

# ***Xylella fastidiosa* infection alters the xylem microbiota in wild and cultivated olive trees**



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4<sup>th</sup> European  
conference on  
***Xylella  
fastidiosa***  
**2023**

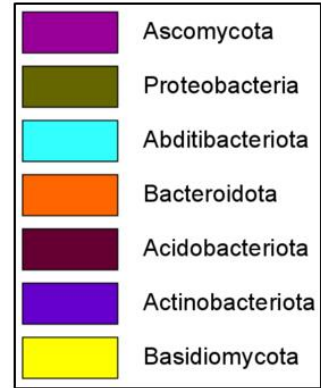
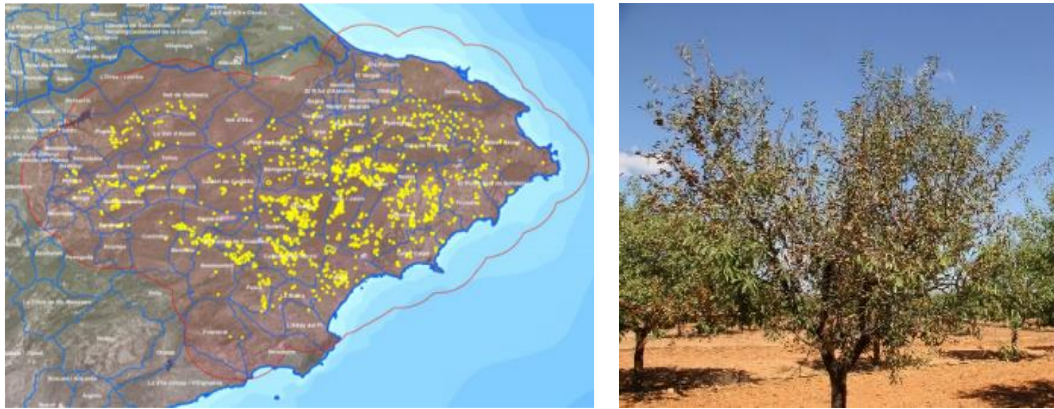


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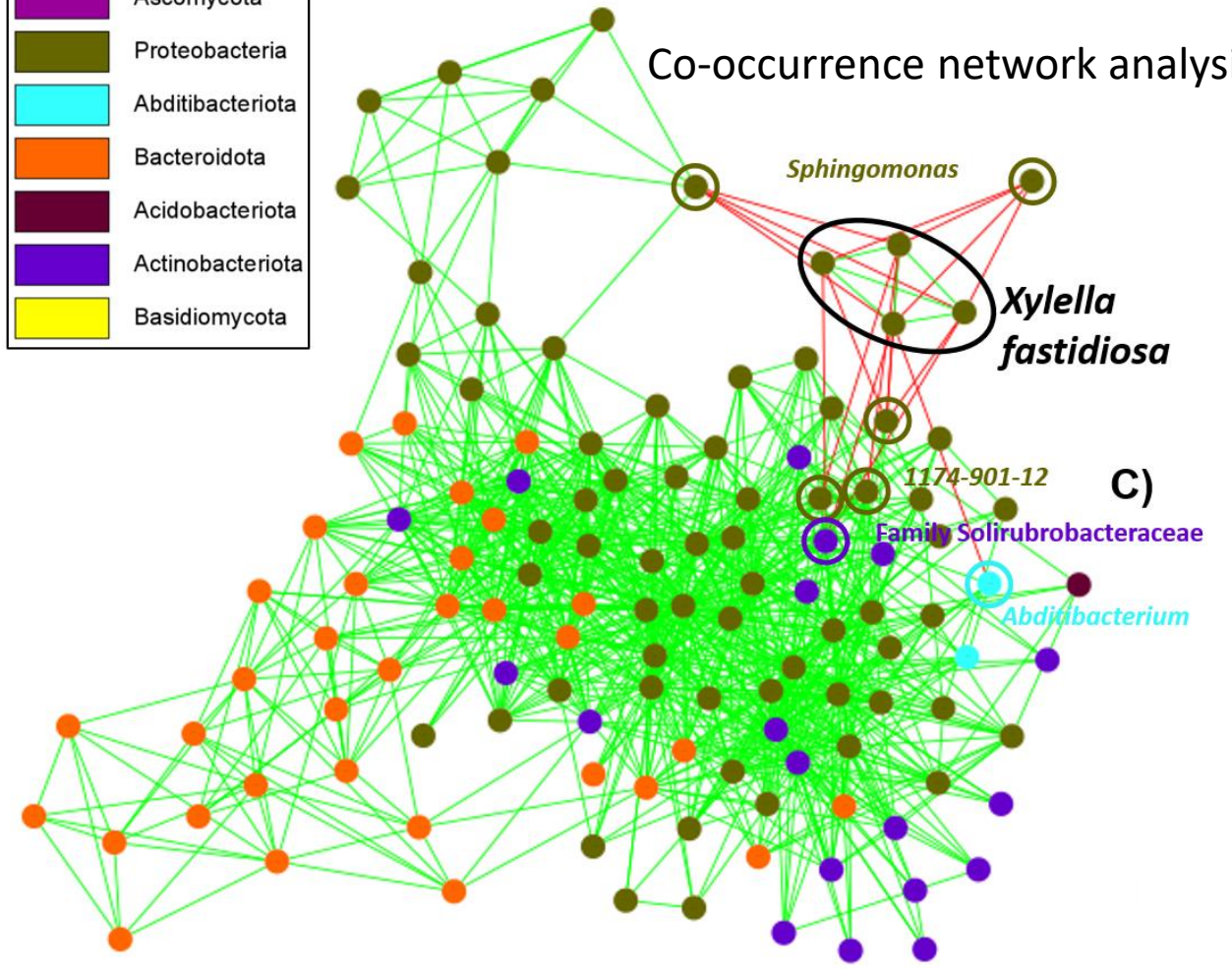
**Lyon, 19 – 20 August 2023**

# *Xylella fastidiosa* infection reshapes microbial composition and network associations in the xylem of almond trees

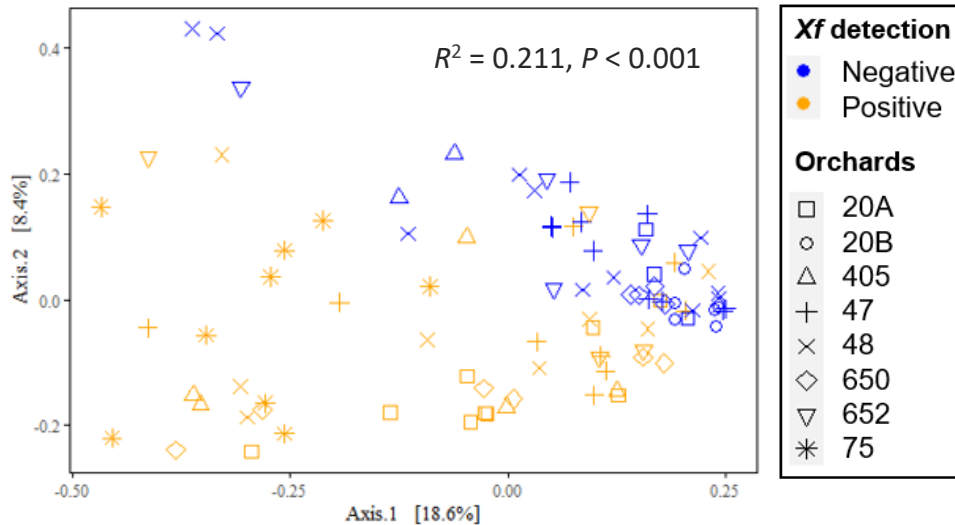
Province of Alicante



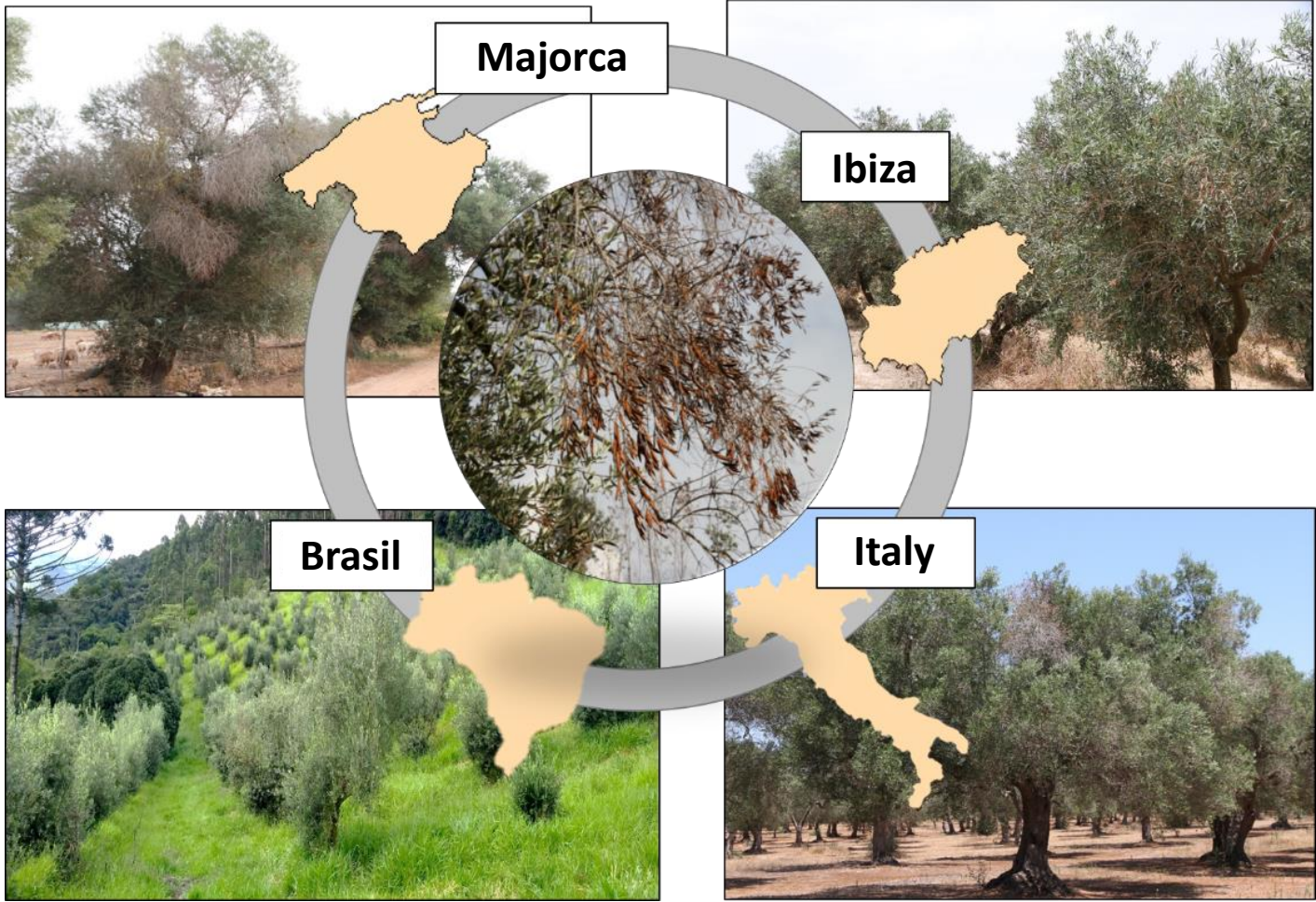
Co-occurrence network analysis



Beta diversity – ASVs Weighted Unifrac

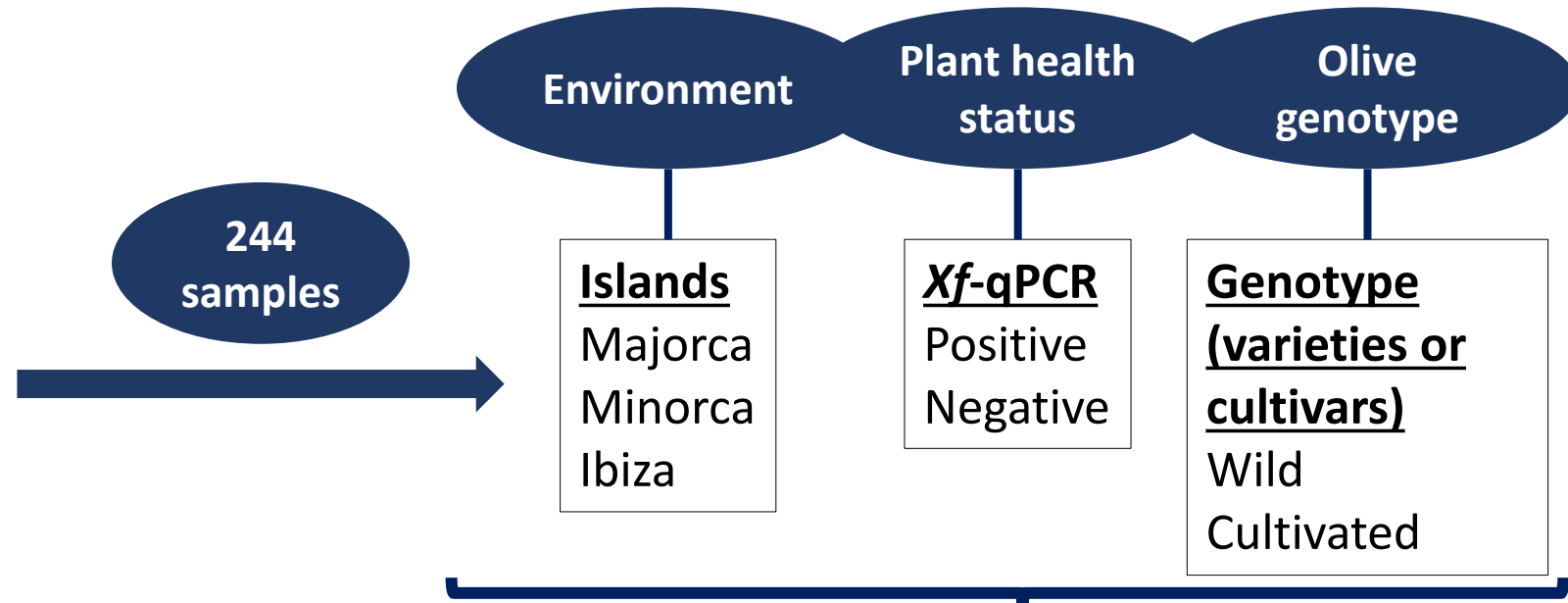
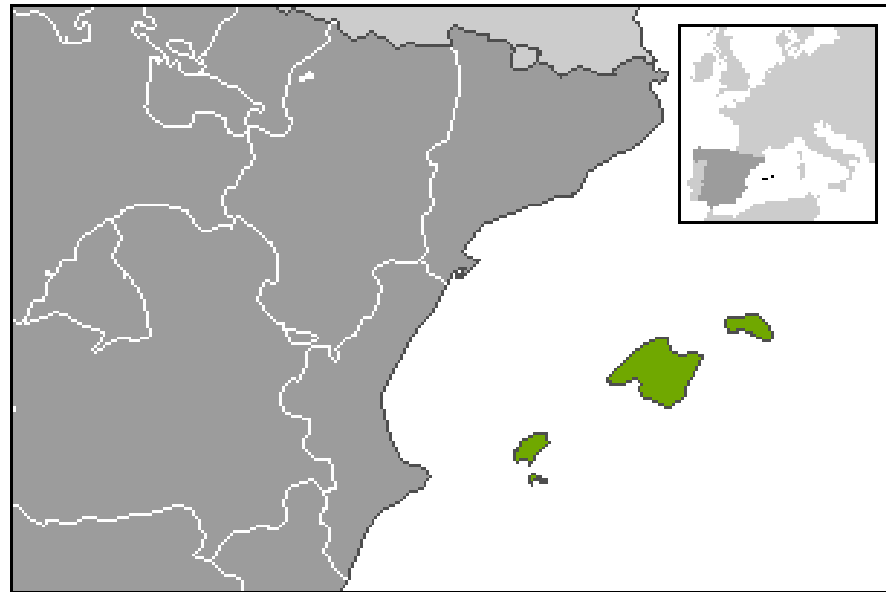


# Is the xylem microbiome involved in the tolerance of olive tree to *Xylella fastidiosa*?



Microbiome comparative research ongoing

# Xylem-inhabiting bacterial communities in different wild and cultivated olive genotypes infected or not by *Xylella fastidiosa* under natural field conditions in the Balearic Islands



Leaf petioles



Differences in the xylem microbiota associated to the factors analysed and EST-SNP marker analysis to identify the olive accession

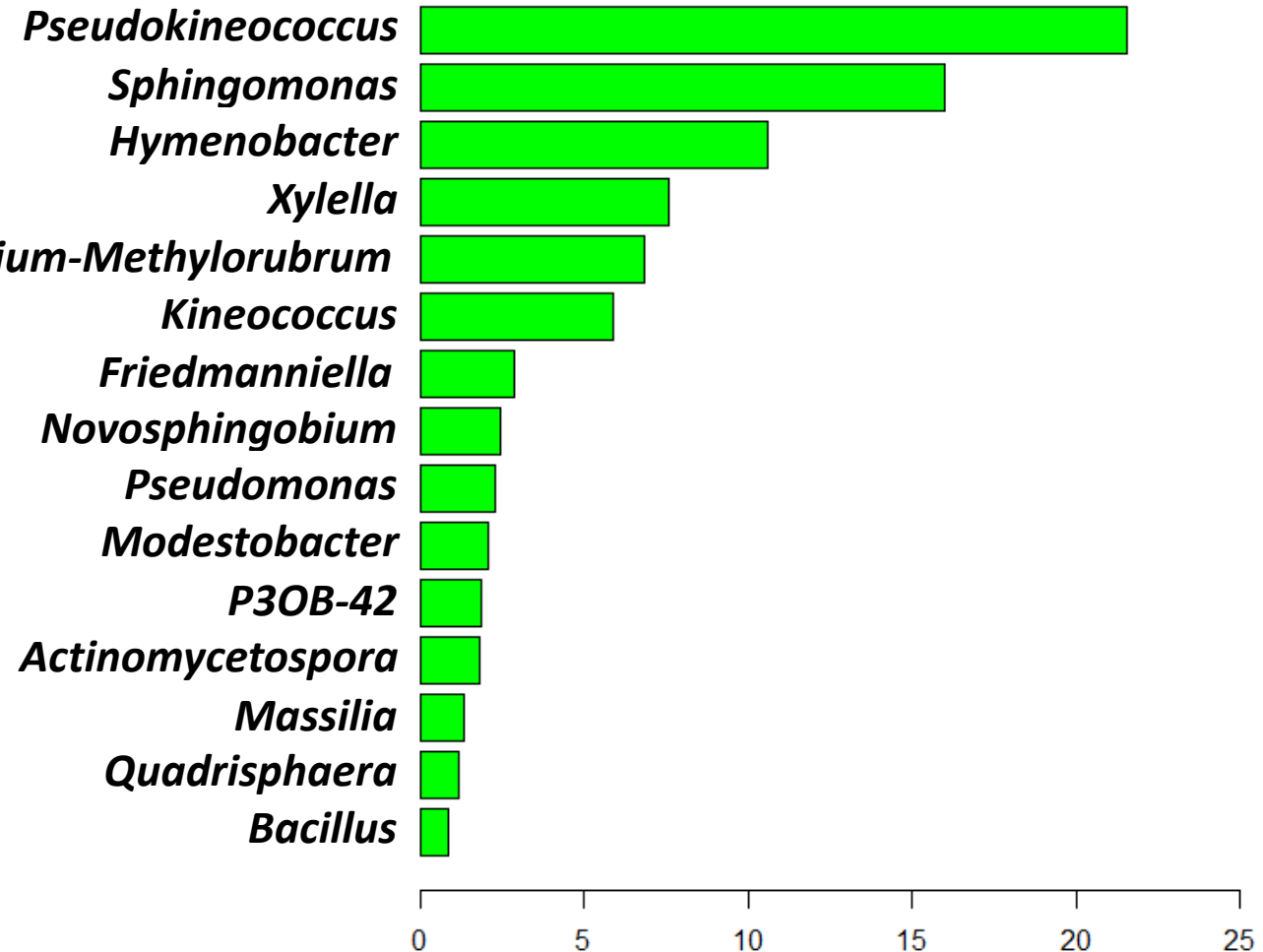
# Differences in the xylem microbiota associated to wild and cultivated olive genotypes

## General overview

Input	11,343,819 reads	
Filtered	7,952,664 reads	
Merged	7,636,478 reads	
Nonchim	7,254,012 reads	→ 5,909 ASVs
Archaea	2	
Eukaryota	0	
Unassigned Phylum	222	
Mitochondria, Chloroplast...	61	
Singletons	150	→ <b>1,119 ASVs</b>
Prevalence 5%	4,355	
	Mean: 26,104 reads/sample	
	Total: 6,291,151 reads Bacteria	

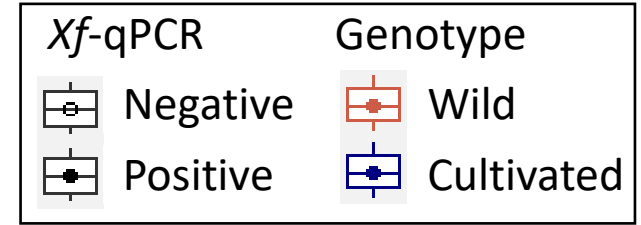
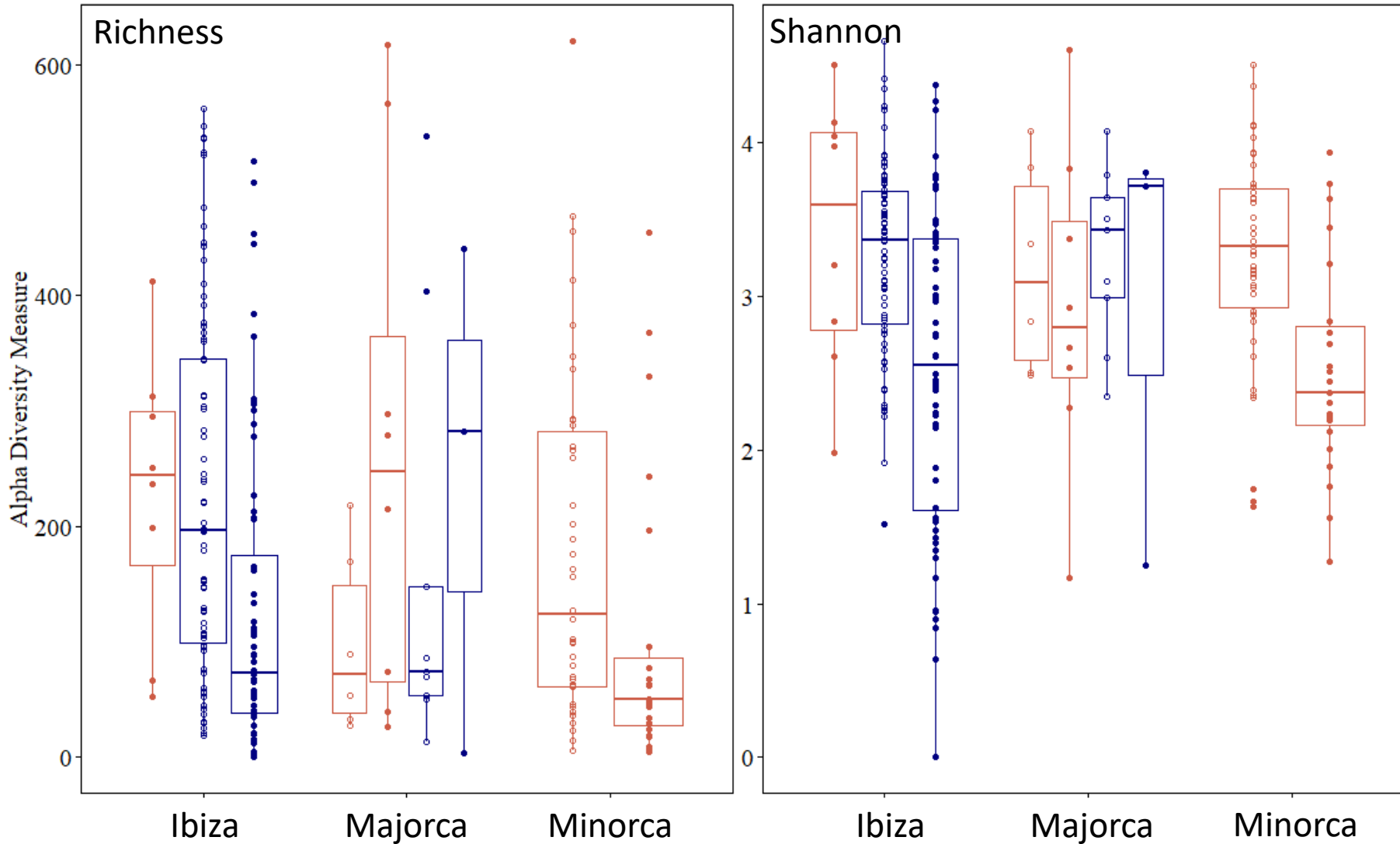
**ASV: 1,119**  
**Genera: 257**

## Relative Abundance - Genus level



# Differences in the xylem microbiota associated to wild and cultivated olive genotypes

## Alpha Diversity



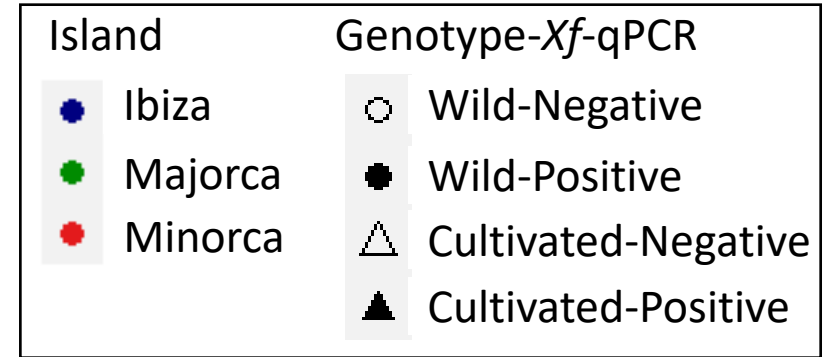
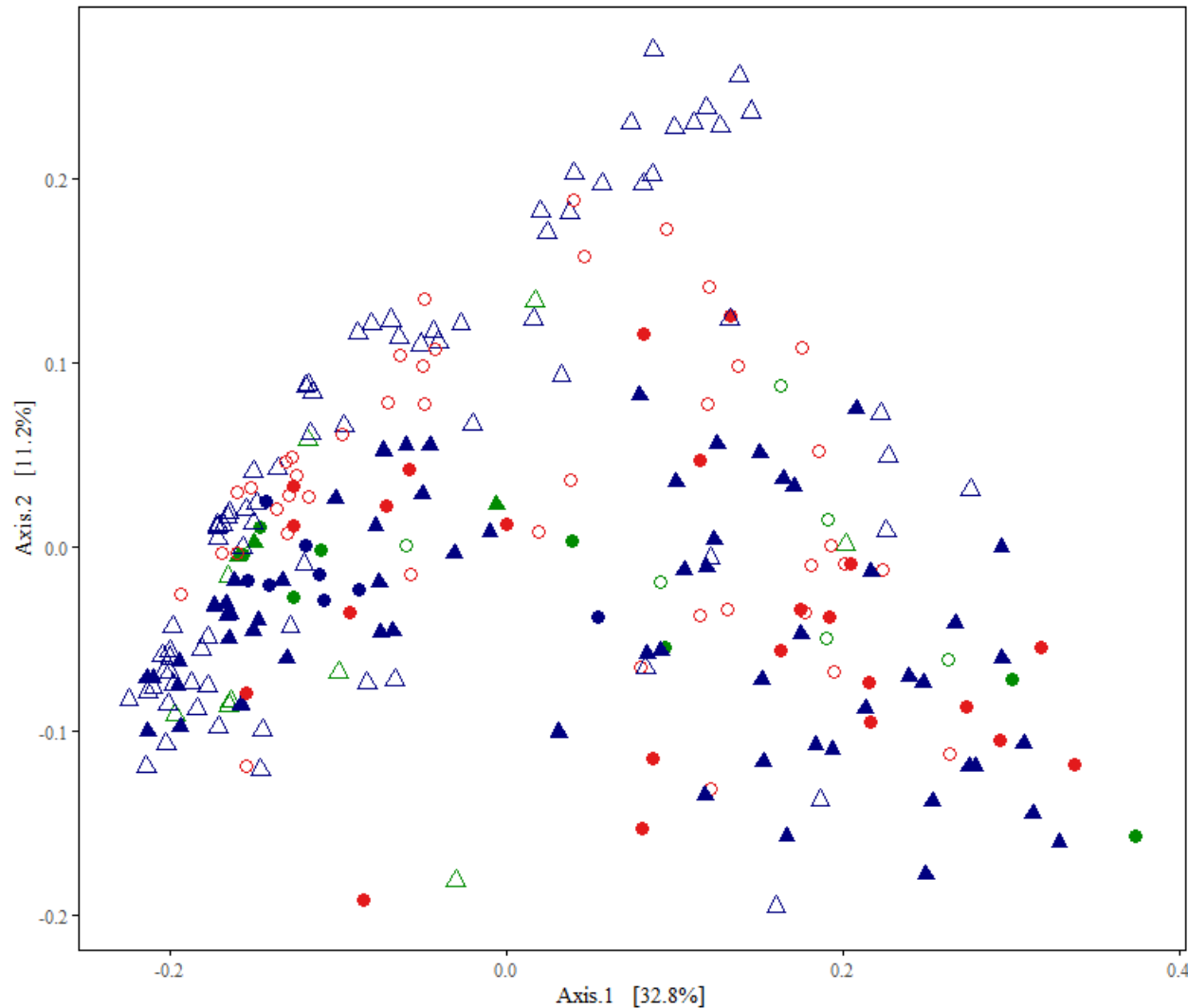
### Kruskal-Wallis Test - ASVs

Factor	Richness	
	H	P-value
Island	3.4919	0.1745
Genotype	1.2862	0.2567
<i>Xf</i>	11.353	<b>0.0007</b>

Factor	Shannon	
	H	P-value
Island	0.6265	0.7310
Genotype	0.2540	0.6142
<i>Xf</i>	26.454	<b>0.0001</b>

# Differences in the xylem microbiota associated to wild and cultivated olive genotypes

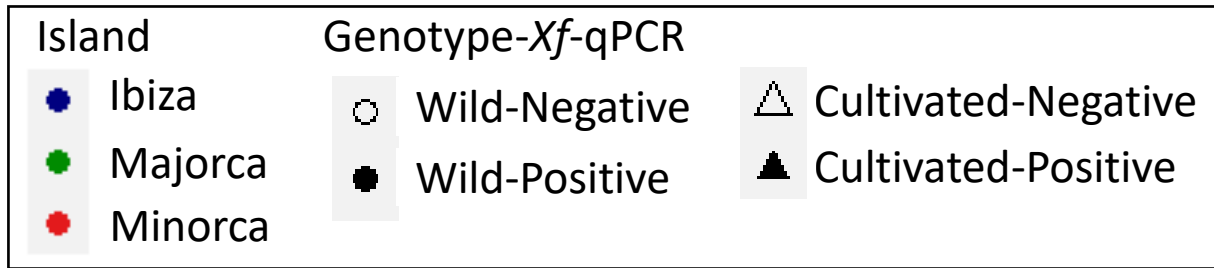
## Beta Diversity – Weighted Unifrac



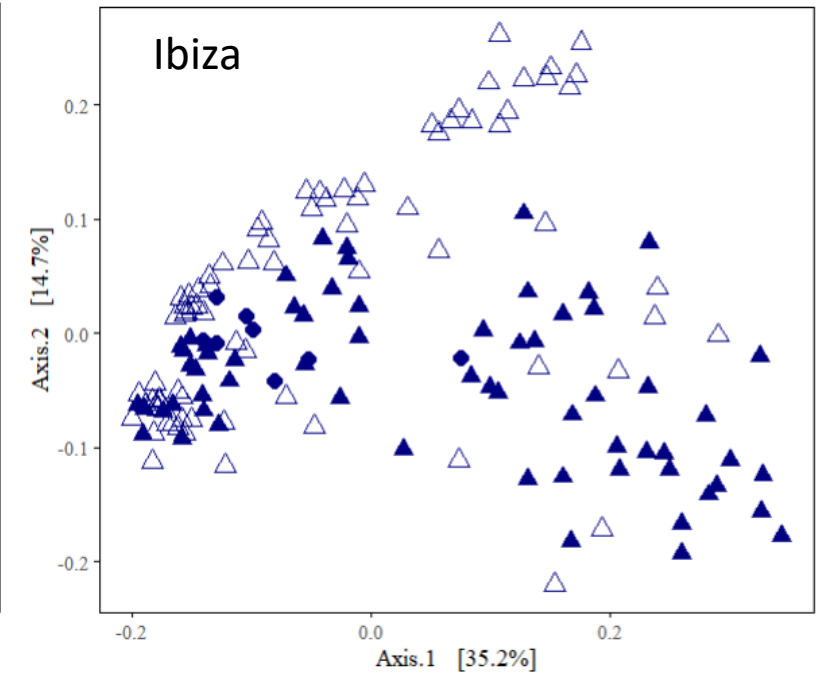
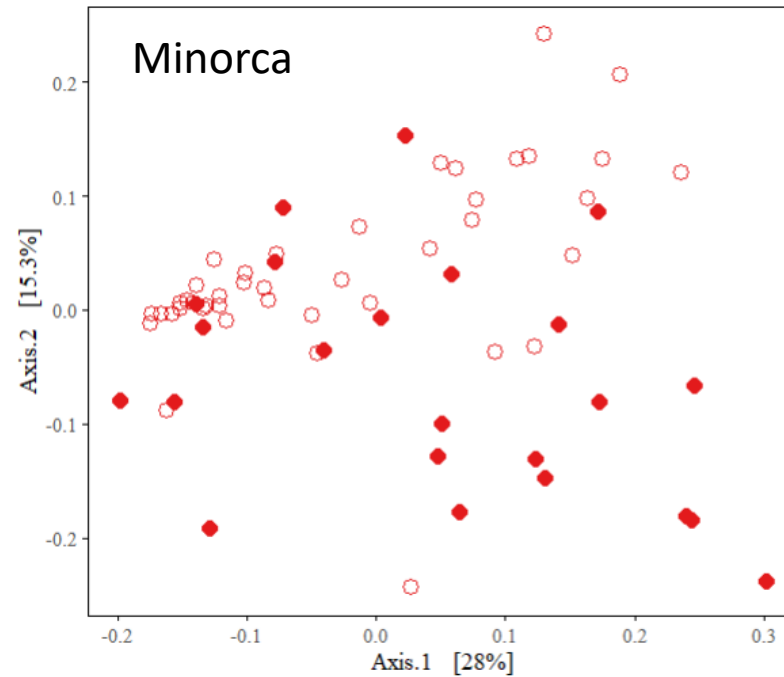
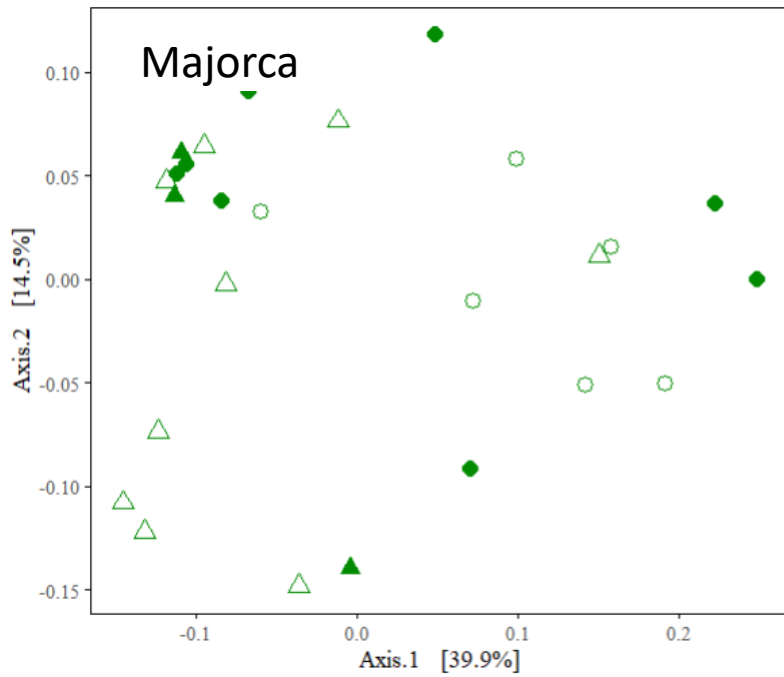
## Permanova

Factor	$R^2$	$P$ -value
Island	0.029	0.001
Genotype	0.006	0.120
<i>Xf</i>	0.049	0.001
Island*Genotype	0.016	0.001
Island* <i>Xf</i>	0.018	0.008
Genotype* <i>Xf</i>	0.003	0.393

# Differences in the xylem microbiota associated to wild and cultivated olive genotypes



## Beta Diversity – Weighted Unifrac



Factor	$R^2$	$P$ -value
Genotype	0.130	<b>0.005</b>
<i>Xf</i>	0.079	0.061
Genotype* <i>Xf</i>	0.036	0.343

Factor	$R^2$	$P$ -value
<i>Xf</i>	0.062	<b>0.003</b>

Factor	$R^2$	$P$ -value
Genotype	0.014	<b>0.036</b>
<i>Xf</i>	0.074	<b>0.001</b>



# Differences in the xylem microbiota associated to wild and cultivated olive genotypes

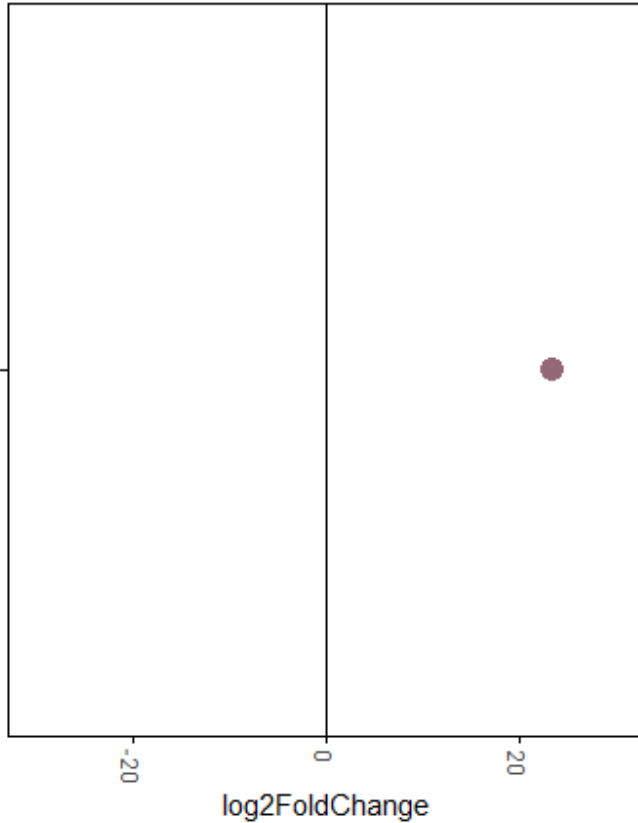
## Differential significant abundance (DESeq2)

According to genotype

### Majorca

Cultivated

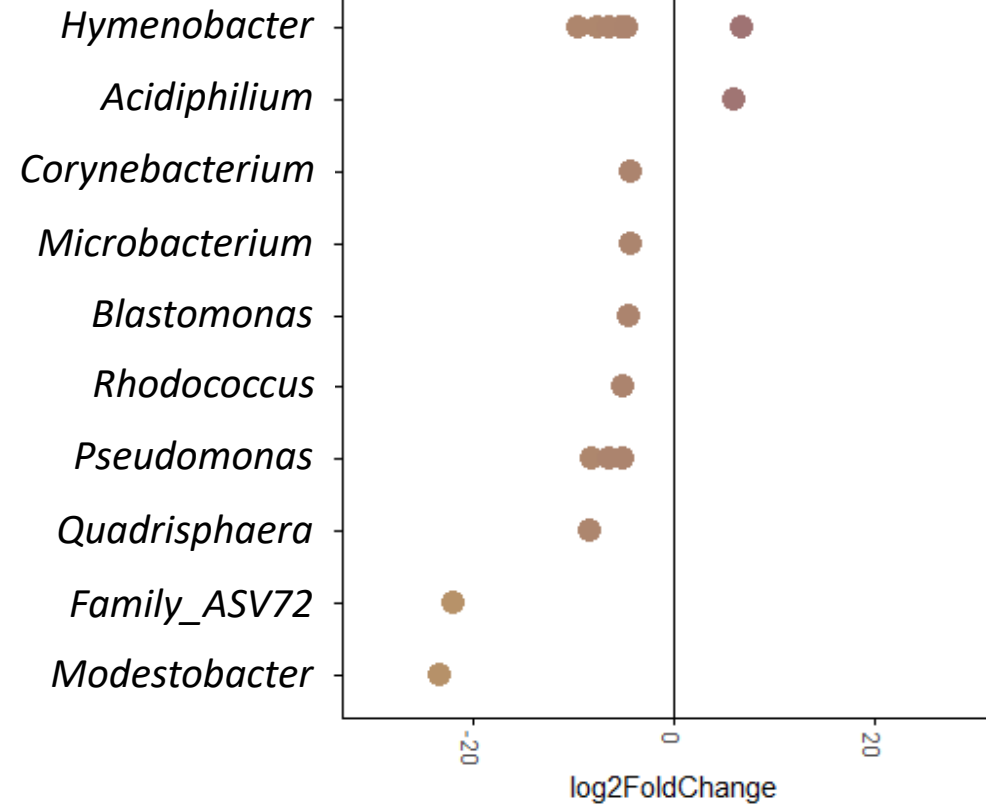
Wild



### Minorca

Cultivated

Wild

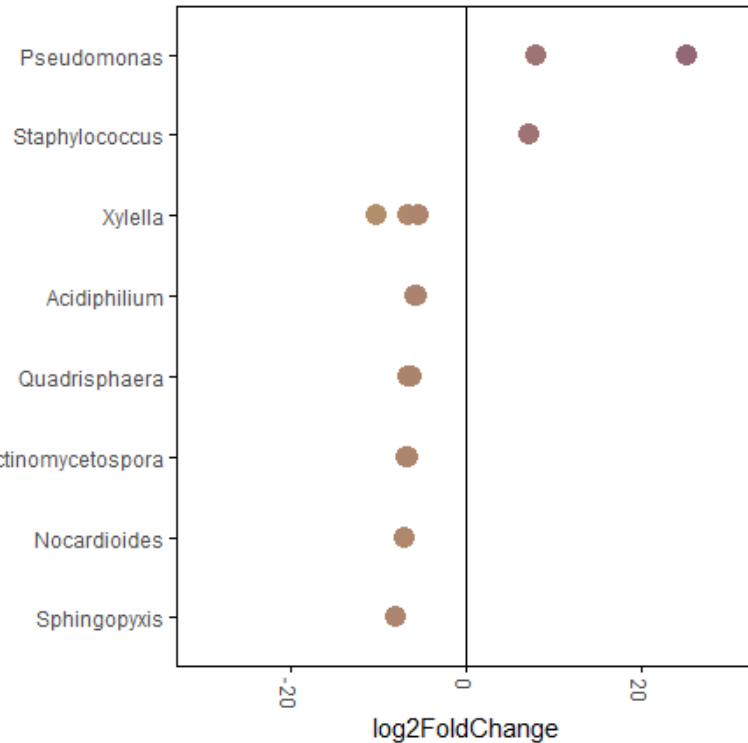


# Differences in the xylem microbiota associated to wild and cultivated olive genotypes

According to *Xf*-qPCR

## Majorca

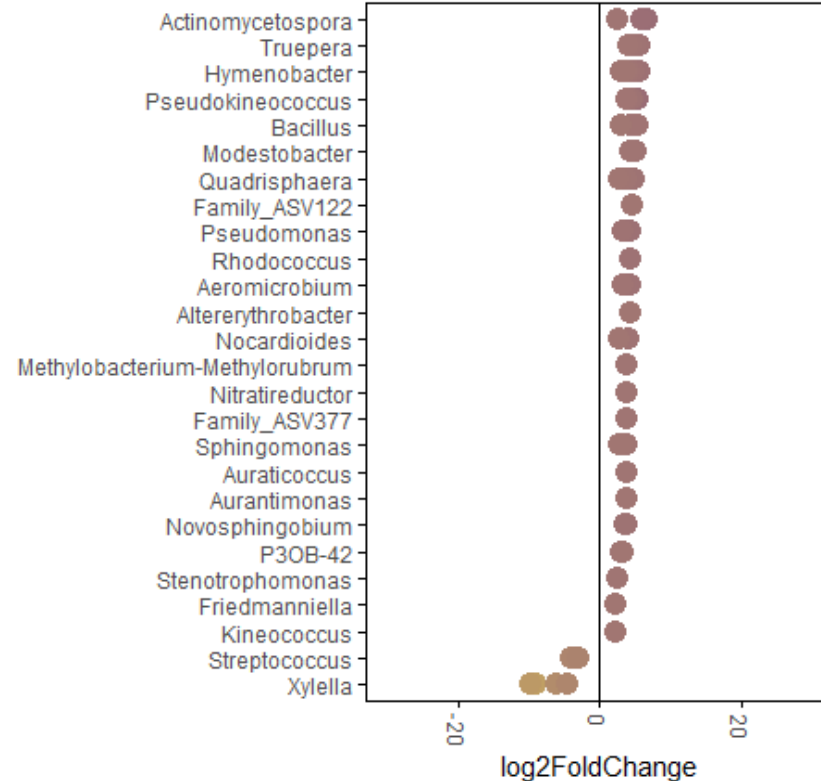
Positive Negative



Differential significant abundance (DESeq2)

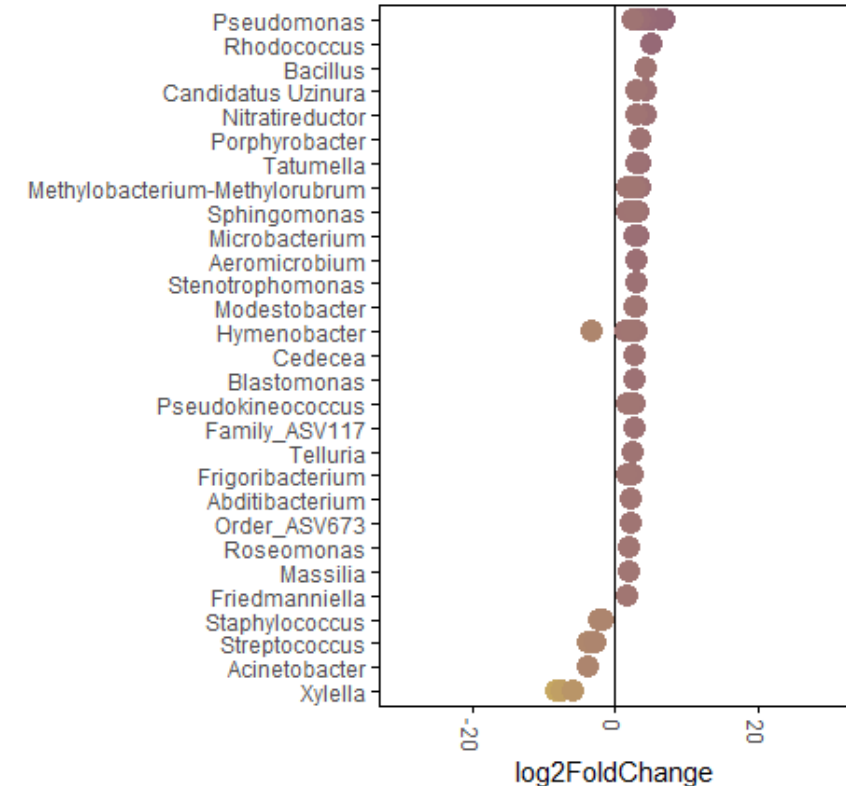
## Minorca

Positive Negative

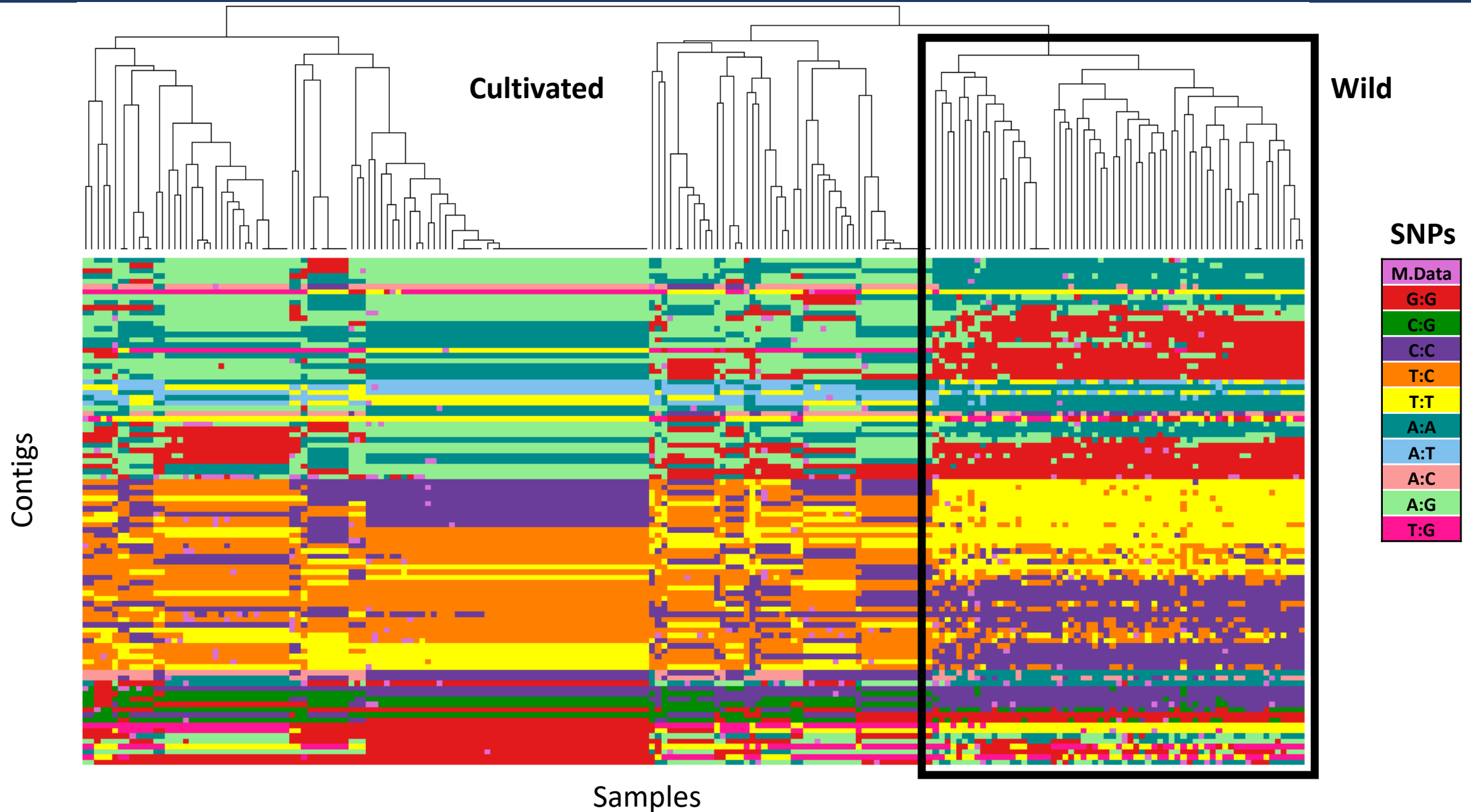


## Ibiza

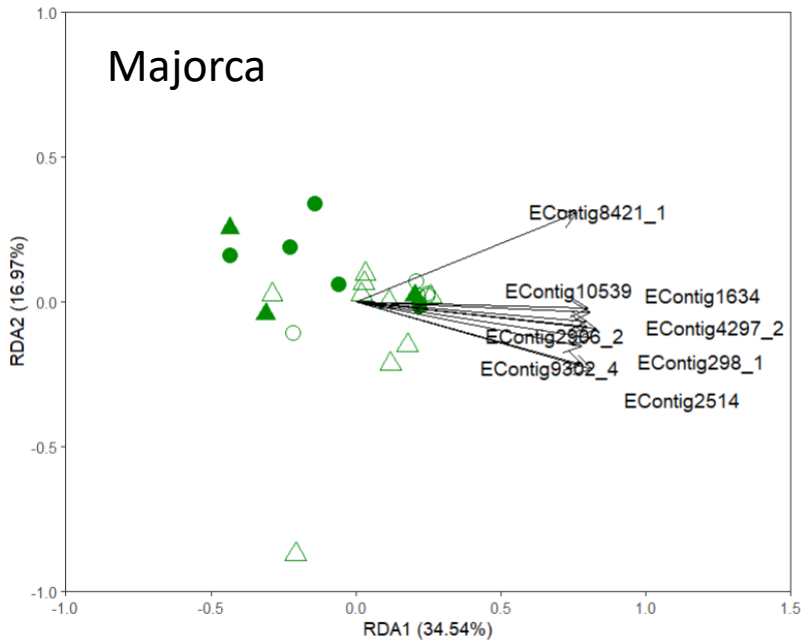
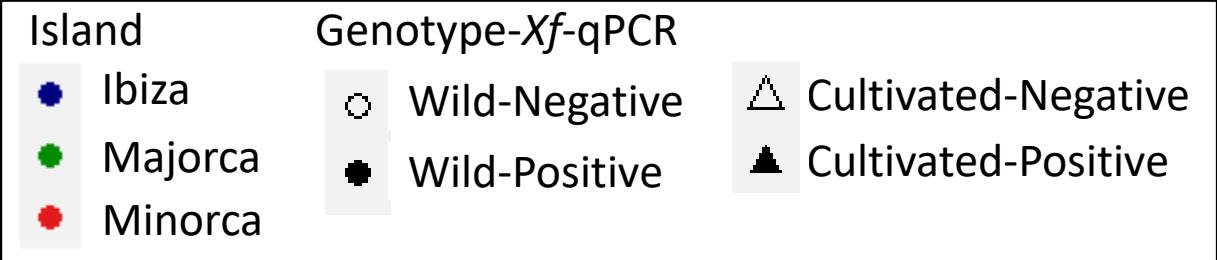
Positive Negative



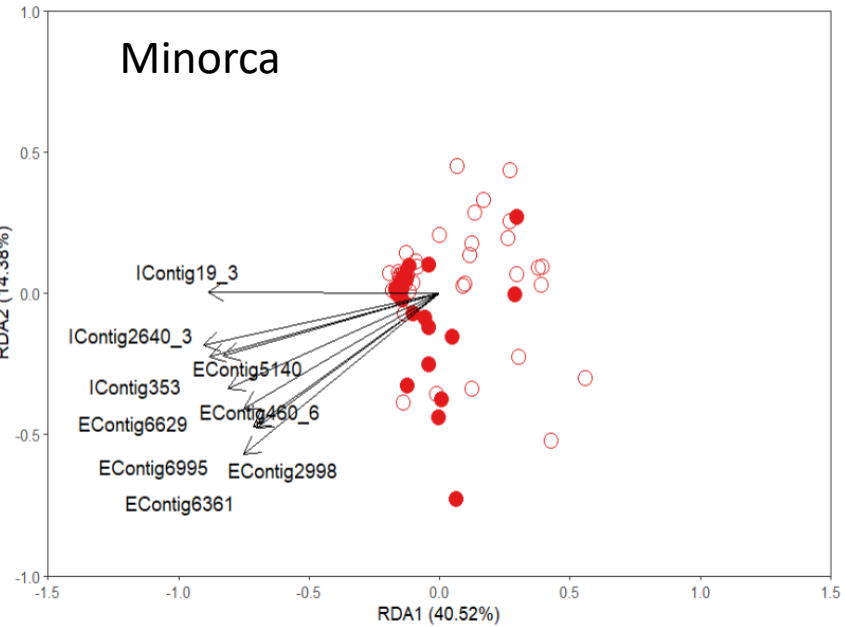
# Olive genotype characterization by EST-SNP marker analysis



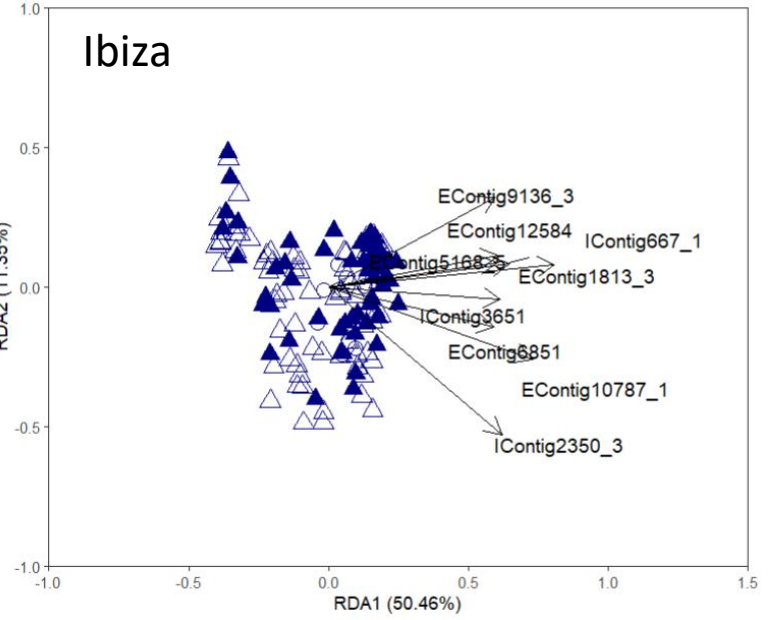
# Diversity of xylem microbiome of cultivated and wild olive genotypes according to their genetic closeness



Mantel statistic  $R^2$ : 0.2355  
 P-value: 0.0056



Mantel statistic  $R^2$ : -0.001516  
 P-value: 0.4709



Mantel statistic  $R^2$ : 0.01103  
 P-value: 0.3376

# Conclusions

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- ▶ Alpha diversity (richness and Shannon) of bacterial communities differed significantly according to the *Xylella fastidiosa* infection and was independent of the olive genotype or environment (Islands).
- ▶ Globally, the Beta diversity of the bacterial communities varied mainly according to the environment followed by *Xylella fastidiosa* infection. When each environment (Island) was analyzed independently, there was a significant effect of the olive genotype.
- ▶ DESeq2 analysis identified key bacterial genera that could be differentially associated with the presence or absence of *Xylella fastidiosa* in the xylem vessels of olive.
- ▶ The genetic profile of the olive trees sampled explained the diversity of the xylem microbial communities in Majorca, but not in Minorca and Ibiza probably due to different confounding factors (different environments (climate, soil, agronomic practices, etc.) and sampling dates).

# *Xylella fastidiosa* infection alters the xylem microbiota in wild and cultivated olive trees

## THANKS

### Research Collaborators:

- Angelina Belaj
- Diego Olmo
- Juan A. Navas-Cortés
- Blanca B. Landa



4<sup>th</sup> European conference on  
*Xylella fastidiosa*  
2023



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