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Article

Different Functional and Taxonomic Composition of the Microbiome in the Rhizosphere of Two Purslane Genotypes

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Abstract: Soil microbial communities have an important role in plant establishment and health. Particularly, the role of the soil microbiome in agriculture is of current interest. The study of microbial communities associated with purslane could open questions about the rational exploitation of the microbiota for sustainable agricultural purposes. In this study, the composition of the fungal and bacterial communities and the bacterial metabolic functions, associated with the rhizospheres of two purslane genotypes (one commercially available and one collected from the wild in Spain) were evaluated. The results showed a clear effect of purslane genotype on fungal and bacterial community composition and functional profiles. The bacterial community of the commercial purslane rhizosphere was characterized by more numerous metabolic pathways, mainly pathways related to Terpenoids and Polyketides, Carbohydrate, Lipid, and Amino Acid metabolism. By contrast, the rhizosphere bacterial community of the Spanish (wild) genotype was characterized by the enrichment of functions related to cellular processes such as cell motility and transport. We hypothesize that these differences could be due to differential effects of root exudate composition on the microbial functional community composition. This finding points out the need to consider differences in the functional characteristics of plant genotypes when selecting the beneficial microorganisms to be used as biofertilizers aiming to maximize plant growth and resistance to environmental stressors.

Keywords: *Portulaca oleracea*; genotypes; ilumina sequencing; bacterial community; fungal community; functional composition

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1. Introduction

In the interface between plant root and soil (rhizosphere), complex interactions occur between the soil microbiome and plants through root exudation [1]. There is increasing evidence suggesting that the quantity and quality of these rhizodeposits greatly influence the diversity, composition, and activity of the rhizosphere microbiomes [2]. Roots secrete a plethora of photosynthesis-derived organic compounds to the rhizosphere that serve as resources for microbial growth. In return, they provide beneficial services to the plant such as enhanced nutrient acquisition, improved water uptake, nitrogen fixation, solubilisation of mineral phosphates, pathogen resistance, and stress tolerance [3]. Moreover, the plant–microbe communication is mediated by means of plant molecular signals, especially secondary metabolites which are also secreted into the rhizosphere [2].

Previous studies conducted with different crops have shown that plant species traits such as genotype, physiological functions, developmental stage, and plant traits may

influence rhizosphere microbiome composition by favoring microorganisms with specific functions for hosts [1].

The microorganisms are considered a fundamental component of the soil ecosystem, since they perform numerous functions allowing plant growth and health by fixation of nutrients, fighting diseases, inducing resistance to drought, expanding root tissues, and decomposing organic material [4].

Purslane (*Portulaca oleracea* L.) is acknowledged as one of the most important medicinal herbs [5]. It is also an important palatable vegetable crop with significant health properties related to the high contents of omega-3 (α-linolenic acid) fatty acid and antioxidants [6,7]. It can be found worldwide and grow well under various environmental conditions, while it has been suggested that its medicinal properties and secondary metabolites can change depending on environmental conditions and genotype [8,9]. In spite of the research carried out in purslane aboveground traits, as far as we know, no studies have focused on the influence of purslane on the functions of soil microbiome. Considering the important role of soil microbiome for plants and ecosystems, understanding the major factors that shape its community assembly and deciphering the molecular mechanisms underlying plant-microbial community associations will be crucial steps towards the rational exploitation of the microbiota for sustainable agricultural purposes and will also help to identify potential targets for future crop breeding and management.

Therefore, the present experiment aimed to investigate how purslane genotypes from different geographical areas may affect the associated soil microbial community composition and function. We hypothesize that, because of specific plant traits, plant genotype drives the microbial community composition and regulates specific metabolic functions.

2. Materials and Methods

2.1. Design of the Experiment

The soil used in the experiment came from the CEBAS-CSIC Experimental Farm (Santomera, Murcia, Spain 38°06′14.0″ N 1°02′00.1″ W). The soil was classified as Lithic xeric haploxeroll. The chemical characteristics of the soil were total N 0.57 g/kg, available P 6.0 mg/kg, available K 33.9 mg/kg, organic matter 12.6 g/kg, $CaCO_3$ 3 g/kg, pH 7.14 and EC 0.10 dS/m. Two kilograms of soil mixed with sand and vermiculite (1:1:1; *w*:*w*:*w*) were put in 2 L pots (15.7 cm diameter, 12.5 cm height). In April 2021, seeds of purslane (*Portulaca oleracea* L.; Hortus Sementi Srl., Budrio, Italy; 2020 production lot) were provided by the Department of Agriculture Crop Production and Rural Environment (University of Thessaly, Greece) and seeds of wild purslane plants collected from semiarid areas of the Southeast of Spain were directly sown in the pots in order to obtain one plant per pot after thinning. Before sowing, seeds were surface sterilized using 1% hypochlorite/H_2O solution under gentle agitation for 5 min and washed 4 times with excess of sterile water. The experiment consisted of a mesocosm assay with seven pots (n = 7) for each plant genotype. Each plant was fertilized with 100 mL of nutrient solution (300:100:100 ppm N:P:K ratio) per pot by manual irrigation once a week.

The experiment was maintained for three months after May 2021 (from seed sowing) under greenhouse conditions at CEBAS-CSIC Experimental Farm (Santomera, Murcia, Spain). Day/night temperature was 35 °C/25 °C. Plants were irrigated regularly with water to keep 60% of soil field capacity.

At experiment completion, plants were harvested, and rhizosphere soil samples were stored at −20 °C for DNA sequencing. Fresh and dry (air-dried at 105 °C for 5 h) shoot biomass was measured.

2.2. Analyses of Plant Tissue

Dry shoot biomass was measured after drying fresh samples at 105 °C for 5 h.

2.3. DNA Extraction and Illumina Sequencing

Genomic DNA was extracted from 0.25 g of rhizosphere soil from each sample by using the DNeasy PowerSoil DNA Isolation kit (Qiagen, Hilden, Germany), following the manufacturer protocol. DNA yield and quality were checked both by electrophoresis in 0.8% (*w*/*v*) agarose gels stained with GelRed and visualized under UV light, and by using a Qubit 3.0 fluorometer (Life Technologies, Grand Island, NY, USA). DNA from each individual sample was sequenced using the Illumina MiSeq platform at the genomics service of the Institute of Parasitology and Biomedicine "López Neyra" (CSIC), Granada, Spain. Prokaryotic libraries were constructed by amplifying the hyper-variable V3–V4 regions of the 16S rRNA gene using the primer pair 341F (5′-CCTACGGGNBGCASCAG-3′) and 806R (5′-GACTACNVGGGTATCTAATCC-3′) according to Takahashi and coauthors [10]. These amplicons were tagged to be attached to PNA PCR clamps to reduce plastid and mitochondrial DNA amplification [11]. Fungal libraries were constructed by amplifying the ITS2 region using the primer pair ITS4 (5′-TCCTCCGCTTATTGATATGC-3′) [12] and fITS7 (5′-GTGARTCATCGAATCTTTG-3′) [13]. Both runs were sequenced using a paired-end 2 × 300 bp (PE 300) strategy.

2.4. Sequencing Data Processing

Raw sequence data were analyzed by following the DADA2 v.1.16 analytical pipeline, adapted for ITS data in the case of the fungal run (DADA2 ITS Pipeline Workflow v.1.8) [14]. Briefly, forward and reverse primers were excised and cutadapt [15]. A quality filtering and dereplication of sequences were carried out using standard DADA2 parameters. The rate error model was inferred and used to implement the sample inference algorithm. Forward and reverse reads were merged, and chimeric sequences were removed. To further curate for possible sequencing errors, we applied the LULU algorithm [16]. In order to correct for mistagging, Amplicon Sequence Variants (ASVs) occurring at a frequency below 0.01% in each sample were removed. Taxonomic assignment was determined using the RDP algorithm implemented in DADA2 against the UNITE fungal database v.8.2. [17] for fungi and the 16S/18S SILVA release 132 for bacteria. ASVs not assigned to a known fungal phylum level were discarded as conducted for ASVs not assigned to the bacteria kingdom for fungi and bacteria datasets, respectively.

Bacterial metagenome prediction was performed on the basis of the ASV table using PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) [18]. PICRUSt is used to estimate the bacterial genes present in the metagenomes of a microbial community under study, using 16S rRNA data and to estimate the profile of the potential microbial functions associated with each of the groups. A normalization of each ASV was carried out dividing each ASV by the known 16S copy number abundance in a sample basis. The functional profile of the genes was determined with the identification in Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways [19].

2.5. Statistical Analyses

We normalized the data by rarefying the samples to the sequence number of the lowest sample. A non-metric multidimensional scaling (NMDS) ordination based on the Bray–Curtis distance was performed to visually compare the taxonomic composition of the bacterial and fungal communities independently, using the "metaMDS" function implemented in "vegan" package for R [20]. To test the effect of the different plant genotypes, on the rhizosphere microbial community composition and structure, a permutational multivariate analysis (perMANOVA) using 999 permutations was conducted using Bray–Curtis distance as a measure of dissimilarity with the "adonis" function in vegan.

An indicator taxon analysis (ISA) was conducted using the phylum and family abundance data (indicspecies R package, [21]).

The influence of the plant genotype on bacteria functional profiles was evaluated individually for each function by using the Kruskal–Wallis test. The Benjamini–Hochberg false discovery rate (FDR) [22] correction method was applied to the results and all features

with a p value ≥ 0.05 were discarded. The statistical procedures were carried out using the package STAMP [23].

2.6. Data Availability

The sequences retrieved in this study were submitted to the NCBI Sequence Read Archive repository (www.ncbi.nlm.nih.gov/sra (accessed on 20 April 2023)) and are accessible in the BioProject PRJNA934288.

3. Results and Discussion

The composition of the rhizosphere fungal and bacterial communities varied depending on the plant genotype ($F = 3.68$, $p < 0.05$, and $F = 2.95$, $p < 0.05$, respectively) according to perMANOVA results. These differences were easily visualized in the NMDS ordination plot (Figures 1 and 2) where it has been shown the important role of a plant genotype as key determinant of the microbial assemblage. Similar results were shown in different specie varieties of maize [24], barley [25], wheat [26], soybean [27], cotton [28], or rice [29]. Nonetheless, there was no significant effect of the purslane genotype on alpha diversity (Shannon index and ASV richness), either for bacteria or fungi, except for fungal richness that was significantly higher in the Spanish (wild) purslane rhizosphere ($F = 18.4$, $p < 0.001$). In this way, Hartmann and Widmer suggested that changes in the microbial community composition may not necessarily result in changes in diversity and abundance because the shifts in some microbial taxa may be compensated by others [30].

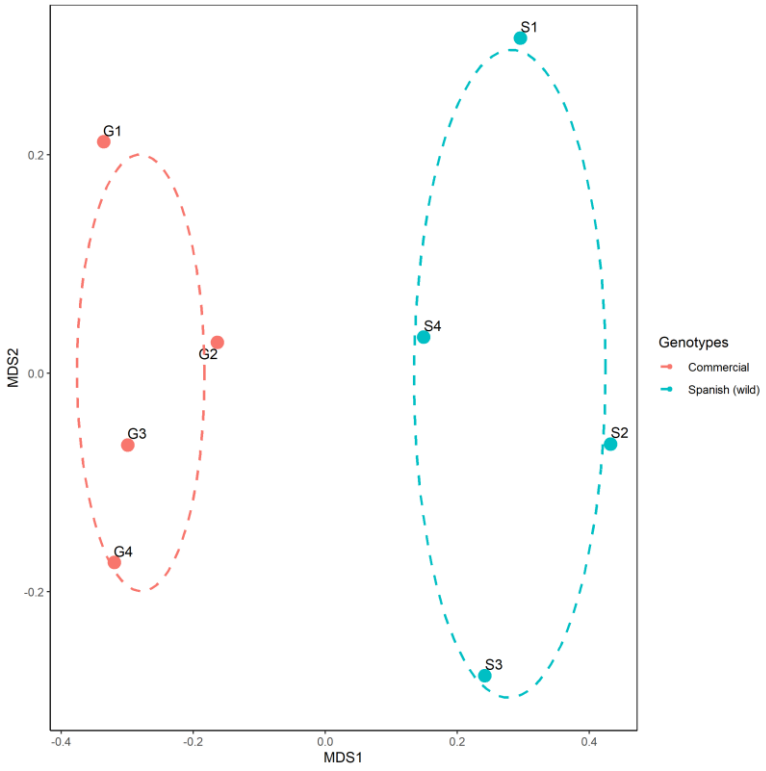

Figure 1. Nonmetric multidimensional scaling (NMDS) analysis on a Bray–Curtis dissimilarity matrix based on the ASVs dataset retrieved from the fungal communities of the rhizospheric soil of purslane from commercial and Spanish (wild) genotypes. Ellipsoids represent 95% confidence for each treatment mean.

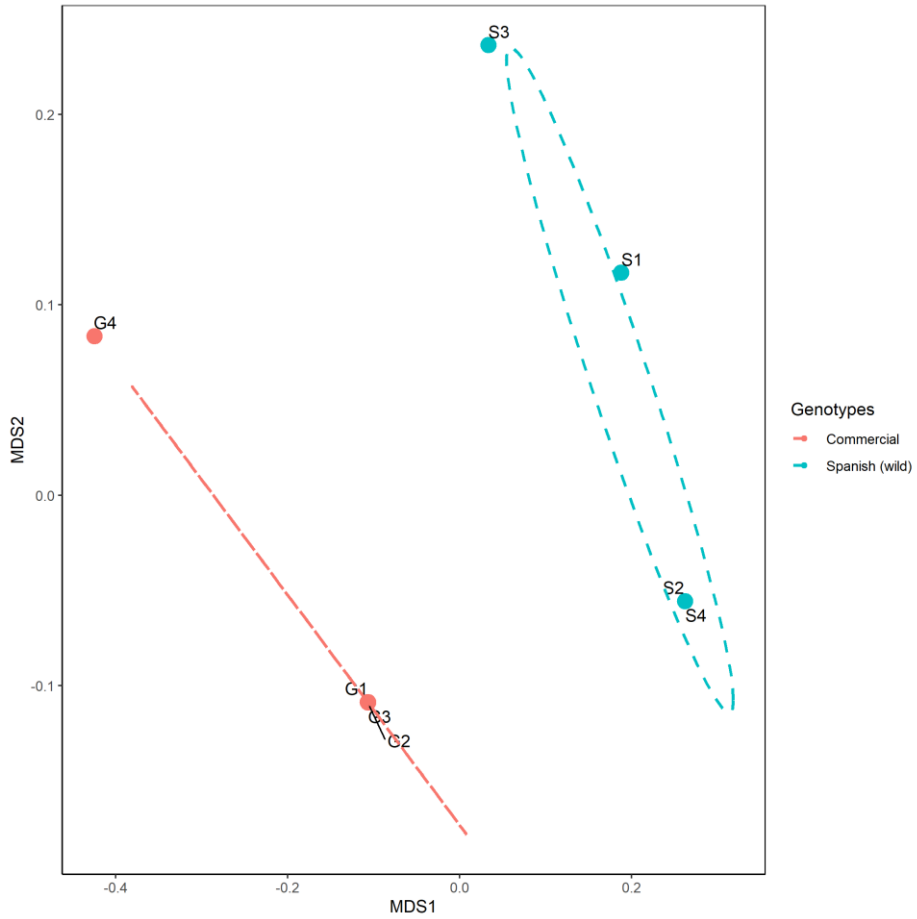

Figure 2. Non-metric multidimensional scaling (NMDS) analysis on a Bray–Curtis dissimilarity matrix based on the ASVs dataset retrieved from the bacterial communities of the rhizospheric soil of purslane from commercial and Spanish (wild) genotypes. Ellipsoids represent 95% confidence for each treatment mean.

We found significant differences (F = 18.2, $p < 0.01$) in the plant growth (dry leave biomass) between both plant genotypes (2.43 $\pm$ 0.32 commercial genotype; 1.37 $\pm$ 0.32 Spanish (wild) genotype). Semchenko and coauthors demonstrated a positive relationship between the aboveground photosynthetical processes and the rhizodeposition or the amount of root exudates and the utilization of carbon belowground for bacterial metabolism [31]. This could indicate that, keeping the soil and environmental conditions constant, the recorded changes in microbiome composition could be related to the root rhizodeposition [24]. Attending to microbial metabolic capacities, PICRUST as a functional pathway analysis showed differences between both purslane rhizospheres. This analysis showed that the relative abundance of 49 pathways out of the total 231 found, differed significantly between both plant genotype rhizospheres according to Kruskal–Wallis t-test (Figure 3). The bacterial community of the commercial purslane rhizosphere was characterized by a higher increase of metabolic pathways, mainly pathways related to Terpenoids and Polyketides, Carbohydrate, Lipid, and Amino Acid metabolism. These pathways, in particular lipids and carbohydrates, are associated with energy production than facilitate plant growth and development. Carbohydrates act as one of the major reservoirs of readily available energy and carbon compounds, while lipids are organic compounds with an essential structural role in cell membranes, considered important energy sources that act as signaling molecules in intracellular communication [32].

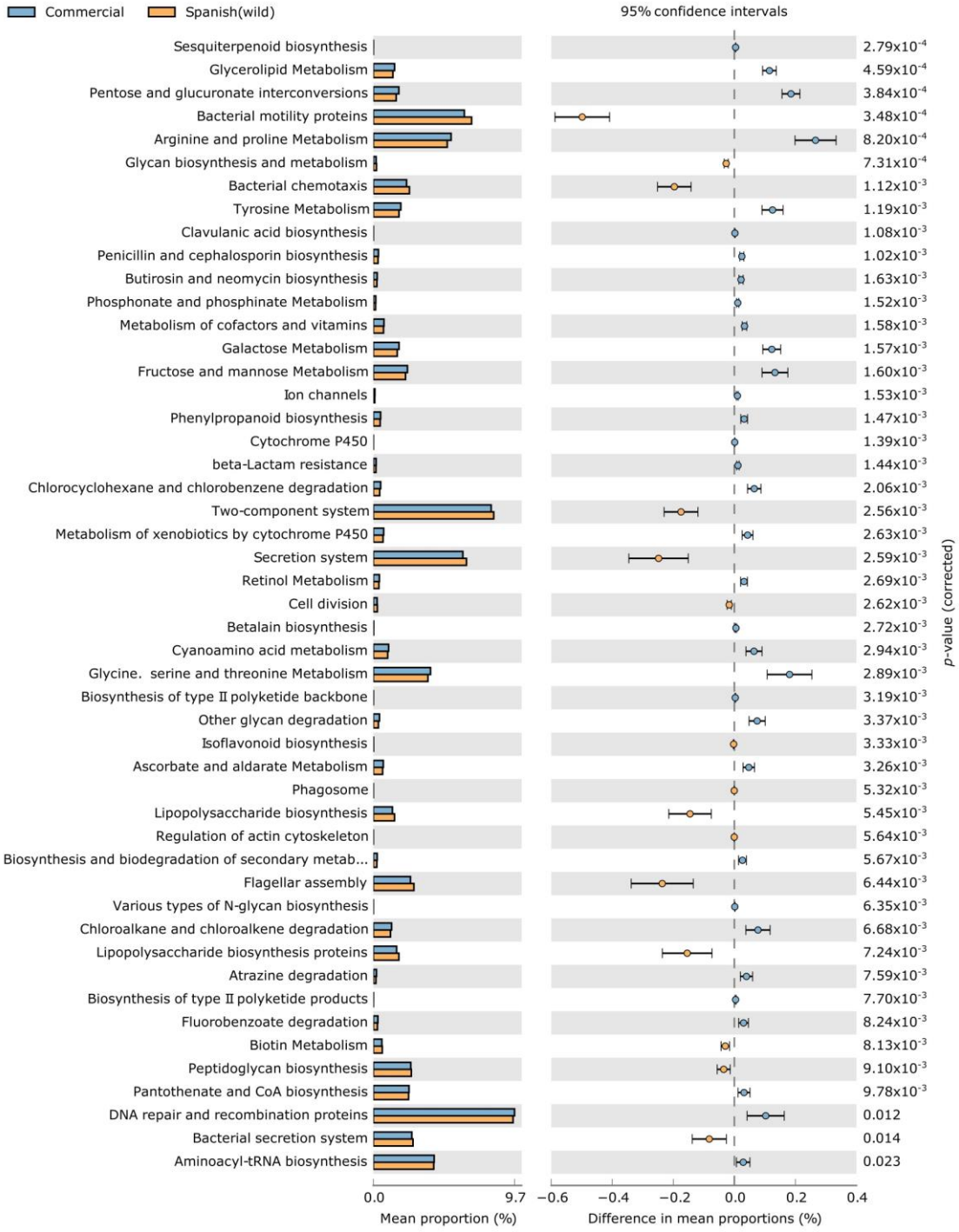

Figure 3. Relative abundance of pathways predicted by PICRUSt that were significantly different in the bacterial communities of commercial and Spanish (wild) purslane rhizosphere according to a two-sided Welch's *t*-test with Benjamini–Hochberg multiple testing correction (q-value < 0.05).

Biosynthetic pathways of secondary metabolites such as Phenylpropanoid, Penicillin, cephalosporin, and Betalain as well as Xenobiotics Biodegradation were also enriched in the microbial community of the commercial genotype. Previous reports have suggested that the antibiotic activity of bacteria in the rhizosphere is particularly important when plants are attacked by pathogens [26,33]. By contrast, the bacterial community of the Spanish (wild) genotype rhizosphere was characterized especially by the enrichment of functions related to cellular processes such as cell motility and transport (Figure 3).

With respect to the predicted nitrogen pathway, an enrichment of functional genes related to N-cycling (*amoA*, *amoB*, and *amoC*) was observed for the commercial genotype rhizosphere (Figure 4), which contributes significantly to ammonia oxidation [34], probably due to an increase in the nitrification process within the rhizosphere of this particular genotype. On the other hand, the Spanish (wild) genotype rhizosphere was enriched by genes related to the N-fixation and denitrification process. Predictive C-cycling genes encoding cellulolytic activity, beta glucosidase (bglX), and alpha-glucosidase (malZ) and also hemicellulose hydrolysis, Alpha-L-fucosidase (FUCA) showed the highest abundance in the case of the commercial genotype rhizosphere. Several authors [35,36], have shown that organic exudates from the rhizosphere can increase C-degrading pathways. Also, Zuo and coauthors found differences in the microbial enzymes associated with nitrogen and carbon metabolism in response to different wheat genotypes [37]. The authors attributed that these differences could be due to differences in the root phytochemicals, which could have also occurred in our study.

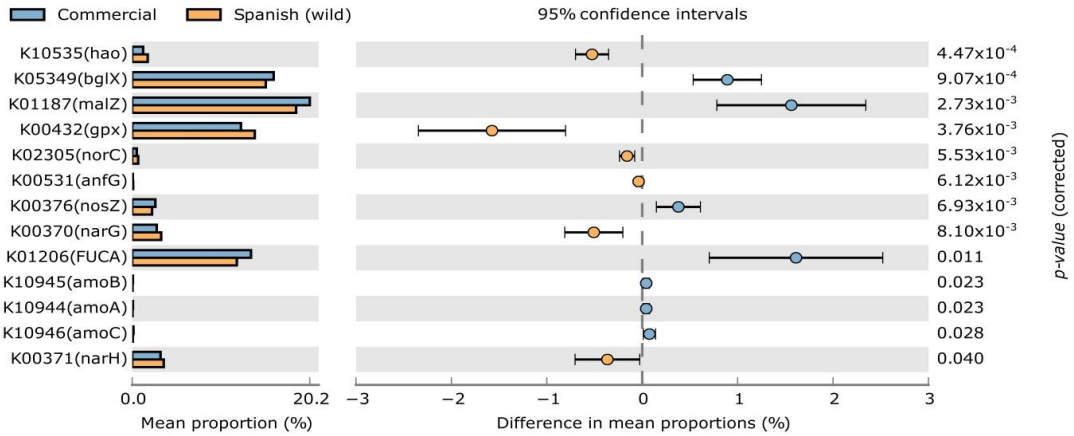

Figure 4. Predicted nitrogen and carbon metabolism pathway genes that were significantly different in the rhizosphere of commercial and Spanish (wild) purslane according to a two-sided Welch's *t*-test with Benjamini–Hochberg multiple testing correction (*q*-value < 0.05). C genes (*bglX*, *malZ*, *gpx*, *FUCA*) and N genes *(hao*, *amoA*, *amoB*, *amoC*, *norC*, *anfG*, *nosZ*, *narG*, and *narH*).

In line with Semchenko and coauthors, the root exudations could be one of the main channels by which the variation in plant functional traits translate into changes in soil microbial activity [31]. In fact, the higher activation of the rhizosphere microbial activity was observed in the commercial genotype rhizosphere which also showed the higher biomass yield.

We also found an increase of enzymes that are considered indicators of the soil microbial activity, since they catalyze the biological oxidation of organic matter, thus providing energy to the soil microorganisms [38]. Among them, the hydrolytic enzyme β-glucosidase (EC:3.2.1.21) degrades complex organic substrates, providing nutrients available to plants and it is involved in the C cycling. The enzyme Catalytic peptidase such as Peptidyldipeptidase Dcp (EC:3.4.15.5) produced by microorganisms with important functions in the recycling of soil organic N, and oxidoreductases enzymes such as NADH dehydrogenase (EC:1.6.5.3) that catalyses the biological oxidation of organic matter, providing energy to the soil microbiota (Figure 5). Thus, all these metabolic functions could be able to lead to a higher increase in the availability of nutrients and energy to mobilize nutrients that would be absorbed by root providing higher biomass yield.

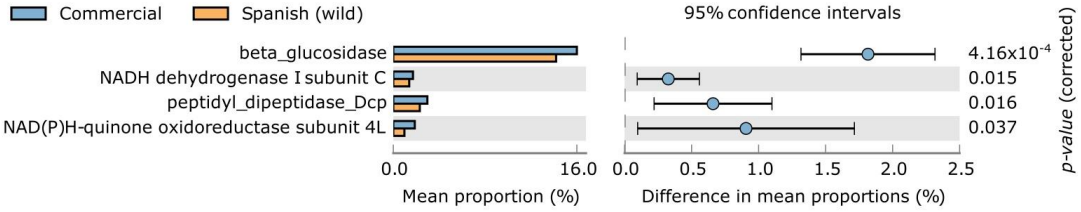

Figure 5. Predicted enzymes that were significantly different in the rhizosphere of commercial and Spanish (wild) purslane according to a two-sided Welch's *t*-test with Benjamini–Hochberg multiple testing correction (*q*-value < 0.05).

The fungal community was composed of 11 fungal phyla. Ascomycota was the most abundant fungal phylum (67%), followed by *Mortierellomycota* (13%) and *Basidiomycota* (12%). The rest of the fungal phyla accounted for less than 5% of the total relative abundance. Only the *Mortierellomycota* phylum was significantly different from the studied purslane genotypes ($F = 23.0$, $p < 0.01$) (Figure S1). In the case of the bacterial community, it was composed of 21 bacterial phyla. *Proteobacteria* (26%), *Actinobacteria* (25%), and *Chloroflexi* (22%) were the most abundant and the nineteen remaining phyla counted less than or equal to 6% of the total relative abundance (Figure S2).

The ISA was performed to find specific phyla and genera associated with different plant genotypes. The highest ISA was associated with the Spanish (wild) genotype, as shown in Table 1. *Proteobacteria* (28.2%), *Acidobacteria* (6.8%), and *Gemmatimonadetes* (2.4%) were the indicator bacterial phylum with the highest relative abundance in the rhizosphere soil of the Spanish (wild) purslane. *Patescibacteria* (6.2%) and *Deinococcus* (<1%) were the only indicator phyla for the commercial genotype. Attending to genera a more balanced figure was found for both purslanes, sixteen bacterial indicators were found for the Spanish (wild) purslane and fourteen for the commercial one (Table 1). For the Spanish (wild) purslane, *Blastococcus* and *Candidatus Alysiosphaera* genera were observed with higher relative abundance (both 0.8%). For the commercial purslane, *Streptomyces* and *Lechevalieria* showed the highest relative abundance with 3.4% and 2.9%, respectively. It is noteworthy that the indicator genera in the rhizosphere of commercial purslane showed higher relative abundance than indicator genera in Spanish (wild) purslane. Streptomyces is considered a well-described plant growth promoting rhizobacteria (PGPR) with an important role in plant adaptation and performance, since it promotes activities such as IAA and siderophore production, phosphate solubilisation and induced systemic resistance [33]. Thus, the highest abundance of Streptomyces as indicator taxa in the commercial genotype rhizosphere could have contributed to the found functional differences in metabolic pathways related with the secondary metabolites between the tested purslane genotypes. In fact, it has been found that various species of Streptomyces genus produce antimicrobial secondary metabolites [39] and have important roles in disease control [40]. *Lechevalieria* was the second most abundant bacterial genera indicator of the commercial genotype rhizosphere. This genus has been previously identified and isolated from the rhizosphere of wheat [41]. Custer and coauthors also found *Lechevalieria* and *Streptomyces* as the most abundant genera in rhizosphere soils under *Solanum tuberosum*, in accordance with our results [42]. Although these are known to produce antibiotics [43], their role in host plant and functions in soil still remains elusive.

Table 1. Indicator value (IndVal) and associated significance value (*p*) of indicator species analysis (ISA) of bacterial taxa at phyla and genera level of two different genotypes of purslane. Relative abundances (RA) of each phylum and genus in the rhizospheric soil of purslane from commercial and Spanish (wild) genotypes.

	Bacterial Phyla	**IndVal**	***p*-Value**	**RA (%)**
Spanish (wild) purslane	*Elusimicrobia*	0.905	0.0298 *	0.07
	Gemmatimonadetes	0.825	0.0298 *	2.39
	Firmicutes	0.823	0.0298 *	0.19
	WS2	0.807	0.0298 *	0.19
	Acidobacteria	0.745	0.0298 *	6.80
	Proteobacteria	0.740	0.0298 *	28.2
Commercial purslane	*Deinococcus-Thermus*	1.000	0.0298 *	0.10
	Patescibacteria	0.784	0.0298 *	6.20
	Bacterial genera	**IndVal**	***p*-value**	**RA (%)**
Spanish (wild) purslane	*Bauldia*	1.000	0.0296 *	0.09
	Craurococcus	1.000	0.0296 *	0.09
	Candidatus Captivus	0.968	0.0296 *	0.27
	Hirschia	0.945	0.0296 *	0.10
	Quadrisphaera	0.887	0.0296 *	0.18
	OM27 clade	0.885	0.0296 *	0.23
	Haloactinopolyspora	0.869	0.0296 *	0.11
	AKYG587	0.855	0.0296 *	0.23
	Sva0996 marine group	0.853	0.0296 *	0.11
	Amaricoccus	0.850	0.0296 *	0.61
	Nordella	0.846	0.0296 *	0.38
	Pseudonocardia	0.830	0.0296 *	0.35
	Blastococcus	0.823	0.0296 *	0.83
	Pedomicrobium	0.815	0.0296 *	0.63
	Candidatus Alysiosphaera	0.811	0.0296 *	0.81
	SWB02	0.808	0.0296 *	0.45
Commercial purslane	*Brevundimonas*	1.000	0.0296 *	0.44
	Truepera	1.000	0.0296 *	0.05
	Leptolyngbya EcFYyyy.00	0.991	0.0296 *	0.004
	Tychonema CCAP_1459.11B	0.990	0.0296 *	1.90
	Lechevalieria	0.975	0.0296 *	2.89
	Aeromicrobium	0.958	0.0296 *	0.68
	Shinella	0.929	0.0296 *	0.70
	Allorhizobium	0.916	0.0296 *	0.43
	Aridibacter	0.886	0.0296 *	0.28
	Streptomyces	0.881	0.0296 *	3.39
	Nocardioides	0.881	0.0296 *	1.26
	Herpetosiphon	0.873	0.0296 *	1.02
	Altererythrobacter	0.872	0.0296 *	1.87
	Pseudarthrobacter	0.792	0.0296 *	1.02

* Significant at $p < 0.05$.

Regarding fungi, both plant genotypes showed only one indicator fungal phylum; *Rozellomycota* for Spanish purslane and *Mortierellomycota* for commercial purslane (Table 2). As in the case of bacteria, the highest number of indicator fungal taxa at the genera taxonomic level was detected in the Spanish genotype. Of the eighteen indicator genera detected under the Spanish genotype, the most abundant genus was *Fusarium* (relative abundance 27.5%), while the rest of indicator genera accounted less than 3%. In the commercial purslane rhizosphere six indicator genera were identified, being *Mortierella* (relative abundance 19.4%) the most abundant fungal genus. It was followed in abundance by the genera *Ulocladium* (5.6%) and *Chrysosporium* (3.7%). The rest of the genera counted less

than 1.2%. Our results suggest an extremely dominant role for *Fusarium* in the Spanish genotype microbiome that it is a rhizosphere-resident genus where some strains can be identified as plant growth promoting fungi (PGPF) [44]. It is known to improve plant performance and resistance through the solubilisation and mineralization of soil nutrients, and the production of defense-related enzymes, defensive/volatile compounds, and phytohormones [44]. Therefore, this fungus could have played the most important role in the growth of Spanish genotype plants. In the rhizosphere soil of commercial purslane, *Mortierella* was the predominated indicator fungi. It is a filamentous fungus, in which some strains belong to the PGPF, and in recent years has triggered the scientific interest due to various agricultural benefits such as the increase of the nutrient uptake efficiency, the positive effect in crop adaptation against adverse conditions, and the reduction of the inputs of chemical fertilizers and pesticides [45]. The abundance of *Mortierella* could be affected by the higher enrichment of the bacterial metabolic pathways implied in the carbohydrates metabolism for the commercial genotype rhizosphere due to their important role in the utilization of carbon sources [45]. Also, Li and coauthors found that *Mortierella* promoted the maize growth by stimulating metabolic-related genes that are involved in sugars export and lipids import-transport [46].

Table 2. Indicator value (IndVal) and associated significance value (*p*) of indicator species analysis (ISA) of fungal taxa at phyla and genera level of two different genotypes of purslane. Relative abundances (RA) of each phylum and genus in the rhizospheric soil of purslane from commercial and Spanish (wild) genotypes.

	Fungal Phyla	**IndVal**	***p*-Value**	**RA (%)**
Spanish (wild) purslane	*Rozellomycota*	0.860	0.0298 *	1.45
Commercial purslane	*Mortierellomycota*	0.879	0.0298 *	19.52
	Fungal genera	**IndVal**	***p*-value**	**RA (%)**
Spanish (wild) purslane	*Byssochlamys*	1.000	0.0298 *	0.06
	Metarhizium	0.970	0.0298 *	0.09
	Wardomycopsis	0.957	0.0298 *	0.60
	Aspergillus	0.956	0.0298 *	0.11
	Liua	0.950	0.0298 *	1.23
	Microascus	0.947	0.0298 *	0.61
	Purpureocillium	0.939	0.0298 *	1.40
	Auxarthron	0.938	0.0298 *	0.08
	Stephanonectria	0.936	0.0298 *	0.06
	Powellomyces	0.935	0.0298 *	0.44
	Cladorrhinum	0.933	0.0298 *	0.51
	Scopulariopsis	0.930	0.0298 *	0.14
	Saksenaea	0.898	0.0298 *	0.14
	Agaricus	0.897	0.0298 *	0.42
	Chaetomium	0.887	0.0298 *	2.96
	Naganishia	0.868	0.0298 *	1.89
	Talaromyces	0.865	0.0298 *	0.08
	Fusarium	0.800	0.0298 *	27.51
Commercial purslane	*Lachancea*	1.000	0.0298 *	0.02
	Gibberella	0.996	0.0298 *	1.12
	Ulocladium	0.988	0.0298 *	5.57
	Alternaria	0.981	0.0298 *	0.86
	Chrysosporium	0.915	0.0298 *	3.73
	Mortierella	0.879	0.0298 *	19.42

* Significant at $p < 0.05$.

4. Conclusions

The results presented in this study showed that purslane genotypes coming from different geographical areas such as Greece and Spain may greatly modify the community composition and functional capacities of the microbial communities in their rhizospheres.

We hypothesized that these differences could be due to the effect of different metabolites and compounds in exudates excreted by roots on the bacterial and fungal functional community composition. This finding points out the need of considering differences in the functional characteristics of plant genotypes when selecting the beneficial microorganisms to be used as biofertilizers aiming to maximize plant growth and resistance to environmental stressors.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy13071795/s1. Figure S1: Relative abundances of the dominant fungal phyla of the rhizospheric soil of purslane from commercial and Spanish (wild) genotypes; Figure S2: Relative abundances of the dominant bacterial phyla of the rhizospheric soil of purslane from commercial and Spanish (wild) genotypes.

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Data Availability Statement: Data available upon request to M.d.M.A. The sequences retrieved in this study were submitted to the NCBI Sequence Read Archive repository (www.ncbi.nlm.nih.gov/sra (accessed on 20 April 2023)) and are accessible in the BioProject PRJNA934288.

Conflicts of Interest: The authors declare no conflict of interest.

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