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Supplementary Table S1. Primers for 16S and 18S rRNA amplification.

Primer	Primer sequence (5' → 3')	Target and size of the amplicon	Reference
515R	CCTACGGGAGGCAGCAG	Bacterial 16S rRNA gene 174 bases	(López-Gutiérrez *et al.*, 2004)
341F	ATTACCGCGGCTGCTGGCA		
Arch967F	ATTGGCGGGGGAGCAC	Archaeal 16S rRNA gene 140 bases	(Cadillo-Quiroz *et al.*, 2006)
Arch1060R	GGCCATGCACCWCCTCTC		
FR1	AICCATTCAATCGGTAIT	Fungal 18S rRNA gene 340 bases	(Vainio and Hantula, 2000)
FF390	CGATAACGAACGAGACCT		

Supplementary Table S2. Formulae for Biolog index calculations.

Index	Definition	Formulae	Notes
AWCD	Sum of the corrected OD value	$\sum_{i=1}^{n} \frac{ODi}{31}$	OD_i = absorbance of the response well
H	Richness diversity	$-\sum pi(\ln pi)$	p_i = ratio between OD_i and OD_i sum
E	Evenness calculated from H	*H* / lnS	S = Number of wells

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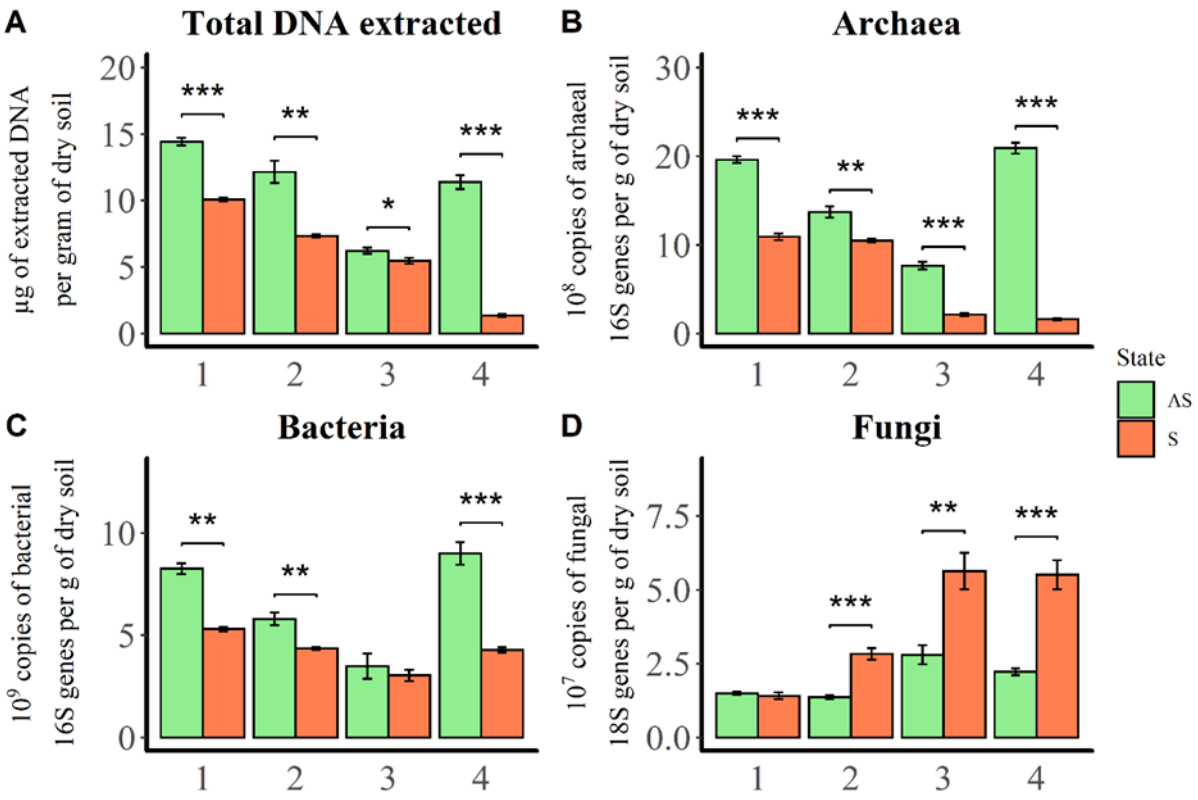


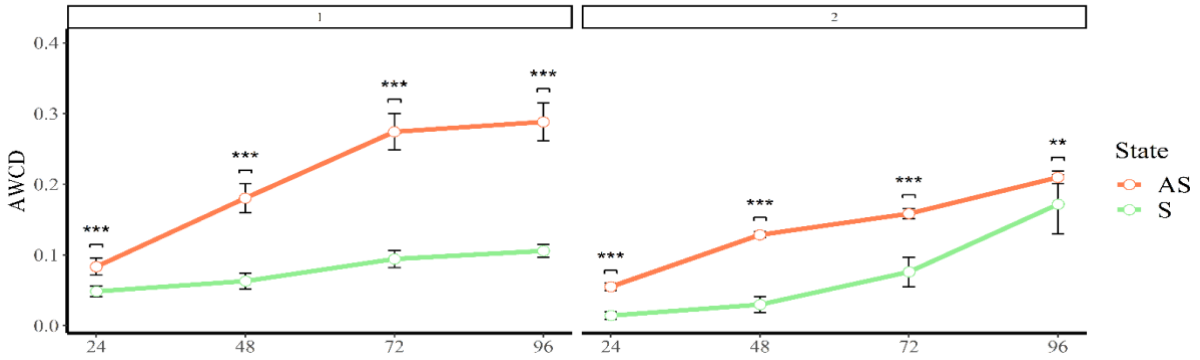
Supplementary Figure S1. Quantifications of (A) crude extracted DNA, (B) archaeal 16 rRNA genes, (C) bacterial 16S rRNA genes, and (D) fungal 18S rRNA genes in asymptomatic (AS = green) and in symptomatic (S = orange) soils among plots 1, 2, 3, and 4 during autumn. Bars represent means ± SE (n = 5). Significance differences corrected with Bonferroni method were detected through pairwise t or Wilcoxon tests after ANOVA or Kruskal test. To facilitate the graph reading, usual letters were replaced with $P < 0.05$ (*), $P < 0.01$ (**), and $P < 0.001$ (***).

SUPPLEMENTARY DATA

Romain Darriaut, Guilherme Martins, Coralie Dewasme, Séverine Mary, Guillaume Darrieutort, Patricia Ballestra, Elisa Marguerit, Philippe Vivin, Nathalie Ollat, Isabelle Masneuf-Pomarède, Virginie Lauvergeat (2021). Grapevine decline is associated with difference in soil microbial composition and activity. *OENO One*, *55*(3). https://doi.org/10.20870/oeno-one.2021.55.3.4626

Supplementary Table S3. Bacterial and fungal numbers of isolates from the soils within the plots 1 and 2 with (S) and without (AS) dieback symptoms during autumn period. Means ± SE are presented (n = 5). Asterisks represent significant differences between S and AS soils with $P < 0.05$ (*), $P < 0.01$ (**), and $P < 0.001$ (***).

Terroir	Graves			
Plots	1		2	
State	S	AS	S	AS
Bacterial counts (log (CFU / g of soil))	7.14 ± 0.03	7.42 ± 0.03	6.78 ± 0.04	7.44 ± 0.03
	*		***	
Fungal counts (log (CFU / g of soil))	6.67 ± 0.05	6.51 ± 0.08	6.60 ± 0.06	6.39 ± 0.09
	*		**	
AUC	2.49 ± 0.03	3.36 ± 0.06	2.33 ± 0.04	2.91 ± 0.01
	***		***	
E	0.915 ± 0.008	0.927 ± 0.013	0.878 ± 0.003	0.890 ± 0.004
	ns		*	
R	13 ± 2	22 ± 1.73	14	17 ± 1
	***		***	



Supplementary Figure S2. Eco-Plates™ measurements representing microbial activities represented by Average Well Colour Development of metabolized substrates based on 96h incubation (n = 3) in symptomatic (S = orange) and in asymptomatic (AS = green) soils of decline among for plots 1 and 2 during autumn. Points on the curves represent means ± SE (n = 3). Asterisks represent significant differences between S and AS soils with $P < 0.05$ (*), $P < 0.01$ (**), and $P < 0.001$ (***).

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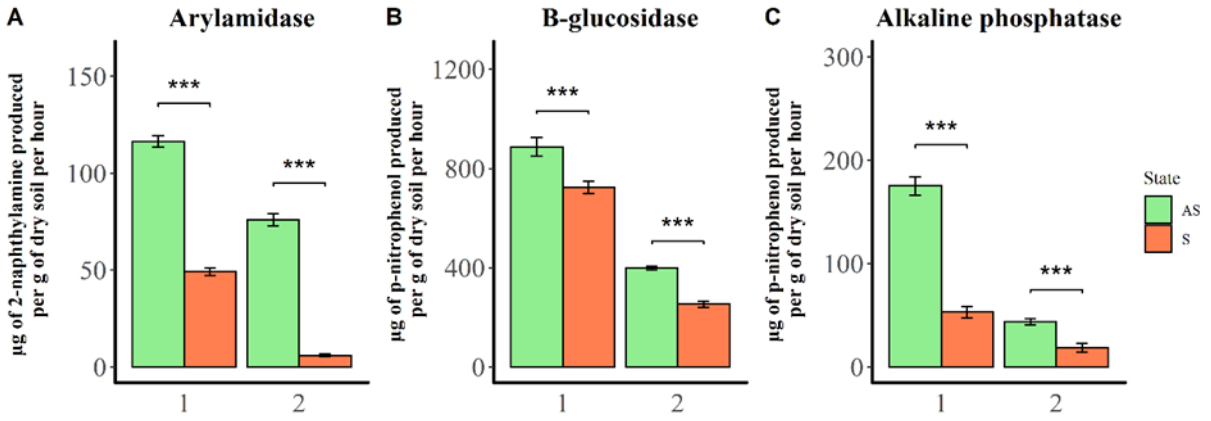

Supplementary Figure S3: Enzymatic activities in asymptomatic (AS = green) and in symptomatic (S = orange) soils among plots 1 and 2. Soils were assayed for the activity of (A) arylamidase in µg of 2-naphthylamine per g dwt h^{-1} of soil, (B) β-glucosidase, (C) alkaline phosphatase in µg of p-nitrophenol produced per g of dry soil per hour during autumn. Bars represent means ± SE (n=5). Significance differences corrected with Bonferroni method were detected through pairwise t or Wilcoxon tests after a ANOVA or Kruskal test. To facilitate the graph reading, usual letters were replaced with $P < 0.05$ (*), $P < 0.01$ (**), and $P < 0.001$ (***).

Supplementary Table S4. Ratios between 16S bacterial and 18S fungal genes and also between cultivable bacterial and fungal CFUs from the soils within the 4 studied plots with (S) and without (AS) dieback symptoms during autumn period. Means ± SE are represented (n = 5). Asterisks represent significant differences between S and AS soils with $P < 0.05$ (*), $P < 0.01$ (**), and $P < 0.001$ (***).

Terroir	Graves				Médoc			
Plot	1		2		3		4	
Soil	S	AS	S	AS	S	AS	S	AS
(*B* / *F*) molecular	384 ± 63	551 ± 37	158 ± 30	425 ± 40	54 ± 4	122 ± 17	80 ± 18	411 ± 88
	*		***		***		***	
(*B* / *F*) cultivable	3.03 ± 0.48	4.17 ± 0.89	1.52 ± 0.17	8.93 ± 1.60	nd	nd	nd	nd
	*		***					

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Supplementary Table S5. Statistical results testing the effects of season (autumn and spring), terroir (Médoc and Graves) on enzymatic (arylamidase, B-glucosidase, acid, and alkaline phosphatases), molecular (total DNA, archaeal and bacterial 16S and fungal 18S), and microbial (Eco-Plates® measurements, and cultivable bacteria and fungi) variables. Asterisks represent significant differences between S and AS soils with $P < 0.05$ (*), $P < 0.01$ (**), and $P < 0.001$ (***). Annotations with "nd" were due to the absence of samplings and data for Médoc terroir during autumn.

Parameter	Terroir		Period		Terroir*Period	
	F	*P*	*F*	*P*	*F*	*P*
Arylamidase	12.98	***	10.50	**	nd	nd
β-glucosidase	13.38	***	122.13	***	nd	nd
Alkaline phosphatase	38.57	***	61.60	***	nd	nd
DNA	17.20	***	25.08	***	1.48	0.23
Archaeal 16S	9.53	**	11.23	**	6.42	*
Bacterial 16S	20.59	***	25.92	***	16.08	***
Fungal 18S	1.00	ns	0.23	ns	39.83	***
Cultivable bacteria	0.02	ns	61.06	ns	nd	nd
Cultivable fungi	0.04	ns	49.83	ns	nd	nd
AWCD	1.04	ns	83.37	***	nd	nd
SEI	0.01	ns	69.23	***	nd	nd
Richness	2.57	ns	37.43	***	nd	nd
Amines	0.68	ns	139.73	***	nd	nd
Amino acids	0.58	ns	104.29	***	nd	nd
Carbohydrates	0.83	ns	197.63	***	nd	nd
Carboxylic acids	5.33	*	289.77	***	nd	nd
Phenolic compounds	1.05	ns	59.96	***	nd	nd
Polymers	5.22	*	134.33	***	nd	nd