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1. Chemical composition of the grapevine leaf extract used to make the Grapevine Leaf-based Agar (GLA) culture medium

The nutritional analyses showed that the sugar levels in the grapevine-leaf extract were very low, with a value <2 g/100 g and the pH was acidic, with a value of 3.5 (Table S1). The levels of all the amino acids were also very low with the highest being 0.04 g/100 g for glutamic acid. The sum of all the amino acid content taken together amounts to <0.4 g/100 g and the overall protein content was also low, with a value of <0.5 g/100 g. In terms of vitamin and mineral content, the extract was rich in potassium and β-carotene (Table S2). Using a dosage of 50 mL (equivalent to 49.4 g) of the extract to make 1 L of the GLA makes it a very nutritionally poor medium when compared with the other media used in the study.

The analysed amino acid content of the GLA alongside the estimated amino acid content in the conventional media is summarised in Table S3. According to the manufacturer, 1 L of the TSA used for isolating bacteria, contained 17 g of the pancreatic digest of casein and 3 g of the papaic digest of soybean meal which contributes together to a total amino acid content that is approximately 84 times higher than the GLA. It also contained 2.5 g of dextrose[1] making the sugar content higher as well. The LBA was diluted 1/10 and for 1 L of diluted medium, it contained 1 g of tryptone and 0.5 g of yeast extract which when combined is still higher than the overall amino acid content than the GLA by a factor of about 6. The small quantity of the yeast extract present in the dil. LBA contributed a larger variety of B vitamins overall when compared to the GLA.

Similarly, the MEA used for isolating yeasts and filamentous fungi was nutritionally richer than the GLA. According to the manufacturer's technical data sheet, it contained 80 % maltose and 10 % dextrin[2] making the eventual sugar levels available in the medium much higher. It also contained 9.3 g/100 g of total amino acids. At the dose of 15 g per litre of culture medium, the amino acid content was higher than the GLA by a factor of about 7.

[1] https://www.solabia.com/biokar-diagnostics/product/papaic-digest-of-soybean-meal-usp/?documentation=1852&_wpnonce=f8c5af56a9
[2] https://www.solabia.com/biokar-diagnostics/product/bacteriological-malt-extract/?documentation=4754&_wpnonce=f8c5af56a9

Table S1. Nutritional analyses of grapevine leaf extract used to make the grapevine leaf-based agar (GLA) medium from AQUANAL (Pessac) carried out on 01/03/2024.

	Parameter	Result	Units
Nutritional analyses	Calories	<5	kcal/100 g
	Energy value	<25	kJ/100 g
	Lipids (Fats)	<0.3	g/100 g
	Sugars	<2	g/100 g
	Total dietary fibre	<0.5	g/100 g
	Proteins (N × 6,25)	<0.5	g/100 g
	Ash	0.28	g/100 g
	Moisture at 103 °C	98.26	g/100 g
pH	pH	3.5	
Metals/minerals	Calcium	47.9	mg/100 g
	Copper	33.0	µg/100 g
	Iron	0.19	mg/100 g
	Potassium	143	mg/100 g
	Magnesium	12.4	mg/100 g
	Manganese	0.25	mg/100 g
	Sodium	2.25	mg/100 g
	Phosphorous	23.7	mg/100 g
	Zinc	0.11	mg/100 g
	Lead	<0.005	mg/kg
	Selenium	<0.5	µg/100 g

Table S2. Vitamin content of grapevine leaf extract used to make the grapevine leaf-based agar (GLA) medium from AQUANAL (Pessac) carried out on 01/03/2024. Estimated vitamin content of yeast extract[1] which is an ingredient in the dil. LBA based on technical sheets from manufacturers. NA indicates that the information was not available.

Vitamins	Estimates for yeast extract	Results for grapevine leaf extract	Units
β-carotene	NA	132	µg/100 g
Vitamin B1	2.1	0.05	mg/100 g
Vitamin B2	12.5	NA	mg/100 g
Vitamin B3	60.0	NA	mg/100 g
Vitamin B5	10.5	NA	mg/100 g
Vitamin B6	2.4	NA	mg/100 g
Vitamin B7	0.4	NA	mg/100 g
Vitamin B9	0.6	NA	mg/100 g
Vitamin B12	NA	<0.05	µg/100 g

[1] https://www.solabia.com/biokar-diagnostics/product/yeast-extract/?documentation=2335&_wpnonce=f8c5af56a9

Table S3. Individual amino acid content of grapevine leaf extract used to make the grapevine leaf-based agar (GLA) medium from AQUANAL (Pessac) carried out on 01/03/2024. Estimated amino acid content of individual ingredients in conventional media used based on technical sheets from manufacturers. For TSA – pancreatic digest of casein[1] and papaic digest of soybean meal[2]; for dil. LBA – tryptone[3] and yeast extract[4]; for MEA – malt extract[5]. NA indicates that the information was not available.

Amino acid	Estimates for pancreatic digest of casein	Estimates for papaic digest of soybean meal	Estimates for tryptone	Estimates for yeast extract	Estimates for malt extract	Results for grapevine leaf extract	Units
Aspartic acid	6.4	7.2	6.9	6.5	0.9	0.02	g/100 g
Threonine	3.4	2.5	3.3	2.6	0.4	<0.02	g/100 g
Serine	4.2	3.4	4.1	2.4	0.4	<0.02	g/100 g
Glutamic acid	17.4	13.2	18.5	11.5	1.6	0.04	g/100 g
Proline	8.4	4.2	9.0	2.3	0.6	<0.02	g/100 g
Glycine	1.9	2.9	3.2	3.0	0.4	<0.02	g/100 g
Alanine	2.6	2.9	3.1	4.8	0.4	<0.02	g/100 g
Valine	5.1	4.6	6.1	4.1	0.6	<0.02	g/100 g
Cystine	NA	NA	NA	NA	NA	<0.01	g/100 g
Methionine	2.4	0.8	2.4	0.9	0.2	<0.01	g/100 g
Isoleucine	4.3	3.0	4.9	3.1	0.5	<0.02	g/100 g
Leucine	7.2	5.2	8.1	4.2	0.6	<0.02	g/100 g
Tyrosine	2.0	1.3	1.5	1.1	0.3	<0.03	g/100 g
Phenylalanine	4.1	3.4	4.9	2.6	0.7	<0.03	g/100 g
Lysine	6.5	4.6	7.6	4.6	0.6	<0.02	g/100 g
Histidine	2.7	1.9	2.9	1.4	0.6	<0.02	g/100 g
Arginine	3.1	4.2	3.2	3.2	0.5	<0.03	g/100 g
Tryptophan	1.2	1.1	1.2	0.9	NA	<0.01	g/100 g
Total	87.6	57.9	90.9	59.2	9.3	<0.4	g/100 g

[1] https://www.solabia.com/biokar-diagnostics/product/pancreatic-digest-of-casein-codex/?documentation=1839&_wpnonce=f8c5af56a9

[2] https://www.solabia.com/biokar-diagnostics/product/papaic-digest-of-soybean-meal-usp/?documentation=1852&_wpnonce=f8c5af56a9

[3] https://www.solabia.com/biokar-diagnostics/product/tryptone-usp/?documentation=2199&_wpnonce=f8c5af56a9

[4] https://www.solabia.com/biokar-diagnostics/product/yeast-extract/?documentation=2335&_wpnonce=f8c5af56a9

[5] https://www.solabia.com/biokar-diagnostics/product/bacteriological-malt-extract/?documentation=4754&_wpnonce=f8c5af56a9

2. Taxa of interest for biocontrol within collection

Table S4. Bacteria of interest for their biocontrol potential *in vitro* or *in planta* across various plant and pathogen species from published culture-dependent studies.

Microorganism	Number of isolates in collection	Biocontrol potential as described in literature	References
Arthrobacter globiformis	1	Potential biocontrol effects against *Fusarium verticillioides*.	Cavaglieri *et al.* (2004)
Aureimonas sp.	1	Potential for suppression of ash dieback.	Burghard *et al.* (2023)
Bacillus pumilis	2	Potential for biocontrol of grapevine downy mildew and *Fusarium* wilt in tomato. Biocontrol of fungal phytopathogens like *Fusarium oxyposum*, *Sclerotine sclerotiorum*, and *Fagopyrum esculentum*.	Dobrzyński *et al.* (2023); Heidarzadeh & Baghaee-Ravari (2015); Zhang *et al.* (2017)
Bacillus thuringiensis	2	Biocontrol potential in various agricultural systems with strain-dependent anti-insect, anti-bacterial and anti-fungal activity.	Pohare *et al.* (2021); Raddadi *et al.* (2009)
Duganella sp.	3	Known for anti-fungal effects against *Fusarium graminearum*.	Haack *et al.* (2016)
Erwinia billingiae	9	Potential for biocontrol of fire blight in pears.	Mikiciński *et al.* (2020)
Erwinia persicina	10	Specific strain showed biocontrol potential against *Fusarium* head blight in wheat.	Deroo *et al.* (2022)
Flavobacterium sp.	3	Potential biocontrol of crown rot of "Embul" banana.	Niroshini Gunasinghe & Karunaratne (2009)
Frigoribacterium sp.	19	Specific strain may potentially limit growth of *P. infestans* in-vitro.	Bruisson *et al.* (2019)
Frondihabitans sp.	5	May have a role in inhibiting attachment of *Saprolegniato* (oomycete) to salmon eggs.	Liu *et al.* (2014)
Janthinobacterium sp.	1	Known for anti-fungal effects in-vitro against *Fusarium graminearum*.	Haack *et al.* (2016)
Microbacterium sp.	1	In-vitro biocontrol of *Botrytis cinerea*.	Pacifico *et al.* (2019)
Microbacterium foliorum	1	In-vitro biocontrol of *Botrytis cinerea* and growth promotion of lettuce plants.	Suárez-Estrella *et al.* (2023)
Mycolicibacterium sp.	1	Potential biocontrol agent against *Pythium aphanidermatum*in lettuce. Catalyses aflatoxin degration produced by *Aspergillus* species, responsible for contamination of food crops.	Stouvenakers *et al.* (2023); Taylor *et al.* (2010)
Paenibacillus xylanexedens	2	Biocontrol potential against *Botrytis cinerea*, *Plasmopara viticola*, and *Xiphinema index* nematodes in grapevine. Specific strains show biocontrol of hairy root disease in tomato.	Pacifico *et al.* (2019); Vargas *et al.* (2021)

Pantoea agglomerans	12	Antagonistic activity against *Phytophthora infestans* and *Botrytis cinerea* in-vitro. Biocontrol of post-harvest diseases in apples.	Bruisson *et al.* (2019); Nunes *et al.* (2002); Pacifico *et al.* (2019)
Pantoea vagans	6	Specific strain capable of biocontrol of fire blight in apple and pear.	Kamber *et al.* (2012)
Priestia megaterium	5	Potential biocontrol of *Aspergillus flavus* in stored rice and *Botrytis cinerea* in-vitro (combined treatment with aldehydes).	Abanda-Nkpwatt *et al.* (2006); Mannaa & Kim (2018)
Pseudomonas fluorescens group	39	Some species classified among plant growth promoting rhizobacteria (PGPR). In-vitro biocontrol of *Rhizoctonia solani*, *Botrytis cinerea*, and other soil-borne phytopathogens.	Couillerot *et al.* (2009); Pacifico *et al.* (2019); Soltani *et al.* (2011)
Pseudomonas graminis	17	Specific strain showed potential for biocontrol of fire blight and *Listeria monocytogenes* in fresh-cut fruit.	Iglesias *et al.* (2018); Mikiciński *et al.* (2011)
Pseudomonas viridiflava	7	Specific strains capable of selective herbicidal activity (vineyard weeds).	Samad *et al.* (2017)
Rahnella sp.	1	*R. aquatilis* showed biocontrol potential against crown gall in grapevine.	Bouaichi *et al.* (2019); Habbadi *et al.* (2017)
Rhodococcus corynebacteroides	1	Mild disease suppression against *Pseudomonas syringae* pv. tomato.	Hong *et al.* (2015)
Sphingomonas echinoides	1	Potential biocontrol of *Phytophthora infestans* in-vitro.	Bruisson *et al.* (2019)
Sphingomonas melonis	3	Potential biocontrol *Pseudomonas syringae* pv. tomato.	Innerebner *et al.* (2011)
Staphylococcus warneri	1	Specific strain showed mild inhibition of *Phytophthora infestans* in-vitro.	Bruisson *et al.* (2019)
Staphylococcus epidermidis	4	Specific strain showed mild inhibition of *Botrytis cinerea* in-vitro.	Bruisson *et al.* (2019)
Stenotrophomonas rhizophila	19	Biocontrol of *Fusarium proliferatum* (fruit rot disease) on muskmelon.	Rivas-Garcia *et al.* (2019)
Streptomyces sp.	8	Specific species known to be endophytic to *V. vinifera*, growth promoters and confers resistance against *Botrytis cinerea*.	Loqman *et al.* (2009); Vatsa-Portugal *et al.* (2017)

SUPPLEMENTARY DATA
Jaswa, A., Vallance, J., Fournier, P., Martin, V., Masneuf-Pomarède, I., Labarthe, S., … Vacher, C. (2026). Developing a culturomic approach to build a collection of grapevine foliar microorganisms with potential applications in disease biocontrol. *OENO One*, *60*(1).
https://doi.org/10.20870/oeno-one.2026.60.1.9588

Table S5. Yeast of interest for their biocontrol potential *in vitro* or *in planta* across various plant and pathogen species from published culture-dependent studies.

Microorganism	Number of isolates in collection	Biocontrol potential as described in literature	References
Aureobasidium pullulans	89	Potential role as a biocontrol agent of fungal trunk pathogens. Biocontrol of *Botrytis cinerea* and sour rot.	Galli *et al.* (2021); Gramaje *et al.* (2022)
Candida friedrichii	3	Non-fermentative yeast that reduces vegetative growth of ochratoxin A producing fungus *A. carbonarious* in grape must.	Fiori *et al.* (2014)
Cystofilobasidium infirmominiatum	22	Post-harvest biocontrol agent for apples and citrus during cold storage.	Vero *et al.* (2011)
Filobasidium oeirense	4	Biocontrol of *Botrytis cinerea* in fruits by production of volatile organic compounds (VOCs). Biocontrol of *Penicillium expansum*.	Reyes-Bravo *et al.* (2021); Ruiz-Moyano *et al.* (2020)
Leucosporidium scottii	4	Post-harvest biocontrol agent for apples and citrus during cold storage.	Vero *et al.* (2011)
Metschnikowia sp.	5	Post-harvest biocontrol of table grapes. Among the genera of non-*Saccharomyces* yeasts that can influence the organoleptic characteristics of the wine in spontaneous fermentations.	Lombardo *et al.* (2023); Vicente *et al.* (2020)
Meyerozyma guilliermondii	2	Potential biocontrol of soft rot of kiwifruit. Wild grape-associated isolate showed promising biocontrol of grape decaying molds. Specific strain showed post-harvest biocontrol agent of *Penicillium expansum* and *Penicillium digitatumin* apples and lemons.	Agirman & Erten (2020); Cordero-Bueso *et al.* (2017); Pan *et al.* (2022)
Papiliotrema flavescens	4	Biocontrol of *Fusarium* head blight in wheat.	Shude *et al.* (2022)
Papiliotrema terrestris	1	Specific strain showed potential for in-field and post-harvest biocontrol of fruit.	Castoria *et al.* (2021); Lima *et al.* (1998)
Rhodotorula babjevae	5	Potential post-harvest, antifungal activity via biosurfactant production against *Botrytis cinerea* and *Penicillium expansum*.	Sen *et al.* (2017); Stanevičienė *et al.* (2021)
Sporobolomyces roseus	3	Specific strain potential for post-harvest biocontrol of blue mold on apples and pears.	Filonow *et al.* (1996); Janisiewicz (1994)
Udeniomyces pyricola	2	Negative effect on growth of *Erysiphe necator* (grapevine powdery mildew) in controlled conditions.	Pauvert *et al.* (2020)
Vishniacozyma victoriae	4	Biocontrol of *Botrytis cinerea* in kiwifruit. Specific strain showed post-harvest fungal disease biocontrol in organic pears.	Gorordo *et al.* (2022); Nian *et al.* (2023)

Table S6. Filamentous fungi of interest for their biocontrol potential *in vitro* or *in planta* across various plant and pathogen species from published culture-dependent studies.

Microorganism	Number of isolates in collection	Notes on life mode and/or diseases caused	Biocontrol potential as described in literature	References
Alternaria alternata	2	Leaf spot in soybean	Capable of inhibiting sporulation of *Plasmopara viticola* (grapevine downy mildew)	Li *et al.* (2023); Molnár *et al.* (2023); Musetti *et al.* (2006)
Bjerkandera adusta	3	Apple tree dieback	Biocontrol of *Fusarium graminearum* in wheat by strain *B. adusta* M1	Jacobs *et al.* (2024); Li *et al.* (2022)
Clonostachys rosea	2	Wood decay, root rot in grapevine	Biocontrol effect on *Fusarium graminearum* and mycotoxin detoxification in oat	Jayawardena *et al.* (2018); Khairullina *et al.* (2023)
Epicoccum nigrum	8	–	*Plasmopara viticola* (grapevine downy mildew) antagonist	Jayawardena *et al.* (2018); Kortekamp (1997); Taguiam *et al.* (2021)
Plectosphaerella cucumerina	7	Fruit rot, root rot, collar rot in horticultural crops	Biocontrol of potato cyst nematodes. Potential as bioherbicide against *Cirsium arvense*	Bailey *et al.* (2017); Carlucci *et al.* (2012); Jacobs (2000)
Trametes versicolor	6	Ubiquitous wood-inhabiting fungi, which most likely only play subordinate roles as primary decomposers in grapevine therefore pathogenic significance probably small	Potential biocontrol of *Fusarium langsethiae* in cereals	Fischer & González García (2015); Parroni *et al.* (2019)

3. Subcloning colonies obtained initially on GLA on conventional media to check for improvement in MALDI-TOF MS analyses

Table S7. MALDI-TOF MS analyses on bacteria initially isolated on GLA and subcultured on richer media to improve identification (ID). The names of any additional taxa identified by changing the media are indicated by symbols and listed below the table.

Plot pair	Plot name	Sampling zone	Total isolates on GLA	Identification of bacteria across different media with MALDI-TOF MS						
				Medium used for reculturing	Same ID on GLA and reculturing medium	Better taxonomic level of ID on medium of origin	Improved taxonomic level of ID with change in medium	No ID on GLA; ID on reculturing medium only	ID on GLA only; no ID on reculturing medium	No ID on any media
E2M	Pompignac	CEN	24	LBA	9	0	0	0	0	15
E2M	Pompignac	UC1	25	YPD	3	0	0	0	1	16
				LBA 1/10th	5		0	0		
E2M	Baron	CEN	19	LBA	2	0	5*	1*	0	8
				YPD	2		0	1*		
E2M	Baron	UC1	29	TSA	12	0	5°	10°,#	0	2

* *Erwinia bilingiae*

° *Curtobacterium flaccumfaciens*

¤ *Curtobacterium flaccumfaciens* (*n* = 9)

Pseudomonas sp. (*n* = 1)

SUPPLEMENTARY DATA
Jaswa, A., Vallance, J., Fournier, P., Martin, V., Masneuf-Pomarède, I., Labarthe, S., … Vacher, C. (2026). Developing a culturomic approach to build a collection of grapevine foliar microorganisms with potential applications in disease biocontrol. *OENO One*, *60*(1). https://doi.org/10.20870/oeno-one.2026.60.1.9588

Table S8. MALDI-TOF MS analyses on yeast initially isolated on GLA and subcultured on richer media to improve identification (ID). The names of any additional taxa identified by changing the media are indicated by symbols and listed below the table.

				Identification of bacteria across different media with MALDI-TOF MS						
Plot pair	**Plot name**	**Sampling zone**	**Total isolates on GLA**	**Medium used for reculturing**	**Same ID on GLA and reculturing medium**	**Better taxonomic level of ID on medium of origin**	**Improved taxonomic level of ID with change in medium**	**No ID on GLA; ID on reculturing medium only**	**ID on GLA only; no ID on reculturing medium**	**No ID on any media**
ME1	121M	CEN	6	MEA	1	0	0	0	0	5
		UC1	11	MEA	1	0	0	0	1*	9
ME1	68M	CEN	10	MEA	1	0	0	0	0	9
		UC1	10	MEA	0	0	0	1*	0	9
ME2	33CS	CEN	7	MEA	0	0	0	0	0	7
		UC1	5	MEA	0	0	0	0	0	5
ME2	62CS	CEN	8	MEA	0	0	0	0	0	8
		UC1	8	MEA	0	0	0	0	1¤	7

* *Filobasidium magnum*

¤ *Metscnikowia* sp.

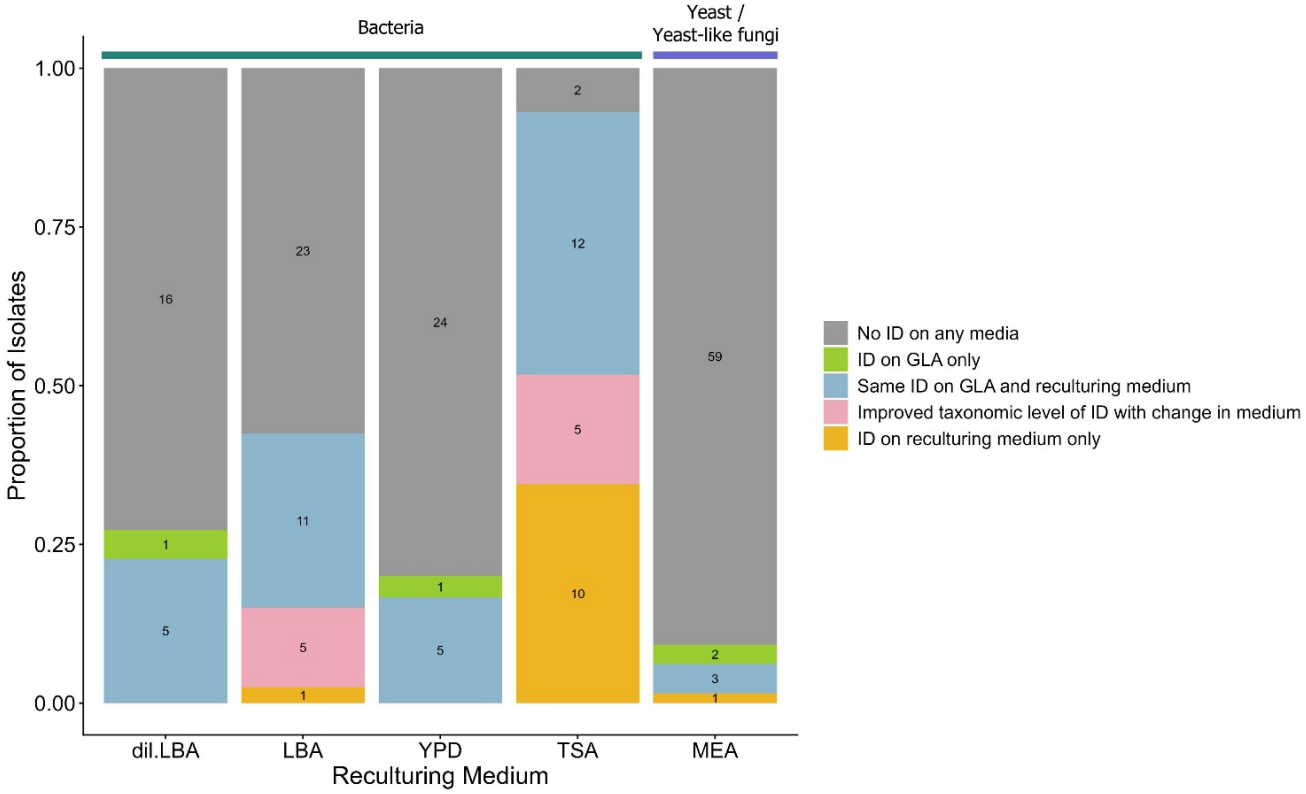


Figure S1. Proportion of isolates identified using MALDI-TOF MS analyses on bacteria and yeast initially isolated on GLA subcultured on richer media to improve identification (ID). Isolates that were initially identified only to the genus level on GLA but identified to the species level with a change in culture media are represented as "Improved taxonomic level of ID with change in medium".

4. Colony growth while subcloning colonies obtained initially on GLA on conventional media

We observed that the colonies obtained on the GLA were smaller and translucent or lighter in colour compared to the conventional and diluted media. We tested subcloning on different media for a subset of colonies of bacteria obtained from leaf washings from different plot pairs with contrasted levels of Downy mildew incidence and severity. We subcloned colonies originally obtained on GLA by streaking on richer media like LBA, LBA diluted 1/10th, TSA and YPD (Yeast Extract Peptone Dextrose Agar, Sigma-Aldrich, France). We observed that a few colonies showed weak growth or no growth at all on the richer media even with a prolonged incubation period (Table S9).

Table S9. Bacterial colonies obtained on GLA from leaf washings on plot pair E2M (Entre-deux-Mers) planted with Merlot grape variety showing contrasted levels of downy mildew incidence and severity. Colonies recultured on nutritionally richer media including dil. LBA, undiluted LBA, TSA and YPD to assess growth. Normal growth indicated colony development comparable to medium of origin after 72 hours of incubation. Weak growth indicated sparser colony development five days post-incubation and no growth indicated zero colony development five days post-incubation.

Plot pair	Plot name	Downy mildew incidence and severity	Sampling zone	Colonies on GLA	Reculturing bacteria isolated on GLA on different media to check growth			
					Medium used for reculturing	Normal growth	Weak growth	No growth
E2M	Pompignac	Low	CEN	24	LBA	20	4	0
E2M	Pompignac	Low	UC1	25	YPD	9	2	10
					LBA 1/10th	25	0	0
E2M	Baron	High	CEN	19	LBA	17	2	0
					YPD	10	0	9
E2M	Baron	High	UC1	29	TSA	29	0	0

5. Statistical analyses

Table S10. Effect of culture medium used on number of colonies obtained per sample.

	Model			Culture medium
	N	**R^2c**	**R^2m**	***p***
Bacteria	62	0.914	0.014	**0.01087**
Filamentous fungi and yeast	48	0.513	0.029	0.109

A negative binomial generalised linear mixed-effects model (GLMM) with the CFU/mL as the dependent variable and the culture medium as a fixed factor. The sampling location (*i.e.* the zone within each plot) was included as a random effect to account for the non-independence of plates inoculated with the same leaf washing solution. N corresponds to the number of plates counted, R^2m and R^2c correspond to the marginal and conditional coefficients of determination of the model respectively. Chisq and DF denote the chi squared value and degrees of freedom respectively for the Type II Wald chi square test and *p* corresponds to the *p*-value. The threshold for statistical significance was set at $p = 0.05$ and significant *p*-values are indicated in bold.

Table S11. Pairwise comparisons for culture media.

Pairwise contrasts	**Estimate**	**SE**	***Z* ratio**	***p***
GLA – dil. LBA	–0.264	0.0887	–2.981	**0.0081**
GLA – TSA	–0.100	0.0894	–1.122	0.5002
dil. LBA – TSA	0.164	0.0897	1.829	0.1600

Computing contrasts of estimated marginal means for pairwise comparison of media used for bacteria with Tukey method for *p*-value adjustment. SE indicates standard error and *p* indicates the *p*-value. The threshold for statistical significance was set at $p = 0.05$ and significant *p*-values are indicated in bold.

Table S12. Comparison of Shannon index for taxonomic diversity across culture media.

Response variable	**Fixed effects**	**DF**	***F* value**	***p***
Shannon index for bacteria	Culture medium	2	7.3684	**0.006514**
	Plot_zone	7	4.9809	**0.005227**
Shannon index for filamentous fungi and yeast	Culture medium	1	0.8333	0.3917
	Plot zone	7	0.5500	0.7757

Linear Models (LM) with culture medium and the sampling location (*i.e.* the zone) within each plot as fixed factors. The threshold for statistical significance was set at $p = 0.05$ and significant *p*-values are indicated in bold.

Table S13. Pairwise comparisons for culture media.

Pairwise contrasts	Estimate	SE	*t* ratio	*p*
GLA – dil. LBA	–0.4037	0.139	–2.911	**0.0288**
GLA – TSA	0.0987	0.139	0.712	0.7607
dil. LBA – TSA	0.5024	0.139	3.623	**0.0073**

Computing contrasts of estimated marginal means for pairwise comparison of media used for bacteria with Tukey method for *p*-value adjustment. SE indicates standard error and *p* indicates the *p*-value. The threshold for statistical significance was set at $p = 0.05$ and significant *p*-values are indicated in bold.

Table S14. Pairwise comparisons for sampling locations.

Pairwise contrasts	Estimate	SE	*t* ratio	*p*
121M_CEN – 121M_UC1	0.5983	0.226	2.642	0.2190
121M_CEN – 33CS_CEN	0.7758	0.226	3.426	0.0599
121M_CEN – 33CS_UC1	–0.0366	0.226	–0.161	1.0000
121M_CEN – 62CS_CEN	0.6286	0.226	2.776	0.1781
121M_CEN – 62CS_UC1	–0.0943	0.226	–0.417	0.9998
121M_CEN – 68M_CEN	0.5302	0.226	2.341	0.3377
121M_CEN – 68M_UC1	0.0561	0.226	0.248	1.0000
121M_UC1 – 33CS_CEN	0.1775	0.226	0.784	0.9914
121M_UC1 – 33CS_UC1	–0.6349	0.226	–2.803	0.1705
121M_UC1 – 62CS_CEN	0.0303	0.226	0.134	1.0000
121M_UC1 – 62CS_UC1	–0.6927	0.226	–3.058	0.1125
121M_UC1 – 68M_CEN	–0.0682	0.226	–0.301	1.0000
121M_UC1 – 68M_UC1	–0.5422	0.226	–2.394	0.3139
33CS_CEN – 33CS_UC1	–0.8124	0.226	–3.587	0.0451
33CS_CEN – 62CS_CEN	–0.1472	0.226	–0.650	0.9972
33CS_CEN – 62CS_UC1	–0.8702	0.226	–3.842	0.0286
33CS_CEN – 68M_CEN	–0.2457	0.226	–1.085	0.9500
33CS_CEN – 68M_UC1	–0.7198	0.226	–3.178	0.0919
33CS_UC1 – 62CS_CEN	0.6652	0.226	2.937	0.1375
33CS_UC1 – 62CS_UC1	–0.0578	0.226	–0.255	1.0000
33CS_UC1 – 68M_CEN	0.5667	0.226	2.502	0.2694

33CS_UC1 – 68M_UC1	0.0926	0.226	0.409	0.9999
62CS_CEN – 62CS_UC1	–0.7229	0.226	–3.192	0.0897
62CS_CEN – 68M_CEN	–0.0984	0.226	–0.435	0.9998
62CS_CEN – 68M_UC1	–0.5725	0.226	–2.528	0.2595
62CS_UC1 – 68M_CEN	0.6245	0.226	2.757	0.1833
62CS_UC1 – 68M_UC1	0.1504	0.226	0.664	0.9968
68M_CEN – 68M_UC1	–0.4741	0.226	–2.093	0.4623

Computing contrasts of estimated marginal means for pairwise comparison of media used for bacteria with Tukey method for *p*-value adjustment. SE indicates standard error and *p* indicates the *p*-value.

Table S15. Pairwise comparison of taxonomic composition of cultivable communities (beta diversity) across culture media (GLA *vs* MEA) for fungi.

	DF	Sum of squares	R^2	F	p
Model	1	0.9502	0.23448	4.2882	**0.005**
Residual	14	3.1023	0.76552		
Total	15	4.0526	1.00000		

PERMANOVA with the compositional dissimilarity (Bray–Curtis dissimilarity) as the dependent variable and the culture medium as a fixed factor. DF denotes degrees of freedom and R^2 denotes the coefficient of determination. Permutations were constrained within each sampling location (*i.e.* the zone within each plot) using the *strata* option to account for the non-independence of communities cultivated from the same leaf washing solution. The number of permutations = 255. The threshold for statistical significance was set at $p = 0.05$ and significant *p*-values are indicated in bold.

Table S16. Pairwise comparison of taxonomic composition of cultivable communities (beta diversity) across culture media (GLA *vs* dil. LBA) for bacteria.

	DF	Sum of squares	R^2	F	p
Model	1	0.2465	0.06828	1.026	0.14
Residual	14	3.3637	0.93172		
Total	15	3.6102	1.00000		

PERMANOVA with the compositional dissimilarity (Bray–Curtis dissimilarity) as the dependent variable and the culture medium as a fixed factor. DF denotes degrees of freedom and R^2 denotes the coefficient of determination. Permutations were constrained within each sampling location (*i.e.* the zone within each plot) using the *strata* option to account for the non-independence of communities cultivated from the same leaf washing solution. The number of permutations = 255.

Table S17. Pairwise comparison of taxonomic composition of cultivable communities (beta diversity) across culture media (GLA *vs* TSA) for bacteria.

	DF	Sum of squares	R^2	F	p
Model	1	0.6130	0.13877	2.2559	**0.01**
Residual	14	3.8045	0.86123		
Total	15	4.4175	1.00000		

PERMANOVA with the compositional dissimilarity (Bray–Curtis dissimilarity) as the dependent variable and the culture medium as a fixed factor. DF denotes degrees of freedom and R^2 denotes the coefficient of determination. Permutations were constrained within each sampling location (*i.e.* the zone within each plot) using the *strata* option to account for the non-independence of communities cultivated from the same leaf washing solution. The number of permutations = 255. The threshold for statistical significance was set at $p = 0.05$ and significant *p*-values are indicated in bold.

Table S18. Pairwise comparison of taxonomic composition of cultivable communities (beta diversity) across culture media (dil. LBA *vs* TSA) for bacteria.

	DF	Sum of squares	R^2	F	p
Model	1	0.4898	0.12042	1.9166	**0.01**
Residual	14	3.5776	0.87958		
Total	15	4.0673	1.00000		

PERMANOVA with the compositional dissimilarity (Bray–Curtis dissimilarity) as the dependent variable and the culture medium as a fixed factor. DF denotes degrees of freedom and R^2 denotes the coefficient of determination. Permutations were constrained within each sampling location (*i.e.* the zone within each plot) using the *strata* option to account for the non-independence of communities cultivated from the same leaf washing solution. The number of permutations = 255. The threshold for statistical significance was set at $p = 0.05$ and significant *p*-values are indicated in bold.

6. Representativeness of the collection

To gauge how representative our collection is of the true range of microorganisms present in the grapevine phyllosphere and endosphere, we analysed the overlap between the taxa in the collection and the taxa obtained by metabarcoding analyses on samples collected simultaneously at the same locations as in our study. For the bacteria at the genus level, we found a 12.5 % overlap between the metabarcoding and culturomic datasets (Figure S2), which decreased to 12 % when excluding the GLA (Figure S3). At the species level, we found a 6.6 % overlap (Figure S4), which decreased to 5.9 % when excluding GLA (Figure S5). For the fungi at the species level, we found 14.6 % overlap (Figure S6), which decreased to 9.9 % when excluding GLA (Figure S7).

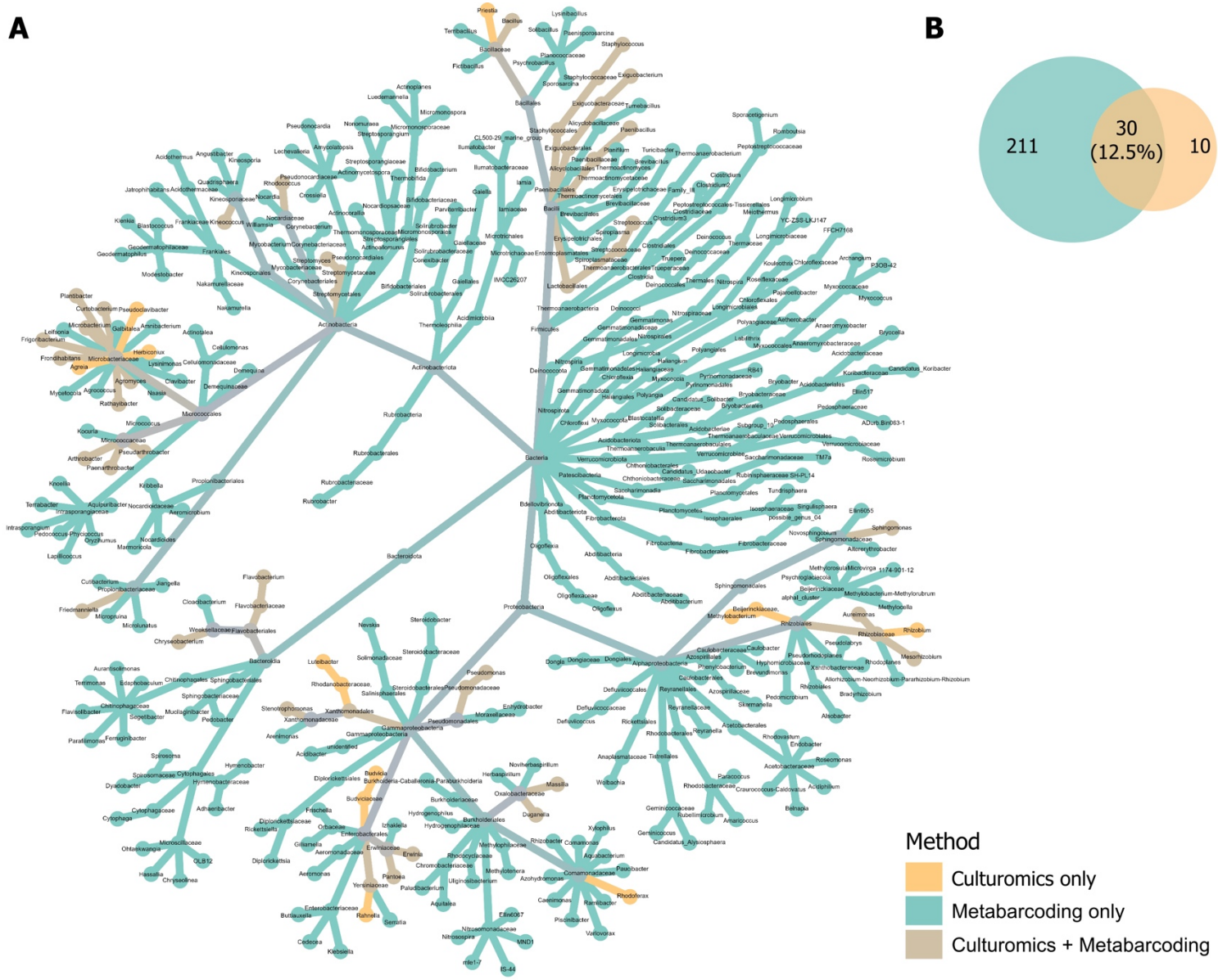


Figure S2. (A) Taxonomic tree showing overlap between the metabarcoding and culturomics datasets for bacterial genera obtained on three culture media – GLA, dil. LBA, and TSA. (B) Venn diagrams show the number of taxa obtained by each method as well as the percentage of overlap between both methods.

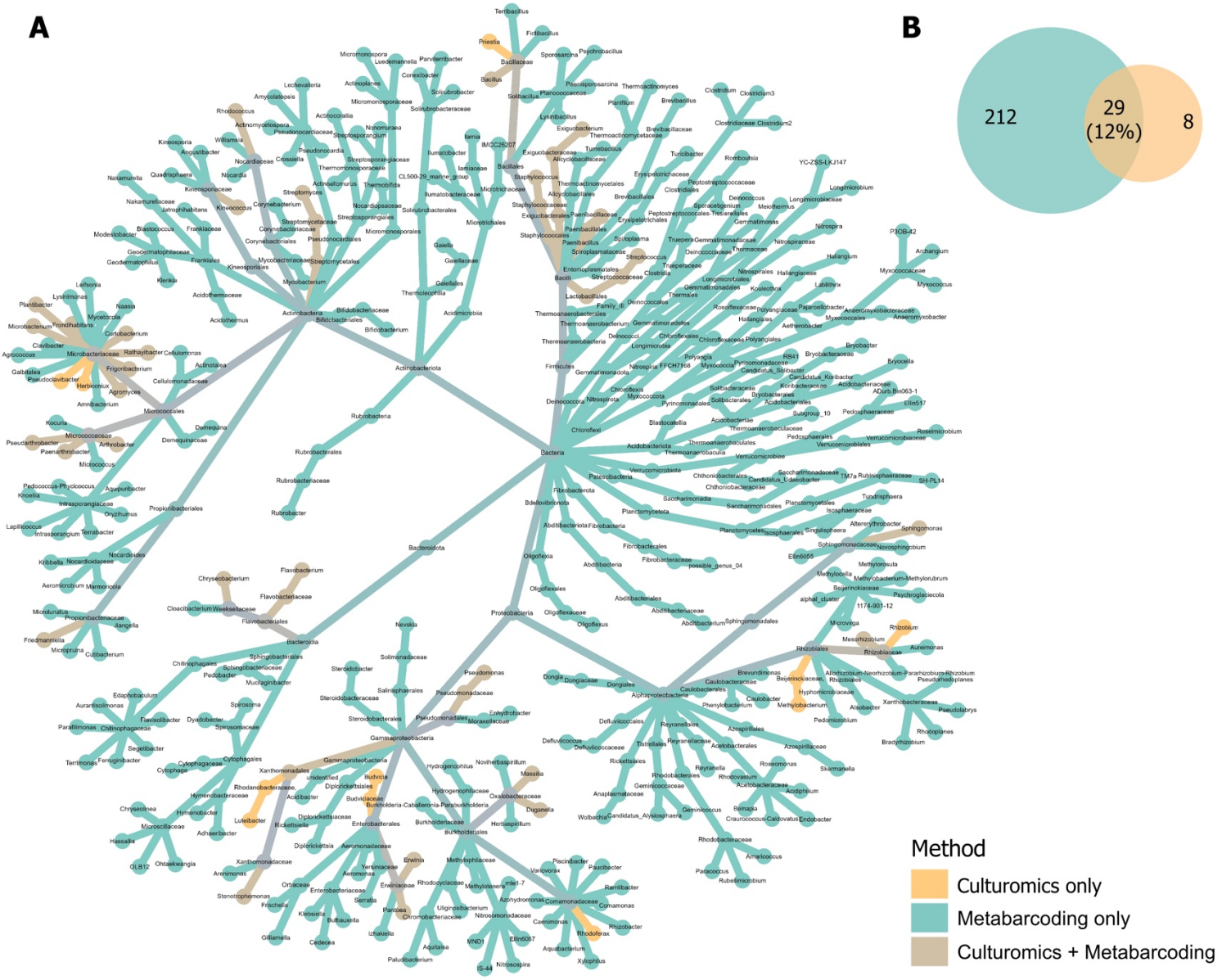


Figure S3. (A) Taxonomic tree showing overlap between the metabarcoding and culturomics datasets for bacterial genera obtained on two conventional culture media – dil. LBA and TSA. (B) Venn diagrams show the number of taxa obtained by each method as well as the percentage of overlap between both methods.

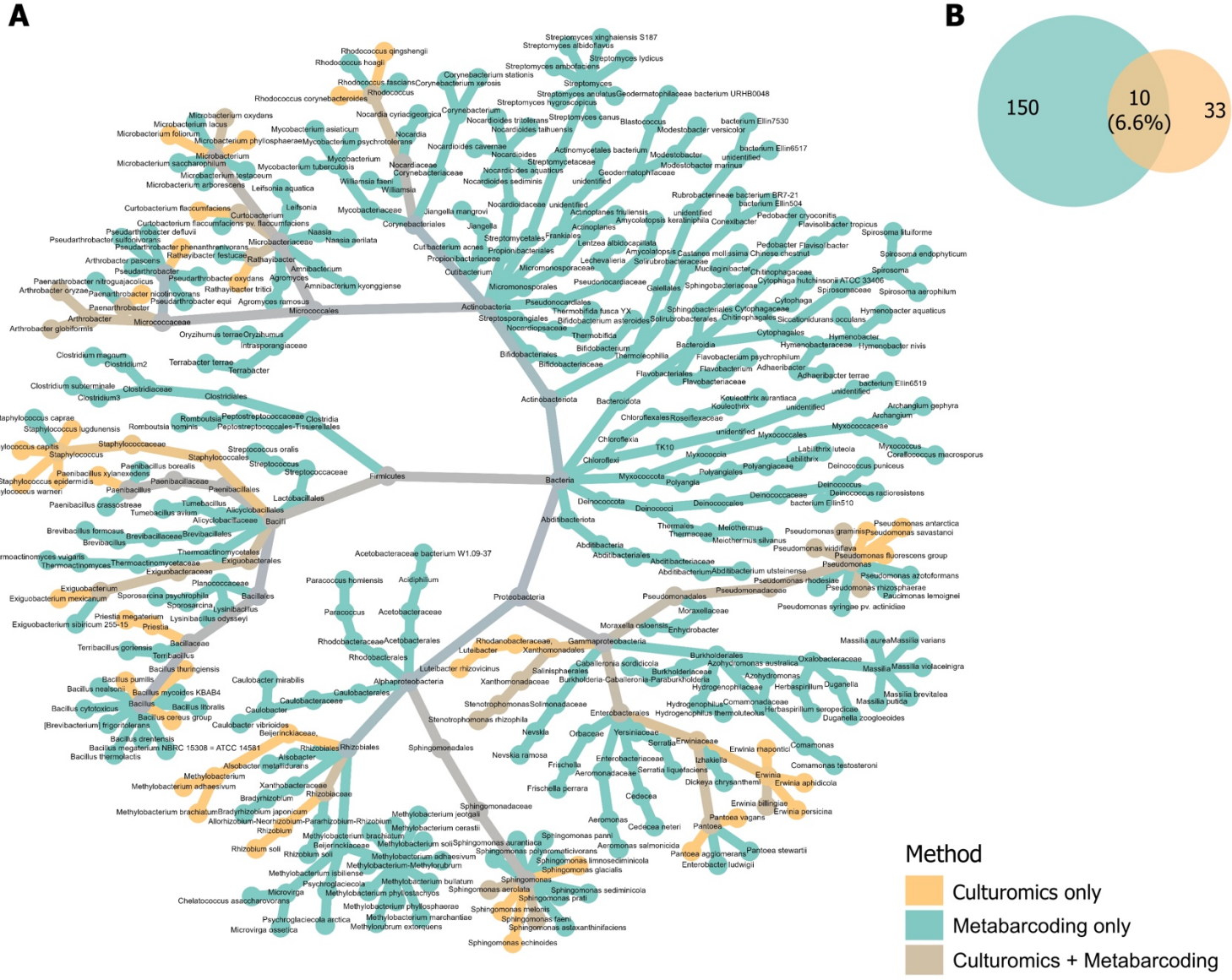


Figure S4. (A) Taxonomic tree showing overlap between the metabarcoding and culturomics datasets for bacterial species obtained on three culture media – GLA, dil. LBA, and TSA. (B) Venn diagrams show the number of taxa obtained by each method as well as the percentage of overlap between both methods.

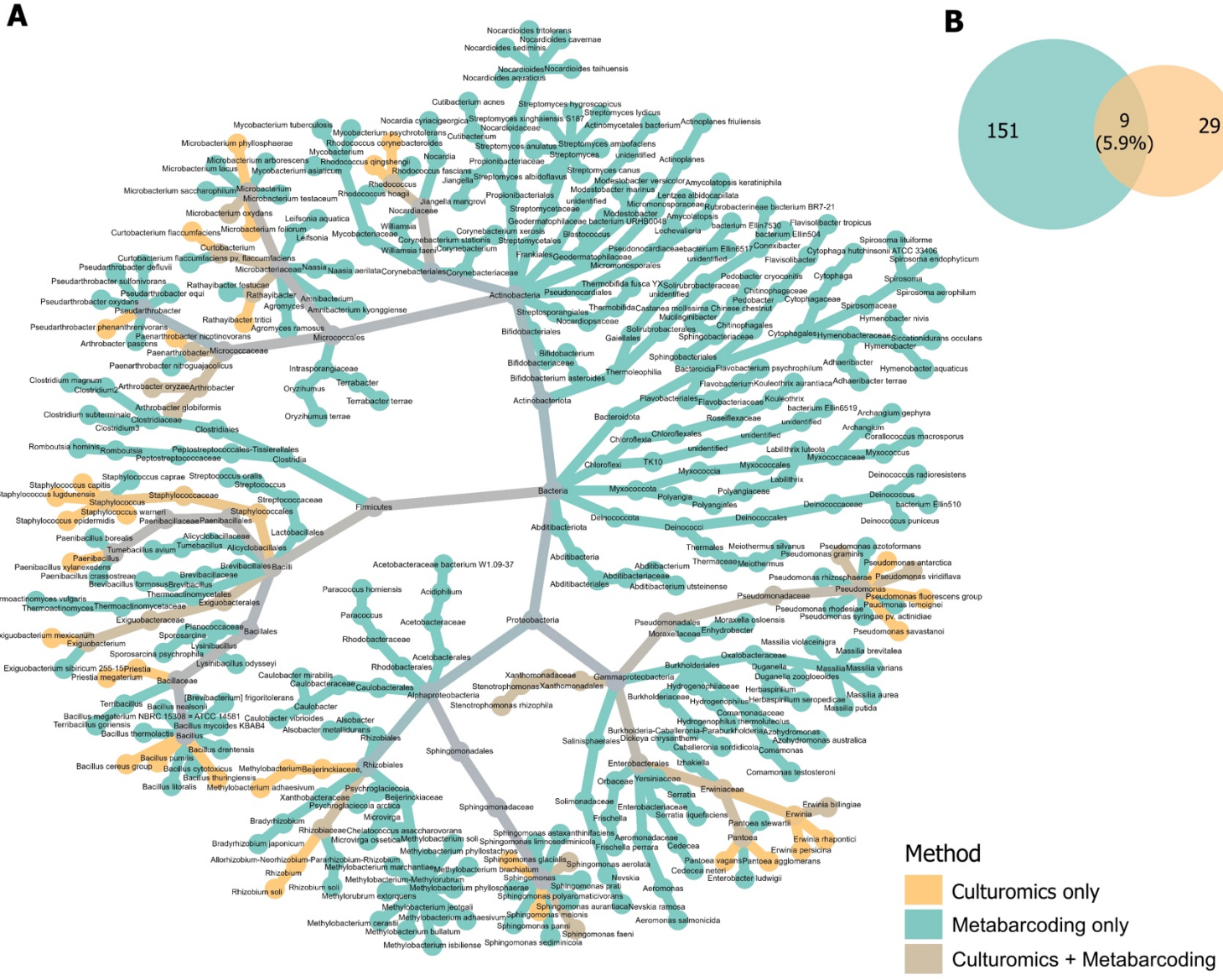


Figure S5. (A) Taxonomic tree showing overlap between the metabarcoding and culturomics datasets for bacterial species obtained on two conventional culture media – dil. LBA and TSA. (B) Venn diagrams show the number of taxa obtained by each method as well as the percentage of overlap between both methods.

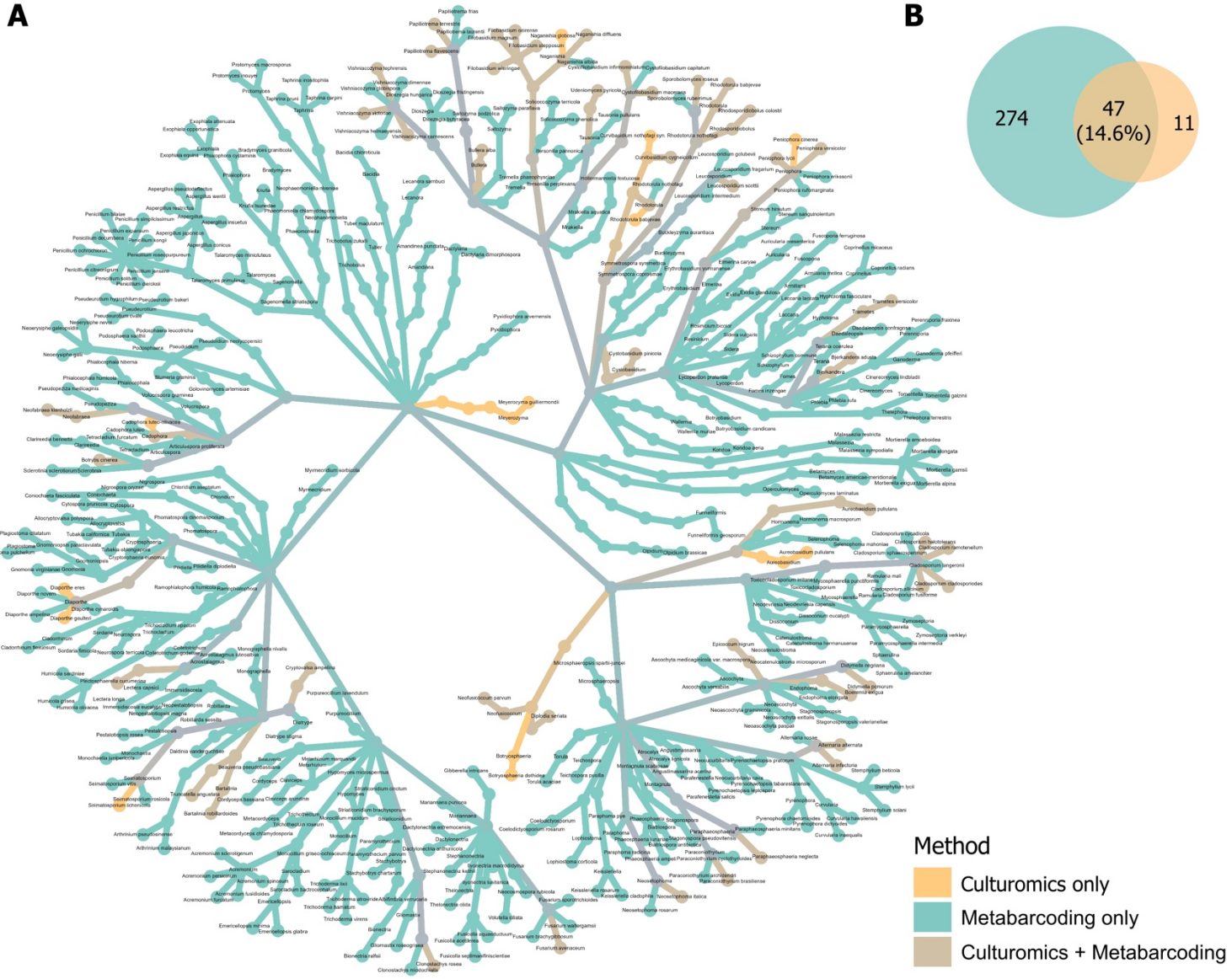


Figure S6. (A) Taxonomic tree showing overlap between the metabarcoding and culturomics datasets for fungal species obtained on two culture media – GLA and MEA. (B) Venn diagrams show the number of taxa obtained by each method as well as the percentage of overlap between both methods.

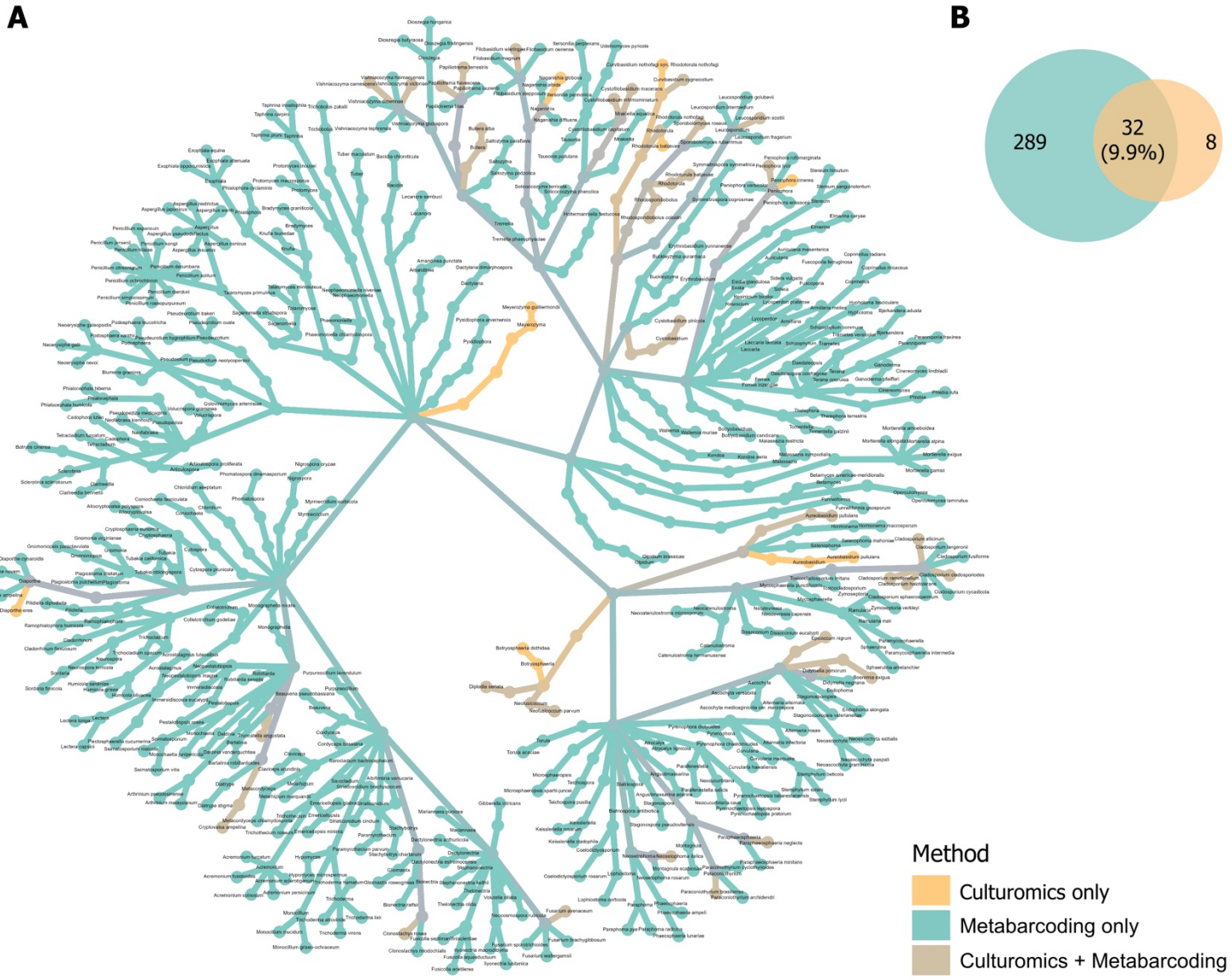


Figure S7. (A) Taxonomic tree showing overlap between the metabarcoding and culturomics datasets for fungal species obtained on conventional culture medium – MEA only. (B) Venn diagrams show the number of taxa obtained by each method as well as the percentage of overlap between both methods.

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