

Microbiome manipulation of potato with biostimulator *Rhodococcus qingshengii* VKM Ac-2784D

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Motivation and Aim: Plants' microbiome helps them to adapt to the environment conditions and keep the organism healthy. Microbiome consists of vast range of microorganisms, which form the trophic chain, keeping stable when environment conditions change. Microbiome changing can infer into trophic chains and impact negatively to the health of the plant host. Bacteria of genus *Rhodococcus* are typical rhizosphere inhabitants. Like other actinomycetes they synthesize a broad range of bioactive compounds: biosurfactants, phytohormones, siderophores, antibiotics. In our previous studies we isolated the strain *Rhodococcus qingshengii* VKM Ac-2784D, which can digest the alkanes and surface-active substances [1, 2] and it has lactonase activity, which infers the quorum sensing (also called quorum quenching) [3]. We suggest that the strain can be used as the fertilizer agent, it will impact on the rhizosphere and endosphere microbiome. The complete genome of *Rhodococcus qingshengii* VKM Ac-2784D is available NCBI GenBank [4]. Genome analysis with antiSMASH revealed a number of biosynthetic gene clusters of siderophores and some antibiotics: monensin, rifamorpholine, thiolutin, acyldepsipeptide 1, tetronasin, hygromycin A, kirromycin, diisonitrile antibiotic SF2768. To evaluate the diversity shift of rhizosphere and endosphere communities we performed the amplicon sequencing study.

Methods and Algorithms: We used the “Lugovskoy” variety in this study as it common for the region. Tubers were treated for 24 h by bacterial suspension of *Rhodococcus qingshengii* VKM Ac-2784D. The secondary treatment was performed on plant flowering period (21 July 2023). Sample collection was performed at three stages: seedling, plant flowering and potato harvesting. DNA was isolated from rhizosphere soil, leaves and tubers samples (38 samples in total). PCR product was further sequenced on BGISEQ platform at shared access center “Genomica” (Novosibirsk). Taxonomic profiling was performed using USEARCH/SINTAX algorithm (RDP 16S database).

Results: After treatment the mean number of tubers per plant increased by 70 % and total yield increased by 55 %, however the mean size (44 × 30 mm) and mass (33–36 g) of tubers stayed almost the same. Microbiome analysis showed that representatives of phylum Proteobacteria, Acidobacteria, Bacteroidetes, Actinobacteria and Firmicutes predominated in the soil samples. Preliminary data indicate that treatment with *Rhodococcus* cell suspension led to a decrease in the

abundance of Proteobacteria and Bacteroidetes. In contrast, the content of Acidobacteria, Firmicutes, and Verrucomicrobia increased (Fig. 1). These results have common features with other inoculation practices, that are described in the literature [5], but other factors – soil type, irrigation regime, pathogens influence has to be evaluated.

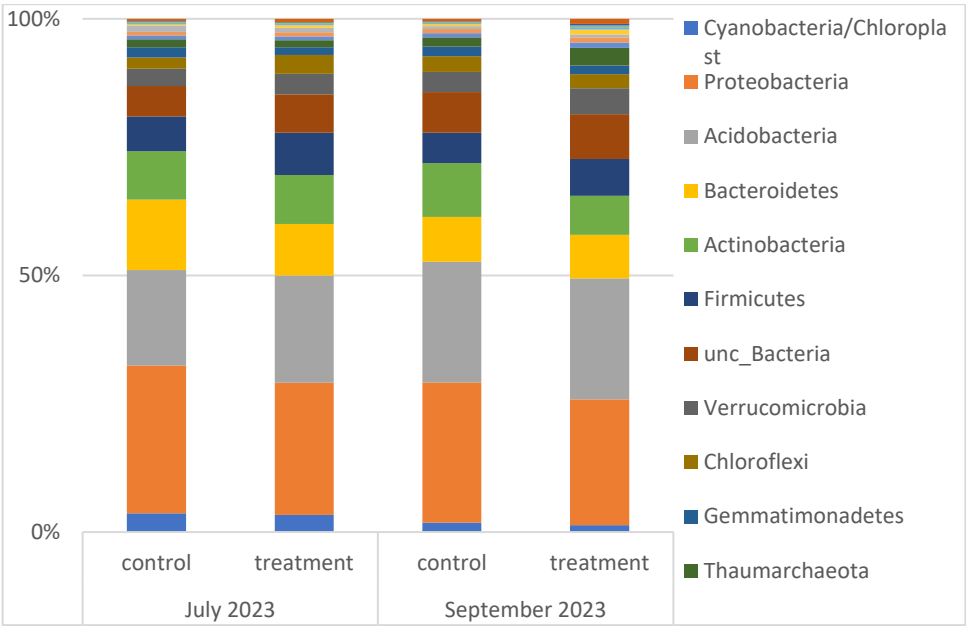


Fig. 1. Potato rhizosphere microbiome taxonomic structure for control and treatment samples; sampling was performed two times: at plant flowering and harvesting

Conclusion: As a result of our study, we got the knowledge of influence of *Rhodococcus qingshengii* VKM Ac-2784D after using it as the fertilizer agent. The samples from potato rhizosphere and endosphere could be used as the source of microorganisms’ communities to form the collections for further study.

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