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Figure 1

Table

Species	genotype/cv
<i>A. macrosperma</i>	Ma183; Ma176
<i>A. arguta</i>	Miss green (MG)
<i>A. polygama</i>	Polygama 70 (Pol)
<i>A. deliciosa</i>	Hayward (Hw)

Background Kiwifruit Vine Decline Syndrome (KVDS) (Fig. 1) is one of the most important diseases of *Actinidia* within Italian sector. Aetiology is still debated as KVDS is considered a disbiosis, primarily caused by Oomycetes (Savian et al., 2022). Since there aren't any effective control strategies, the most promising tool to overcome KVDS is the use of resistant species, being candidate rootstocks or for breeding purposes. Thus, *Actinidia* genotypes (Table) with different behaviour to KVDS have been identified in the field (Mian et al., 2022).

Aims The aims of this research were to understand the Oomycetes species involved in KVDS and how this patho-community can be influenced and modified by plant genotype. For this purpose, a metabarcoding approach was used.

Planting Time
12/15/2020
8 replicates for each genotype (Table)

WORKFLOW

Three waterlogging cycles:
11 -14 -17 May 2021



Symptoms onset
26/05/2021



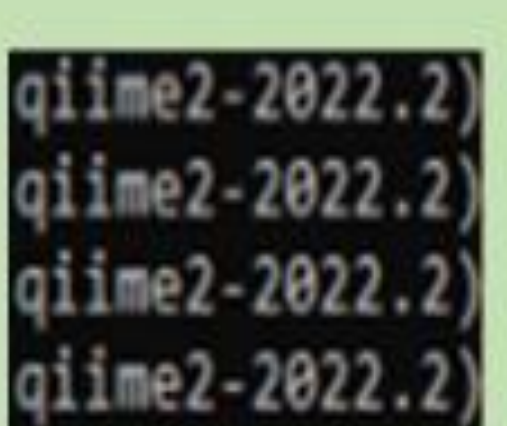
Collapsed plants
(Sampling time and symptoms evaluation)
03/06/2021



DNA endosphere processing:
extraction,
quantification,
amplification
(primers: Riit et al., 2016)
and Illumina seq



Bio informatic analysis:
Qiime2



Results

- At sampling time only cv. Hayward and *A. polygama* showed root-rot symptoms (55-75%) (Fig. 2).
- *Phytophthora* sp. was the predominant oomycete, together with *G. intermedium* (Fig. 3).
- *G. intermedium* was especially found in resistant species, while *Phytophthora* sp. on sensitive ones (Fig. 3).

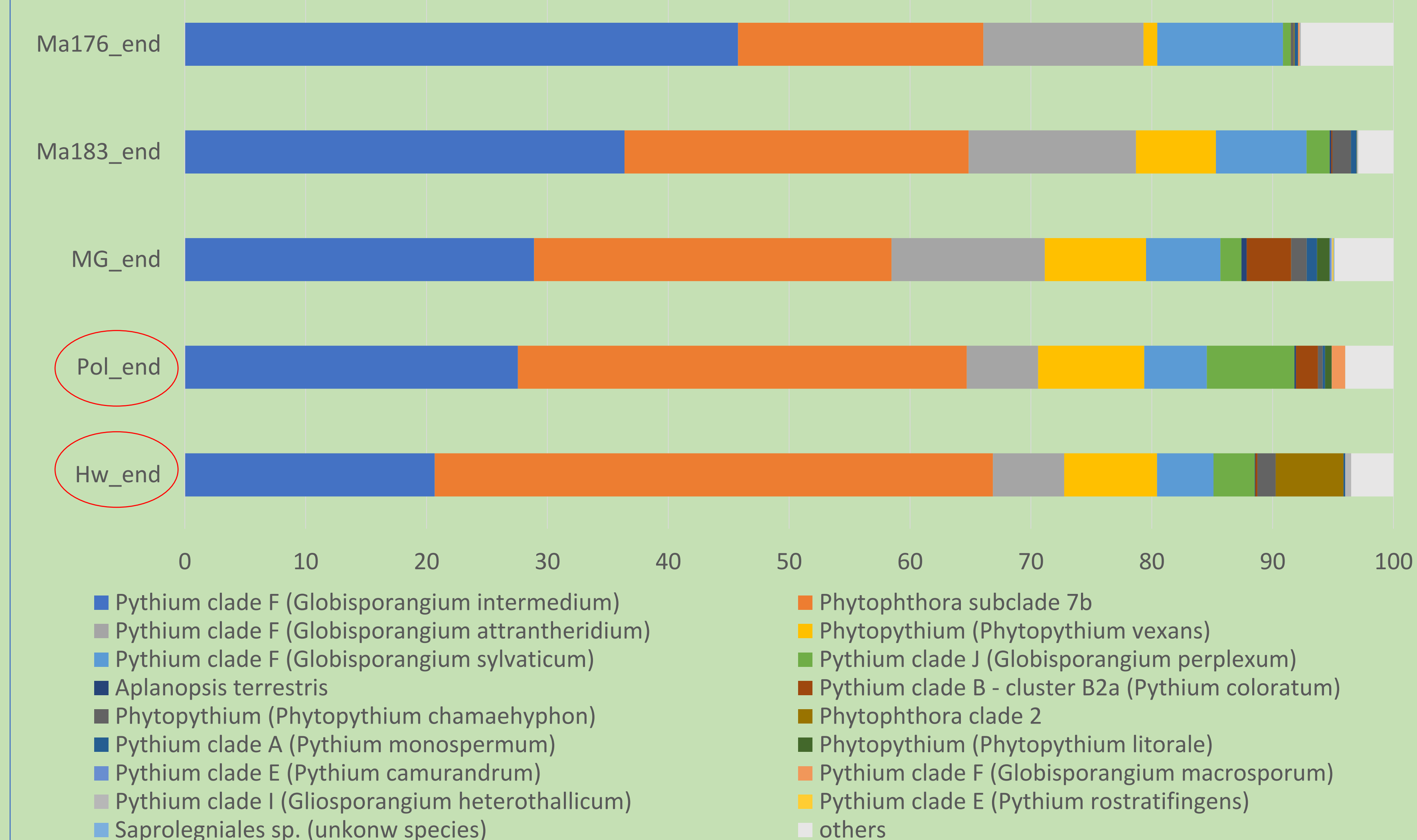
Figure 2

Root Symptoms Incidence (%)



Figure 3

Endosphere relative abundance compositions (%)



Conclusions: we found significant differences (data not shown) between genotypes in terms of oomycetes detected in the endosphere, which correlated with the symptoms displayed. Resistance of *A. macrosperma* and *A. arguta* to KVDS seems to be related to their ability to shape the root pathobiome. In our conditions, *Phytophthora* sp. subclade7b (Yang et al., 2017) was predominant in sensitive genotypes. On the other hand, *Pythium* clade F (*Globisporangium intermedium*) was mainly detected in asymptomatic plants confirming studies of Türkkan et al., 2022 and suggesting that might compete with *Phytophthora* sp. recruitment in resistant plants.