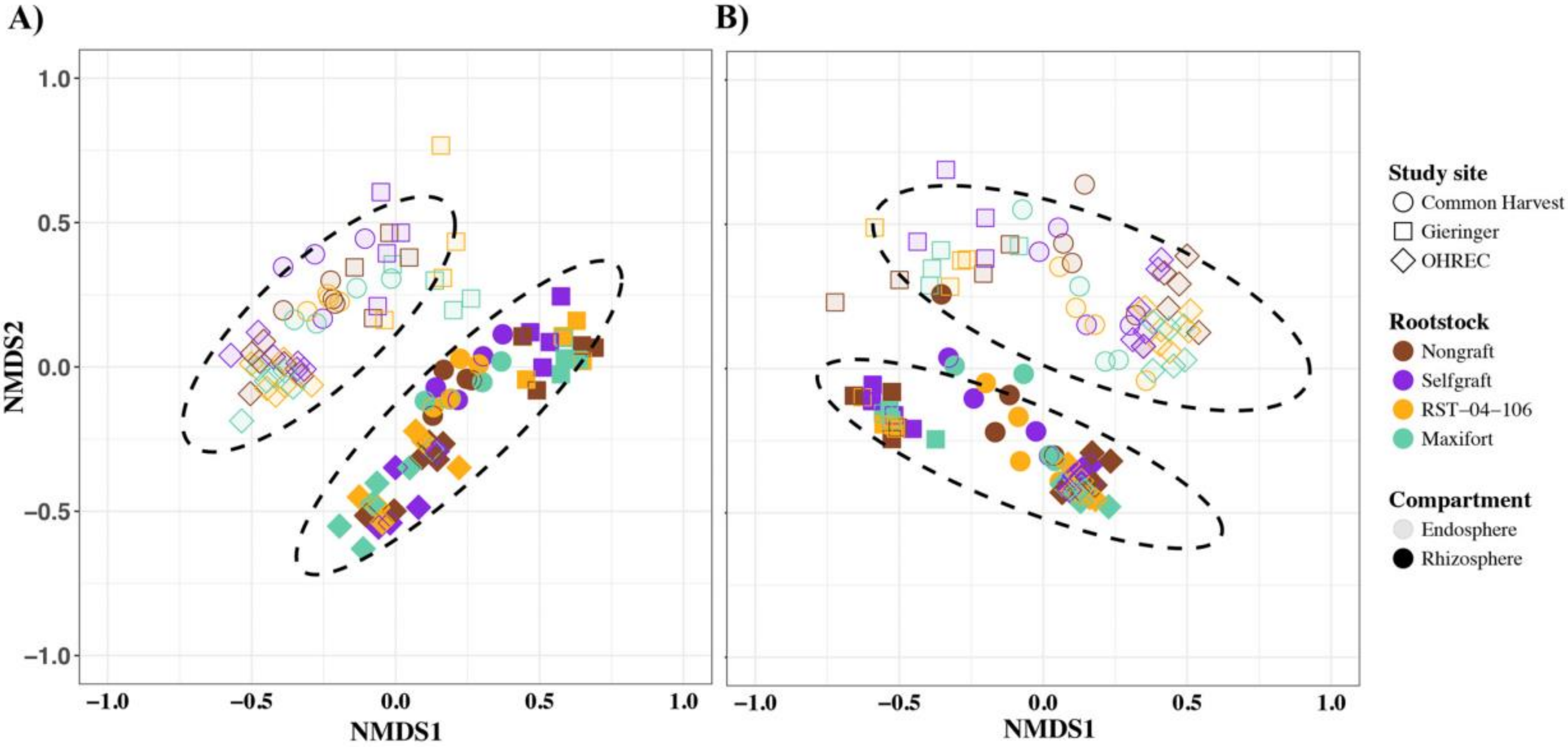
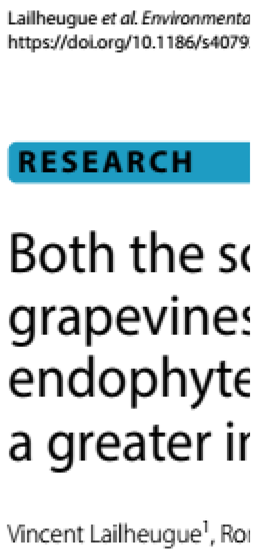


FIG 3 Nonmetric multidimensional scaling (NMDS) ordination of samples from tomato rootstock treatments. NMDS ordination of samples was based on the Bray-Curtis dissimilarity matrix of OTUs from bacterial communities inhabiting the endosphere and rhizosphere compartments in the years 2014 (A) and 2015 (B). Color indicates rootstock treatment (two hybrid rootstocks (RST-04-106 and Maxifort) and nongrafted and self-grafted controls (BHN589)), shape represents study site, and solid and lighter fill colors represent the rhizosphere and endosphere compartments, respectively. Ellipses indicate 95% confidence regions around the centroids of the endosphere and rhizosphere samples.

Ma

- **And**



Lailheugue *et al. Environmenta*
https://doi.org/10.1186/s4079

RESEARCH

Both the sc
grapevines
endophyte
a greater ir

Vincent Lailheugue[1], Ro

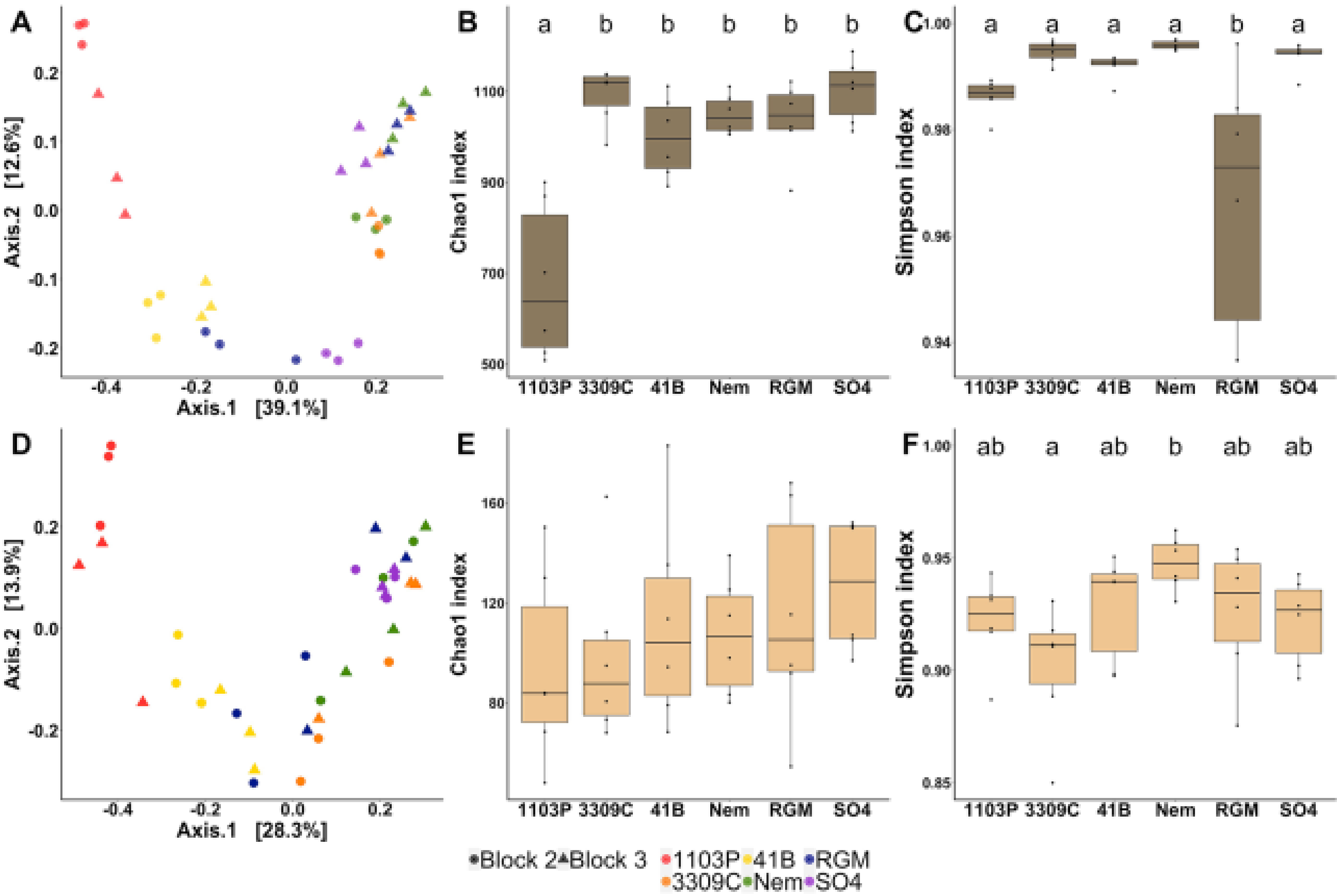


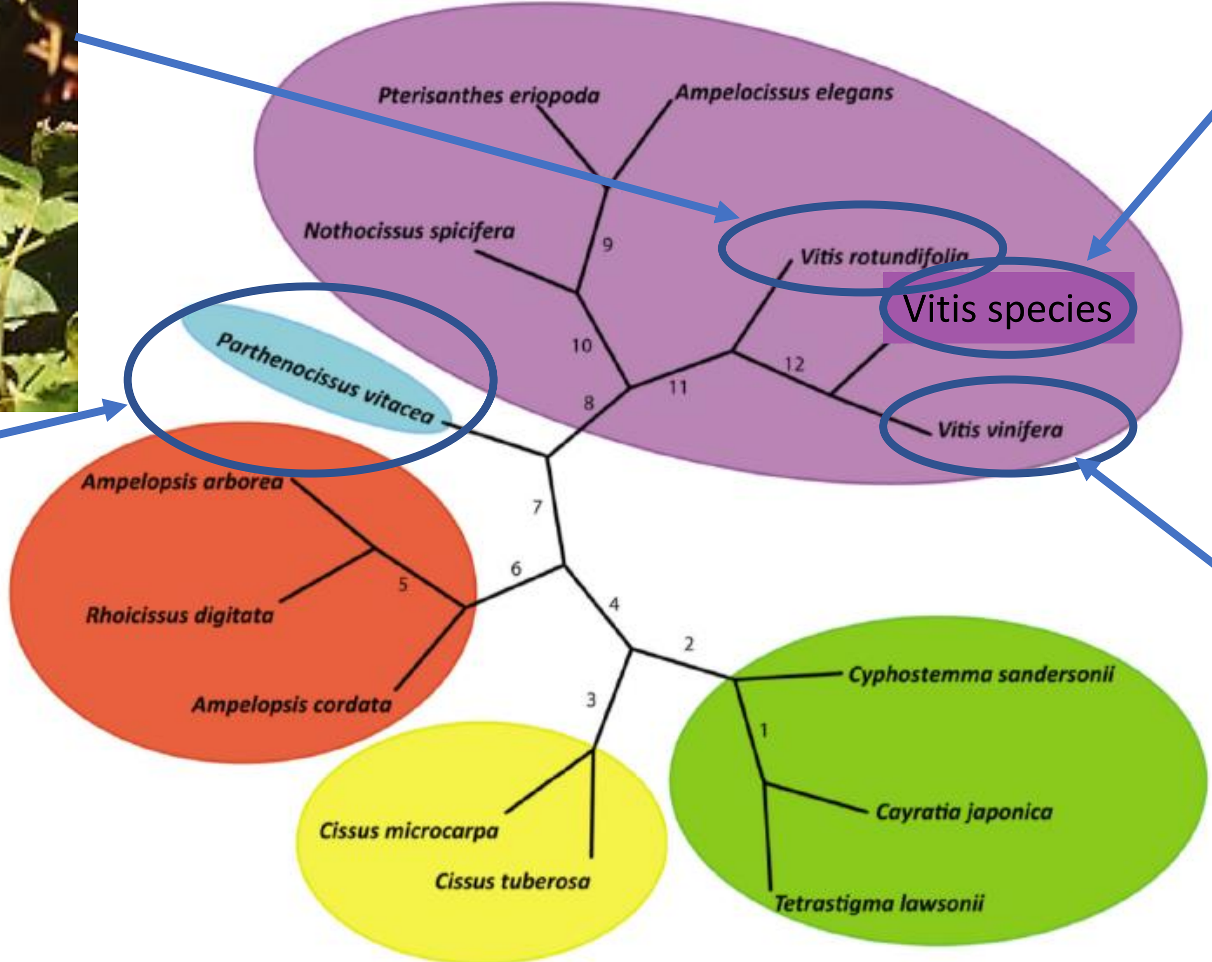
Fig. 2 Comparison of bacterial communities in the rhizosphere (dark brown, top panel) and the root endosphere (light brown, bottom panel) between the 6 rootstock genotypes grafted onto CS ($n = 6$). Comparison of bacterial communities by principal coordinate analysis (PCoA) based on Bray–Curtis dissimilarity matrices in the rhizosphere (**A**) and the root endosphere (**D**). Comparison of bacterial richness (Chao1) and diversity (Simpson) in the rhizosphere (**B, C**) and the root endosphere (**E, F**). *P*-values were calculated using Pairwise-Student tests with Bonferroni correction and were considered as significant when the adjusted *p*-value < 0.05

Major factors affecting microbiome

- **And the plant genotype : not as clear for the phyllosphere**

Plant material : *Vitaceae*, *Vitis* species and *Vitis vinifera* cultivars

Species of Vitaceae family



Unrooted tree of 15 species of vitacea based on sequenes at 229 genes (Wen et al, 2013)

What are the main drivers of taxa diversity in grape Phyllosphere ?

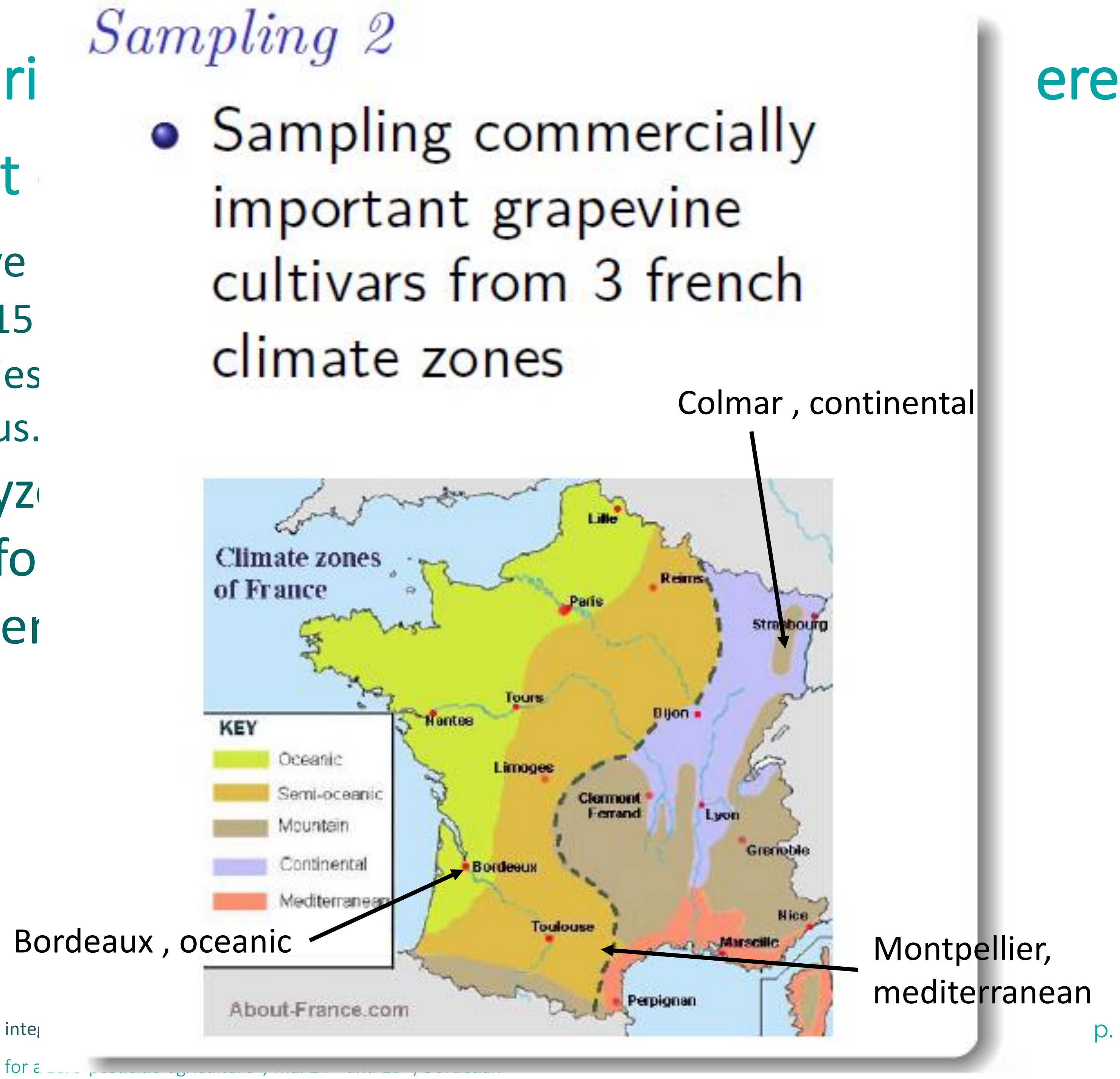
We analyzed different drivers:

- **Genetic identity of scion:** we analyzed different levels of variation
  - At the intraspecies level : 15 individuals from the 3 gene pools
  - Between genus and famillies : V. vinifera, Vitis riparia, Vitis pentagona, Muscadinia rotundifolia, Parthenocissus.
- **Environment** : we analyzed the microbiome during 2 years, at spring and harvest and for few cultivars (CS, Ch, Gre, Sau B, Sy) 3 regions (oceanic, continental, Mediterranean in France)

What are the main dri ere ?

We analyzed different

- **Genetic identity of scion:** we
  - At the intraspecies level : 15
  - Between genus and famillies rotundifolia, Parthenocissus.
- **Environment** : we analyz spring and harvest and fo regions (oceanic, continer



Sampling 2

- Sampling commercially important grapevine cultivars from 3 french climate zones

Colmar , continental

Bordeaux , oceanic

Montpellier, mediterranean

Results: taxonomic data

1. 12875 bacterial and 3413 fungal OTUs
2. Genus level assignment, unassigned taxa were removed
3. 6017 bacterial and 2075 fungal OTUs
4. 542 bacterial & 267 fungal genera

Singh et al, 2018 Frontiers Life Sci. , 11 : 1, 35-46

Results: prevalence of taxa

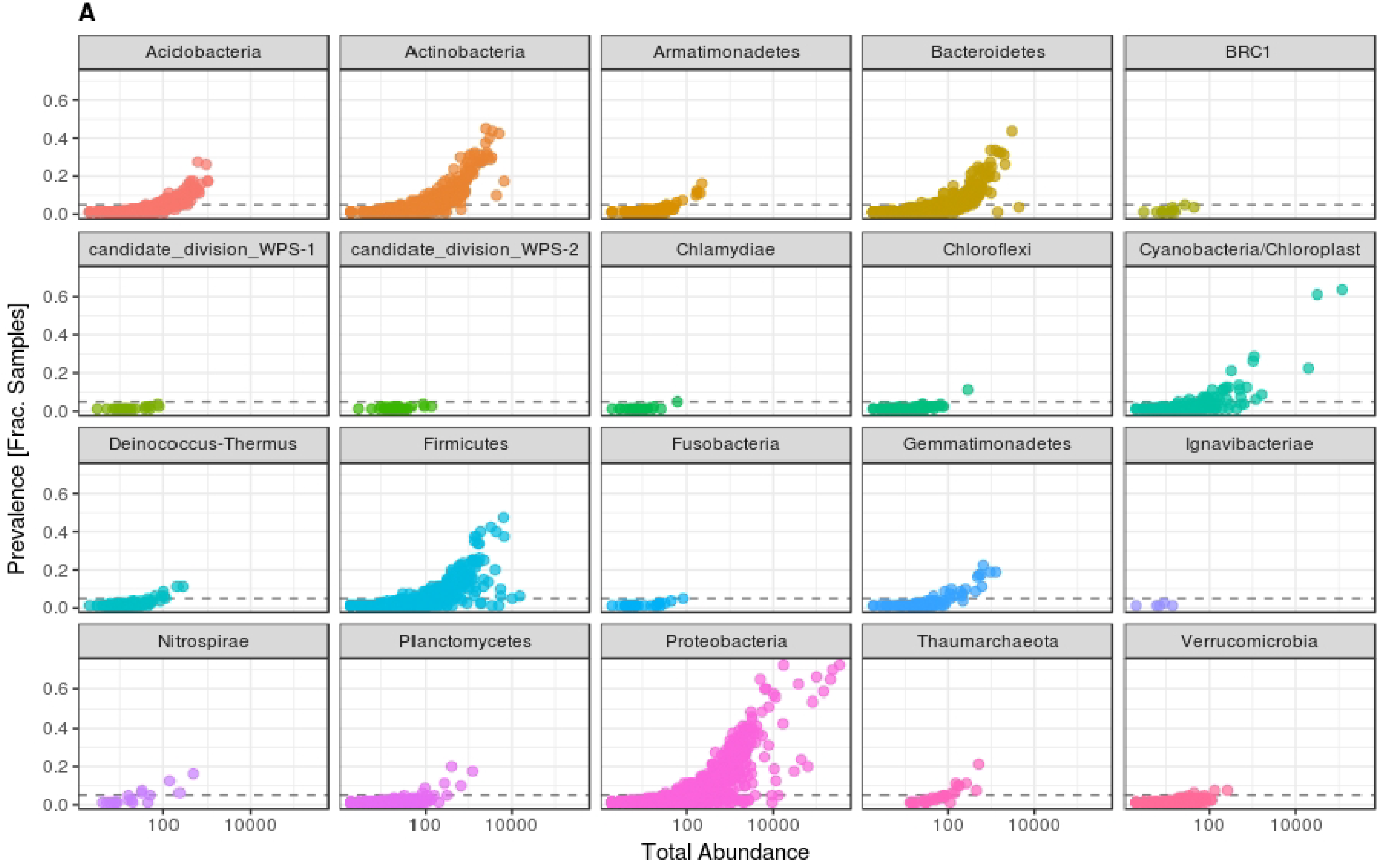


Figure (7) Taxa prevalence versus total counts for 16S data.

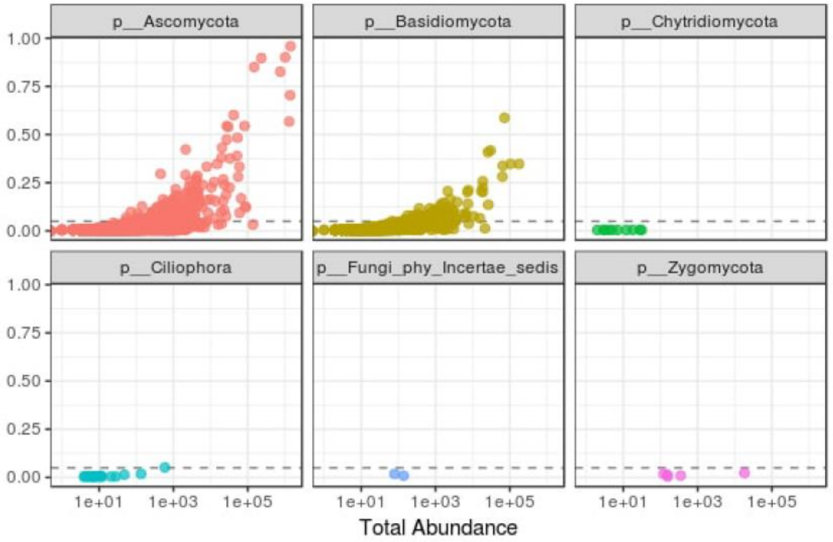


Figure (8) Taxa prevalence versus total counts for ITS data.

Singh et al, 2018 Frontiers Life Sci. , 11 : 1, 35-46

Results: environment is a stronger driver than genetics

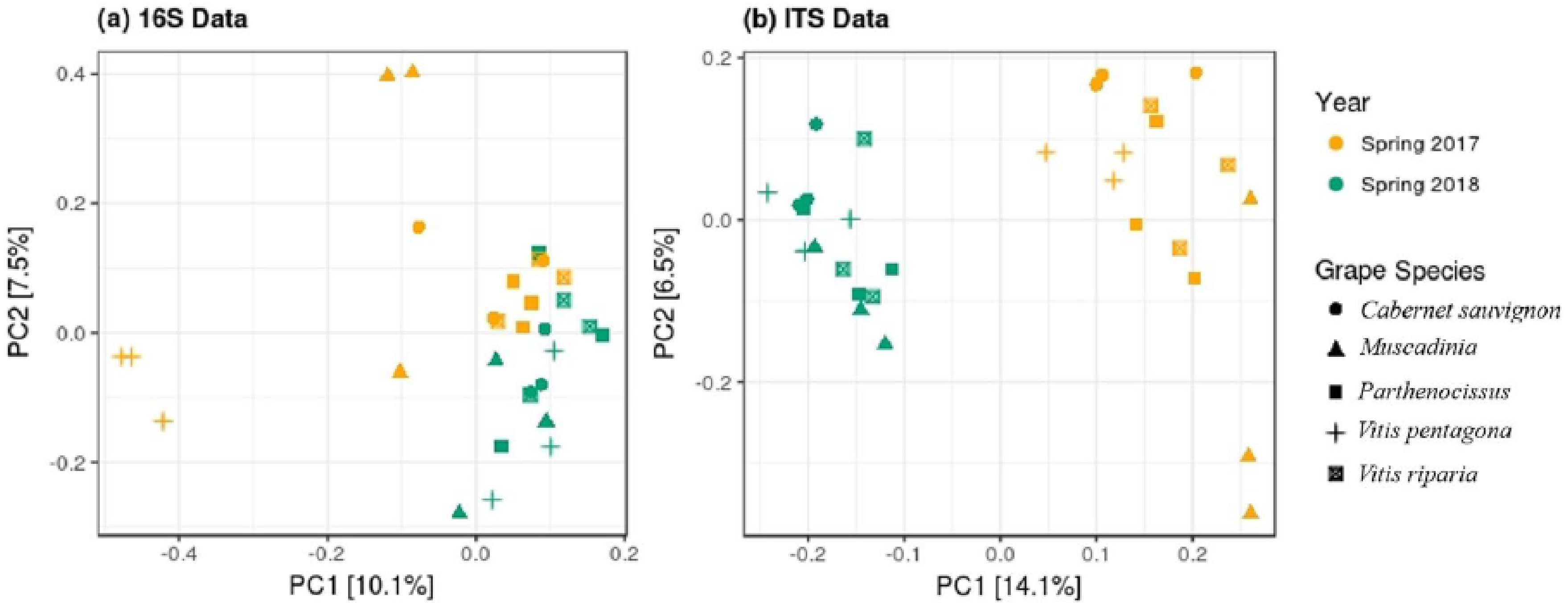


Figure 2. PCoA ordinations of (**a**) bacterial and (**b**) fungal communities derived from leaf phyllosphere at two growing years, using Bray-Curtis distance matrix. Both the axis explains ~20% of variations. The shape represents grape species (N = 30).

Singh et al, 2019, Sci. Reports, 9 : 142941

Results: environment is a stronger driver than genetics

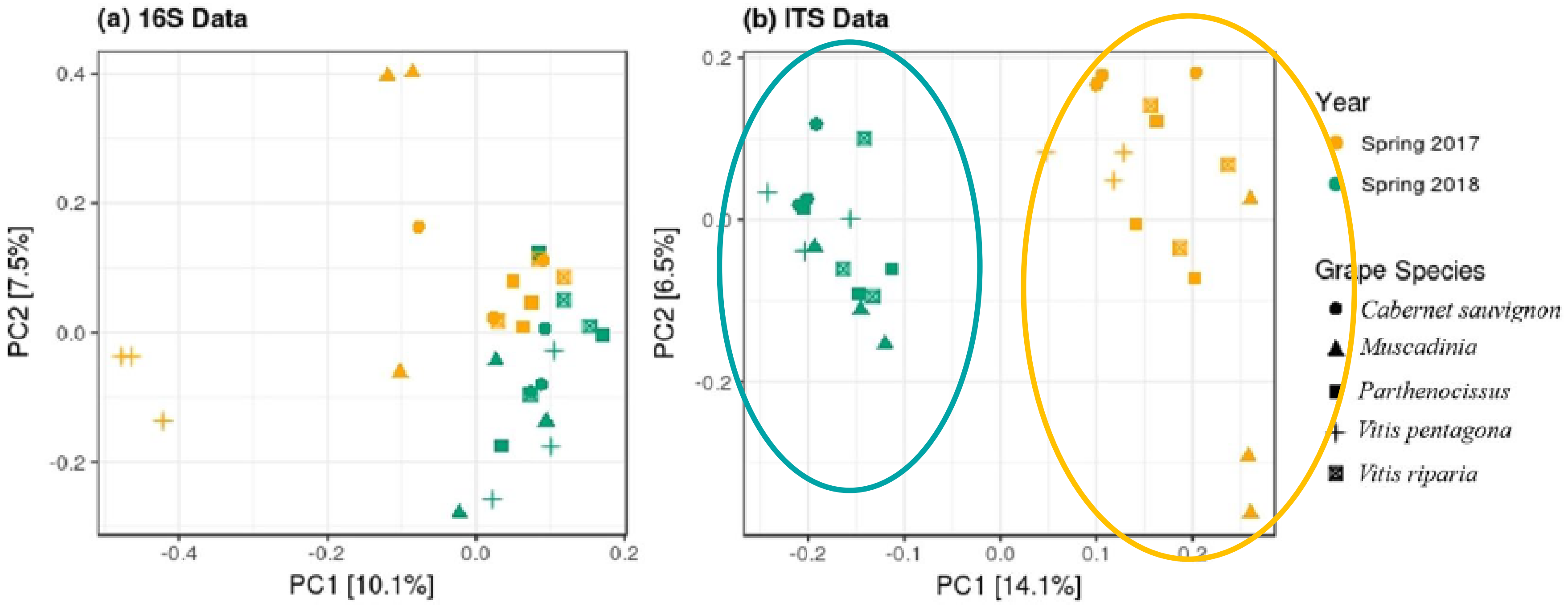
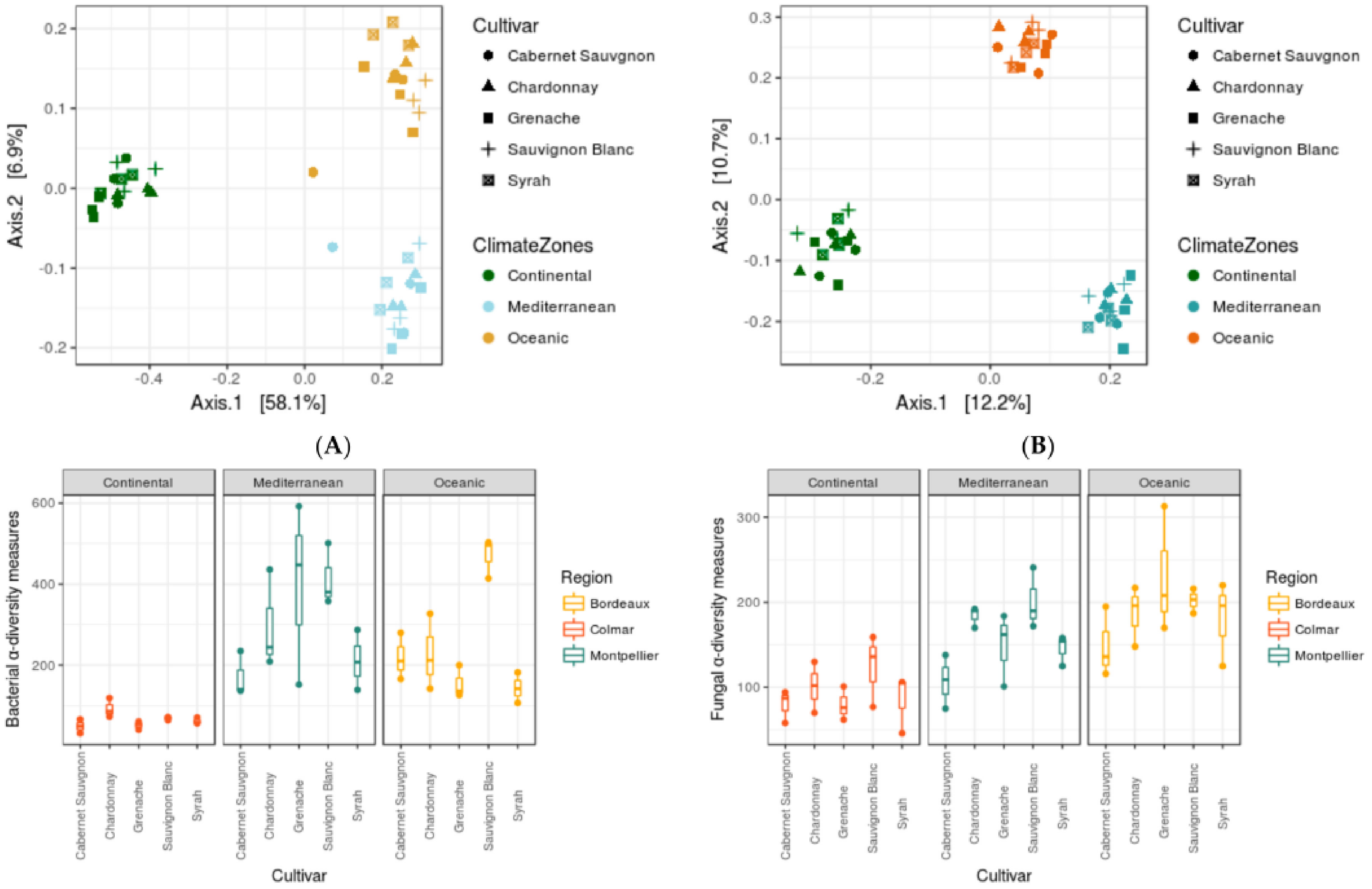


Figure 2. PCoA ordinations of (**a**) bacterial and (**b**) fungal communities derived from leaf phyllosphere at two growing years, using Bray-Curtis distance matrix. Both the axis explains ~20% of variations. The shape represents grape species (N = 30).

Singh et al, 2019, Sci. Reports, 9 : 142941

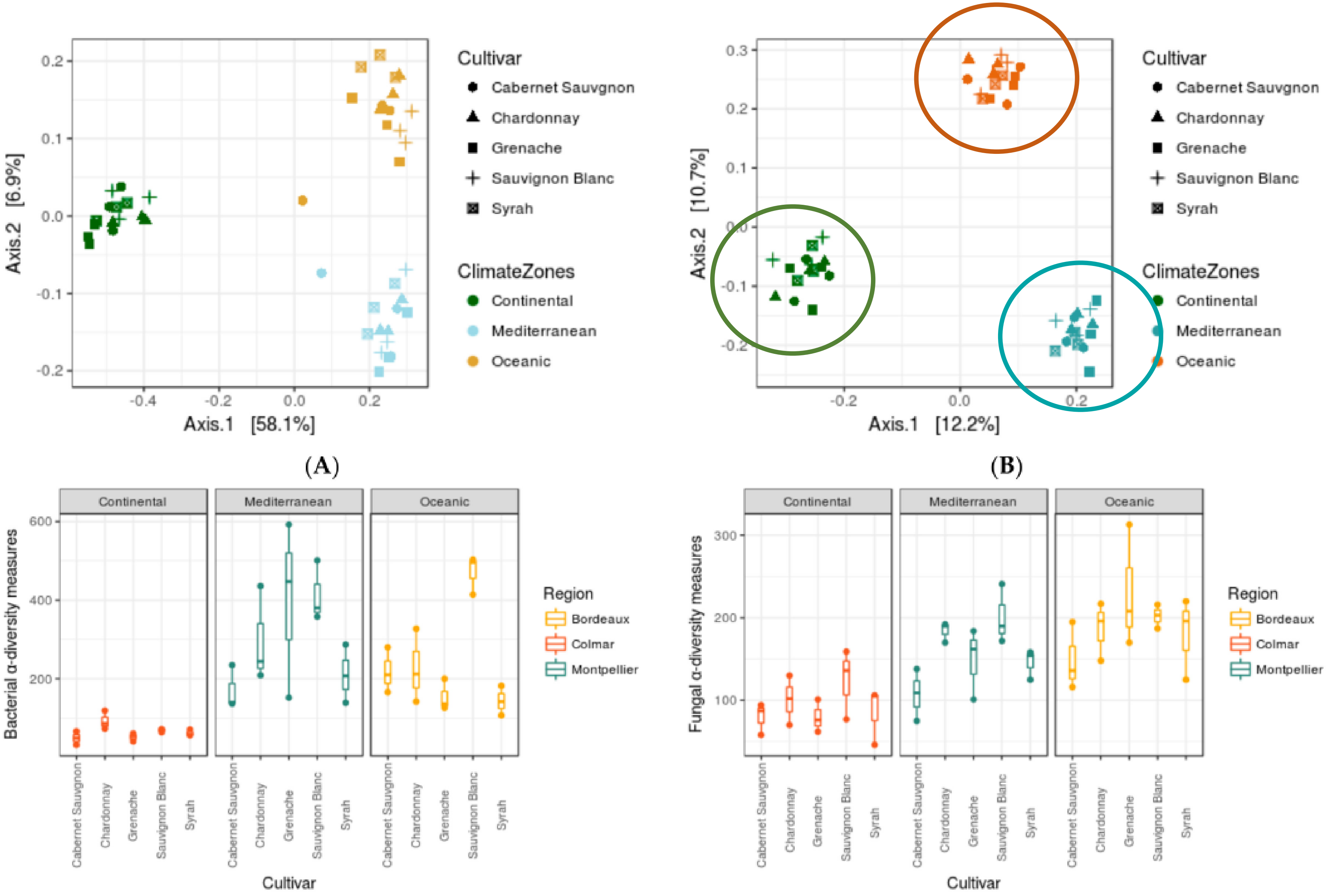
INRAE

Results: environment is a stronger driver than genetics



Singh et al, 2018, microorganisms, 6: 96

Results: environment is a stronger driver than genetics

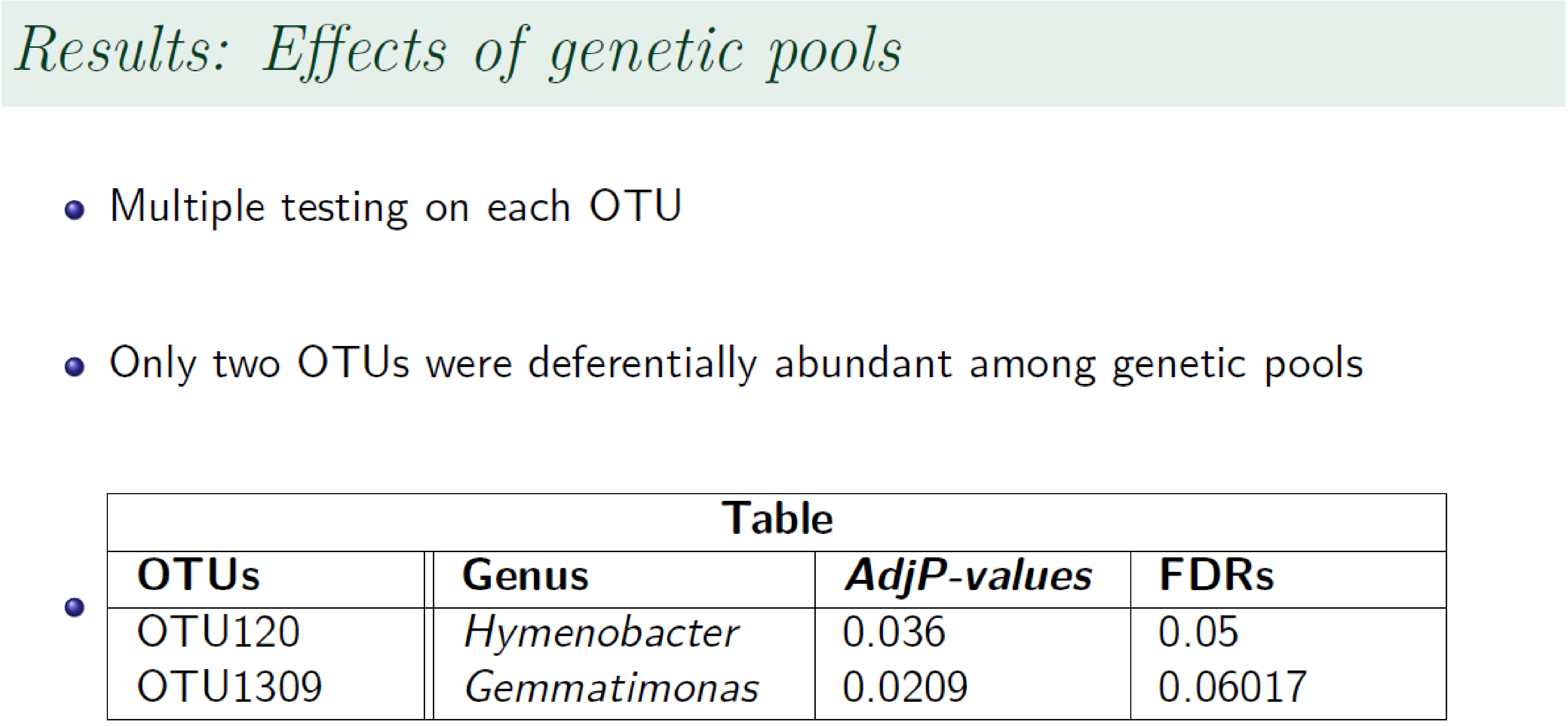


INR

P. This

Singh et al, 2018, microorganisms, 6: 96

Results: environment is a stronger driver than genetics

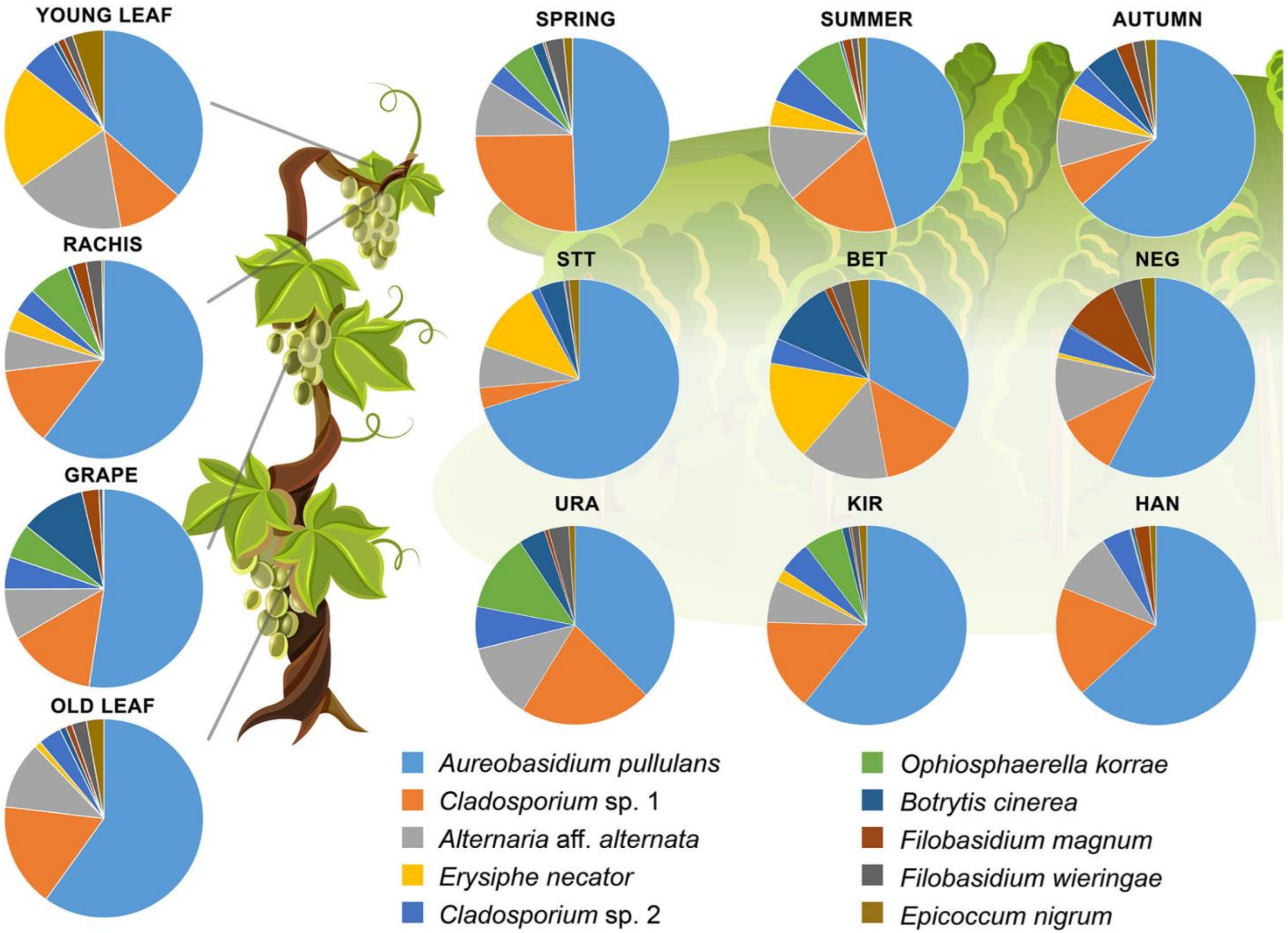


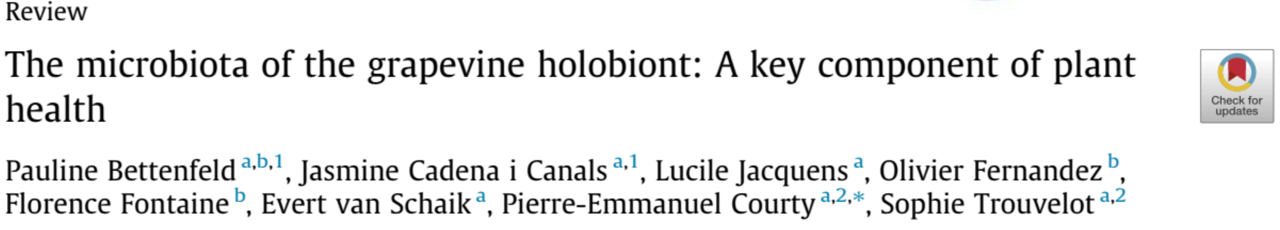
Results: Effects of genetic pools

- Multiple testing on each OTU
- Only two OTUs were deferentially abundant among genetic pools
- **Table**

OTUs	**Genus**	***AdjP-values***	**FDRs**
OTU120	*Hymenobacter*	0.036	0.05
OTU1309	*Gemmatimonas*	0.0209	0.06017

Environment is a strong determinant of leaves and berries endosphere as well





Review

The microbiota of the grapevine holobiont: A key component of plant health

Pauline Bettenfeld[a,b,1], Jasmine Cadena i Canals[a,1], Lucile Jacquens[a], Olivier Fernandez[b], Florence Fontaine[b], Evert van Schaik[a], Pierre-Emmanuel Courty[a,2,*], Sophie Trouvelot[a,2]

What does this mean in term of breeding ?

What does this mean in term of breeding ?

- For many crops, the mains targets for breeding are related to production, quality and tolerance/resistance to biotic and abiotic stresses
  - Example: breeding cultivars resistant to plant disease by intorduction of resistance genes from related wild species

Development of new resistant Varieties : INRA program-Resdur (1, 2 et 3)

ÉCOPHYTO
RÉDUIRE ET AMÉLIORER
L'UTILISATION DES PHYTOS

Initiated in 2000

12 to 25 varieties between 2018 & 2025

Inscription in 2018:

FLOREAL
(référence obtenteur : Col-2007G)

Variété de cuve de la série INRA-ResDur1, à résistance polygénique au mildiou (*Rpv1 + Rpv3*) et à l'oïdium (*Run1 + Ren3*)

Origine / Filiation

Col-2007G = Villaris x Mtp 3159-2-12

Villaris : Variété sélectionnée en 2011 par l'Institut JKI du Geilweilerhof (Allemagne). Elle porte des facteurs de résistance provenant de vignes américaines, principalement *V. rupestris* et *V. oestivalis.*

Mtp 3159-2-12 : Obtention INRA, sélectionnée par A. Bouquet à Montpellier en introgressant la source de résistance *V. rotundifolia.*

VOLTIS
(référence obtenteur : Col-2011G)

Variété de cuve de la série INRA-ResDur1, à résistance polygénique au mildiou (*Rpv1 + Rpv3*) et à l'oïdium (*Run1 + Ren3*)

Origine / Filiation

Col-2011G = Villaris x Mtp 3159-2-12

Villaris : Variété sélectionnée en 2011 par l'Institut JKI du Geilweilerhof (Allemagne). Elle porte des facteurs de résistance provenant de vignes américaines, principalement *V. rupestris* et *V. oestivalis.*

Mtp 3159-2-12 : Obtention INRA, sélectionnée par A. Bouquet à Montpellier en introgressant la source de résistance *V. rotundifolia.*

ARTABAN
(référence obtenteur : IJ 134)

Variété de cuve de la série INRA-ResDur1, à résistance polygénique au mildiou (*Rpv1 + Rpv3*) et à l'oïdium (*Run1 + Ren3*)

Origine / Filiation

IJ 134 = Mtp 3082-1-42 x Regent

Mtp 3082-1-42 : Obtention INRA, sélectionnée par A. Bouquet à Montpellier en introgressant la source de résistance *V. rotundifolia.*

Regent : Variété sélectionnée en 1995 par l'Institut JKI du Geilweilerhof (Allemagne). Elle porte des facteurs de résistance provenant de vignes américaines, principalement *V. rupestris* et *V. oestivalis.*

VIDOC
(référence obtenteur : IJ 58)

Variété de cuve de la série INRA-ResDur1, à résistance polygénique au mildiou (*Rpv1 + Rpv3*) et à l'oïdium (*Run1 + Ren3*)

Origine / Filiation

IJ 58 = Mtp 3082-1-42 x Regent

Mtp 3082-1-42 : Obtention INRA, sélectionnée par A. Bouquet à Montpellier en introgressant la source de résistance *V. rotundifolia.*

Regent : Variété sélectionnée en 1995 par l'Institut JKI du Geilweilerhof (Allemagne). Elle porte des facteurs de résistance provenant de vignes américaines, principalement *V. rupestris* et *V. oestivalis.*

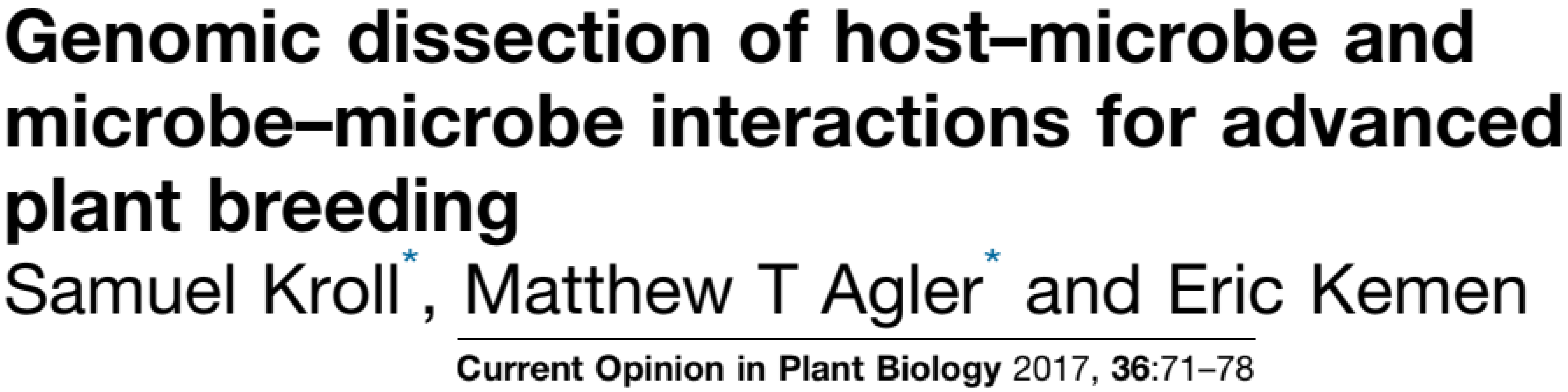
100 hectares in 2019

What does this mean in term of breeding ?

- For many crops, the mains targets for breeding are related to production, quality and tolerance/resistance to biotic and abiotic stresses
  - Until very recently, the selection schemes only took into account the plant and not the holobionte
    - Controlling the microbiota would offer unique opportunities to affect all the traits they have an effect on
      - Considering that the plant microbiome is more genetically plastic than the host plant genome, we can built more plastic plants
- but this will require building our understanding of how plant genotypes impact colonization of specific microorganisms that might help to fix beneficial microbiota-related traits.

P. This: Breeding plant holobionts: how plant microbiomes could be integrated in breeding strategies

The niches theory



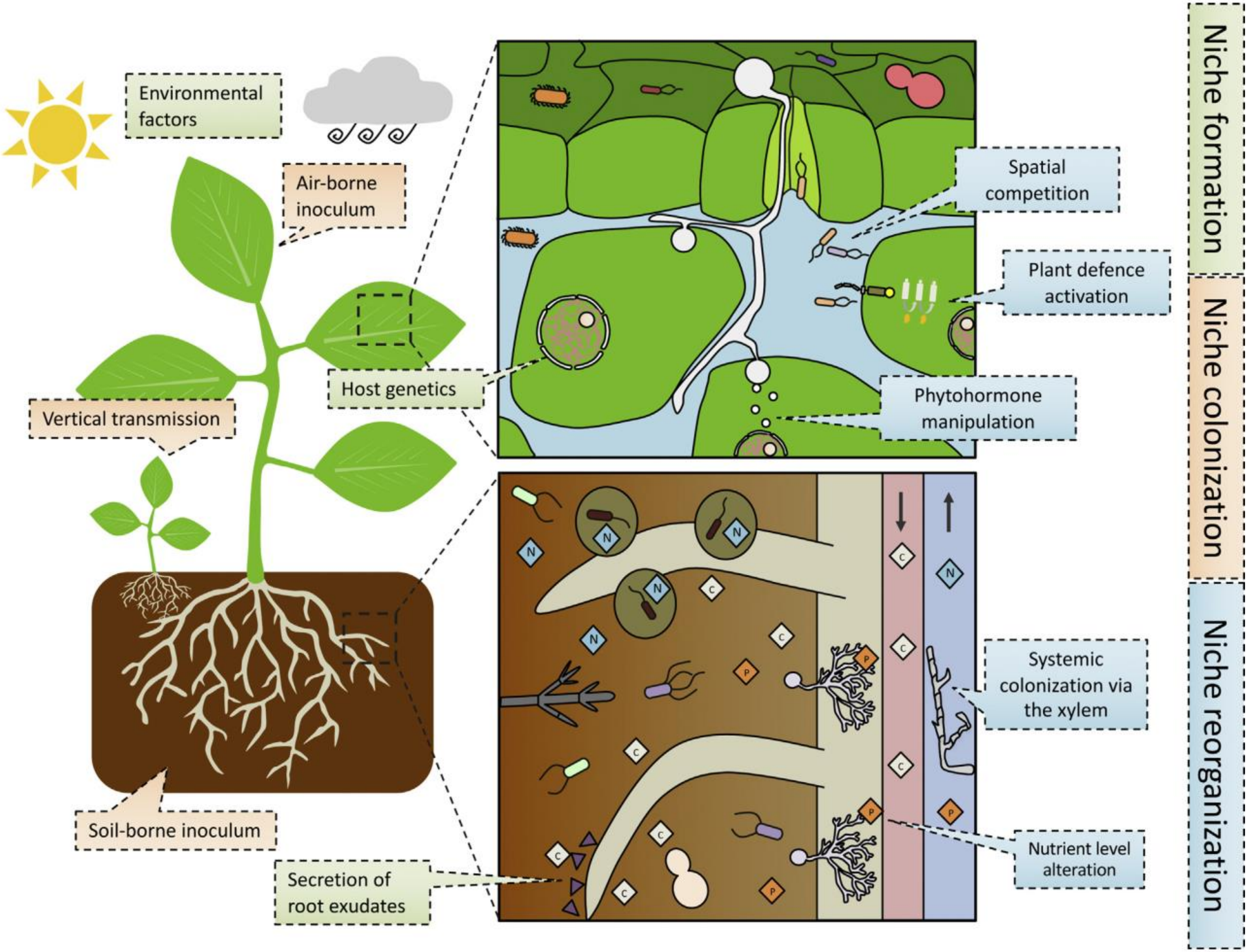
Genomic dissection of host–microbe and microbe–microbe interactions for advanced plant breeding

Samuel Kroll*, Matthew T Agler* and Eric Kemen

Current Opinion in Plant Biology 2017, **36**:71–78

The niches theory

The plant holobiont harbors dynamic niches, with host genes determining the space and primary resources available in each niche



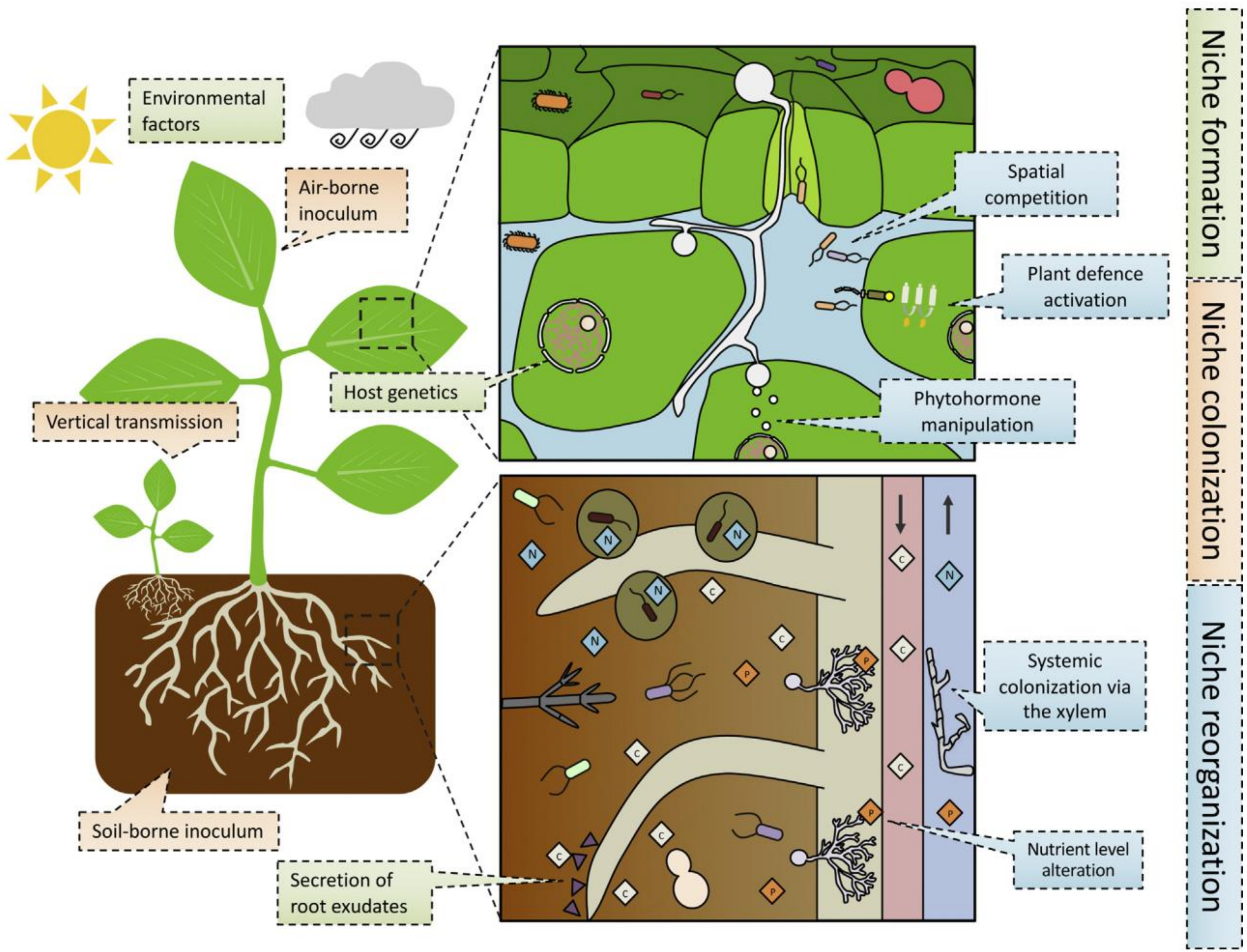
Formation of the plant holobiont. Host genetics together with environmental factors contribute to initial plant niche formation. Those versatile niches are then colonized by a range of microbes, which require different adaptations depending on the colonized tissue type. This results in differential adaptation of microbial genomes and community composition. Apart from tissue specificity, microbes are able to alter a colonized ho niche by, for example, phytohormone manipulation or activation of plant defenses. Dynamics in formation of the holobiont therefore needs consideration.

INRAE

P. This: Breeding plant holobionts: how plant microbiomes co

The niches theory

In plants, alteration of nutrient availability is likely to be an important mechanism by which microbes alter niches in the nutrient-poor plant intercellular spaces

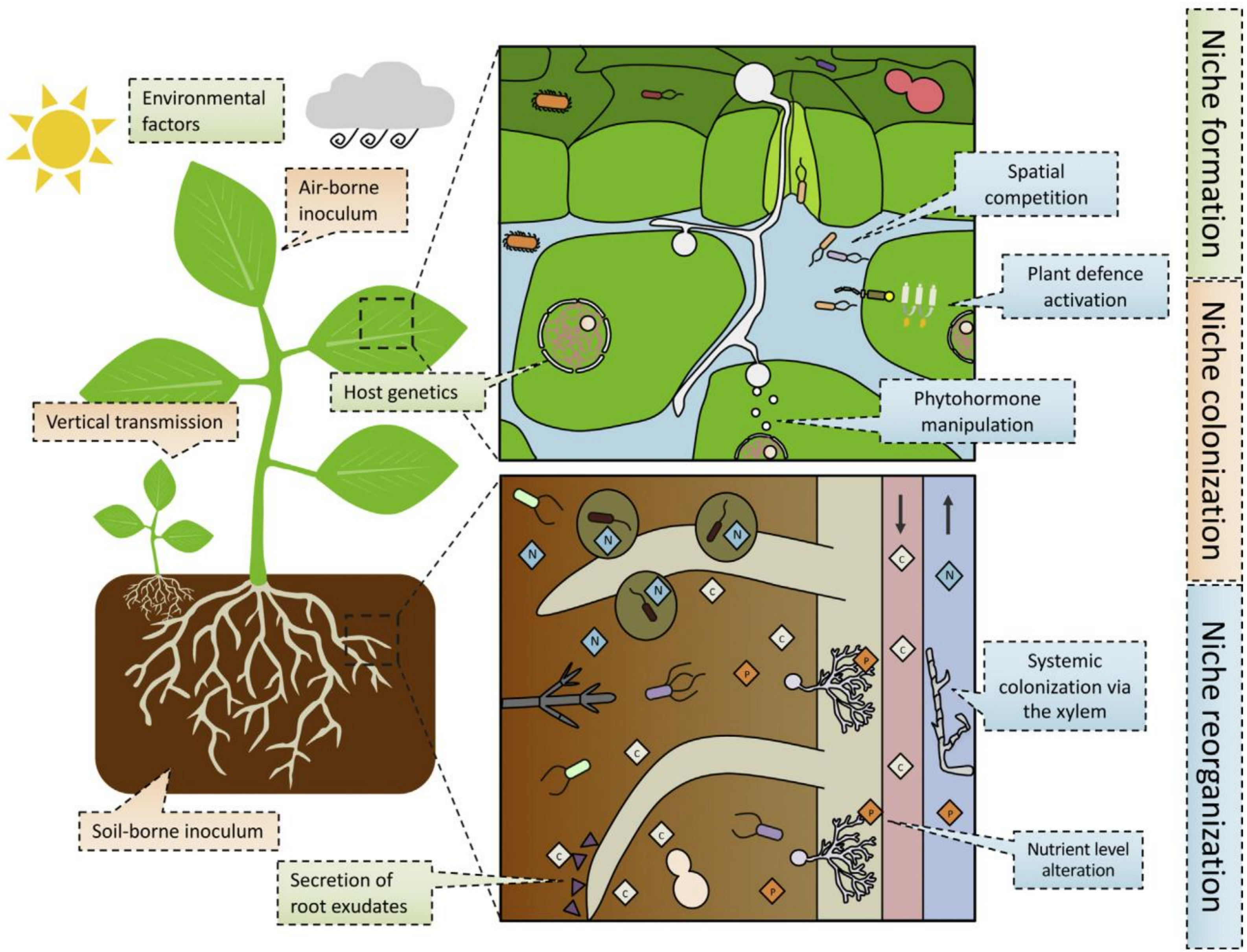


Formation of the plant holobiont. Host genetics together with environmental factors contribute to initial plant niche formation. Those versatile niches are then colonized by a range of microbes, which require different adaptations depending on the colonized tissue type. This results in differential adaptation of microbial genomes and community composition. Apart from tissue specificity, microbes are able to alter a colonized ho niche by, for example, phytohormone manipulation or activation of plant defenses. Dynamics in formation of the holobiont therefore needs consideration.

P. This: Breeding plant holobionts: how plant microbiomes co

The niches theory

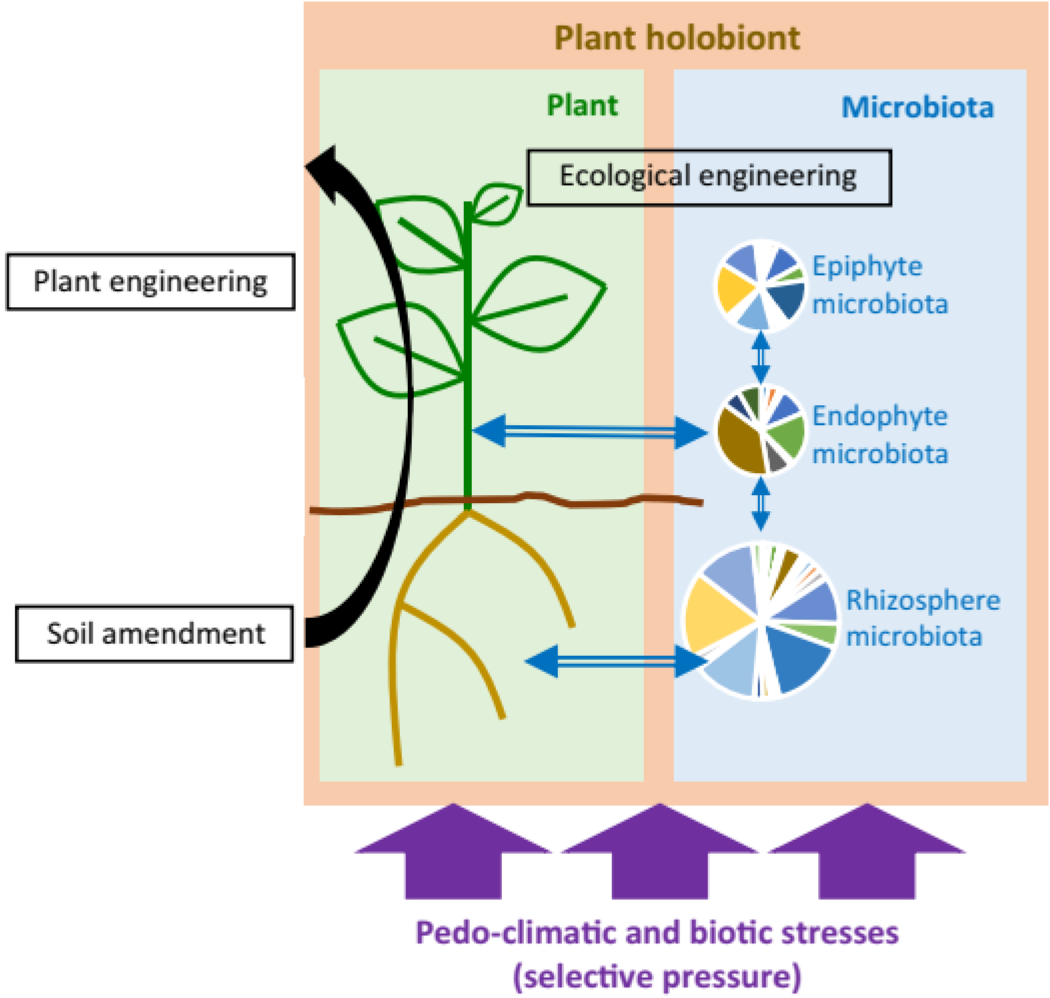
Host genes underlying niche formation represent targets for plant breeding to control the microbiota



Formation of the plant holobiont. Host genetics together with environmental factors contribute to initial plant niche formation. Those versatile niches are then colonized by a range of microbes, which require different adaptations depending on the colonized tissue type. This results in differential adaptation of microbial genomes and community composition. Apart from tissue specificity, microbes are able to alter a colonized ho niche by, for example, phytohormone manipulation or activation of plant defenses. Dynamics in formation of the holobiont therefore needs consideration.

An example

The application of the flagellar peptide flg22 or that of the bacterial to the foliar system of Arabidopsis induced the expression of the malic acid transporter ALMT1,
leading to an **increased malic acid concentration** in the **rhizosphere** of the plants.

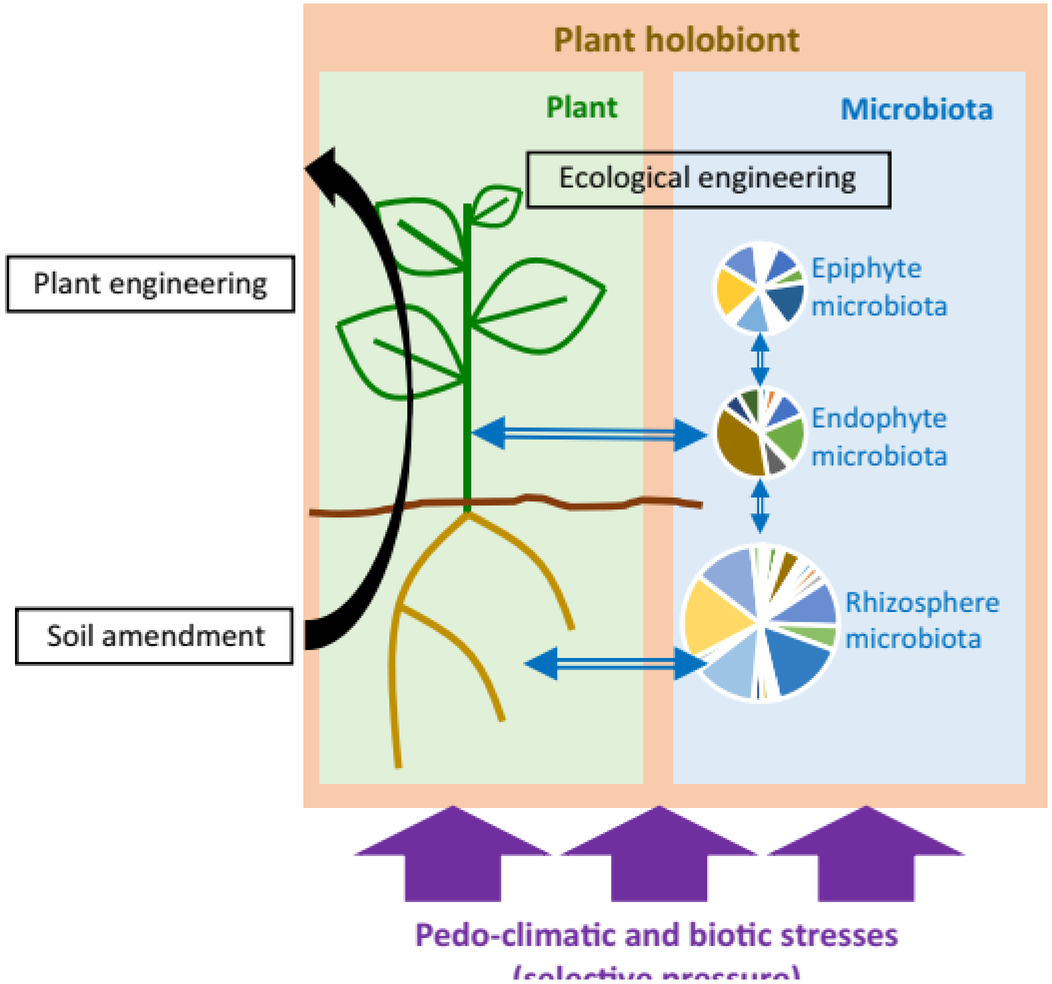


Trends in Plant Science

Yves Dessaux,[1,*] Catherine Grandclément,[1] and Denis Faure[1] Trends in Plant Science 2016

An example

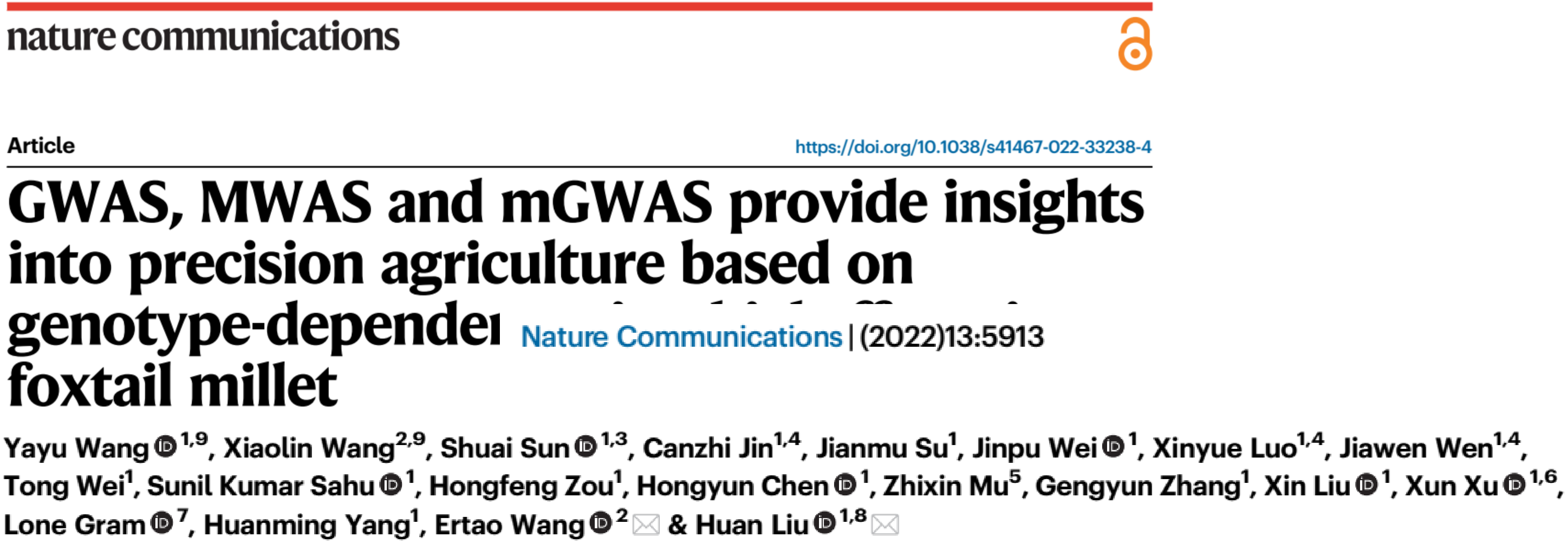
Remarkably, this increased concentration of malic acid beneficiated the PGPR *Bacillus subtilis* strain FB1A7,
the titer of which increased, by 10-fold, causing an induced systemic resistance response in
plants against P. syringae pv. Tomato.



=> Malic acid biosynthesis pathway can be a target

Yves Dessaux,[1,*] Catherine Grandclément,[1] and Denis Faure[1] Trends in Plant Science 2016

How to identify genes involved in recruting microbiome



nature communications

Article

https://doi.org/10.1038/s41467-022-33238-4

GWAS, MWAS and mGWAS provide insights into precision agriculture based on genotype-depende

foxtail millet

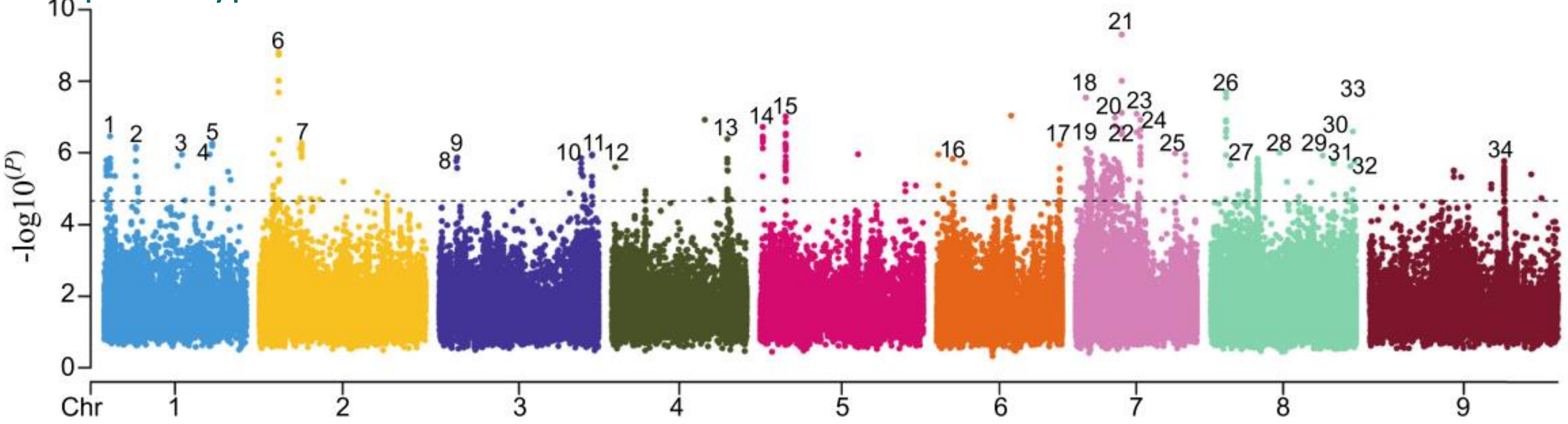
Nature Communications | (2022)13:5913

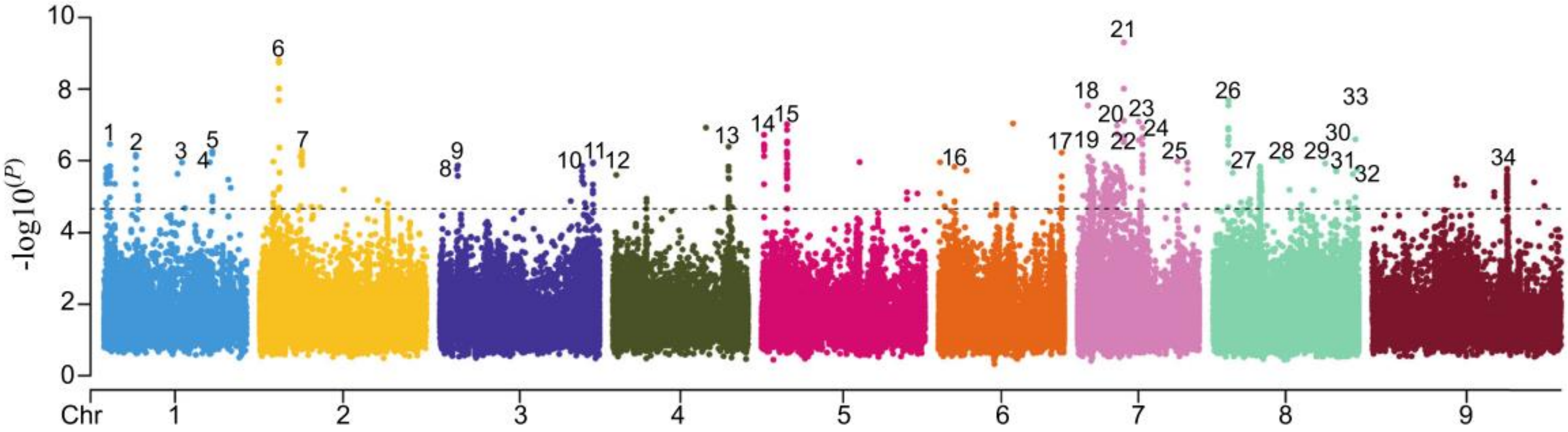
Yayu Wang[1,9], Xiaolin Wang[2,9], Shuai Sun[1,3], Canzhi Jin[1,4], Jianmu Su[1], Jinpu Wei[1], Xinyue Luo[1,4], Jiawen Wen[1,4], Tong Wei[1], Sunil Kumar Sahu[1], Hongfeng Zou[1], Hongyun Chen[1], Zhixin Mu[5], Gengyun Zhang[1], Xin Liu[1], Xun Xu[1,6], Lone Gram[7], Huanming Yang[1], Ertao Wang[2] ✉ & Huan Liu[1,8] ✉

Another example: how to identify genes involved in recruting microbiome

Use the information obtained from the **rhizoplane microbiota of the 827 foxtail millet cultivars**, coupled with the **genome-wide-association** summary statistics for millet growth and yield traits.

=> most of the variations top second leaf width (TSLW), panicle diameter of the main stem (MSPD), main stem panicle weight (MSPW) traits were predicted by rhizoplane microbiota alone, suggesting the important effects of rhizoplane microbiota on host phenotypes.



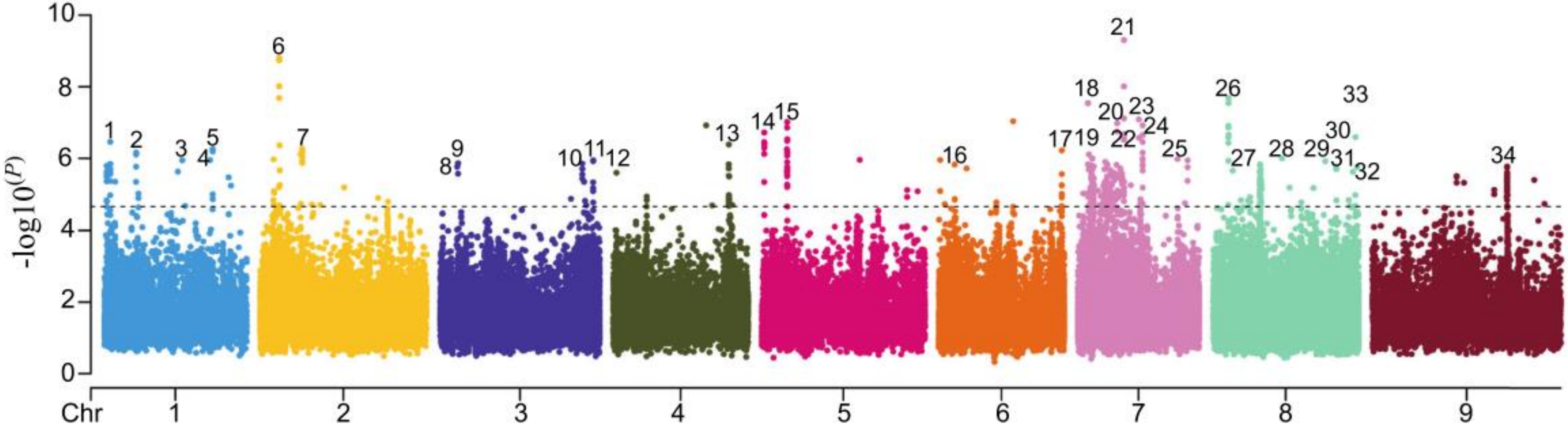


SNPs		Host gene function	Microbial taxa
1	*si1:1723113*	Ca2+/H+ antiporter	OTU_76| Sphingobacteriales
5	*si1:9421763*	transcription factor HBP-1a	OTU_4021| *Niastella*
2	*si1:21809994*	PPR:pentatricopeptide repeat-containing protein	OTU_26564| *Solirubrobacter*
3	*si1:31357983*	Acid phosphatase type	OTU_283| *Nocardia*
4	*si1:32154433*	NIT4:bifunctional nitrilase/nitrile hydratase NIT4	OTU_867| *Curtobacterium*
6	*si2:5642650*	WAK2:wall-associated receptor kinase 2	OTU_643| Gp7;OTU_11652| Gp4
7	*si2:5817610*	CAS1:cycloartenol synthase	OTU_643| Gp7

Fig. 5 | Host genetic variation correlated with common bacterial taxa. Manhattan plots show the significant SNPs for microbial abundance. SNPs located in gene coding regions are labeled with numbers. Details of the associations between the host genes and microbial species are given in the table below. All of these associations of SNP loci and microbial OTUs were significantly lesser than 2.01e−5.

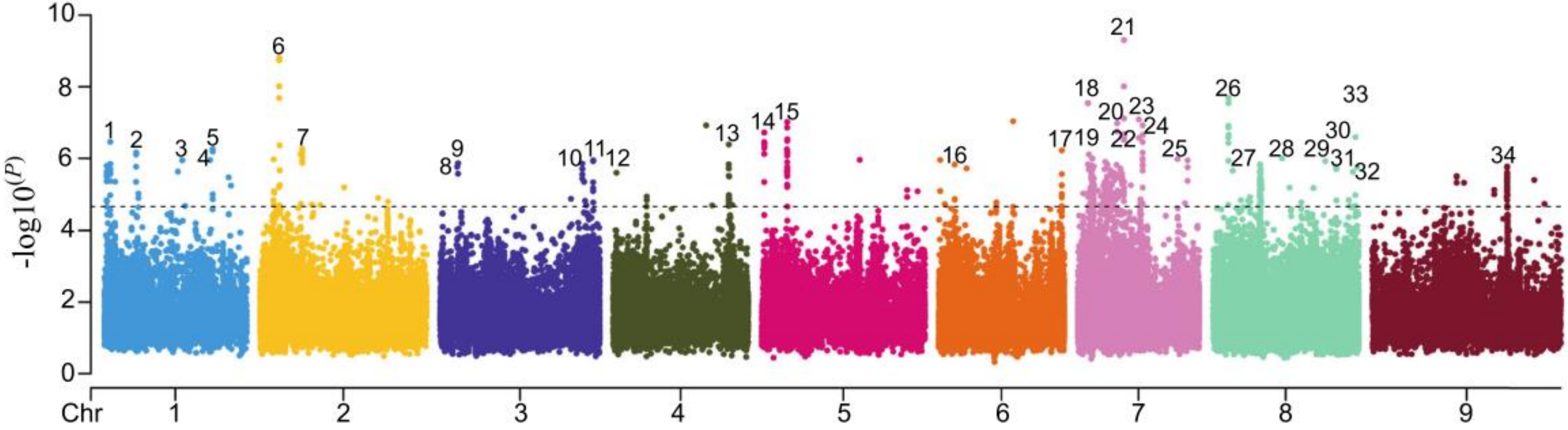
Another example: how to identify genes involved in recruting microbiome

- Thus, it will be important to consider MWAS in studies aiming to improve crop agronomic desirable traits since MWAS can be used to discover rhizobacteria that modulate plant growth.
- In addition, the genes induced by growth promoting bacteria varied among marker strains, indicating that plants have customized responses to different bacteria

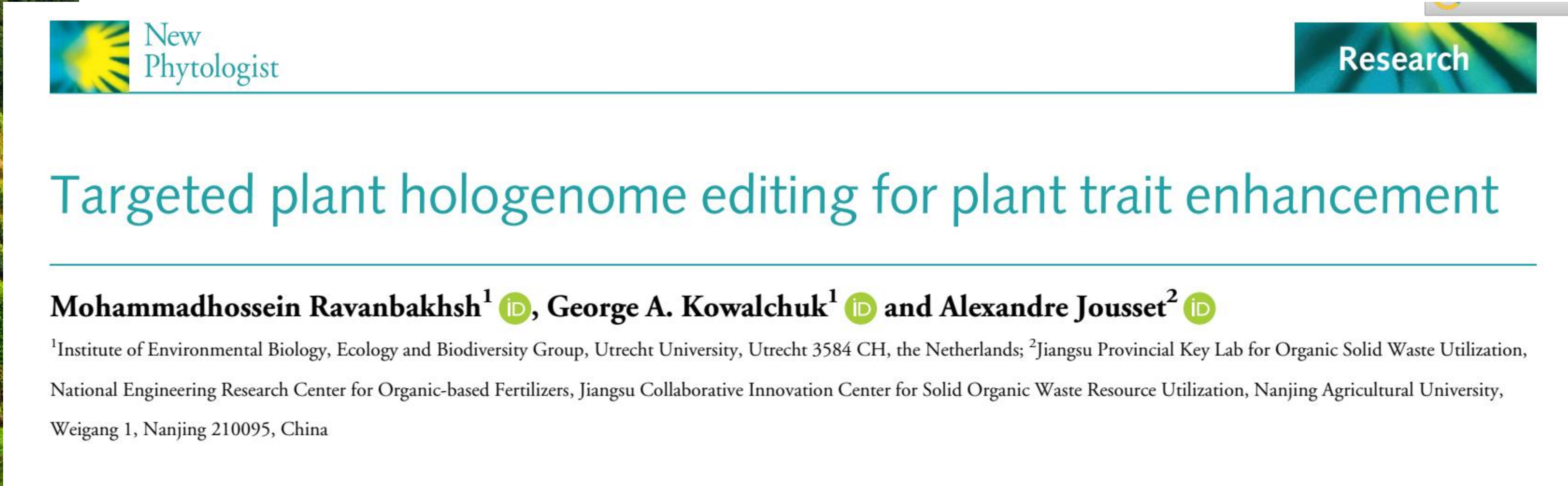


Another example: how to identify genes involved in recruting microbiome

- Host genetics might shape the composition of the root microbiota which in turn shapes the agronomic traits of foxtail millet, similar to the Mendelian randomization relationships among the gut microbiome, short-chain fatty acids and metabolic diseases



What does this mean in term of breeding ?



New Phytologist

Research

Targeted plant hologenome editing for plant trait enhancement

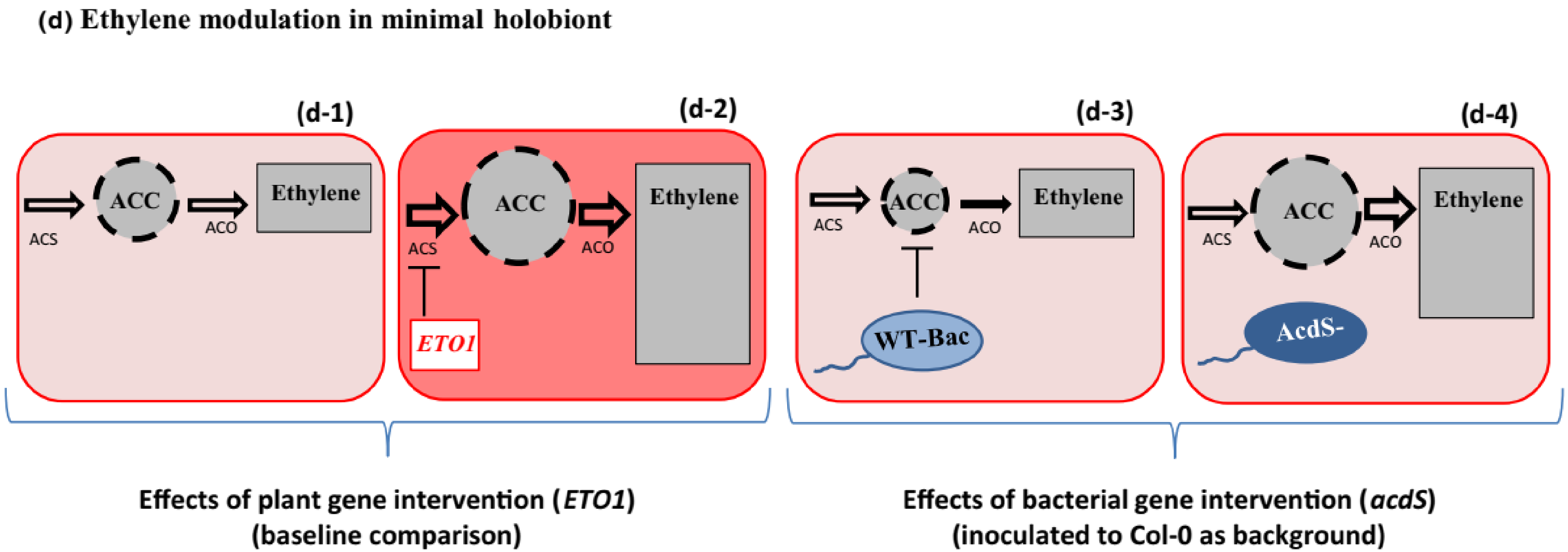
Mohammadhossein Ravanbakhsh[1], **George A. Kowalchuk**[1] and **Alexandre Jousset**[2]

[1] Institute of Environmental Biology, Ecology and Biodiversity Group, Utrecht University, Utrecht 3584 CH, the Netherlands; [2] Jiangsu Provincial Key Lab for Organic Solid Waste Utilization, National Engineering Research Center for Organic-based Fertilizers, Jiangsu Collaborative Innovation Center for Solid Organic Waste Resource Utilization, Nanjing Agricultural University, Weigang 1, Nanjing 210095, China

Ethylene-regulating genes encoded in microbial and plant genomes can have comparable effects on plant growth and stress tolerance (Ravanbakhsh et al., 2019)

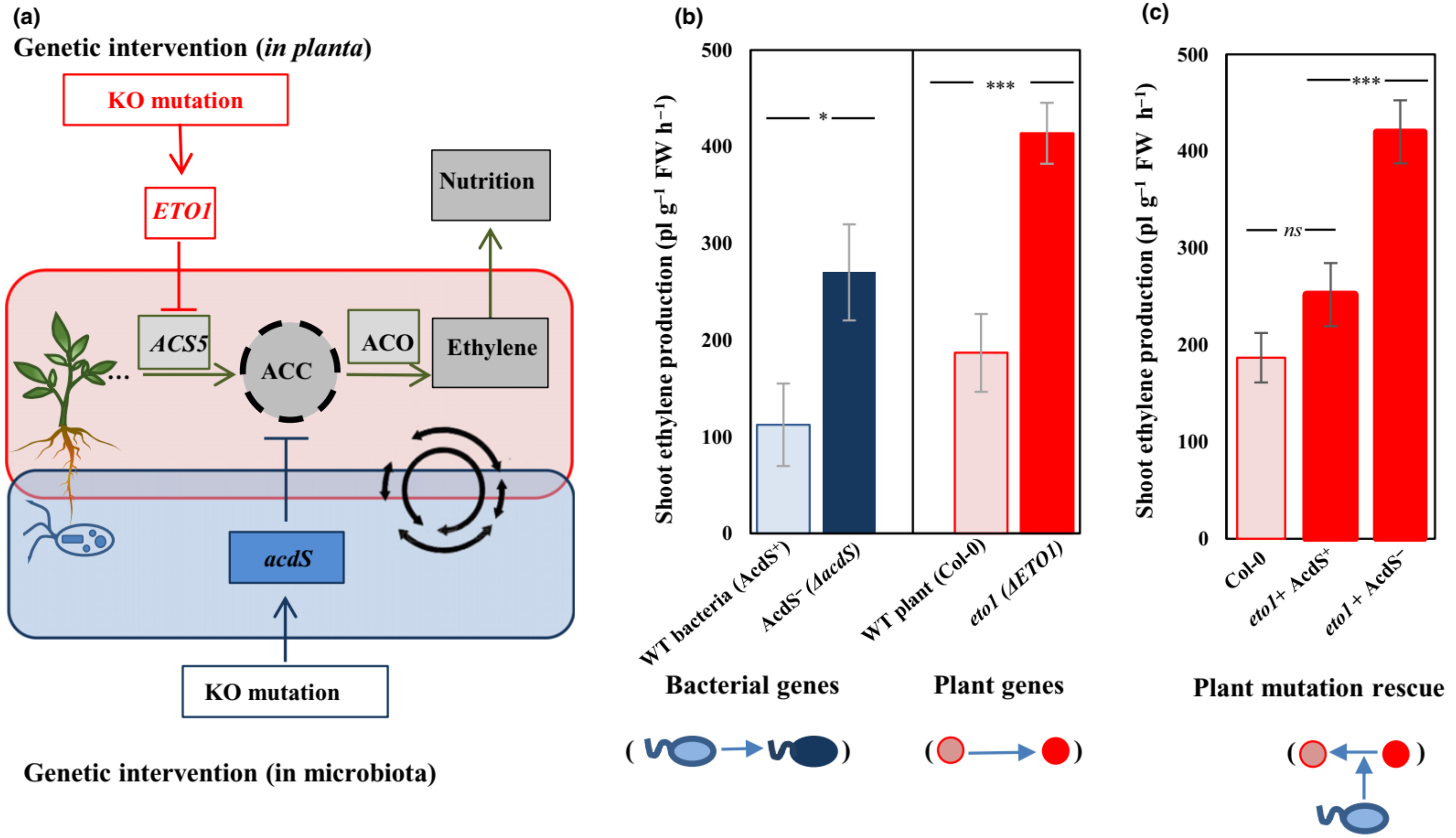
What does this mean in term of breeding ?

Using a minimal holobiont model, they track ethylene production and plant nutritional value in response to alterations in plant ethylene synthesis (KO mutation in ETO1), which induces 1-aminocyclopropane-1-carboxylic acid (ACC) synthase 5 (ACS5), or microbial degradation of ACC (KO mutation in microbial acdS), preventing the breakdown of the plant ACC pool, the product of ACS5



(d) Ethylene modulation in minimal holobiont

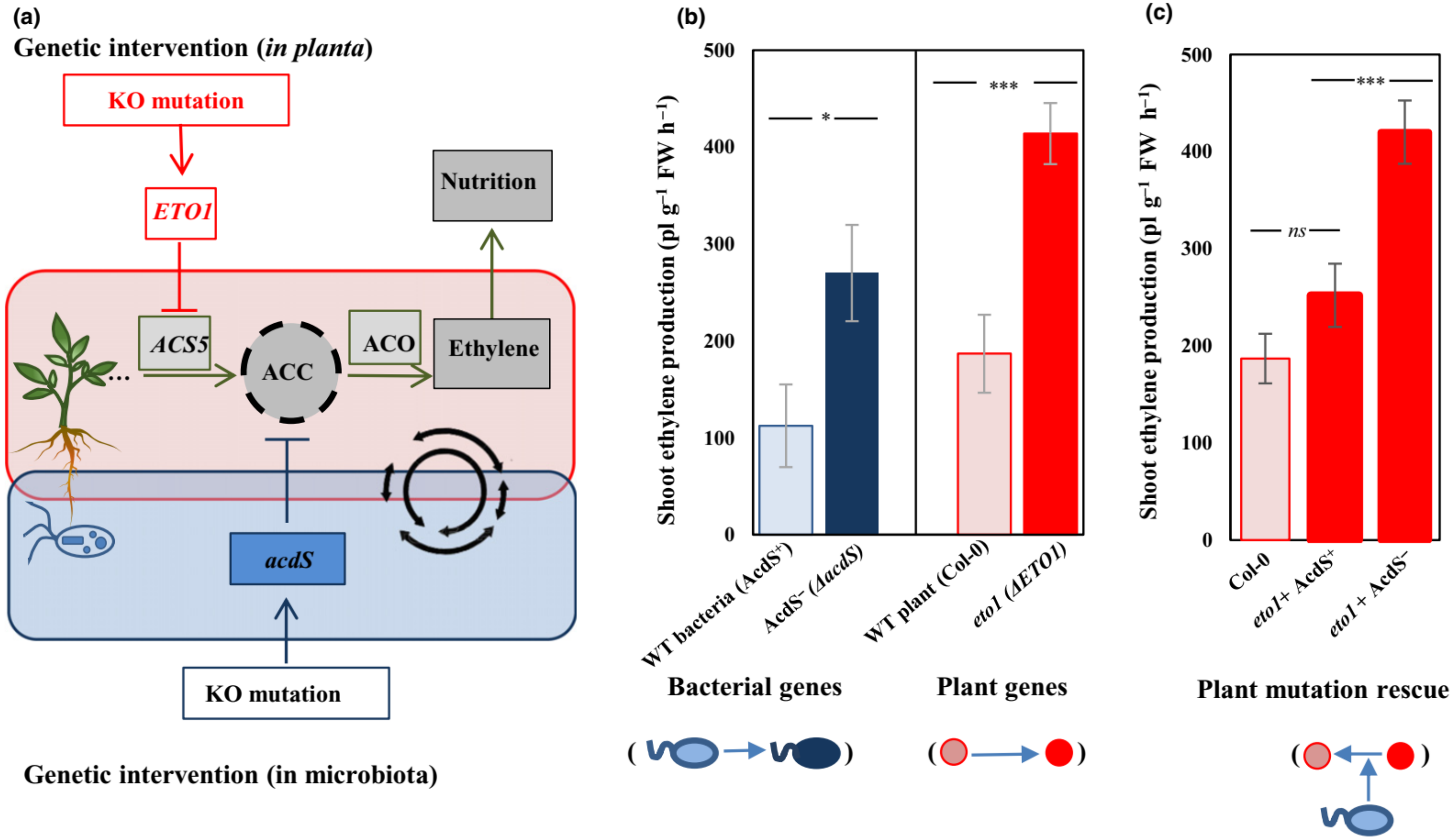
What does this mean in term of breeding ?



Similar plant phenotypes can be generated by either specific mutations of plant-associated microbes or alterations in the plant genome.

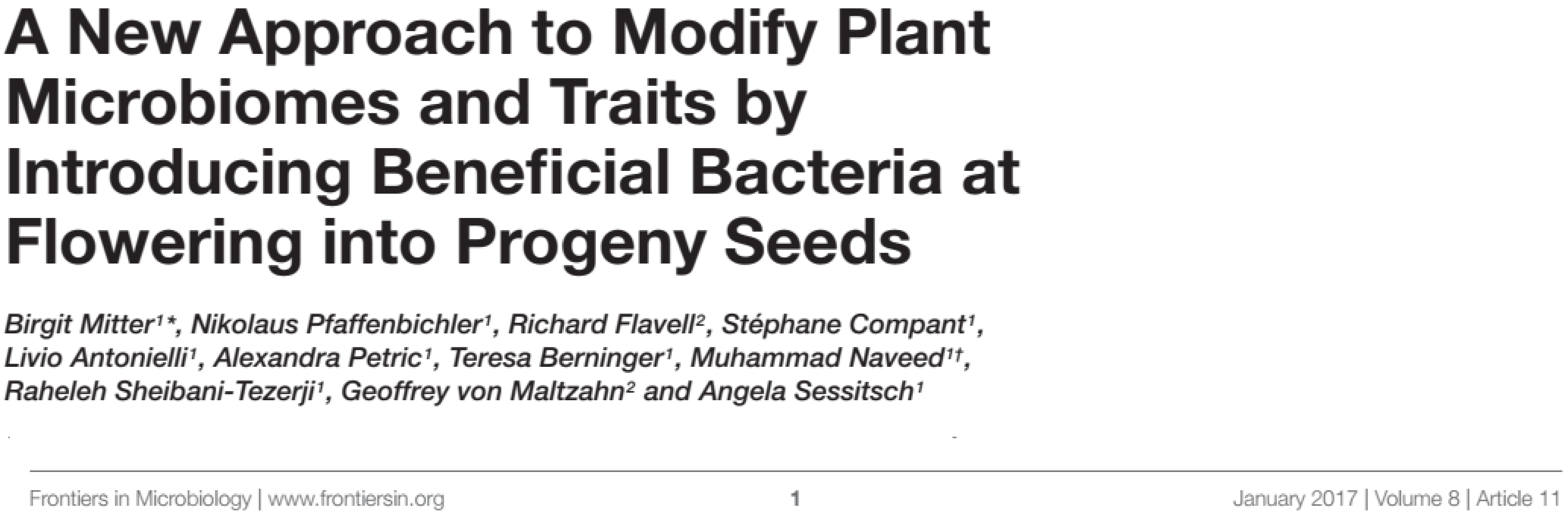
P. This: Breeding plant holobionts: how plant microbiomes could be integrated in breeding strategies

What does this mean in term of breeding ?



Plant and bacterial genes build an integrated plant–microbe regulatory network amenable to genetic improvement from both the plant and microbial sides.

What does this mean in term of breeding ?



A New Approach to Modify Plant Microbiomes and Traits by Introducing Beneficial Bacteria at Flowering into Progeny Seeds

Birgit Mitter[1], Nikolaus Pfaffenbichler[1], Richard Flavell[2], Stéphane Compant[1], Livio Antonielli[1], Alexandra Petric[1], Teresa Berninger[1], Muhammad Naveed[1]†, Raheleh Sheibani-Tezerji[1], Geoffrey von Maltzahn[2] and Angela Sessitsch[1]*

Frontiers in Microbiology | www.frontiersin.org 1 January 2017 | Volume 8 | Article 11

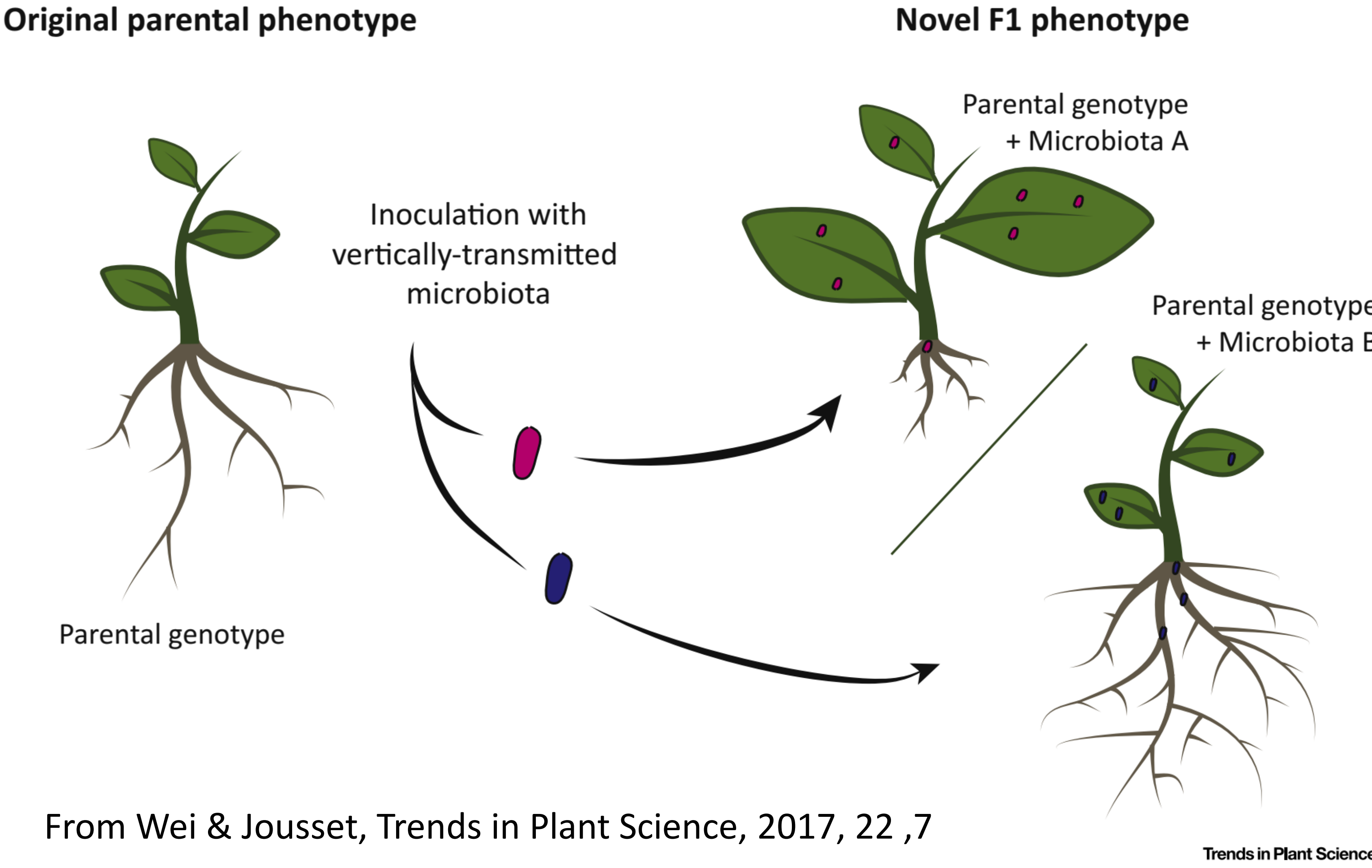
What does this mean in term of breeding ?

Endoendophytic microbes in the flowers, can modify the timing of flowering in wheat

By inoculating flowers with specific microbiota, the team of B. Mitter was able to transfer them reliably into seed material, passing them to the next plant generation

What does this mean in term of breeding ?

The microbes could survive both as endophytes within the plants and from there grow in the rhizosphere.
=> usefulness of this approach by transmitting vertically beneficial microbes that speed up flowering. material, passing them to the next plant generation

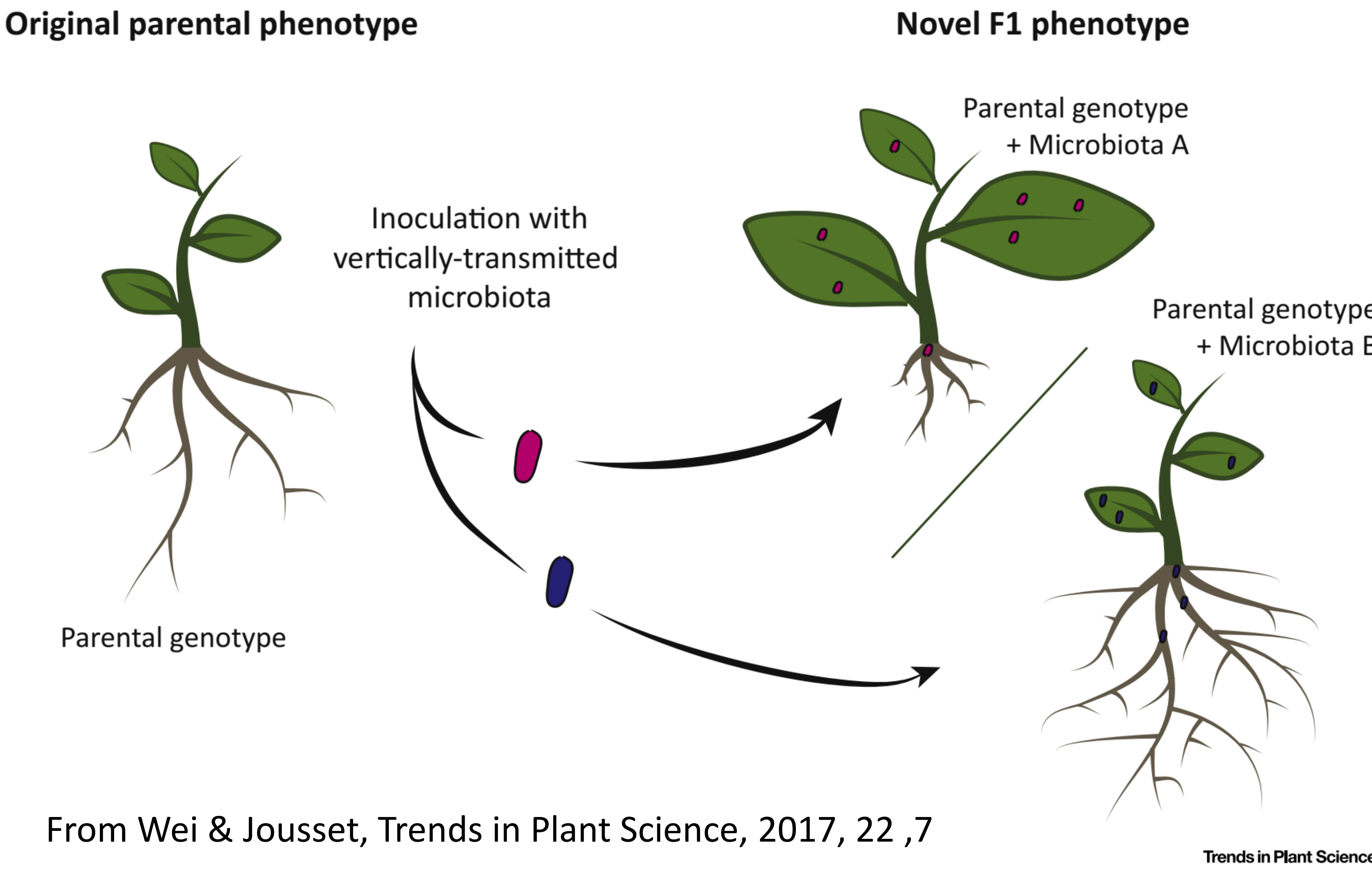


From Wei & Jousset, Trends in Plant Science, 2017, 22 ,7

Figure 1. Conceptual Use of Vertically-transmitted Microbiota as a Basis for a Holobiont-level Breeding. The parental plant genotype can be inoculate with microbes that can modify various life history traits of the plant. Thanks to new developments enabling reliable microbial transmission to the next plant generatio the desired plant phenotype can be obtained by a combination of host- and microbial encoded traits that form together an inheritable unit.

What does this mean in term of breeding ?

By introducing specific endophytic microbes through the flowers, the timing of flowering in wheat could be optimized without manipulating the plant genotype.



From Wei & Jousset, Trends in Plant Science, 2017, 22 ,7

Figure 1. Conceptual Use of Vertically-transmitted Microbiota as a Basis for a Holobiont-level Breeding. The parental plant genotype can be inoculate with microbes that can modify various life history traits of the plant. Thanks to new developments enabling reliable microbial transmission to the next plant generatio the desired plant phenotype can be obtained by a combination of host- and microbial encoded traits that form together an inheritable unit.

Take Home messages

- Holobiont should be considered in breeding, instead of just the plant partner
- Microbiome are involved in many major fonctions of plant nutrition and plant resistance to biotic and abiotic stresses
- Microbiome diversity is important, dependant of the plant organ, affected by many factors (cultivation, environment), genotype notably for rhizosphere
- Since microbiome is involved in major traits, modifing microbiome in plant may have an effect on the phenotype
- This will require building our understanding of how plant genotypes impact colonization of specific microorganisms that might help to fix beneficial microbiota-related traits

Take Home messages (2)

- Host genes underlying niche formation represent targets for plant breeding to control the microbiota
- MWAS (microbiome association genetics) enables to identify targets in the plant with an effect on specific microorganism

- Modifiyng baterial gene by gene editing have similar affect than modifiyng plant genes
- Finally, by introducing specific endophytic microbes through the flowers, the timing of flowering in wheat could be optimized without manipulating the plant genotype.

Thanks for your attention