SUPPLEMENTARY DATA
Biget, M., Mony, C., Aubry, M., Jambon, O., Quaiser, A., Chable, V., Pernet, S., & Vandenkoornhuyse, P. (2021). The drivers of vine-plant root microbiota endosphere composition include both abiotic and plant-specific factors. *OENO One, 55*(3).
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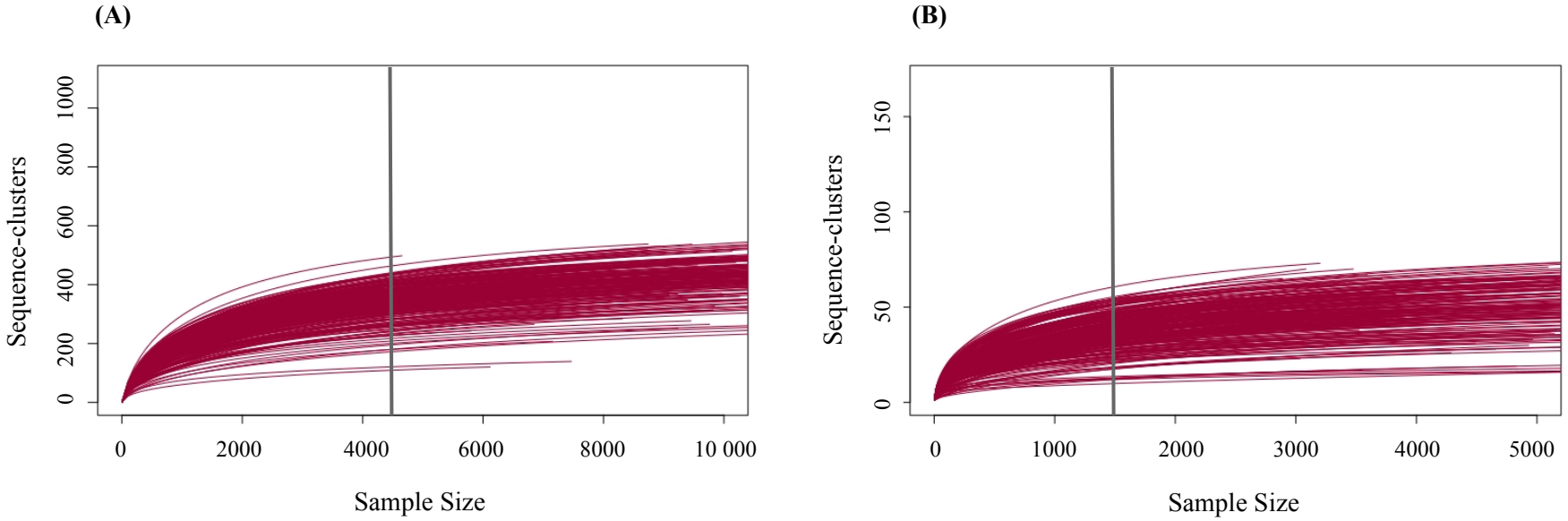


FIGURE S1. Rarefaction curves for (A) "all bacteria" samples and (B) "all fungi" samples.

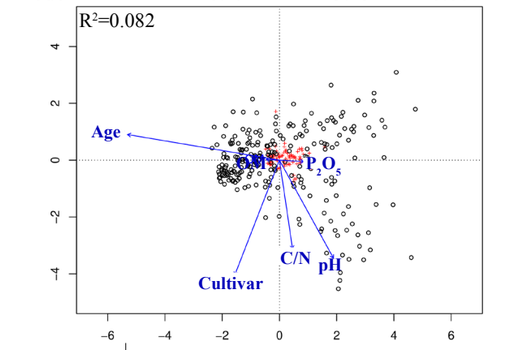
Curves show the total assigned sequence-clusters detected relative to sample size in sequence number.
The vertical line corresponds to the number of sequence-clusters at which data were rarefied.

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(A) Alpha-scale (i) Actinobateria

CCA (sequence-clusterTable~pH+C/N+OM+P_2O_5+Age+Cultivar)

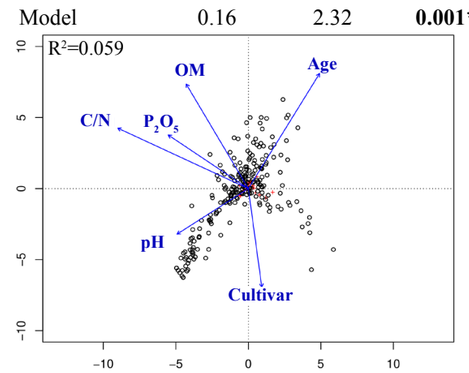
ANOVA	Chisq	F	p-value
Model	0.29	3.45	**0.001*****



Factors	pH	C/N	OM	P_2O_5	Age	Cultivar
F-value (p)	2.66***	2.81***	2.38**	3.09**	6.39***	3.39***

(ii) Acidobacteria

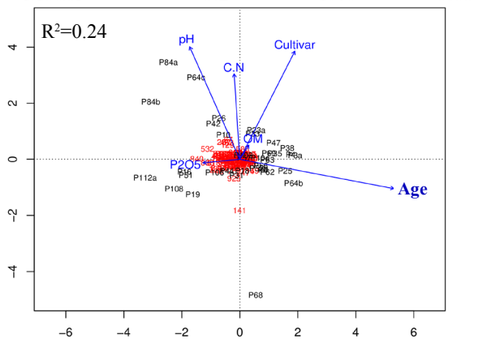
ANOVA	Chisq	F	p-value
Model	0.16	2.32	**0.001*****



	pH	C/N	OM	P_2O_5	Age	Cultivar
F-value (p)	1.82*	1.94*	3.11**	1.72*	3.12***	2.21**

(B) Gamma-scale (i) Actinobateria

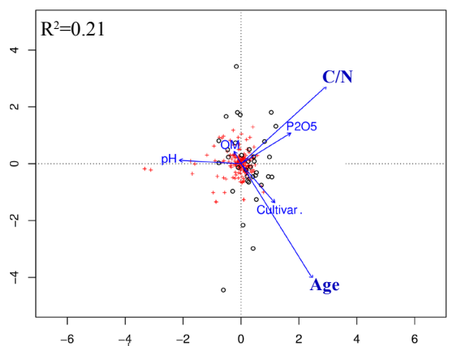
ANOVA	Chisq	F	p-value
Model	0.27	1.40	**0.03***



Factors	Age
F-value (p)	2.39**

(ii) All fungi

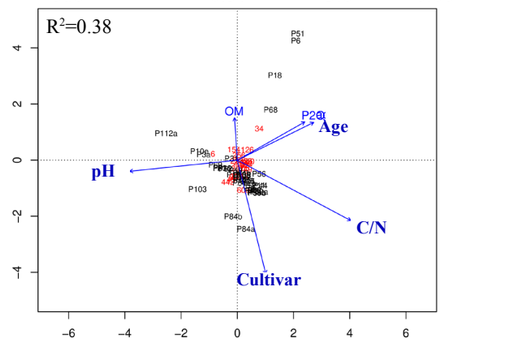
ANOVA	Chisq	F	p-value
Model	0.20	1.27	**0.048***



	C/N	Age
F-value (p)	1.90*	1.80*

(iii) Glomeromycota

ANOVA	Chisq	F	p-value
Model	0.37	3.02	**0.001*****



	pH	C/N	Age	Cultivar
F-value (p)	2.37*	6.06**	3.30*	3.55**

FIGURE S2. Effect of abiotic and plant-specific factors on the composition of the endospheric (A) minor bacterial communities inhabiting the vine plant roots at the α-scale and (B) bacterial and fungal communities inhabiting the vine plant roots at the γ-scale.
Percentages of explained deviance and significance were calculated using ANOVA-like permutation tests with canonical correspondence analysis (CCA).

(A) Results of the CCA at the α-scale for the two minor bacterial phyla. Black dots reprensent the samples and red cross represent sequence-clusters.
(B) Significant results of the CCA at the γ-scale for the bacterial and fungal communities. Black letters reprensent the fields and red numbers represent sequence-clusters.
ANOVA tables show the significance for the CCA model.
Factors tested: age of the vine plant, cultivar (Merlot or Cabernet Sauvignon), OM (Organic Matter), C/N ration (carbon/nitrogen ratio), pH and P_2O_5 Factors which significantly influence the microbial composition are reported on tables.
Values are given (F-value) for the "all bacteria" / "all fungi" communities and the associated phyla when the explained deviance is significant (*, $P < 0.05$; **, $P < 0.01$. ***, $P < 0.001$).

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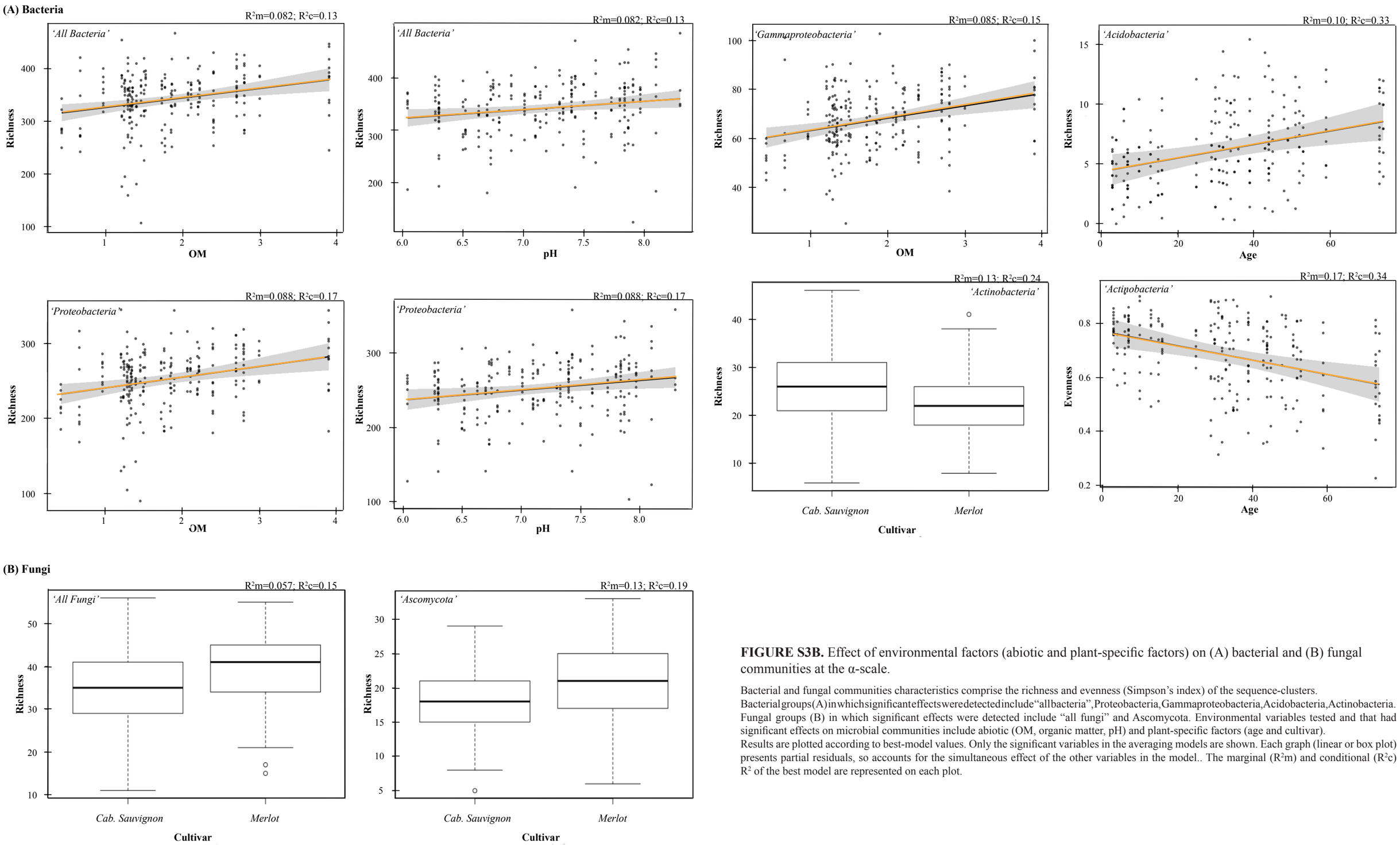


FIGURE S3B. Effect of environmental factors (abiotic and plant-specific factors) on (A) bacterial and (B) fungal communities at the α-scale.

Bacterial and fungal communities characteristics comprise the richness and evenness (Simpson's index) of the sequence-clusters. Bacterial groups (A) in which significant effects were detected include "all bacteria", Proteobacteria, Gammaproteobacteria, Acidobacteria, Actinobacteria. Fungal groups (B) in which significant effects were detected include "all fungi" and Ascomycota. Environmental variables tested and that had significant effects on microbial communities include abiotic (OM, organic matter, pH) and plant-specific factors (age and cultivar).
Results are plotted according to best-model values. Only the significant variables in the averaging models are shown. Each graph (linear or box plot) presents partial residuals, so accounts for the simultaneous effect of the other variables in the model.. The marginal (R^2m) and conditional (R^2c) R^2 of the best model are represented on each plot.