

BACTERIAL COMMUNITIES IN ACIDIC SOIL

Jelena Jovičić-Petrović^a, Mira Milinković^b, Vera Karličić^a, Blažo Lalević^a, Igor Kljujev^a, Vera Raičević^a

^aUniversity of Belgrade, Faculty of Agriculture, Nemanjina 6, 11080 Belgrade, Serbia

^bFruit Research Institute, Kralja Petra I 9, 32000, Čačak, Serbia

INTRODUCTION

Acidification is one of the main types of soil degradation in Serbia, where acidic soils make more than 60%. Besides the effects on plant nutrition and productivity, soil acidity leads to changes in biodiversity. Bacterial diversity in soil is recognized as the main pillar of soil quality, ecosystem stability, climate change resilience, nutrient cycling, and important element of sustainable crop production. The diversity and abundance of soil bacteria are strongly related to various abiotic factors, particularly to soil pH is considered one of the major determinants and predictors of their community structure.

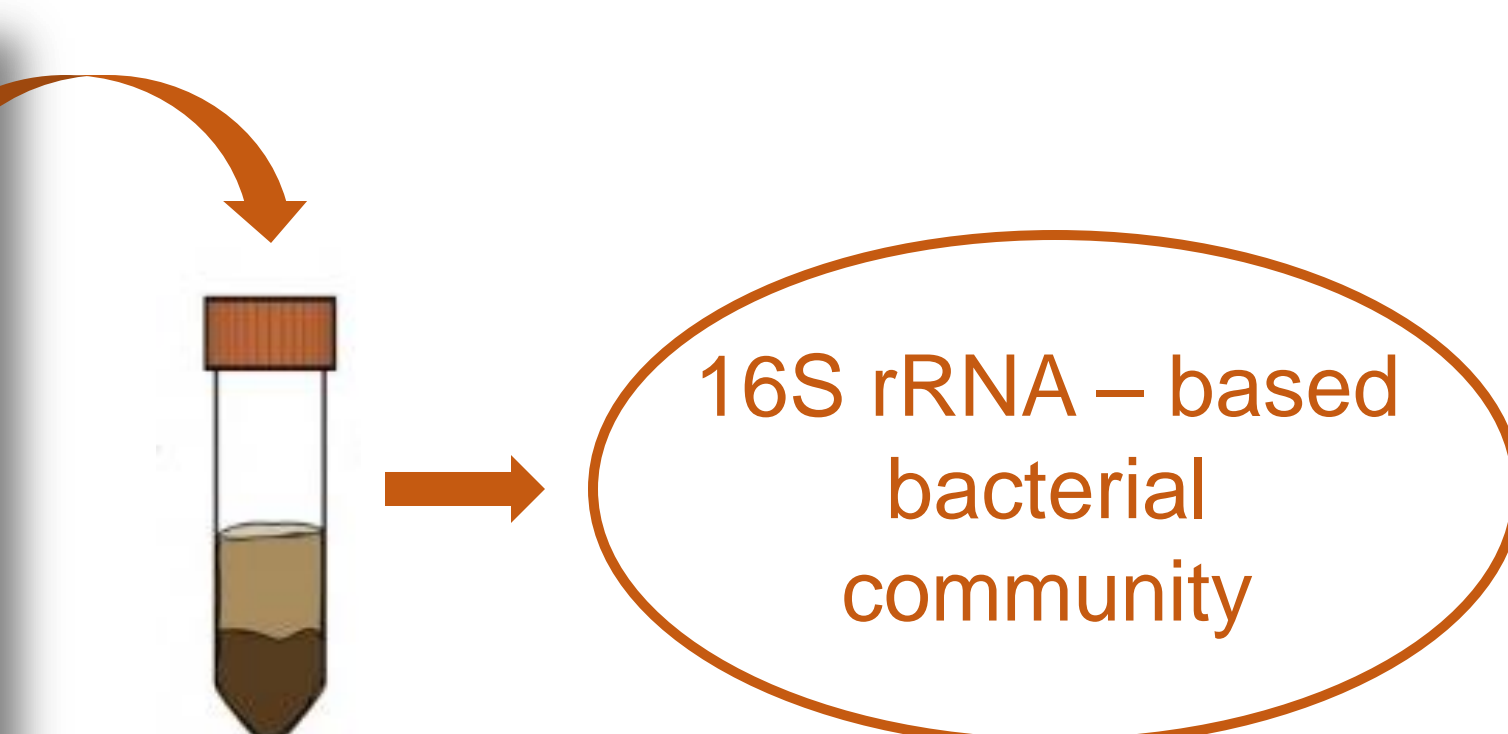
AIM

The main objective of the presented research is to access bacterial community in agricultural acid soil using a metagenomic approach and to relate those results with physico-chemical soil properties.

MATERIAL AND METHODS

16S rRNA gene targeted sequencing was used to determine bacterial community. Soil samples are analyzed by the ZymoBIOMICS® Targeted Sequencing Service for Microbiome Analysis (Zymo Research, Irvine, CA).

Examination of the mechanical composition, physical-chemical parameters, and basic soil fertility was performed using standard procedures.



RESULTS AND DISCUSSION

The obtained microbiome results showed that soil from cornfield (Zaječar) have significantly lower bacterial diversity compared to two soils collected in the Čačak region, which are similar to each other to some level (Figure 1). In all of the studied soils, the most abundant phyla were *Firmicutes*, *Proteobacteria*, and *Actinobacteria* (each above 20%, Fig. 1). Results show that soil mechanical composition significantly affects bacterial diversity, making it scarcer in heavy clay compared to clay loam.

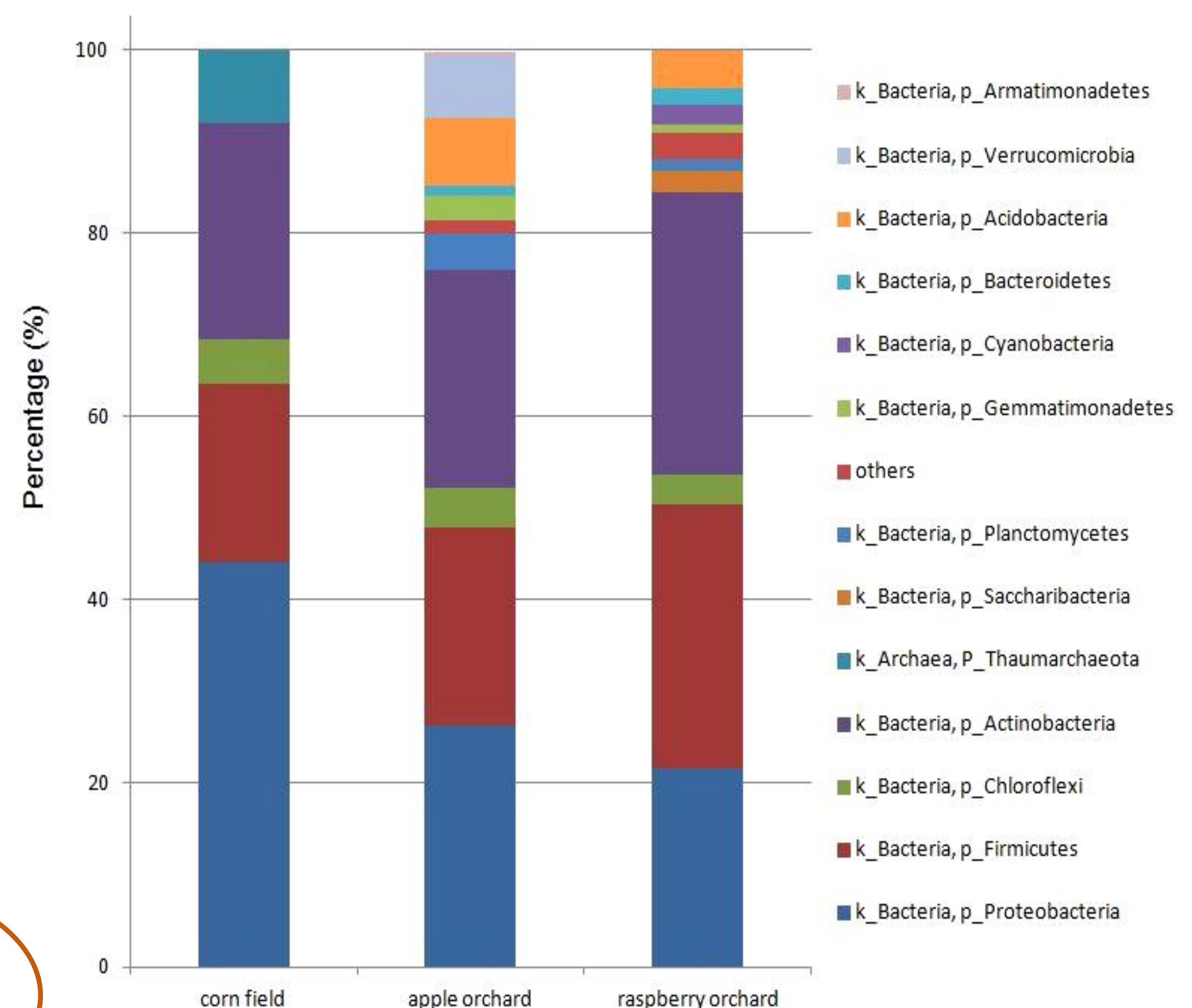


Figure 1. Microbial community composition at phylum level, based on 16S RNA sequences (relative abundance)

Table 1. Hydrolytic and adsorptive complex, basic soil fertility and classification according to the mechanical composition

Samples	H	S	CEC-S	CEC	V (%)	pH/H ₂ O	pH/KCl	CaCO ₃ (%)	Humus (%)	Total N (%)	P ₂ O ₅ mg · 100g ⁻¹	K ₂ O mg · 100g ⁻¹	Classification
	meq · 100g ⁻¹												
Apple orchard	14.95	12.76	9.72	22.48	56.76	5.29	4.21	0.56	2.86	0.14	6.41	37.50	Clay loam
Raspberry orchard	31.25	7.22	20.31	27.53	26.23	4.61	3.84	0.28	4.63	0.23	15.98	35.60	Clay loam
Cornfield	17.00	28.98	11.05	40.03	72.40	5.86	4.90	0.56	4.21	0.21	11.21	37.90	Heavy clay

CONCLUSION

Analyzed acidic soils showed differences in the composition of bacterial communities. Based on physico-chemical analysis, soil from cornfield showed high potential fertility, but significantly high content of the colloid clay affects chemical and microbiological properties, including bacterial community composition. The results indicate that other environmental factors besides pH acting on different geographical locations have additional effects on bacterial diversity in soil.

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* Corresponding author: Jelena Jovičić-Petrović, jelenap@agrif.bg.ac.rs