Special Issue Article

Bacteria associated with wood tissues of Esca-diseased grapevines: functional diversity and synergy with Fomitiporia mediterranea to degrade wood components

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Summary

Fungi are considered to cause grapevine trunk diseases such as esca that result in wood degradation. For instance, the basidiomycete Fomitiporia mediterranea (Fmed) is overabundant in white rot, a key type of wood-necrosis associated with esca. However, many bacteria colonize the grapevine wood too, including the white rot. In this study, we hypothesized that bacteria colonizing grapevine wood interact, possibly synergistically, with Fmed and enhance the fungal ability to degrade wood. We isolated 237 bacterial strains from esca-affected grapevine wood. Most of them belonged to the families Xanthomonadaceae and Pseudomonadaceae. Some bacterial strains that degrade grapevine-wood components such as cellulose and hemicellulose did not inhibit Fmed growth in vitro. We proved that the fungal ability to degrade wood can be strongly influenced by bacteria inhabiting the wood. This was shown with a cellulolytic and xylanolytic strain of the Paenibacillus genus, which displays synergistic interaction with Fmed by enhancing the degradation of wood structures. Genome analysis of this Paenibacillus strain revealed several gene clusters such as those involved in the expression of carbohydrate-active enzymes, xylose utilization and vitamin metabolism. In addition, certain other genetic characteristics of the strain allow it to thrive as an endophyte in grapevine and influence the wood degradation by Fmed. This suggests that there might exist a synergistic interaction between the fungus Fmed and the bacterial strain mentioned above, enhancing grapevine wood degradation. Further step would be to point out its occurrence in mature grapevines to promote esca disease development.

Introduction

Esca, a grapevine trunk disease (GTD), has become a major issue in many viticulture regions in Europe, and even worldwide, in the past two decades. This disease negatively affects vineyard longevity and wine quality (Mugnai et al., 1999; Calzarano et al., 2001, 2004; Pasquier et al., 2013), thereby causing huge economic losses to the viticulture sector. Pathogenic fungi such as Phaeomoniella chlamydospora, Phaeoacremonium minimum and Fomitiporia mediterranea (Fmed) have long been studied for their ability to colonize and degrade wood tissues, causing various types of symptoms in the wood of trunk and stems (Mugnai et al., 1999; Sparapano...
These symptoms include central or sectorial black and/or brown necrotic tissues and also white-rot tissues (Larignon and Dubos, 1997; Mugnai et al., 1999; Serra et al., 2000; Péros et al., 2008; Maher et al., 2012). White rot in grapevine is always associated with basidiomycetes. A considerable number of basidiomycetes have been isolated from different grapevine cultivars worldwide (Mugnai et al., 1999; Fischer, 2006; Cloete et al., 2014; Brown et al., 2020; Mirabolliathy et al., 2021), which are known to degrade the components of cell walls, i.e. lignin, cellulose and hemicellulose.

Fomitiporia mediterranea (Fischer, 2002) is the most common basidiomycete associated with white-rot tissues, typically esca, in grapevine plants in Europe. It is assumed that the development of wood decay, including white-rot, is a long process that takes place over years (Sparapano et al., 2000, 2001). As vineyards age, white rot continues to spread in the trunks and cords of grapevine plants (Fischer, 2000; Fischer and González Garcia, 2015). Recent findings support the idea that white-rot plays a key role in causing esca. In esca-affected plants displaying leaf symptoms, at least 10% of wood had been affected by white rot (Ouadi et al., 2021), and removal of the white-rot led to grapevine recovery (Chole et al., 2021).

It was reported that in asymptomatic young grapevines (10-years-old), the healthy-looking wood was colonized by the three fungal pathogens, P. chlamydospora, P. minimum and F. mediterranea (Bruz et al., 2014, 2020; Kraus et al., 2019). In addition, numerous non-pathogenic fungi were also detected, including some plant-protective microorganisms such as Trichoderma spp. (Fourie et al., 2001; Bruze et al., 2014; Mutawila et al., 2016; Marraschi et al., 2018). Healthy wood tissues exhibited a higher fungal diversity in comparison to the necrotic ones. However, which factors cause necrosis of the healthy and young grapevine woods (10-years-old) after few years (in 15–20-years-old grapevines) are yet unknown.

In this study, we hypothesized that one of these factors influencing wood degradation, in addition to pathogenic fungi, could be the synergistic interaction of these fungi with certain bacteria that colonize the wood of grapevines (Bruz et al., 2015, 2020). This assumption was raised because some authors, such as Clausen (1996) reported that bacteria can affect negatively wood permeability, change wood structure, or work synergistically with other wood-inhabiting bacteria and soft-rot fungi to predispose wood to fungal attack. Therefore, the possible involvement of grapevine wood-colonizing bacteria, alone or in association with GTD-fungal pathogens, could be possible and needs therefore to be further investigated to determine if they are involved in grapevine wood degradation. A multipartite interaction, or a pathobiome, consisting of fungi and bacteria, could be studied further to determine if it can increase the rate of pathogenic fungi-induced wood degradation.

Fungi are generally considered as primary decomposers of wood because of their ability to produce a wide range of extracellular enzymes that degrade major wood polymers, i.e. lignin, cellulose and hemicellulose (Clausen, 1996; Boer et al., 2005; Noll and Jirjis, 2012; Purahong et al., 2016). Due to the limited ability of bacteria to decompose polymeric lignocelluloses, they were thought to play only a minor role in wood decomposition compared to fungi (Cornelissen et al., 2012). However, genomic analyses of certain bacteria revealed the existence of genes encoding lignin-degrading enzymes, suggesting their possible involvement in wood decomposition (Lladó et al., 2017).

Recent studies have reported that some of the wood-colonizing bacteria play a positive role of plant protection by reducing the size of the wood necroses caused by GTD-pathogens (Rezgui et al., 2016; Haidar et al., 2016a; Haidar et al., 2016b). However, some of these bacteria, such as strains of Bacillus pumilus, Xanthomonas sp. and Bacillus licheniformis, might develop synergistic relationships with Neofusicoccum parvum, which is considered as one of the most virulent fungal species associated with GTDs (Laveau et al., 2009; Ubez-Torres and Gubler, 2009). Recently, it was reported that bacterial inoculation favours the pathogenicity of N. parvum by increasing canker length in grapevine stem cuttings (Haidar et al., 2020). However, as regards esca, no study has yet been conducted on the interaction between bacteria and Fmed. The present study was aimed at (i) determining if bacteria isolated from grapevine wood can degrade the wood structure of this plant even minimally, then (ii) we tested the hypothesis that an interaction, possibly synergistic, between wood-colonizing bacteria and Fmed, might eventually lead to increased wood structure degradation.

Results

Characterization of the bacterial strains isolated from the grapevine wood tissues

Identification by 16S rRNA gene sequencing. A total of 237 bacterial strains were isolated from different tissues of grapevine: 59 strains from necrotic (sectorial black streaks) tissues (NT), 62 strains from non-necrotic tissues (NNT), 54 strains from transition tissues between necrotic and non-necrotic zones (TT) and 62 strains from white rot (decaying wood) tissues (WR).

All strains were identified by sequencing a fragment of the 16S rRNA gene (V5–V9 region). Sequences are
available at the GenBank database from accession number MT705336 to MT705572.

The sequences revealed that the 237 isolates belonged to four phyla: Proteobacteria (64% of the isolates), Firmicutes (21%), Bacteroidetes (10%) and Actinobacteria (5%). Furthermore, among the 11 obtained bacterial orders the ones with the highest number of strains were Xanthomonadales, Bacillales and Pseudomonadales with 30.8%, 21.1% and 18.6% of the bacterial strains respectively. Thirty-one genera were also identified. The most frequently occurring genera were Pseudomonas (18.6% of the bacterial strains), followed by Stenotrophomonas (13%), Bacillus (12.6%) and Pseudoxanthomonas (12.6%).

While some strains belonging to genera such as Bacillus, Olivibacter, Pseudomonas and Pseudoxanthomonas were present in all wood tissues, strains of other genera such as Herbiconiux and Kocuria were isolated from only one type of tissue, i.e. white rot tissue, and those of Burkholderia, Curtobacterium, Luteibacter, Pantoea, Rahnella and Rhizobium were isolated only from non-necrotic tissue. Figure 1 shows the distribution of the most abundant genera and according to the wood tissues sampled from trunk or cordon.

**Ability of the selected bacterial strains to decompose wood components.** A total of 59 taxa were defined when sequences were binned into taxa (Gascuel, 1997; Edgar, 2004). One bacterial strain from each taxon was selected for further analyses (Table 1).

None of these strains was able to degrade the Remazol Brilliant Blue R (RBBR) dye, suggesting the absence of ligninolytic activity. Cellulase and xylanase activities were evaluated according to the extent and intensity of hydrolytic clearing zones, classified as moderate (5–40 mm), strong (41–70 mm) and very strong (>71 mm). The screening confirmed 18 strains (30%) showing cellulase and xylanase activity halos with a diameter >5 mm in a Congo Red assay on xylan- and carboxymethyl-cellulose-containing plates (Fig. S1). Ten of these strains were isolated from white rot and eight from trunks. While seven of these 18 strains were isolated from white rot (S136, S158, S159, S190, S23, S283 and S68), only two were isolated from non-necrotic tissues (S241: B. muralis and S293: Paenibacillus amylolyticus) (Table 1). Strain S150 was the only strain (isolated from the transition tissue of one cordon) that showed strong cellulase and xylanase activities.

Only 11 strains (S107, S11, S195, S196, S2, S207, S22, S233, S300, S47 and S5), i.e. 18% of the screened strains, demonstrated cellulolytic activity. Six of these were isolated from non-necrotic tissues. However, eight other strains (S126, S211, S222, S243, S252, S259, S69 and S92) showed only xylanolytic potential by forming zones of clearing on xylan containing plates; none of these strains was isolated from white rot (Table 1).

![Fig. 1. Distribution of bacterial genera in the different wood tissue types. Necrotic tissues (sectorial black streaks) (NT), non-necrotic tissues (NNT), transition tissues between the necrotic and non-necrotic zones (TT) and white rot (decay wood) (WR), a typical necrotic tissue associated with esca. [Color figure can be viewed at wileyonlinelibrary.com]](image-url)
| Test code | Bacterial species | Bacterial origin | Degradation (halo size mm) | Inhibition rate (%) | Dual culture trial | VOCs emission trial |
|-----------|-------------------|------------------|-----------------------------|---------------------|-------------------|--------------------|
|           |                   |                  | Lignin | Cellulose | Xylan |                   |                     |
| S163      | Microbacterium sp. | Necrotic tissue of trunk | 0 | 0 | 0 | 0 | 100 |
| S45       | Pseudomonas sp.    | Non-necrotic tissue of trunk | 0 | 0 | 0 | 52.5 | 75.9 |
| S7        | Sphingomonas sp.   | Intermediate zone of trunk | 0 | 0 | 0 | 2.5 | 46.2 |
| S180      | Stenotrophomonas sp. | Non-necrotic tissue of cordon | 0 | 0 | 0 | 52.3 | 88.8 |
| S273      | Bacillus sp.       | Intermediate zone of trunk | 0 | 0 | 0 | 0 | 66.6 |
| S12       | Stenotrophomonas sp. | Non-necrotic tissue of cordon | 0 | 0 | 0 | 28.8 | 74 |
| S256      | Luteimonas sp.     | Necrotic tissue of trunk | 0 | 0 | 0 | 0 | 81.4 |
| S262      | Achromobacter sp.  | Non-necrotic tissue of trunk | 0 | 0 | 0 | 41 | 85.1 |
| S125      | Brevundimonas sp.  | Intermediate zone of trunk | 0 | 0 | 0 | 0 | 66.6 |
| S64       | Novosphingobium sp. | Non-necrotic tissue of trunk | 0 | 0 | 0 | 55.1 | 100 |
| S62       | Herbiconiux sp.    | White rot of cordon | 0 | 0 | 0 | 0 | 66.6 |
| S46       | Curtobacterium sp. | Non-necrotic tissue of trunk | 0 | 0 | 0 | 45.2 | 100 |
| S261      | Erwinia sp.        | Non-necrotic tissue of trunk | 0 | 0 | 0 | 15 | 88 |
| S174      | Frigotrichobacterium sp. | Intermediate zone of trunk | 0 | 0 | 0 | 49.7 | 66 |
| S172      | Lysinibacillus sp. | Intermediate zone of trunk | 0 | 0 | 0 | 36.3 | 61.1 |
| S146      | Rahelella sp.      | Non-necrotic tissue of trunk | 0 | 0 | 0 | 22.5 | 100 |
| S123      | Erwinia sp.        | Intermediate zone of trunk | 0 | 0 | 0 | 23.4 | 100 |
| S178      | Burkholderia sp.   | Non-necrotic tissue of trunk | 0 | 0 | 0 | 0 | 88.8 |
| S298      | Pseudomonas sp.    | Intermediate zone of cordon | 0 | 0 | 0 | 17.5 | 66.6 |
| S165      | Burkholderia sp.   | Non-necrotic tissue of trunk | 0 | 0 | 0 | 0 | 55.5 |
| S151      | Mycoplana sp.      | White rot of cordon | 0 | 0 | 0 | 26 | 77.7 |
| S259      | Weekellaceae       | Necrotic tissue of trunk | 0 | 0 | 90 | 5.1 | 62.9 |
| S243      | Hafnia sp.         | Non-necrotic tissue of cordon | 0 | 0 | 90 | 16.8 | 83.3 |
| S252      | Stenotrophomonas sp. | Intermediate zone of cordon | 0 | 0 | 90 | 23.7 | 87 |
| S222      | Pantoea sp.        | Non-necrotic tissue of trunk | 0 | 0 | 70 | 44.4 | 75 |
| S92       | Pseudomonas sp.    | Intermediate zone of cordon | 0 | 0 | 60 | 44.1 | 100 |
| S211      | Pseudoxanthomonas sp. | Necrotic tissue of trunk | 0 | 0 | 90 | 2.2 | 0 |
| S69       | Pseudoxanthomonas sp. | Necrotic tissue of trunk | 0 | 0 | 50 | 12 | 100 |
| S126      | Bacillus sp.       | Intermediate zone of trunk | 0 | 0 | 70 | 0 | 72.2 |
| S22       | Achromobacter sp.  | White rot of cordon | 0 | 15 | 0 | 36 | 83.3 |
| S203      | Olivibacter sp.    | Necrotic tissue of trunk | 0 | 20 | 90 | 0 | 62.9 |
| S270      | Paenibacillus sp.  | Intermediate zone of trunk | 0 | 20 | 70 | 4.7 | 64.8 |
| S300      | Rhizobiaceae       | Non-necrotic tissue of cordon | 0 | 20 | 0 | 4.6 | 57.4 |
| S274      | Pigmentifaga sp.   | Intermediate zone of trunk | 0 | 20 | 30 | 0 | 55.5 |
| S107      | Pedobacter sp.     | Necrotic tissue of trunk | 0 | 20 | 0 | 0 | 55.5 |
| S2        | Variovorax sp.     | Non-necrotic tissue of trunk | 0 | 25 | 0 | 32.5 | 55.5 |
| S127      | Luteimonas sp.     | Intermediate zone of trunk | 0 | 30 | 70 | 16.2 | 88.8 |
| S195      | Achromobacter sp.  | White rot of trunk | 0 | 30 | 0 | 23 | 51.8 |
| S207      | Pseudomonas sp.    | Non-necrotic tissue of trunk | 0 | 30 | 0 | 0 | 64.8 |
| S142      | Cedecea sp.        | Necrotic tissue of cordon | 0 | 30 | 60 | 2.3 | 75.9 |
| S233      | Pseudoxanthomonas sp. | Necrotic tissue of cordon | 0 | 35 | 0 | 19.8 | 83.3 |
| S11       | Enterobacter sp.   | Non-necrotic tissue of cordon | 0 | 35 | 0 | -15.8 | 44.4 |
| S47       | Olivibacter sp.    | Non-necrotic tissue of trunk | 0 | 40 | 0 | 12.8 | 55.5 |
| S190      | Bacillus sp.       | White rot of trunk | 0 | 40 | 90 | 4.6 | 88.8 |
| S5        | Bacillus sp.       | Non-necrotic tissue of trunk | 0 | 45 | 0 | -13.4 | 88.8 |
| S231      | Chryseobacterium sp. | Necrotic tissue of cordon | 0 | 50 | 90 | 0 | 9.2 |
| S136      | Pseudomonas sp.    | White rot of cordon | 0 | 50 | 70 | 0 | 66.6 |
| S293      | Paenibacillus sp.  | Non-necrotic tissue of cordon | 0 | 50 | 75 | 0 | 11.1 |
| S196      | Achromobacter sp.  | White rot of trunk | 0 | 50 | 0 | 62.8 | 100 |
| S22       | Xanthomonaceae     | White rot of cordon | 0 | 50 | 60 | 30.1 | 83.3 |

(Continues)
In addition, we tested wood-degrading components ability of the used strain of *F. mediterranea*. This last showed ligninolytic, cellulolytic and xylanase activities.

**In vitro antifungal assays**

The effects of the selected bacterial strains against *Fmed* were evaluated using dual culture tests. Fifty-nine per cent of these bacterial strains (35 of 59 strains) were effective in suppressing *Fmed* (Table 1). Out of the 35 strains, only six (S112, S158, S159, S180, S196 and S45), all of which were isolated from non-necrotic tissues or white rot, showed more than 50% inhibition of radial fungal growth. Interestingly, five strains (S11, S150, S259, S270 and S5) were able to promote the mycelial growth of *Fmed*. Most of the bacterial strains (99%) exhibited antifungal activity against *Fmed* by the secretion of volatile compounds (VOCs) (Table 1).

After 7 days of incubation, there was a 100% inhibition of mycelial growth in *Fmed* due to VOCs produced by nine strains (S112, S123, S146, S163, S196, S283, S46, S69 and S92). Interestingly, eight of these strains (except S163, i.e. *Microbacterium* sp.) reduced the mycelial growth of *Fmed*, by additionally producing diffusible antifungal substances. There was a percentage reduction in mycelial growth ranging from 12% to 62.8%. In addition, 13 other bacterial strains (S127, S178, S180, S190, S22, S23, S233, S243, S252, S256, S261, S262 and S5) showed an inhibition rate of >80%. In conclusion, 34 bacterial strains, which were isolated from different wood tissues (NNT: 13, TT: 9, NT: 3 and WR: 9), exhibited antifungal activity against *Fmed* by producing diffusible and volatile metabolites. However, S150, the strain that exhibited strong cellulase and xylanase activities and promoted mycelial growth of *Fmed*, was selected for exploring the potential synergistic interaction between the two (Table 1).

**Lignin content of grapevine wood exposed to Fmed**

While the average content of Klason lignin was 16.3% in control blocks (throughout the experiment), in blocks exposed to *Fmed* for 2, 7 and 10 months they were about 15.2%, 11.6% and 7.6% respectively (Fig. 2). Thus, the lignin content is significantly reduced by the presence of *Fmed* in grapevine wood.
content of Klason lignin in woodblocks exposed to Fmed decreased significantly with time. While incubation for 2 months showed a non-significant decrease in lignin content, incubation for 7 and 10 months significantly decreased the lignin content. In addition, we observed that the growth of Fmed (diameter of the colony) was improved in the presence of woodblocks, compared to that in control plates containing a culture of Fmed alone (Fig. S2).

Effect of Fmed and/or Paenibacillus sp. (strain S150) on grapevine wood powder in Erlenmeyer flask microcosms

To test the hypothesis that some bacteria synergistically interact with Fmed and that this interaction could be involved in wood degradation, sawdust co-inoculated with Fmed and S150 was analyzed after 2 months of incubation. The choice of this bacterial strain (S150) was based on its cellulolytic and xylanolytic activities and the fact that its metabolites cannot inhibit the growth of Fmed. Moreover, incubation of the fungus with S150 showed an increase in fungal growth. As qualitative indicators of wood degradation (Hervé et al., 2014, 2016), we compared the color and particle size of sawdust with and without Fmed inoculation. We observed that sawdust inoculated with Fmed alone or with Fmed and the bacterial strain showed particles that were smaller in size and lighter in color than control sawdust, 2 months after inoculation (Fig. S3). In addition, carbon and nitrogen concentrations were measured at the end of the experimentation period (2 months after inoculation). The carbon-to-nitrogen (C/N) ratio was significantly higher in sterile sawdust (control) and in sawdust inoculated with S150 only, compared with that in sawdust inoculated with Fmed alone or co-inoculated with S150 (Fig. S3). In addition, the degradation of co-inoculated sawdust was significantly higher compared to sawdust inoculated with Fmed alone, confirming the synergy between the bacterial strain and Fmed and the resulting increase in wood degradation.

Effect of Fmed and/or S150 on grapevine wood powder in Petri plate microcosms

After 8 months of incubation, sawdust from Petri plate microcosms with and without Fmed inoculation was analyzed. The C/N ratio was found to be significantly higher in sterile sawdust (control) compared to other treatments (Fmed, S150 and Fmed with S150) indicating that the chemical composition of wood was altered by the presence of microorganisms during the period of incubation (Fig. 3A). Additionally, when compared to sawdust inoculated with Fmed alone, the degradation of sawdust co-inoculated with Fmed and S150 was significantly higher (Fig. 3A). Furthermore, sawdust co-inoculated with Fmed and S150 was lighter in color compared to those inoculated with Fmed only (Fig. 3B). These results confirmed a synergistic interaction between S150 and Fmed during the incubation period.

Solid-state NMR spectroscopy of wood samples in Petri plate assays

To study the impact of fungi and bacteria on wood degradation, we conducted 13C CP/MAS NMR experiments on intact sterile sawdust (control) and sawdust inoculated with S150 alone, Fmed alone, and co-inoculated with S150 and Fmed (Fig. 3). The peaks observed in these experiments were assigned based on previous NMR studies on wood (Kolodziejski et al., 1982; Haw et al., 1984). Main chemical components of wood (cellulose, hemicellulose and lignin) were distinguished based on their characteristic 13C chemical shifts, although for several regions (e.g. 65–80 ppm), signals overlap due to similar carbohydrate structures. Due to limited overlap in the 81–93 ppm region, the relative intensity of the two structural forms (crystalline and amorphous) of wood cellulose was compared. C-4 resonance of amorphous cellulose was observed at ~85 ppm, whereas crystalline cellulose resonance appeared at ~89 ppm (Park et al., 2009). We derived the cellulose crystallinity index (CrI) by integrating the peaks of the crystalline and amorphous C-4 spectral area after deconvolution, following the procedure described in Davis et al. (1994). An increase in CrI (Fig. 3D) was observed in the sawdust inoculated with S150, changing from 17% ± 1% for the control to 27% ± 1% for that inoculated with S150. A similar effect was observed after inoculation with Fmed, with CrI increasing to 30% ± 1%. These results indicated that S150 and Fmed both had the ability to specifically degrade cellulose. The increase in CrI suggests that fungi and bacteria might have a preferential effect on amorphous cellulose, which is structurally easier to degrade compared to crystalline cellulose. As CrI is calculated as CrI = a/a + b, with a and b being the crystalline and amorphous contribution respectively, a decrease in amorphous cellulose would increase the CrI. Such changes in the relative amount of amorphous cellulose as a result of wood degradation caused by fungi and bacteria are in line with the findings of previous studies (Davis et al., 1994) on Colorado blue spruce. When co-inoculated with S150 and Fmed, CrI further increased to 34% ± 1%, which corresponds to twice the CrI value obtained in the control sample, suggesting a synergistic effect of bacteria and fungi on cellulose degradation.

In addition to the preferential degradation of amorphous cellulose, the CPMAS spectra reveal an overall decrease in aromatic signals of lignin, especially the
guaiacyl C-1 and C-4 contribution at ~146 ppm, in the samples inoculated with *Fmed* and co-inoculated with *Fmed* and S150. This effect was not observed in sawdust inoculated only with S150, suggesting a stronger lignin-degrading effect of the fungus compared to that of the bacterium.

**Genome analysis of S150**

**Genomic features and taxonomic affiliation.** The genome of strain S150 was analyzed and was found to have a total size of 7.45 Mb, as well as an average G + C content of 52.54% (Table 2). The analysis based on 468 markers showed a genome completeness of 99.8% and contamination around 1.59%. The taxonomical analysis could not assign a species to the strain as it did not reach the required 95% ANI threshold for species circumscriptio. The genomic features of the strain are summarized in Table 2.

Table 2. Summary of the genomic feature of strain S150.

| Feature               | S150          |
|-----------------------|---------------|
| Organism              | *Paenibacillus* sp. |
| Length (bp)           | 74 15 460     |
| Coverage              | 229.3607 ± 109.6652 |
| Completeness (%)      | 99.47         |
| GC content (%)        | 52.54         |
| Contigs               | 102           |
| Total genes           | 6,292         |
| Predicted CDS         | 6,200         |
| CRISPR number         | 6             |
| rRNA number           | 6             |
| tRNA number           | 85            |
| tmRNA number          | 1             |

**Genes predicted to be involved in carbohydrate metabolism.** RAST annotation allowed the detection of several genes (230) involved in carbohydrate transport and metabolism, in addition to other clusters of orthologue groups. Seven genes involved in xylose (xyloside) degradation were detected (Table 3), namely, XylA coding for a
xylose isomerase that catalyses the reaction of D-xylose to D-xylulose, XylB coding for a xylulose kinase that catalyses phosphorylation of D-xylulose to D-xylulose 5-phosphate, XynA coding for a beta-xylosidase and XynN coding for endo-1,4-beta-xylanase. A precursor that endohydrolyse (1→4)-beta-D-xylosidic linkages in xylans. XDH was also found that codes for a D-xylose 1 dehydrogenase (catalyses the reaction: D-xylose + NAD (⁺) ↔ D-xylonolactone + NADH). Lastly, XL coding for a xynolactone (catalyses the reaction: D-xylono-1,4-lactone + H₂O ↔ D-xylonate), and XTD coding for a xylonate dehydratase (catalyses the reaction: D-xylonate ↔ 2-dehydro-3-deoxy-D-arabinonate + H₂O) were also detected (Table 3). Genes involved in the pentose-phosphate pathway were further analyzed. They code for transketolase, ribose-phosphate pyrophosphokinase, glucose-6-phosphate 1-dehydrogenase, 6-phosphogluconolactonase, dehydrogenase, xylulose 5-phosphate, fructose 6-phosphate phosphoketolase and transaldolase (Table S1). No gene, possibly involved in lignin degradation (related to lignin-degrading auxiliary enzymes and lignin-modifying enzymes) was detected in the genome of S150 (Tables S1 and S2).

Furthermore, we also analyzed all gene clusters related to carbohydrate-active enzymes (CAZy) to have a better view of the functions of carbohydrate-related genes such as auxiliary activities, carbohydrate-binding modules and encoding carbohydrate esterases, glycoside hydrolases, glycosyltransferases and polysaccharide lyases (Figs 4–5). Among them, several GH families, as well as subfamilies, showed potential cellulase activities (i.e. endo β-1,4-glucanases) and activities on arabinofuranosides, fucosides, mannosides, xyloses and xylans (xylosides), and galactosides and glucuronides (Table S3).

**Table 3.** Protein encoding genes (part of the carbohydrate transport and metabolism) predicted to be involved in xylose (xylosides) degradation pathway of strain S150 determined by RAST.

| Feature                                      | Gene | Functional roles                                                                 |
|----------------------------------------------|------|----------------------------------------------------------------------------------|
| Genes involved in xylose (xylosides)         | XylA | Xylose isomerase (EC 5.3.1.5)                                                   |
| degradation pathway                          |      |                                                                                  |
|                                             | XylB | Xylulose kinase (EC 2.7.1.17)                                                   |
|                                             | XynA | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8)                                  |
|                                             | XDH  | α-xylose 1-dehydrogenase (EC 1.1.1.175)                                          |
|                                             | XL   | Xynolactone (EC 3.1.1.68)                                                       |
|                                             | XTD  | Xylonate dehydratase (EC 4.2.1.82)                                               |

**Genes predicted to be involved in plant–microbe interaction.** The carbohydrate metabolism of S150 and genes in its genome encoding polysaccharide lyases may be correlated to its behavior as an endophyte. In addition, the analysis of its genome also enabled the detection of genes encoding proteins that are predicted to be involved in plant–microbe interaction, including motility and chemotaxis, biofilm, siderophore and iron transport (-Table S4), as well as genes related to oxidative stress and detoxification (Table S5). Interestingly, S150 also possesses genes involved in resisting copper and metalloids (Table S6) but not arsenic. However, a homologous

Fig. 4. (A) Cluster Orthologue Group (COG) categories of *Paenibacillus* sp. (S150), (B): Carbohydrate-active enzymes (CAZymes) related genes of strain S150. AA: auxiliary activities, CBM: carbohydrate-binding modules, CE: carbohydrate esterases, GH: Glycoside hydrolases, GT: Glycosyltransferases, PL: Polysaccharide lyases. [Color figure can be viewed at wileyonlinelibrary.com]
gene of the repressor of the arsenic resistance operon was detected by eggNOG analysis (Table S2).

**Genes predicted to be involved in fungal stimulation.** Several gene clusters involved in the metabolism of vitamins such as thiamin (B1), riboflavin (B2), pyridoxin (B6), biotin (B7), folate (B9), cobalamin (B12), menaquinone (K1), phylloquinone (K2) and ubiquinone (Q10) were detected in S150 (Table S1). As per previous studies, these genes could be involved in fungal stimulation (del Barrio-Duque et al., 2019, 2020). These studies showed several strains of Proteobacteria and Mycobacteriaceae promoting the growth of the mycorrhiza-like fungus *Serendipita indica*. Only a few genes reported to be involved in the provision of nitrogen to the fungus were identified (Table S1).

**Biosynthetic gene clusters involved in secondary metabolite production.** A total of six potential gene clusters involved in secondary metabolite production were identified. These clusters showed no similarity to genes encoding known compounds. However, one cluster encoding a putative nonribosomal peptide synthetase (NRPS) showed 46% similarity to gene cluster responsible of bacillibactin (a catechol based siderophore), and another related to lasso peptide (synthesized and post-translationally modified peptides; RiPPs) showed 100% similarity to most similar known cluster related to paeninodin, which was proposed to serve as a signal molecule, and an antimicrobial and antiviral compound (Zhu et al., 2016; Khurana et al., 2020) (Fig. 6). The draft genome sequence of the strain is available at NCBI, BioProject PRJN643435, with the DDBJ/ENA/GenBank accession number JACBYI000000000.

**Discussion**

Specifically adapted fungi and bacteria both have the ability to colonize grapevine wood tissues (Brez et al., 2014, 2015, 2020; Campisano et al., 2014; Pinto et al., 2014), but based on studies on GTD, fungi were almost exclusively considered responsible for wood degradation leading to necrosis (Larignon and Dubos, 1997; Mugnai et al., 1999; Mostert et al., 2006; Bertsch...
In our study, we tested the hypothesis that synergistic interaction between a pathogenic GTD-fungus *Fmed* (a basidiomycete), and some bacterial strains inhabiting grapevine woods may have an important role in the wood-degradation process, increasing the overall level of degradation.

**Bacteria colonizing wood grapevine**

V5–V9 region of the 16S rRNA gene sequencing was used to identify the bacterial population colonizing the wood trunks and cordons of esca-symptomatic grapevines. These bacterial communities were dominated by members of the phyla *Proteobacteria* and *Firmicutes*. Among the nine families of *Proteobacteria*, *Xanthomonadaceae* was the most abundant. This is in accordance with prior findings in decaying wood of pine (Kielak et al., 2016), beech (Valášková et al., 2009), and in microcosms containing beech sawdust inoculated with *Phanerochaete chrysosporium* (Hervé et al., 2014, 2016). It has also been reported that *Xanthomonadaceae* were able to degrade the lignocellulose (cellulose, hemicellulose and lignin) of different lignocellulose substrates under controlled conditions (Zimmermann, 1990; Behera et al., 2014; Ceballos et al., 2017; Oh et al., 2017). At genus level, the isolated bacterial community was composed primarily of *Pseudomonas*, which aligns with previous results demonstrating this genus as the most abundant in many organs as well as sap of grapevine (West et al., 2010; Martins et al., 2012, 2013; Faist et al., 2016; Deyett et al., 2017; Compton et al., 2019; Deyett and Rolshausen, 2019). An association of *Xanthomonas* and *Pseudomonas* with wood decay processes of *Picea abies* was also reported (Probst et al., 2018).

**Bacterial and fungal degradation of wood components**

In the present study, 59 bacterial strains obtained from various wood tissues, representing various taxa, were screened for their ability to degrade the three main components of wood, i.e. cellulose, hemicellulose and lignin, and their ability to inhibit *Fmed*. While 18 bacterial strains showed cellulolytic and xylanolytic activities, none of the bacterial strains was able to degrade lignin; conversely, the fungus *Fmed* specifically degraded lignin, as shown by CPMAS NMR analysis. Previous studies have also shown that there was no ligninolytic activity in bacterial strains isolated from spruce stumps or in microcosms containing beech sawdust (Murray and Woodward, 2007; Hervé et al., 2016). For further investigations, we therefore selected *Paenibacillus* sp. strain S150, a bacterial strain able to degrade cellulose and hemicellulose, and did not inhibit *Fmed in vitro*. However, none of the selected *Xanthomonas* and *Pseudomonas* strains
(considered as associated with wood decay processes, as described above) has shown the last criteria.

By studying the physicochemical properties of wood-blocks exposed to Fmed, CPMAS NMR showed that Fmed preferentially degrades both lignin and amorphous cellulose. These results are consistent with the findings of a previous study (Bari et al., 2015), which showed that after 120-days exposure of Oriental beech to the white-rot fungi Pleurotus ostreatus and Trametes versicolor, several properties of wood, such as its hardness, and cellulose and lignin content, declined.

Interaction between bacteria and fungi in wood degradation

Bacterial–fungal interaction involved in the wood degradation process has been reported before, but on other plants than grapevine (Hervé et al., 2014, 2016; Kamei, 2017; Harry-asobara and Kamei, 2018). Evaluation of wood degradation was first done by measuring the C/N ratio of grapevine wood. This ratio provides information on changes in chemical composition of organic matter and thus reflects decomposition processes. The C/N ratio has already been identified as an important variable correlated to organic matter mass loss especially during the decomposition process (Eiland et al., 2001; Lehmann et al., 2002; Hervé et al., 2014, 2016; Meriem et al., 2016; Tramoy et al., 2017). Our results demonstrated that when the two microorganisms were co-inoculated on grapevine sawdust, their interaction increased significantly grapevine wood degradation compared to that caused by the fungus alone and by the study of the physicochemical properties of wood by NMR. All results suggested a functional complementation of the two studied microorganisms.

Specific properties of the Paenibacillus strain S150

Several stains of Paenibacillus, isolated from diverse sources such as soil, bamboo leaves, decomposing rice straw and decaying woods, harbour enzymes that are involved in cellulose and xylan degradation (Nelson et al., 2009; Khianngam et al., 2011; Ghio et al., 2012; Madhaiyan et al., 2017). Our genome analysis of S150 revealed no gene involved in lignin degradation but several ones linked to cellulose, and xylose and xylan (xyloside) degradation. This point is of key importance since cellulose and hemicellulose represent up to 20%–35% of the ligno-cellulosic biomass of all plant cell walls (de Vries and Visser, 2001). The major hemicellulose in hardwood biomass is xylan (10%–35%), but it is less abundant in softwood (10%–15%). Xylan is made up of β-1,4-linked xylose residues with side branches of α-arabinofuranose and α-glucuronic acid (Balakshin et al., 2011). We also found several genes responsible for vitamin metabolism that could explain the increased Fmed growth observed in in vitro assays. Additionally, gene clusters involved in plant–microbe interaction were also identified.

Conclusions

In this study, we hypothesized that bacteria inhabiting grapevine wood could synergistically interact with an esca-causing pathogenic fungus, thus enhancing wood degradation. The obtained results confirmed this hypothesis and showed that (i) some bacteria can independently destruct wood components such as cellulose and hemicellulose, and (ii) fungal ability to degrade wood structures can be strongly influenced by some bacteria inhabiting wood. Specifically, the cellulolytic and xylanolytic strain S150 of the Paenibacillus sp. showed a synergistic interaction with the white-rot fungus Fmed. Having evidenced that fungus–bacteria synergistic interaction to promote wood degradation exists for microorganisms colonizing the wood of grapevines, the further step would be to point out its occurrence in mature grapevines and its role in the triggering and development of esca disease.

Experimental procedures

Grapevine material and sampling

Sampling was carried out in three 21-year-old vines of the cultivar Sauvignon blanc (Vitis vinifera L.) grafted onto the rootstock 101-14 MGT. The vines were located in an experimental vineyard near Bordeaux (INRAE, Villenave d’Ornon, France, 44°47’24.8”N, 0°34’35.1”W), planted in 2000. The vines had previously shown esca-foliar symptoms at least twice during a period of 4 years (2012–2016). The sampling method was as follows: plants were sectioned longitudinally to check the status of the wood tissues, i.e. necrotic or healthy, in the cordon and trunks. From the inner part of each organ, i.e. cordon and trunk, four types of wood tissues were sampled: necrotic (sectoral black streaks) tissues (NT), non-necrotic (apparently healthy) tissues (NNT), transition tissues between the necrotic and non-necrotic zones (TT) and white rot (decaying wood) tissues (WR), the typical necrotic tissue associated with esca (Maher et al., 2012; Bruez et al., 2015). A total of 24 samples, each consisting of 30 wood chips (around 5 mm in length), were collected corresponding to two organs (cordon and trunk) from three esca-symptomatic vines, and four tissues of each type (NT, NNT, TT and WR) were collected.

Wood-inhabiting bacterial strains

Isolation of bacteria from wood tissues of esca-symptomatic grapevines. The wood tissue samples were
and then adjusted to a concentration of 20 ng μl⁻¹ (Sigma-Aldrich) amended with 100 mg L⁻¹ cycloheximide (Sigma) and nutrient agar (NA, Carl Roth) supplemented with 100 mg L⁻¹ nalidixic acid and 5 g L⁻¹ glycerol. The plates were incubated at 28 °C for 48 h. A total of 237 bacterial strains were recovered from the 720 wood pieces collected (three symptomatic vines × two organs × four tissues × two media × five wood chips × three plates). After purification on Trypto-Casein-Soy Agar medium (TSA, Biokar Diagnostics) thrice, the strains were maintained at −20 °C on cryogenic storage beads (Viabank™, MWE, Wiltshire, England).

**Identification by sequencing the partial 16S rRNA gene.** From the 237 bacterial strains that were recovered, genomic DNAs were extracted from pellets obtained after the centrifugation of pure cultures grown for 48 h in Tryptone-Soy Broth (TSB, Biokar) using the cetyltrimethylammonium bromide chloroform/isoamyl alcohol (24:1) protocol. DNA extracts were quantified using nanodrop (ND-1000, Thermo Scientific, USA) for sequencing the 16S rRNA gene with the primers 1492r (5'-AACMGGATTAGATACCGG-3') and 907f (5'-GTTACCTTGTTACGACTT-3') (Heuer et al., 1997; Redford et al., 2010; Bruez et al., 2015). For taxa level identification, sequences were compared with the GenBank database (nr/nt nucleotide collection using Megablast) using the BLASTn program (Altschul, 1997), with a >99% similarity cutoff. Sequences were then binned into taxa using the Muscle alignment method (Edgar, 2004) and the BioNJ distance-based phylogeny reconstruction algorithm (Gascuel, 1997) to select representative strains of each taxon for downstream analyses (microbiological functional analyses). A total of 59 taxa were defined. One bacterial strain of each taxon was selected for further analyses (Table 1).

**Fmed strain and culture conditions**

The Fmed isolate (Ph CO 36) used in this study was selected from the INRA-UMR 1065 SAVE collection (Bordeaux, France). This strain was originally obtained in 1996 in Saint Preuil, near Cognac, France. The strain was subcultured on Malt Agar medium (MA) and incubated at 27 °C (12 h light/12 h dark) for 7 days before being used in microcosm experimentations and 15 days before being used in *in vitro* tests (confrontation and volatility tests).

**Wood component decomposition by bacterial strains and Fmed**

**Selective media used.** Three selective media were used for bacteria and Fmed. (i) Xylan medium: a medium containing xylan as the only carbon source [1 g L⁻¹ K₂HPO₄; 1 g L⁻¹ (NH₄)₂SO₄; 0.5 g L⁻¹ MgSO₄·7H₂O; 0.5 g L⁻¹ NaCl; 5 g L⁻¹ beechwood xylan (Apollo scientific); and 20 g L⁻¹ agar] (Hervé et al., 2016); (ii) CMC medium: a medium containing carboxymethyl-cellulose as the sole carbon source [1 g L⁻¹ K₂HPO₄; 1 g L⁻¹ (NH₄)₂SO₄; 0.5 g L⁻¹ MgSO₄·7H₂O; 0.5 g L⁻¹ NaCl; 5 g L⁻¹ carboxymethyl-cellulose sodium salt (CMC, Sigma); and 20 g L⁻¹ agar] (Hervé et al., 2016); (iii) RBBR medium: a Water Yeast Agar medium containing 0.05% RBBR (Sigma) [1 g L⁻¹ NaCl; 0.1 g L⁻¹ yeast extract (Difco); 1.95 g L⁻¹ MES (Sigma); and 20 g L⁻¹ agar; pH 5] (Hervé et al., 2016). The laccase activity of Fmed was determined in Guaiacol medium: Potato Dextrose Agar (Biokar) medium containing 0.02% Guaiacol (Sigma).

**Enzymatic assays.** Petri plates containing the different selective media were inoculated with each pure microbial strain (59 selected bacteria and Fmed) and then incubated at 28 °C for 7 days in the dark. Four plates were replicated for each medium and strain. Lignolysis was indicated by the RBBR medium that turns from blue to pale pink when positive (Murray and Woodward, 2007). The xylanolytic activity on xylan medium and cellulolytic activity on CMC medium were detected using 0.1% Congo red (Sigma) staining for 40 min followed by washing with 1 M NaCl for counterstaining. Each enzymatic activity was measured based on the size (mm) of the clearing/discoloration zones formed around the bacterial or fungal colonies. The production of laccase by Fmed was indicated by the medium turning brown.

**In vitro bacteria-Fmed co-cultures**

**Direct confrontation assays.** A mycelial plug of Fmed (4 mm in diameter) was placed at the centre of MA plates, and after a week of incubation at 25 °C, selected bacterial strains were streaked at the edge of each plate. A set of plates was inoculated with the pathogen only. Three replicates were performed for each combination (bacterial strain/Fmed) tested. The plates were then incubated in the dark at 27 °C. After 1 week, the radial mycelial growth of Fmed was assessed by measuring the radius of the colony in mm (in the direction of the bacterial strain and also in the opposite direction). The mycelial growth inhibition percentage (GI%) was calculated using...
the following equation: GI% = 100 \times (R2 - R1)/R2,
where R1 is the radial distance (mm) grown by Fmed in
the direction of the bacterial strain, and R2 is the radial
distance (mm) grown by the Fmed in the opposite
direction.

Assay of the volatile substances produced by the bacte-
ria. The Fmed strain was grown on MA plates for 7 days
at 27 °C in the dark, and the bacterial strains were grown
on TSA for 24 h at 28 °C. The bottoms of the plates were
then placed face-to-face, with the bacterial culture plate
placed below the Fmed plate, and sealed with Parafilm.
This arrangement prevented physical contact between
the two microorganisms. Plates were incubated at 27 °C
in the dark for 7 days. The control plates consisted of
Fmed plates inverted over sterile TSA medium. Three
replicates were made for each bacterial strain and the
control. The diameters of the fungal colonies were mea-
sured after 7 days of incubation, and the mycelial growth
inhibition was calculated with respect to the control.

Microcosm experimentations

Degradation of lignin by Fmed. Experimental design.
Grapevine cuttings of cv. Cabernet Sauvignon originating
from INRA experimental vineyards near Bordeaux
(Villenave d’Omon, France, 44°47’24.8”N, 0°34’35.1”W)
were used for the microcosm experimentations. After
having removed the bark, wooden rods (30 mm in length,
10 mm in width) were sectioned and sterilized twice for
20 min at 120 °C, in a 2-day interval. Hundred micro-
cosms were then prepared in Petri plates, each con-
taining one wooden rod and a 7-day-old Fmed colony.
Twenty controls were prepared with wooden rods incu-
bated on sterile MA medium. The microcosms were
sealed with Parafilm before being incubated for 2, 7 and
10 months at 25 °C in the dark.

- Lignin content measurement in wooden rods by the
determination of Klason lignin. The lignin content fol-
lowing a short (2 months) and a long (7 and 10 months)
posure time to Fmed was determined using the Klason
method (Kirk and Obst, 1988; Tlaskal et al., 2017).

The lignin content in control rods was also determined.
Five replicate rods were used for each exposure time. All
assays were performed twice.

Effect of bacteria–Fmed co-cultures on wood
degradation. Selected bacteria and bacterial inocula.
For inoculation, the bacterial strain S150 was prepared
as described by Kamei (2017), with slight modifications.
Liquid cultures were obtained by inoculating Erlenmeyer
flasks containing TSB, with bacterial colonies previously
grown on TSA and by incubating them at 27 °C for 24 h
using an orbital shaker at 150 rpm. Liquid cultures were
then centrifuged twice at 5000 rpm for 10 min, and the
pellets were resuspended in sterile water. Bacterial sus-
pensions were quantified by fluorochrome staining
(500 μl Chemsol B16 buffer + 2.5 μl Chemochrome V6
fluorescein acetate; Biomérieux, France) followed by
epifluorescent direct counts using an optical microscope
(Model BH2, Olympus, France). A minimum of 300 cells
was counted in at least 10 different fields of view, and the
average number of fluorescent cells per field was
expressed as CFU ml⁻¹. The bacterial concentrations
obtained were estimated at 10⁻⁷ and 2 × 10⁻⁷ CFU ml⁻¹.

- Experimental design. Two types of microcosms
(in Erlenmeyer flasks and in Petri plates) were used to
study the effect of S150 on wood degradation by Fmed.

- Erlenmeyer flask microcosms. Experimentations
were carried out in 50 ml Erlenmeyer flasks sealed with
adhesive tape containing 0.4 g of sterile sawdust wood
(cv. Cabernet Sauvignon) sieved (mesh size 2 mm) and
autoclaved twice, 2 days apart (for 20 min, at 120 °C). A
mycelial disk (5 mm in diameter) taken from the margin
of a 15-day-old colony, was then placed on sawdust
already inoculated with 400 μl of bacterial cell suspen-
sion. Control flasks were inoculated with 400 μl of sterile
distilled water. Each flask was sealed with a transparent
adhesive tape and then incubated for 60 days at 28 °C in
the dark.

Four treatments with three replicates each were tested:
(i) controls containing sawdust with sterile water;
(ii) Fmed with sterile water; (iii) Fmed and S150; and
(iv) S150.

- Petri plate microcosms. Experimentations were car-
ried out with the strain S150 in 90 mm Petri plates con-
taining 2 g of sterile sawdust wood (Vitis vinifera L),
sealed with adhesive tape. Grapevine sawdust was
sieved (2 mm mesh) and autoclaved (for 20 min, at 120 °C)
twice, with an interval of 2 days in between. Fun-
gal inocula were prepared on grapevine wood rods as
described in Section 6.1.1.1 of this text.

Wooden rods (1 cm long) were colonized with Fmed
for 5 months, then placed on sawdust and inoculated with
5 ml of bacterial cell suspension. Control flasks were
inoculated with 5 ml of sterile distilled water. Each Petri
plate was sealed with transparent adhesive tape and
incubated for 8 months at 28 °C in the dark.

- Assessment of wood degradation. Measurement
of C and N concentrations. After incubation, the C and N
contents of the woods were measured, in three repeti-
tions of each modality, by the Dumas’ method using a
VarioMax cube elemental analyser at the USRAVE

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precincts (USRAVE, INRAE Aquitaine, France). Size and color of the sawdust particles were observed for all assays.

- Solid-state NMR spectroscopy for analysis of the woods. The evaluation of wood components’ degradation in Petri plate microcosms was carried out by using solid-state NMR (ssNMR), performed under magic-angle spinning (MAS) conditions. MAS ssNMR experiments were conducted on a 300 MHz spectrometer (Bruker Avance III) equipped with a double resonance 4 mm DVT MAS probe. MAS frequency was set to 11 kHz. 13C-detected experiments were performed using a 1H–13C cross-polarization (CP) transfer using a contact time of 500 μs, a recycle delay of 2 s, and 100 kHz proton decoupling during acquisition. 20 k scans were used per CP MAS experiment.

Cellulose crystallinity, measured as the crystallinity index (CrI), was calculated from the area of the (a) crystalline (87–93 ppm) and (b) amorphous (81–88 ppm) cellulose C4 signals, by deconvolution using a Lorentzian line shape.

**Genome of Paenibacillus sp. strain S150**

The bacterial genomic DNA was extracted following a phenol-chloroform based protocol after growing the strain in liquid TSB medium for 3 days and harvesting by centrifugation at 6000 rpm for 3 min. The bacterial pellet was resuspended in a lysis buffer (0.2 mg ml−1 Proteinase K, 50 mM Tris-Cl, 1% SDS, 5 mM EDTA at pH 8 and 0.5 M NaCl) and incubated overnight (at 65 °C; 400 rpm). DNA was extracted twice using phenol–chloroform–isoamylalcohol at a ratio of 25:24:1 and collected by centrifugation at 6,000 rpm for 3 min as described in a previous study (del Barrio-Duque et al., 2020). Genomic DNA was then purified with Amicon Ultra 0.5 ml 30K Centrifugal Filter Units (Millipore, Cork, Ireland) and resuspended in distilled sterile water. Whole-genome shotgun sequencing was performed on an Illumina NovaSeq 6000 mode S2 (GATC Biotech, Konstanz, Germany), producing approximately 6.2 million paired-end reads of 150 bp. The Illumina reads were then screened for the presence of PhiX using Bowtie 2 (v2.3.4.3) (Langmead and Salzberg, 2012); adapters were trimmed and quality filtering was accomplished with FASTP (v0.19.5) (Chen et al., 2018). Sequence length distribution and quality were checked via FastQC (Andrews, 2010). Genome assembly was performed with SPAdes v3.13.0 (Bankevich et al., 2012), and low-abundant (≤2×) and short (<500 bp) contigs were discarded. Contigs were roughly checked for the presence of contaminants using BlobTools v.1.1.1. The quality of genome assembly was determined using QualiMap v2.2 (Okonechnikov et al., 2015) and QUAST v5.0.0 (Gurevich et al., 2013), and then genome completeness of the reconstructed genome was evaluated using CheckM v1.0.18 (Parks et al., 2015). Gene annotation was carried out using Prokka v1.12 (Seemann, 2014) and NCBI Prokaryotic Genome Annotation Pipeline (PGAP). The presence of plasmids was ascertained by using Mash v2.1 against the PLSDB database (Galata et al., 2019). Putative plasmid contigs were screened for the presence of genes coding for replication initiator proteins, repA. For this purpose, a curated FASTA file with ~8,000 repA genes was generated from plasmid genome sequences in NCBI. These repA gene sequences were used to build a database against which the selected contigs were aligned using BLAST+ v2.10.0. These repA gene sequences were used to build a database against which the selected contigs were BLASTed. Functional annotation was performed using the ClassicRAST (Rapid Annotation using Subsystem Technology) webserver (http://rast.nmpdr.org) (Aziz et al., 2008), and the hierarchical orthology framework EggNOG 4.5 (Huerta-Cepas et al., 2016). CAZY families were ascertained with dbCAN2 based on the HMMER database. Annotation of proteins was based on the CAZY database (Lombard et al., 2014). Biosynthetic gene clusters and secondary metabolites were further predicted using antiSMASH version 4.0.2 (Weber et al., 2015). To assign objective taxonomic classifications to the genome, the software toolkit GTDB-Tk v0.3.2 was used (Parks et al., 2018; Chaumeil et al., 2020).

**Statistical analyses**

The experimental data obtained from in vitro or microcosm assays were compared using an analysis of variance (ANOVA) followed by Newman–Keuls’ test (P ≤ 0.05). These analyses were carried out with the StatBox software (Version 6.6, Grimmer© Logiciels, Paris).

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**Supporting Information**

Additional Supporting Information may be found in the online version of this article at the publisher’s web-site:

**Table S1.** RAST annotation of S150.

**Table S2.** eggNOG annotation of S150.

**Table S3.** Glycoside hydrolases genes present in the genome of strain S150. GH: Glycoside hydrolases.

**Table S4.** protein encoding genes predicted to be involved in plant-microbe interaction by strain S150 determined by RAST.

**Table S5.** protein encoding genes predicted to be involved in oxidative stress and detoxification of strain S150 determined by RAST.

**Table S6.** protein encoding genes predicted to be involved in resistance to antibiotics and toxic compounds of strain S150 determined by RAST.

**Fig. S1.** Degradation of wood component by A: *F. mediterranea* a) cellulose b) xylan c) lignin; B) bacteria; a) cellulose b) xylan c) lignin (absence of halo)

**Fig. S2.** Effect of the presence of wooden rods on the growth rate of *F. mediterranea*. Three days culture of *F. mediterranea* on MA with (A) or without wooden rod (B).