The background features a dark, abstract design. On the left, a large, semi-transparent sphere is partially visible. Overlaid on this and the rest of the background is a complex network graph. The graph consists of numerous small circular nodes connected by thin, light-colored lines. Some nodes are highlighted with larger, glowing circles. A prominent, thick, magenta-colored line curves from the bottom right towards the center, passing through several nodes. The overall aesthetic is scientific and data-driven.

Exploratory biological DATASET of grapevine fungal diseases among *terroirs* and seasons

• Carla Mota Leal

Data Research Assistant

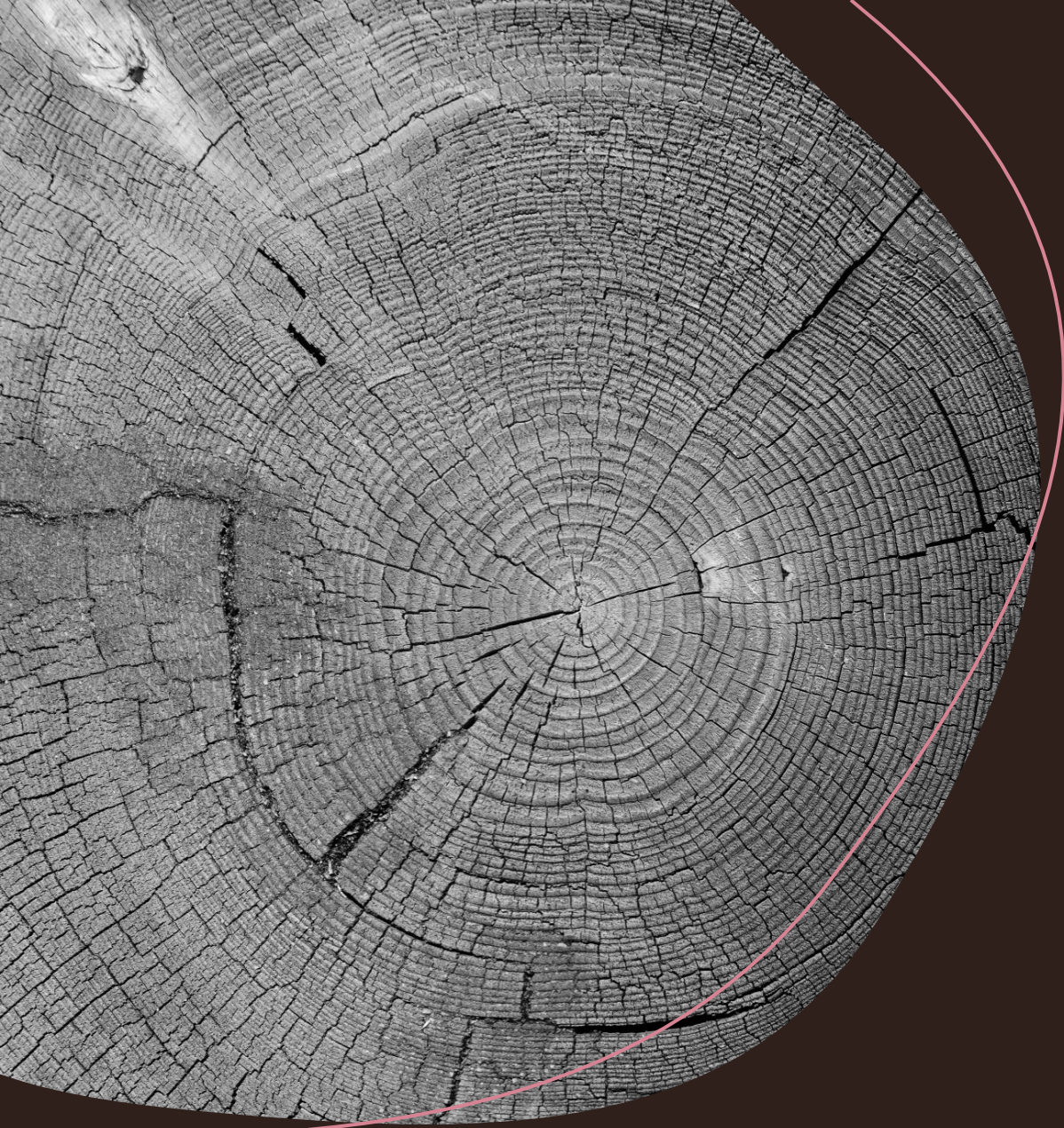


Sampling / wood
tissue



Dataset Introduction

- Living woody tissue samples from field were DNA sequenced and return with a data base of raw DNA sequences (~50,000 sequences)
- DNA data came from three *terroirs* sampled in late Winter and late Summer of 2020



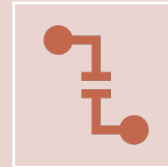
Main OBJECTIVE

- Analyze the compositional dynamics of fungi in woody tissue of grapevine (source), with emphasis on fungi associated grapevine trunk diseases (GTDs – main trunk diseases known)

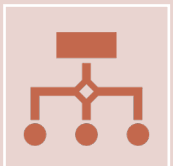
Bioinformatic / Data Cleaning step



Raw DNA seq were processed with DADA2 R package



Truncated to 250 bp forward and 200 bp for reverse, denoised, chimera filtered, merged and clustered into amplicon sequence variants (ASVs)



Taxonomic assignments were made based on the UNITE DATABASE (2021) using USEARCH v. 11



Functionality assignment using FungalTraits v.12 reference DATABASE

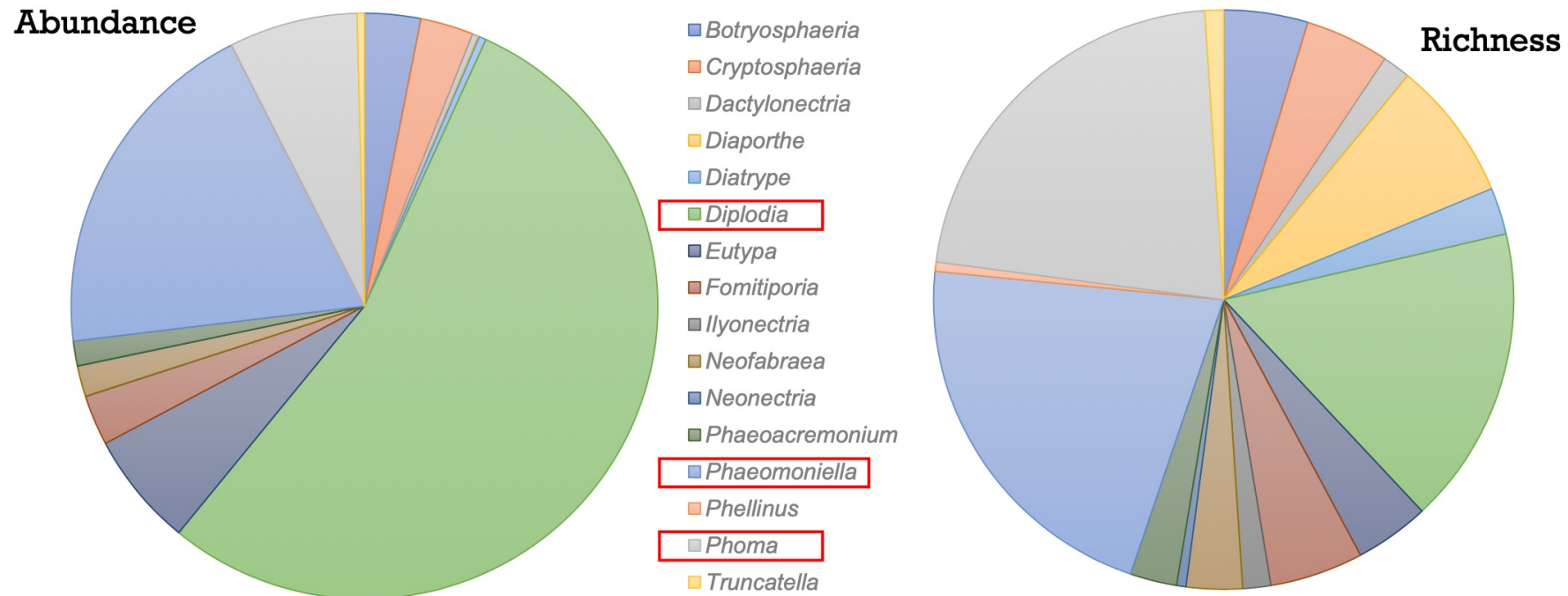
Exploratory and Statistical analyses

ANOVA, non-metric multidimensional scaling (NMDS), PerMANOVA and cooccurrence networks were performed in R.

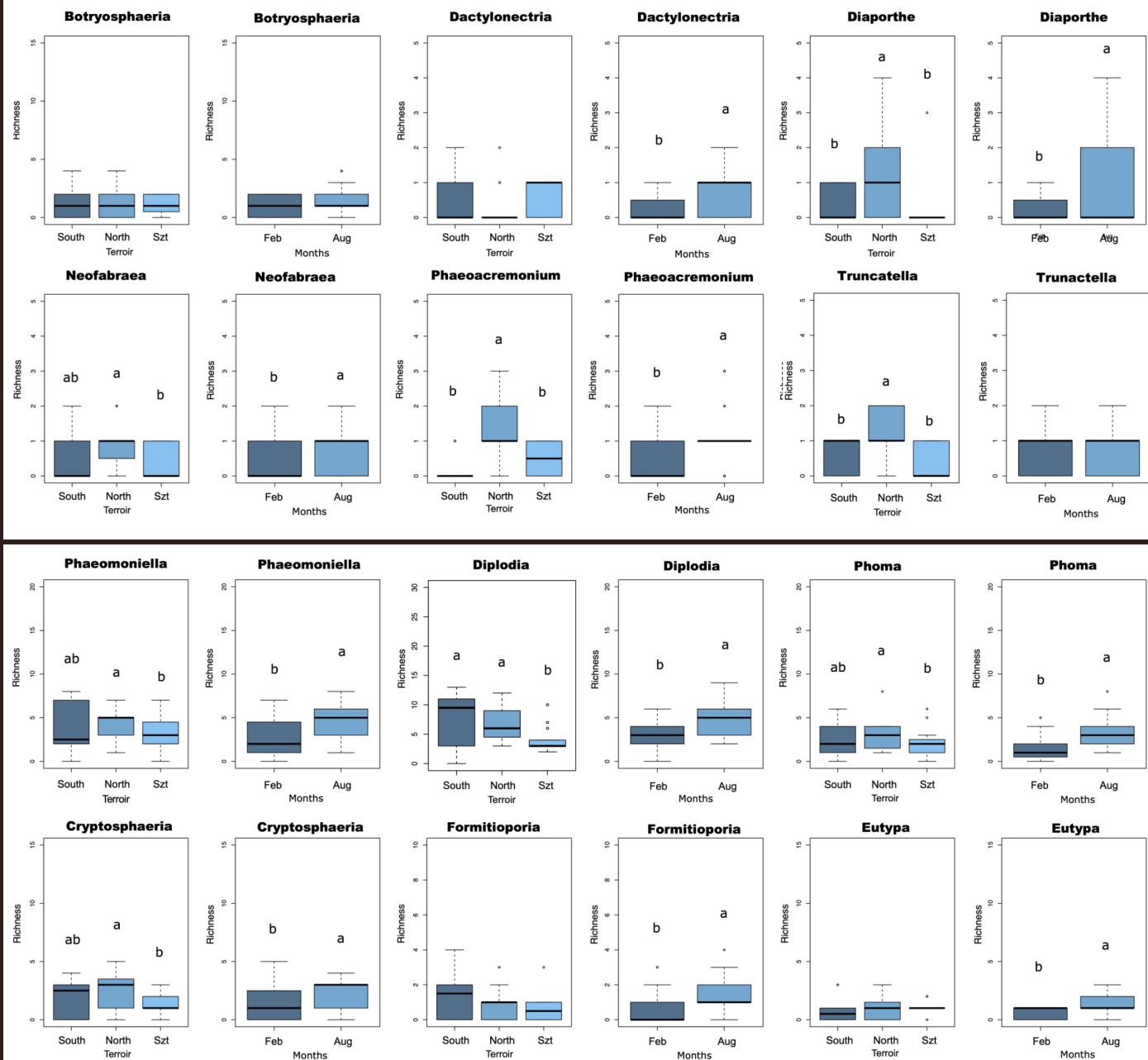


Exploratory and Statistical analyses

- Out of 494 plant pathogenic ASVs, 192 ASVs (38.8%) represented 15 fungal genera known to be associated with GTDs



Pie chart showing the proportional **read abundance** (left) and proportional **richness** (right) of GTD-associated fungal genera



Comparison of **genotypic richness** (number of ASVs) of GTD-associated fungal genera found in three *terroirs* and two seasons. Means were compared using ANOVA and Tukey's HSD tests, with letters denoting significant differences.

Exploratory and Statistical analyses

Exploratory and Statistical analyses

Eight GTD-associated fungal genera showed significant differences among *terroirs* and/or seasons:

Cryptosphaeria
Diaporthe
Diplodia
Neofabraea
Phaeoacremonium
Phaeomoniella
Phoma
Truncatella

	<i>Terroirs</i>	Season
All GTDs	0.0721	2.68e-05
<i>Phaeomoniella</i>	0.0349	0.00298
<i>Diplodia</i>	0.0310	0.00116
<i>Phoma</i>	0.0245	6.69e-05
<i>Phaeoacremonium</i>	2.58e-06	2.44e-05
<i>Eutypa</i>	0.63852	0.00724
<i>Botryophaeria</i>	0.7516	0.0567
<i>Cryptosphaeria</i>	0.04009	0.00935
<i>Fomitiporia</i>	0.0873	0.0192
<i>Diatrype</i>	0.4962	0.0509
<i>Ilyonectria</i>	0.111	0.315
<i>Dactylonectria</i>	0.1849	0.00446
<i>Diaporthe</i>	0.00599	0.01881
<i>Neofabraea</i>	0.0175	0.0113
<i>Neonectria</i>	0.613	0.921
<i>Truncatella</i>	0.00196	0.33865

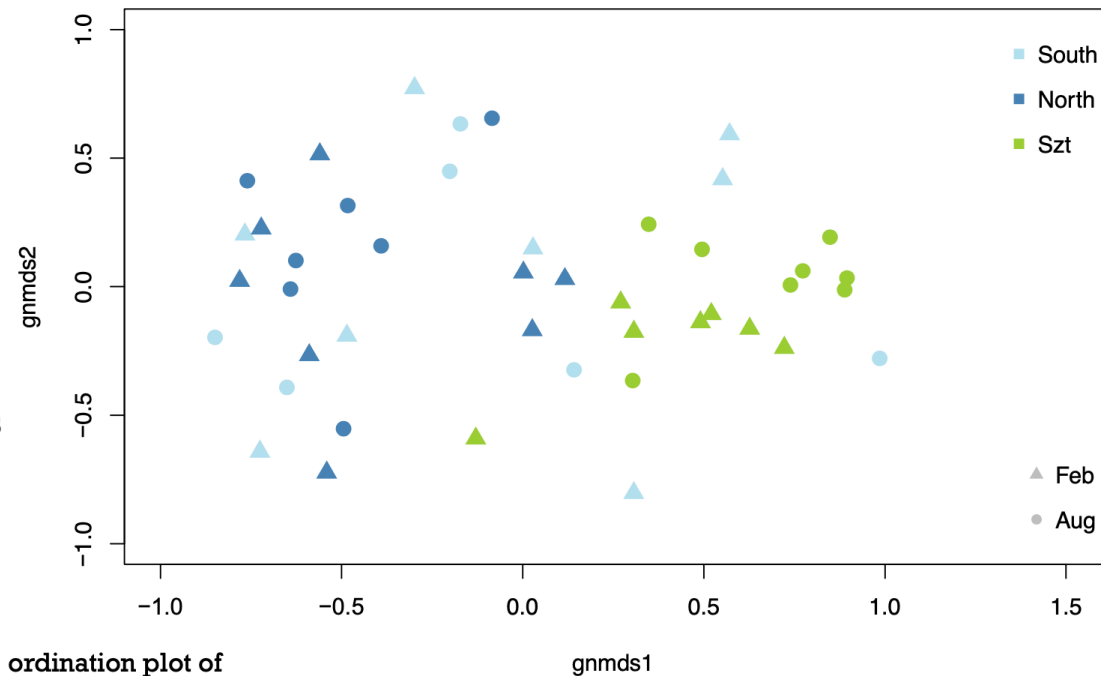
Analysis of variance (ANOVA) showing the *p* values of significant differences among GTD-associated fungal genera with respect to richness in different *terroirs* and seasons in the Tokaj wine region. Significant results are in bold.

Exploratory and Statistical analyses

- The composition of GTD-associated fungal community differs among *terroirs* and seasons
- No difference between grapevines with and without Esca symptoms

Non-metric multidimensional scaling (NMDS) ordination plot of the GTD-associated fungal community in the sampled *terroirs* and seasons based on Hellinger-transformed data.

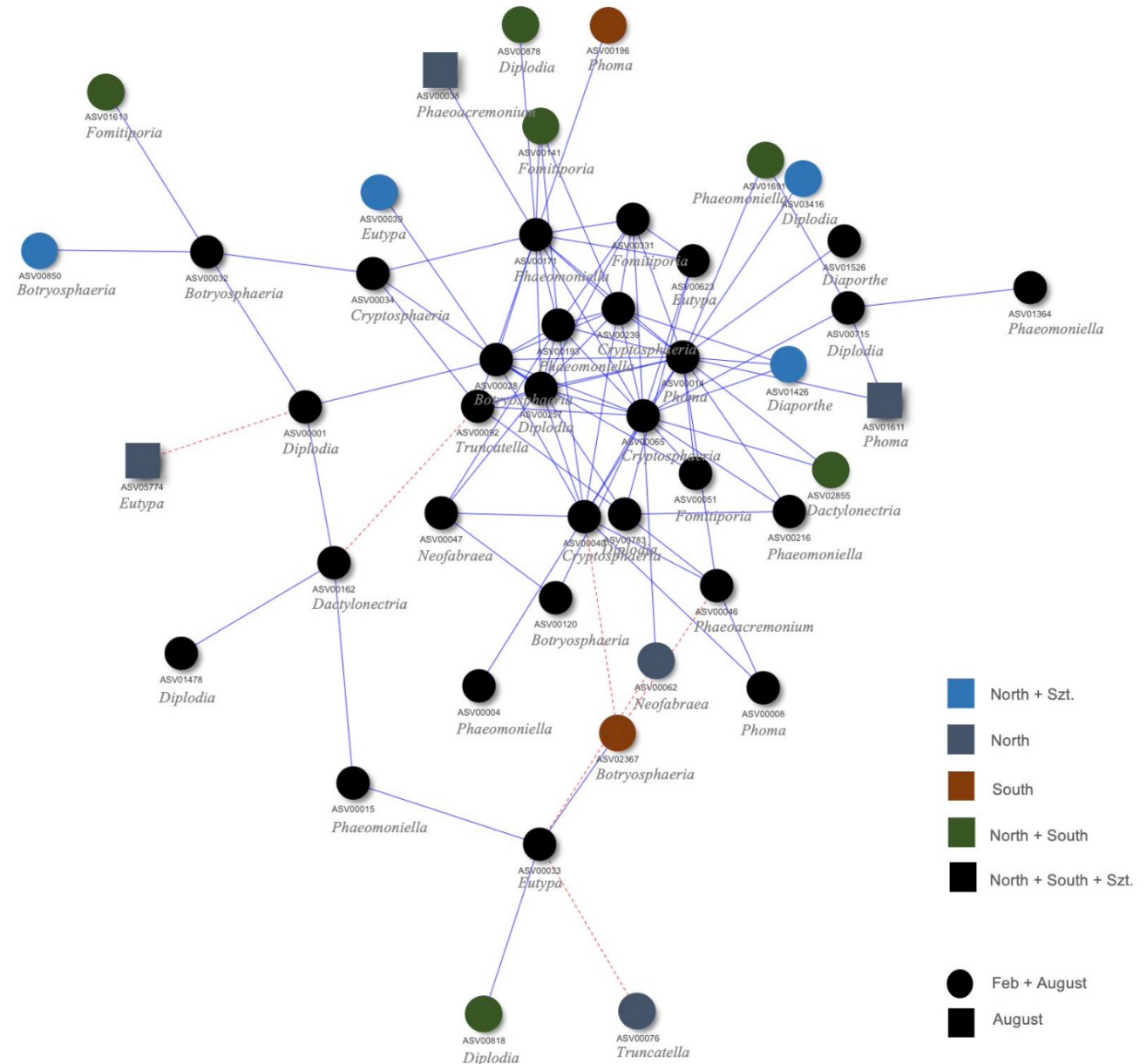
Proportion of variation (%) in GTD-associated fungal community composition explained by *terroir* and season calculated with permutational multivariate analysis of variance. Significant results are in bold. Significance codes: 0 '***' 0.001 '**' 0.01.



	<i>Terroir</i>	<i>Season</i>	<i>Terroir:Season</i>
	%	%	%
GTD fungi	11.46 ***	6.05 **	0.02
All fungi	9.16 ***	4.34 **	7.23

Exploratory and Statistical analyses

- Network graph showing significant positive (blue lines) and negative (red dotted lines) correlations among GTD-associated plant pathogenic fungal ASVs
- Only ASVs present in at least 10 samples included
- Most correlations among genotypes (ASVs) are positive
- Different pairs of ASVs of the same genus pairs can show positive or negative correlations
- ASV pairs with only negative correlations: *Eutypa*-*Diplodia*, *Truncatella*-*Dactylonectria*, *Botryosphaeria*-*Neofabraea*, *Phaeoacremonium*-*Neofabraea*



- Composition of GTD-associated plant pathogenic fungal communities primarily influenced by site-species environmental factors (“microbial *terroir*”) and less by seasonality
- The relatively stable inner wood microhabitat still is influenced by mesoclimatic and edaphic conditions (pH, soil moisture, nutrient contents etc)
- No significant difference in resident plant pathogenic fungi in grapevines with and without disease symptoms
- Most GTD-associated fungi show positive cooccurrence (shared microniche and/or synergism?)
- Some GTD-associated fungi show negative cooccurrence (distinct microinch or antagonism or avoidance of competition?)
- Studies testing for influence of specific environmental factors and management related variables are needed to better understand fungal composition dynamics in grapevines affected by GTDs

Data Output Discussion

- Currently working on more data of this project

```
mirror_mod = modifier_ob.  
#set mirror object to mirror  
mirror_mod.mirror_object =  
operation == "MIRROR_X":  
mirror_mod.use_x = True  
mirror_mod.use_y = False  
mirror_mod.use_z = False  
operation == "MIRROR_Y":  
mirror_mod.use_x = False  
mirror_mod.use_y = True  
mirror_mod.use_z = False  
operation == "MIRROR_Z":  
mirror_mod.use_x = False  
mirror_mod.use_y = False  
mirror_mod.use_z = True
```

```
#selection at the end -add  
mirror_ob.select= 1  
modifier_ob.select=1  
context.scene.objects.active  
= ("Selected" + str(modifier_ob.name))  
mirror_ob.select = 0  
= bpy.context.selected_objects  
data.objects[one.name].select  
print("please select exactly one mirror")
```

--- OPERATOR CLASSES ---

```
bpy.types.Operator):  
X mirror to the selected  
object.mirror_mirror_x"  
mirror X"
```

```
context):  
context.active_object is not None
```