Does plant diversity determine the diversity of the rhizosphere microbial community?

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Abstract

The rhizosphere community represents an “ecological interface” between plant and soil, providing the plant with a number of advantages. Close connection and mutual influence in this

communication allow to talk about the self-adjusting “plant-rhizosphere community” system, which should be be studied in connection. Diversity estimation is one of the ways of describing both bacterial and plant communities. Based on the literature, there are two assumptions of how the diversity of plant communities related to the diversity of bacterial communities: 1) an increase in the species richness of plants leads to an increase in the number of available micro-niches, and increasing of microbial diversity, 2) an increase in the species richness of plants is accompanied by the predominant development of bacteria from highly productive specific taxa and decreasing in the diversity of microorganisms. Experimental studies show controversial results.

We analyzed field sites (rye crop field and two fallow sites), using DNA isolation of both the plant root mass (followed by sequencing of the ITS1 region) and rhizosphere microorganisms (followed by sequencing of the 16s rDNA V4 region). This allowed us to 1) accurately determine the abundance and taxonomic position of plant communities; 2) extract information about both plant and microbial communities from the same sample.

There was no correlation between alpha-diversity indices of plants and rhizosphere communities. Alpha-diversity connection should be explored in similar plant communities, such as synusia. We hypothesize, that the significant differences in plant abundances lead to significant changes in exudation profiles, and the loss of diversity connection. The beta-diversity between rhizosphere communities and plant communities is highly correlated, in particular in terms of the abundance of taxa. This can be explained by a potential correlation (as reported in the literature) or by the presence of statistical artifacts.

42

43 **Introduction**

44 As the formation of a specific microbial community near the plant root, the phenomenon of
45 the rhizosphere effect has been the subject of many works of both classical and modern biology.

46 The rhizosphere community represents an “ecological interface” between plant and soil, providing
 47 the plant with a number of advantages such as growth stimulation, protection from pathogens,
 48 nutrition, among others [1, 2]. The source of the rhizosphere microbiome is both the microbial
 49 community of plant seeds [3] and the community of soil microorganisms [4]. The composition and
 50 abundance of plant root exudates determine the formation of the bacterial community [5, 6]. The
 51 source of the microbiome, and the development of it, thus forms the final community.

52 Diversity in both sources and ways of development lead to the specificity of the rhizosphere
 53 microbiome. Several factors can affect the composition of rhizosphere communities. In addition to
 54 the type and agrochemical properties of the soil, the genotype of the plant (species [7, 8] and
 55 cultivar [9]) is a significant factor for microbiome development. This can be explained by the
 56 specific exudation spectrum from various plants, as the spectrum of secreted substances depends not
 57 only on the species or cultivar but also on the developmental phase, physiological state, etc. [10,
 58 11]. In turn, the microbial communities themselves affect the metabolic status of the plant [12],
 59 which allows us to talk about the “plant-rhizosphere community” system as a self-adjusting system
 60 (a kind of “gut-brain axis” in plants). This system is additionally complicated by the high diversity
 61 of plant species, which is natural in indigenous plants populations.

62 Diversity estimation is one of the ways of describing both bacterial and plant communities. As
 63 self-adjusting systems, rhizosphere microbiomes and plant communities are connected, and
 64 therefore, the following question arises: is the diversity of plant communities related to the diversity
 65 of bacterial communities? Based on the literature, there are two assumptions: 1) an increase in the
 66 species richness of plants leads to an increase in the number of available micro-niches, which leads
 67 to an increase in microbial diversity, 2) an increase in the species richness of plants is accompanied
 68 by the predominant development of bacteria from highly productive specific taxa, which leads to a
 69 general decrease in the diversity of microorganisms [13]. Experimental studies of this relationship
 70 show controversial results: some studies indicate the absence or negative correlation between plant

71 and bacterial richness [14, 15], whereas others show the presence of a positive relationship [16].
72 Beta diversity indices show an unambiguous positive correlation between the distances of plant and
73 bacterial communities [17].

74 There are examples of research of similar relationships between the diversity of plants and the
75 associated microorganisms. A close relationship was demonstrated in a study of the diversity of the
76 rhizobial soil community (by the *nodA* gene) and the diversity of their symbiotic hosts (the *NFR5*
77 and *K1* genes of leguminous plants), allowing the authors to formulate the hypothesis of
78 "evolutionary molding", where the plant community plays the role of the rigid matrix and the
79 microbial community acts as a "molding" substance. The whole process not only links diversities,
80 but even phylogenetic topologies; for the description of the last phenomenon, the concept of beta-
81 topological diversity has been introduced [18]. Another example is the close relationship between
82 the diversity of *Galega* rhizobia and their two hosts, *G. orientalis* and *G. officinales*, revealed at the
83 level of genomic AFLP fingerprints [19]. However, for less closely integrated systems with
84 indigenous plant communities, analyzed by taxonomic rather than functional markers, such a
85 relationship has not yet been shown.

86 One of the reasons for the uncertainty in this area is, most likely, the problem of the correct
87 estimation of plant diversity, for which the same algorithms that are used today for the analysis of
88 microbial diversity could be applied. The development of NGS methods for the estimation of
89 microbial diversity, from DNA extraction methods to statistical analysis of libraries (16S, ITS), has
90 led to the rise of this area observed today [20]. However, in most papers, plant diversity is
91 determined using geobotanical methods [13, 15], but this approach is not accurate enough in both
92 determining the species in the communities and their abundances [21]. In addition, in the context of
93 the aim of this study, there is a question about the correspondence between the "aboveground" and
94 "belowground" plant diversities, which can be quite different [22].

Therefore, in this work, we analyzed the diversity of the plant population via direct DNA isolation of the plant root mass, followed by NGS sequencing of the ITS1 region; rhizosphere soil samples were taken from the same root sample. This allowed us to 1) accurately determine the abundance and taxonomic position of plant communities; 2) extract information about both plant and microbial communities from the same sample; 2) analyze plant diversity using the same NGS approaches as used for the rhizosphere community of microorganisms. Thus, we were able to use the same algorithms and metrics to analyze both communities.

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103 **Materials and Methods**

Samples were collected on July 21, 2017, on fields of the Pskov Research Institute of Agricultural Sciences and Rodina State Farm in the Pskov region, Russia (coordinates of the collection point are 57.845611 N 28.201028 E). We select one site within a rye crop field (referred to as Monoculture Rye or MonoR) and two fallow sites outside the field border from two locations, dominated by cereals (Polyculture Cereal or PolyC) and *Galium* and *Dactylis* species (Polyculture Galium, or PolyG). In each site, three samples were taken. The photo and the geobotanical description of the sampling sites is provided in the S1 Table and S1 Fig.

Bricks of topsoil (about 15 x 15 x 10 cm) were collected and stored in individual packages not longer than 48 hours. In the laboratory, bulk soil was gently removed manually by shaking, and 30 g of the root mass was intensively shaken with 50 ml of 0.005M Na-phosphate buffer in a Pulsifier II (Microgen, UK) in provided bags (PUL512 Bags) for 1 min. The liquid fraction was centrifuged, and the pellet was used to isolate the total rhizosphere DNA. The root mass was used to isolate plant DNA.

Procaryotic DNA from the pellet was isolated using the MN NucleoSpin Soil Kit (Macherey-Nagel, Germany) and a Precellus 24 homogenizer (Bertin, USA). Quality control was carried out by

119 PCR and agarose gel electrophoresis. Sequencing of the V4 variable region of the 16S rRNA gene
120 was performed on an Illumina MiSEQ sequencer, using the primers F515
121 (GTGCCAGCMGCCGCGGTAA) and R806 (GGACTACVSGGGTATCTAAT) [23].

122 Plant DNA from roots was isolated using mechanical destruction in liquid nitrogen, followed
123 by phenol extraction; the quality of the DNA was also checked via agarose gel electrophoresis.
124 Sequencing of the ITS1 variable region was performed on an Illumina MiSEQ sequencer, using the
125 primers ITS-p5 (YGAATCTCGGCAACGGATA) and ITS-u2
126 (GCGTTCAAAGAYTCGATGRTTC) [24].

127 The general processing of sequences was carried out in R 3.6.4, using the dada2 (v. 1.14.1)
128 [25] and phyloseq (v. 1.30.0) [26] packages. For taxonomic annotation, the databases SILVA 138
129 [27] and PLANITS [28] were used.

130 The main alpha- and beta-metrics were calculated using the phyloseq and picante [29]
131 packages. For the mean p-distance in a library, we used the home-brew script with following steps:
132 1) make multiple alignment for reference sequences; 2) extract p-value for every pair of sequence;
133 3) multiple this p-value to abundance of both sequences; 3) sum all values. Correlations between
134 diversity indices were calculated using Spearman correlation. Significant differences in abundances
135 of taxa between sites were determined using theDeSEQ2 package [30].

136 All reads were submitted to SRA (PRJNA649486) and are available under the link
137 <https://www.ncbi.nlm.nih.gov/sra/PRJNA649486>.

138

139 Results

140 The ITS1 sequencing of plant DNA yielded 230 ASVs. The taxonomic position at genus level
141 was defined for 217 of them; the number of reads per sample after rarefaction was 14,210.
142 Regarding 16s rDNA, we found 5,284 ASVs, with 15,487 reads per sample.

Fig 1 shows the taxonomic composition of the communities. The geobotanic description

(provided in the S1 Table) corresponded with the composition structure according to ITS1

sequencing (Fig 1A). Almost all reads from MonoR libraries were attributed as *Secale*; PolyC

(samples from the cereal synusia) had about half the reads from *Poa*, followed by *Elymus* and

Dactylis. PolyG (samples from *Galium* and *Dactylis* synusia) was more diverse; most reads were

attributed as *Galium*, *Poa*. Despite the geobotanical description of this synusia as mixed *Galium*

and *Dactylis*, there was no evidence of a great amount of *Dactylis* in the PolyG libraries, which can

be explained by difficulties in describing the gramineae vegetation outside the flowering phase.

Fig 1. Relative abundances of plant and bacterial communities in the experimental fields

The bacterial communities from the samples (Fig 1B) were typical for rhizosphere

microbiomes [11]. The communities from the two fallow sites (PolyC, PolyG) were similar,

whereas the communities from the rye site (MonoR) contained more *Gammaproteobacteria*

(*Proteobacteria*) and *Bacteroidia* (*Bacteroideta*). Differential abundance analysis allowed us to find

584 microbial taxa, which significantly differed between two sites, with information about

abundance in repeats. When comparing PolyC and PolyG, none of the OTUs was marked as

significantly different. The results of the pairwise comparison of PolyC and PolyG with MonoR are

shown in Fig 2 at the order level.

Fig 2. Mean abundances of bacterial orders with different inter-source abundances

(according to DeSEQ2)

In this comparison, the most abundant OTUs in rye crop rhizosphere microbiomes were from

Proteobacteria (orders *Pseudomonadales*, *Sphingomonadales*, *Enterobacteriales*), followed by

Armatimonadota (*Fimbriimonadales*), *Acidobacteriales* (*Bryobacterales*), and *Actinobacteriota*

(*Micrococcales*). In fallow root microbiomes, *Verrucomicrobia* (*Chthoniobacteriales*),

Acidobacteria (*Blastocatellales*), and *Actinobacteria* (*Pseudonocardiales*) were more abundant.

For all samples, the most common alpha-diversity indices, observed OTUs, Shannon, Simpson, mpd (mean pairwise distance), and p-dist (mean p-distance, restored from alignment, see Materials and Methods), were calculated at different taxonomic levels (Fig 3).

Fig 3. Alpha-diversity indices for plant and bacterial communities (significance for ANOVA in groups; ns – non-significant, * - $p < 0.05$, ** $p < 0.01$, * $p < 0.005$)**

The plant communities were highly diverse at different levels and indices (Fig 3A). The observed OTU index was not useful because of the presence of weedy plants in the rye crop. Weighted indices, such as mpd or p-dist, were more suitable; the differences between sample sites were significant for both indices up to the order level.

The bacterial communities were less diverse. The observed OTUs as well as the p-dist and mpd indices showed that communities from the PolyC site were more diverse, mostly at low taxonomical levels (OTUs, genus). Interestingly, samples from rye roots (MonoR) were significantly less diverse at phylum level, whereas at other taxonomical ranks, there were no such differences.

For each index on the OTU taxonomic level, the correlation between plant diversity indices and microbial diversity indices was calculated. We observed no significant correlations between plant and rhizosphere microbial diversity.

Fig 4 shows the beta-diversity indices (Bray distance and weighted UniFrac). According to the weighted UniFrac index (Dunn index for roots 0.316, for microorganisms 0.821), the samples were mixed (Fig 4A). Samples from rhizosphere communities from PolyC and PolyG were mixed in one cluster. While the MonoR and PolyC samples were close, the PolyG samples were different. This might be connected to the phylogenetic composition of the population; *Secale* and *Poa*, the two main genera from these sites, both belong to the *Poaceae* family, whereas *Galium* belongs to the Rubiaceae family (Fig 1A).

Fig 4. Beta-diversity indices for plant and bacterial communities

According to the Bray distance (Dunn index for roots 0.832, for microorganisms 0.909), all communities, from plants and from rhizospheres, formed their own clusters (Fig 3B).

The correlation between the distance matrix in plant and bacterial communities was high for the Bray distance ($R = 0.866$, $p = 0.01$) and not significant for the weighted UniFrac index. Fig 5 shows the results of the beta-distance correlation, excluding the intra-cluster distance (distance between repeats of the same sample).

Fig 5. Correlation between beta-diversity indices

Discussion

The aim of this work was to determine the potential connection between the diversity of plant communities and the diversity of rhizosphere microbiomes. For this purpose, we used three sites with different plant communities (synusiae) in the same location: a rye crop monoculture (MonoR) and two polyculture fallow sites, dominated by cereals (PolyC) and *Galium* and *Dactylis* (PolyG). Despite differences in crop species and tillage, soil type, water regime, and main soil properties were similar for all three sites, minimizing the influence of these factors on microbial communities.

The novel approach to estimate plant community composition (ITS1 sequencing) is highly effective. Almost all (217 of 230) determined ASVs were annotated, and the composition and abundance of plant genera fit the geobotanical description. In addition, this method allows 1) to characterize plant communities via their underground parts (which interact with rhizosphere microorganisms); 2) use the same sample for both plant and microbiome analysis (therefore, each rhizosphere library matches with the plant library); 3) use standard approaches for processing and calculating diversity indices and generating bar graphs.

For samples obtained from same soil and location, the most important factor shaping the microbial community of the rhizosphere is the plant community structure. We hypothesize that the

variation in the spectrum of exudates could be one of the possible mechanisms responsible for the diversity of the rhizosphere microbial community. This spectrum is specific for various plant species and genotypes, and therefore, in the case of the whole plant community, we can talk about an “exudome” of the community, whose structure depends on the abundance of plants in the community. This exudome can be described by the number of the individual plant spectra and by their weights (amount of exudate spectra of exact plant species in all exxudome), according plant abundances. In the comparison of two polycultures, the number of plant species is the same (as shown in Fig 3A), with variations in abundance; it therefore seems logical that the exudomes of these communities also will differ not in the number of different spectra but in their weights. In contrast, when comparing monoculture plants communities with polyculture ones, there are differences in the number of plant species. In this case, exudomes of plant communities will differ in the number of different spectra and in their weights.

In this study, using modern approaches, we found no correlation between different alpha-diversity indices. According to all indices, rhizosphere communities in the monoculture site (MonoR) were as diverse as those in the polycultures (PolyR, PolyC), whereas the plant community diversity in the monoculture was obviously lower. Regarding the polyculture (and mpd and p-dist indices), more diverse plant communities (PolyG) showed a less diverse rhizosphere microbial community. This might be evidence of a negative connection, as suggested by Goberna and coauthors [13], but this connection can be found only in plant communities with close exudomes (differing in abundance by not in the number of spectra). Significant differences in exudomes can lead to different microbial response and a loss of similarity, when environmental factors override the realistic relationship. Perhaps, this variation in exudome abundance allowed Schlatter and colleagues to show that in artificial plant communities, there is a decrease in bacterial diversity with increasing richness (1, 4, 8, 16 species) [31].

239 Despite the expected main difference in plant diversity between poly- and monocultures, with
 240 a moderate variation between polycultures, both alpha- and beta-diversity of the plants showed
 241 significant variations between synusiae. In the community of different cereals, PolyG in most cases
 242 is significantly more diverse by all alpha-diversity indices, and shows inter-sample variability
 243 (sample PolyG.3). This effect is also clear at higher taxonomic levels (family or order).

244 Differential abundance analysis did not show any difference between rhizosphere
 245 communities of polycultures. Similarly, OTUs and Shannon indices of these samples were also not
 246 significantly different. Only phylogenetic-related indices (mpd and p-dist) were significantly
 247 different, leading us to infer that the phylogenetic composition of communities varies in the
 248 rhizospheres of similar plant communities. However, further elaboration of this theory is
 249 recommended.

250 In contrary, when comparing the microbial communities of the polyculture sites with those of
 251 the monoculture, there was a significant difference in the observed OTUs, whereas phylogenetic-
 252 related indices (mpd, p-dist) showed no clear pattern. Differential abundance analysis enabled us to
 253 identify taxa with significant differences in relative diversity, most likely because of significant
 254 differences in exudome profiles and the loss of similarity between plant-microbial systems.

255 This idea also fits well with the beta diversity plots. Indeed, the distances between samples
 256 from polycultures were small for both plant and bacterial communities (about 17% of the explained
 257 variance in PcoA plots for plants and 8% for microorganisms). The distances between samples from
 258 mono- and polycultures were large (about 60% of the explained variance in PcoA plots). This
 259 allowed us to estimate a correlation for Bray distances only (due to the taxonomic similarity
 260 between rye and cereal, the correlations between weighted Unifac distances were not significant).
 261 This correlation might be a true correlation, as observed in previous studies [17], or a statistical
 262 artifact (caused by the large distance between monoculture and polyculture clusters).

263 The significant distance in beta-diversity is connected to the differences in the abundances of
 264 the different taxa. Hypothesized as a molding matrix, differences in abundances between plant
 265 communities are not useful, whereas abundances of microbial taxa represent the specificity of
 266 rhizosphere taxa in different plant communities (at the order level, as shown in Fig 2). Some of
 267 them have previously been reported as rhizosphere taxa. *Sphingomonadales* and *Enterobacteriales*
 268 are typical for plant rhizosphere communities [32], and *Fimbriimonadales* has previously been
 269 described as a bacterial taxon from the *Anthurium andraeanum* rhizosphere community [33]. In the
 270 same case, *Blastocatellales* has previously been described as an oligotrophic, slightly acidophilic to
 271 neutrophilic mesophile from arid soils [34]. However, these data are controversial, as they can
 272 describe a novel location of this microorganism or a biased database. More precise data can be
 273 obtained by functional or full-genomic analyses of rhizosphere communities.

274 Despite the absence of a clear correlation between plant and bacterial diversity, comparing the
 275 results with the previously mentioned concept of evolutionary molding, where the plant population
 276 "molds" in the microbial population and where the correlation between plant and microbial
 277 diversities is clear, is challenging. The reasons are as follows: 1) the symbiotic system itself is
 278 tighter than the rhizosphere community interaction; 2) in this work, we used regular taxonomic
 279 marker genes, not specific plant or bacterial genes. A closer interaction could be revealed with the
 280 use of genes directly involved in plant-rhizosphere communication processes. This could be plant
 281 genes involved in plant root exudation and responses to bacterial signals (for example,
 282 strigolactone-processing genes) and bacterial genes involved in the decomposition of those exudates
 283 by microorganisms. Also, it is important to characterize the structure and composition of common
 284 exudation profiles of different plant communities.

285

286 **Conclusions**

287 1. Sequencing of the ITS1 region is highly effective for the taxonomical annotation of plant
288 communities. Almost all ASVs were attributed; abundances of taxa fairly corresponded to the
289 geobotanical descriptions.

290 2. There was no correlation between alpha-diversity indices of plants and rhizosphere
291 communities. Alpha-diversity connection should be explored in similar plant communities, such as
292 synusia. Significant differences in plant abundances lead to significant changes in exudation
293 profiles, different microbial responses, and the loss of diversity connection.

294 3. In contrast, the beta-diversity between rhizosphere communities and plant communities is
295 highly correlated, in particular in terms of the abundance of taxa. This can be explained by a
296 potential correlation (as reported in the literature) or by the presence of statistical artifacts.

297 4. In future studies, the diversity connection should be analyzed by searching for functionally
298 related genetic regions of plants and soil microorganisms.

299

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421 **Supporting information**

422

423 **S1 Fig. General view, current location and root samples.** MonoR — rye crop field; PolyC -
 424 forb and cereal meadow dominated by cereals ; PolyG - forb and cereal meadow dominated by
 425 *Galium* and *Dactylis* species. Samples are: 1 — MonoR.1; 2 — MonoR.2; 3 — MonoR.3; 4 —
 426 PolyG.1; 5 — PolyG.2; 6 — PolyG.3; 7 — PolyC.1; 8 — PolyC.2; 9 — PolyC.3;

427 **S1 Table. Geobotanical description of the sampling sites.**

Fig 2

A. Plant diversity

B. Bacterial diversity

Fig 3

A. Weighted UniFrac

B. Bray distance

Fig 4

A. Plant diversity

B. Bacterial diversity

Fig 1