SUPPLEMENTAL MATERIAL:

Resilience of the natural phyllosphere microbiota of the grapevine to chemical and biological pesticides

FIGURE S1. Culturable microorganisms of grapevine leaves. Bacterial (white) and fungal (black) colony forming units (CFU) present in the leaf-washing suspensions (CFU mL^{-1}) were obtained from untreated plants (UNT) and plants treated with penconazole (PEN) or with *Lysobacter capsici* AZ78 (AZ78) in Udine (UD), San Michele all'Adige (SM1) and San Michele all'Adige protected from rain (SM2). Mean values and standard errors from three replicates are presented for each sample. Different letters indicate significant differences among treatments and locations, according to Tukey's test (α = 0.05). *Lysobacter* spp. colonies were distinguishable indicating the viability of AZ78 in the collected samples. Morphology of bacterial and fungal colonies indicated that the cultivable microorganisms represent only a minor part of total diversity of the phyllosphere populations.

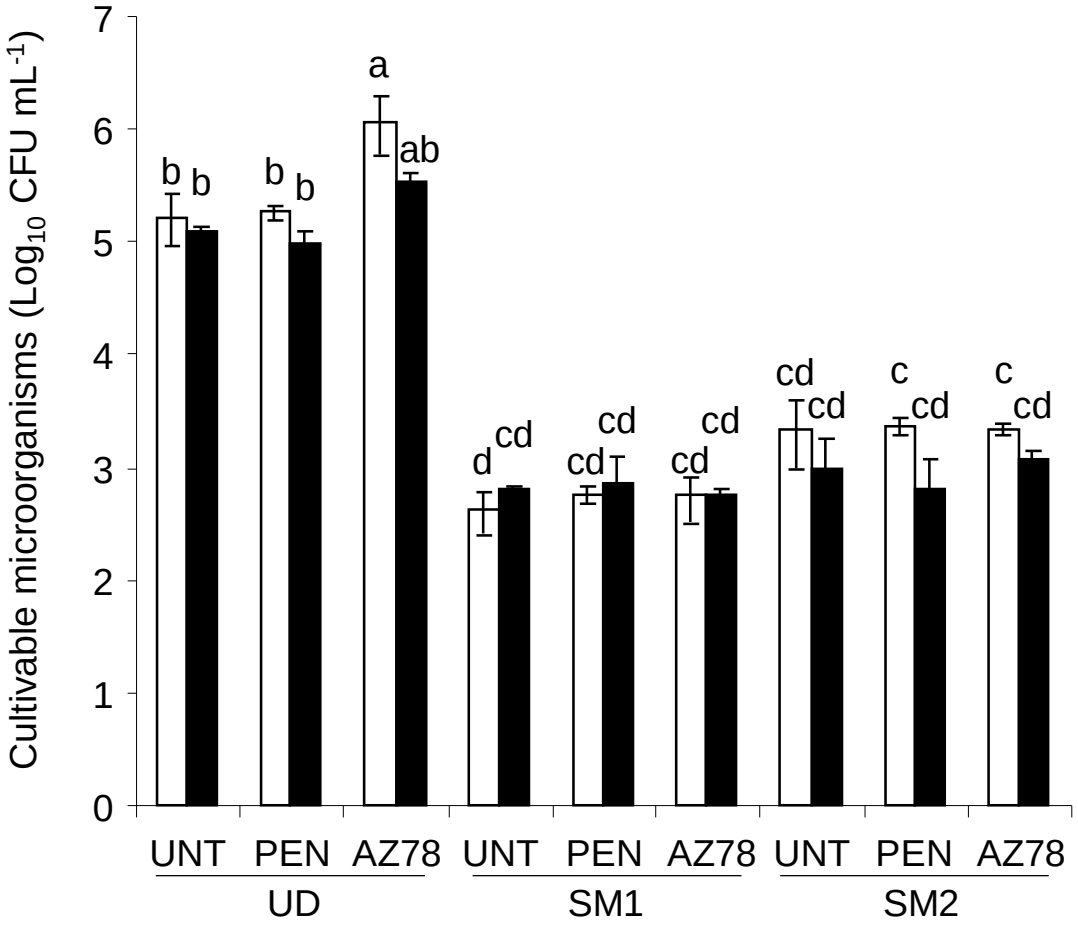
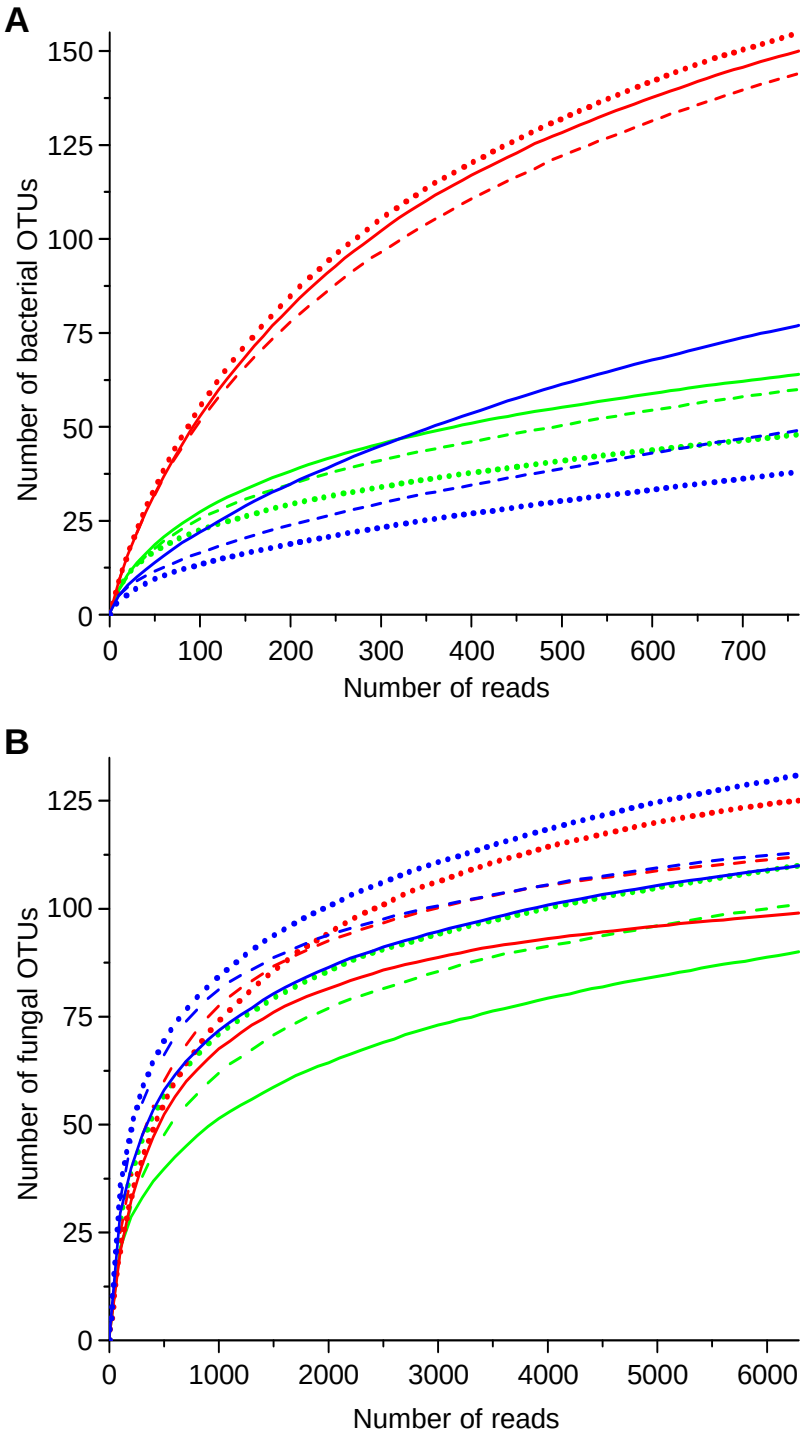


FIGURE S2. Rarefaction curves of bacterial (**A**) and fungal (**B**) communities identified on grapevine leaves. Reads of three replicates were merged and curves were obtained by random re-sampling without replacement with Mothur for samples collected from untreated plants (UNT; solid lines), plants treated with penconazole (PEN; dotted lines) or with *Lysobacter capsici* AZ78 (AZ78; dashed lines) in Udine (UD; green), San Michele all'Adige (SM1; red) and S. Michele all'Adige protected from rain (SM2; blue). Data were normalized and curves were rarefied to the lowest number of filtered reads for bacteria (762 in SM2-AZ78) and fungi (6,290 in SM2-PEN) respectively.



SUPPLEMENTAL TABLES

Data are reported in the Supplemental Excel file named:

Perazzolli et al SuppMaterialSampleDataset (TableS1-S5).xls

TABLE S1. Fusion primers for pyrosequencing. Sequences of primer pairs used for amplification and sequencing of the 16S rRNA gene (799-f and 1520-r) and ITS fragment (ITS5-f and ITS4-r) are reported, including the multiplex identifier (MID) codes for each DNA sample.

TABLE S2. Number of total filtered reads, identified operational taxonomic units (OTUs), richness estimators (Good's coverage, Chao1 and ACE) and Shannon index (H´) obtained for bacteria and fungi collected from grapevine leaves. The 16S rRNA and ITS fragments were amplified from DNA extracted from leaf-washing suspensions of untreated plants (UNT), plants treated with penconazole (PEN) or with *Lysobacter capsici* AZ78 (AZ78) in Udine (UD), San Michele all'Adige (SM1) and San Michele all'Adige protected from rain (SM2). Data of three replicates (named from A to C) and the results obtained by merging data of replicates (Merged) are reported for each sample. OTUs belonging to the Xanthomonadaceae family (which includes the reads of AZ78) were removed (Bacteria except Xanthomonadaceae) in PCoA analysis of bacterial data.

TABLE S3. Coefficients of Spearman's correlation calculated among replicates of bacterial and fungal data. Spearman's correlation coefficients ($P < 0.01$) are based on read counts of bacterial and fungal OTUs identified in each replicate (named from A to B) of leaves collected from untreated plants (UNT), plants treated with penconazole (PEN) or with *Lysobacter capsici* AZ78 (AZ78) in Udine (UD), San Michele all'Adige (SM1) and San Michele all'Adige protected from rain (SM2).

TABLE S4. Bacterial operational taxonomic units (OTUs) identified on grapevine leaves. Read counts are reported for each OTU identified using the GreenGenes database at 97% of sequence similarity for each replicate (named from A to C) of leaf samples collected from untreated plants (UNT), plants treated with penconazole (PEN) or with *Lysobacter capsici* AZ78 (AZ78) in Udine (UD), San Michele all'Adige (SM1) and San Michele all'Adige protected from rain (SM2). Taxonomy indicates kingdom (K), phylum (P), class (C), order (O), family (F), genus (G), and species (S) of identified OTUs.

TABLE S5. Fungal operational taxonomic units (OTUs) identified on grapevine leaves. Read counts are reported for each OTU identified using the Unite database at 97% of sequence similarity, for each replicate (named from A to C) of leaf samples collected from untreated plants (UNT), plants treated with penconazole (PEN) or with *Lysobacter capsici* AZ78 (AZ78) in Udine (UD), San Michele all'Adige (SM1) and San Michele all'Adige protected from rain (SM2). Taxonomy indicates kingdom (K), phylum (P), class (C), order (O), family (F), genus (G), and species (S) of identified OTUs.