Effect of site and phenological status on the potato bacterial rhizomicrobiota

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Supplementary information file

Dataset S1: Table reporting the amplicon sequence variants (ASVs) detected, their taxonomic assignment and occurrence; .csv file.

Table S1: Table containing, sample codes, locality, phenological stage, fast1 file name, the number of total input reads from fastq files and the number of reads that passed the filtering parameters; .xlsx file.

Table S2: Table containing the physicochemical features of soil samples; .xlsx file.

Table S3: Table of Good's coverage values. Good's coverage was estimated on the amplicon sequence variant (ASV) table for each sample after removing chimeras; .csv file.

Table S4: List of richness, diversity and evenness indices; .csv file.

Table S5. Results of Permutational Multivariate Analysis of Variance (PERMANOVA) test performed on alpha diversity indicates; .csv file.

Table S6: List of p values calculated through a Permutational Multivariate Analysis of Variance (PERMANOVA) test performed on the phyloseq object after a centered log ratio (CLR) transformation; .csv file.
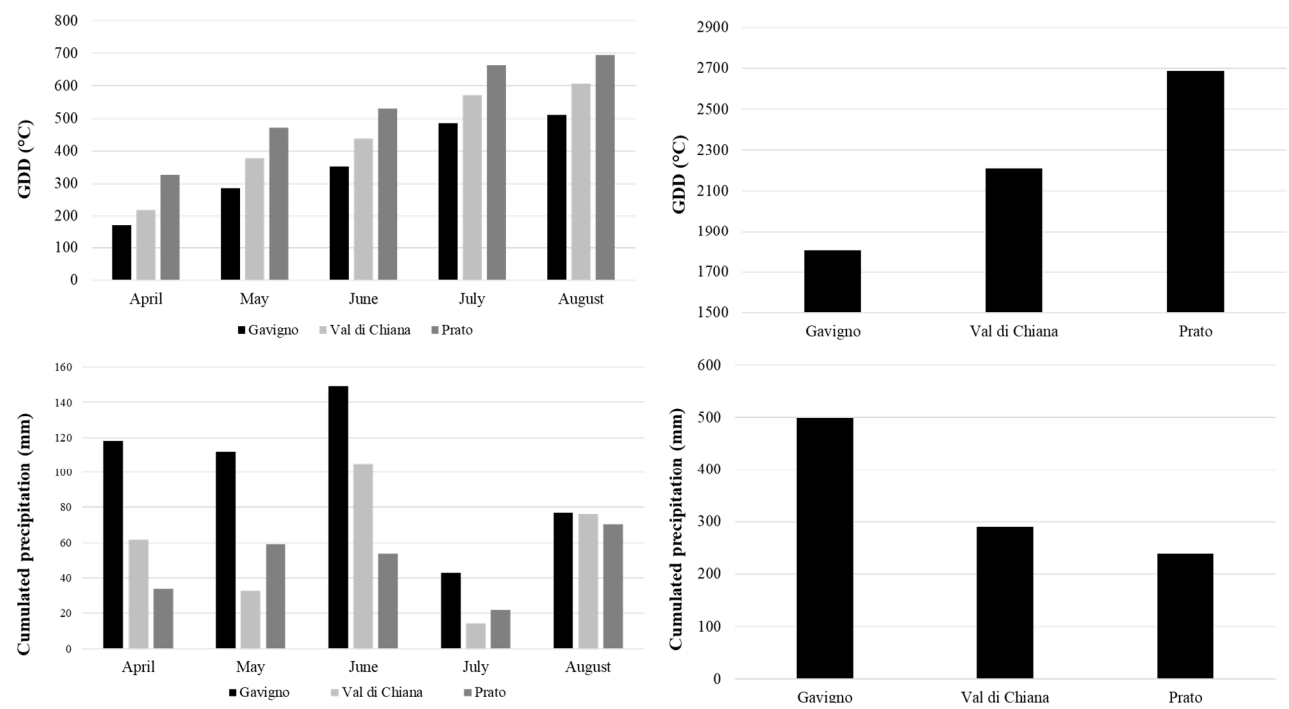
Table S7: Results of DeSeq2 on ASVs mostly differing among localities; .csv file.

Table S8: List of all identified metabolic pathways present in the taxa retrieved in the bacterial community; .xlsx file.

Figure S1: Climatic conditions. The cumulated growing degree days (GDD; °C) (top row) and the cumulated precipitation (mm) (bottom row) are reported. Results were calculated on a monthly basis (April-August) (left panel) and for the entire growing season (from sowing to maturity) (right panel).

Figure S2: Rarefaction curve of all soil samples. The x axis indicates the number of sequences found for each sample, while the y axis indicates the species richness.

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