Theme 1
Status and trends of global soil nutrient budget

Microbial source shapes the community of endophytic bacteria in rice roots

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Introduction

Plants interact with their immediate environment, thus cohabiting with the diverse soil microbiome.

The soil is regarded as the major environmental ***source*** of ***endophytic bacteria*** – a subgroup of soil bacteria that colonize the internal tissues of plants and form endosymbiotic relationships.

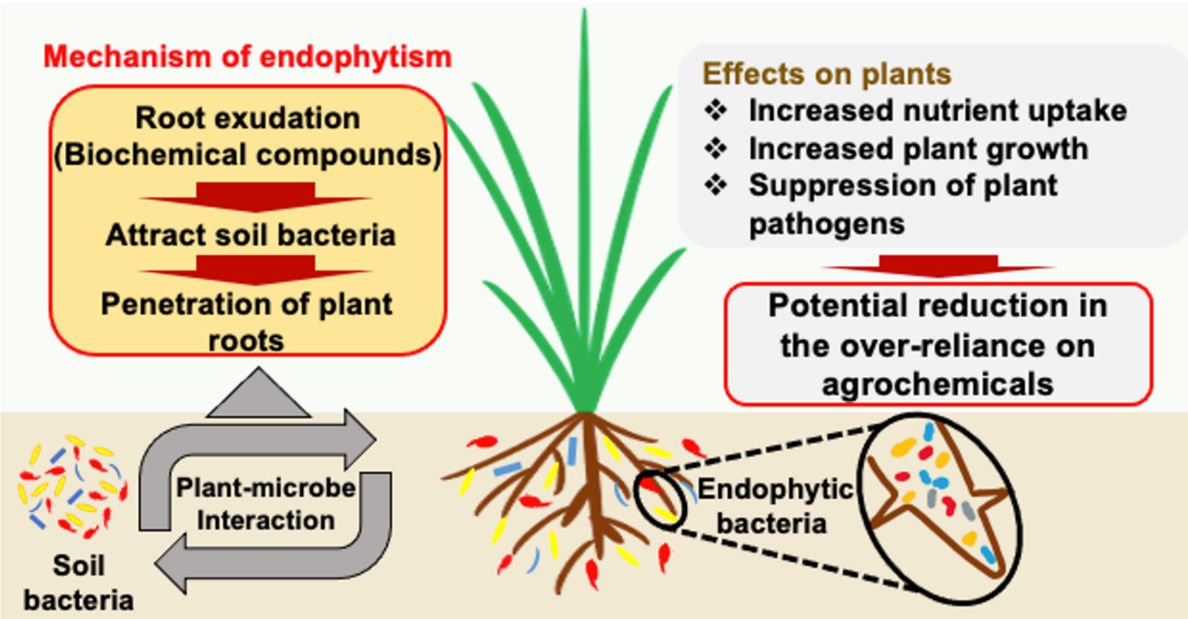

Fig. 1: Illustration of the interaction between a rice plant and the underground community of microorganisms

❖ However, little is known about the effect of the microbial source as an individual factor on endophytic assemblage

Hypothesis: Distinct endophytic bacterial communities will be assembled from different microbial sources

Methodology

Transplantation of 21-day-old sterile rice seedlings into different experimental set-ups, inoculated with 5 different soil types obtained from across Japan and pre-incubated (*n*=3).

❖ The different soil types were named as microbial *Source_A to E*

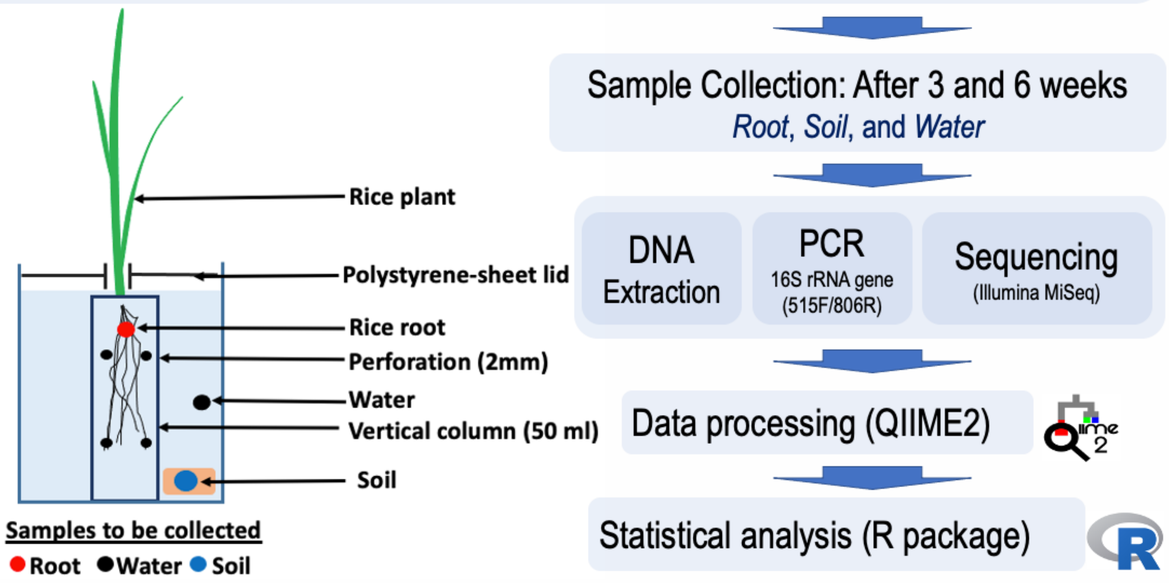

Fig. 2: Experimental set-up

Table1: Characteristics of the five soil types used in this study as the different microbial sources A to E

M. Source	Prefecture	Land Use	Classification	K^+	Ca^{2+}	Mg^{2+}	Na^+	pH
				(mg/100gds)				
Source_A	Aichi	Paddy	Gray upland	5.92	105.26	48.73	6.49	5.17
Source_B	Nagano	Paddy	Andosol	8.88	82.06	12.83	5.10	5.66
Source_C	NU, Niigata	Forest	Sand dune	13.50	39.30	16.50	3.62	5.87
Source_D	Shibata, Niigata	Paddy	Gray lowland	19.05	64.34	17.76	5.57	5.44
Source_E	Shindori, Niigata	Paddy	Gley lowland	21.40	84.40	37.70	9.28	5.05

NU: Niigata University; M. Source: Microbial source

Results

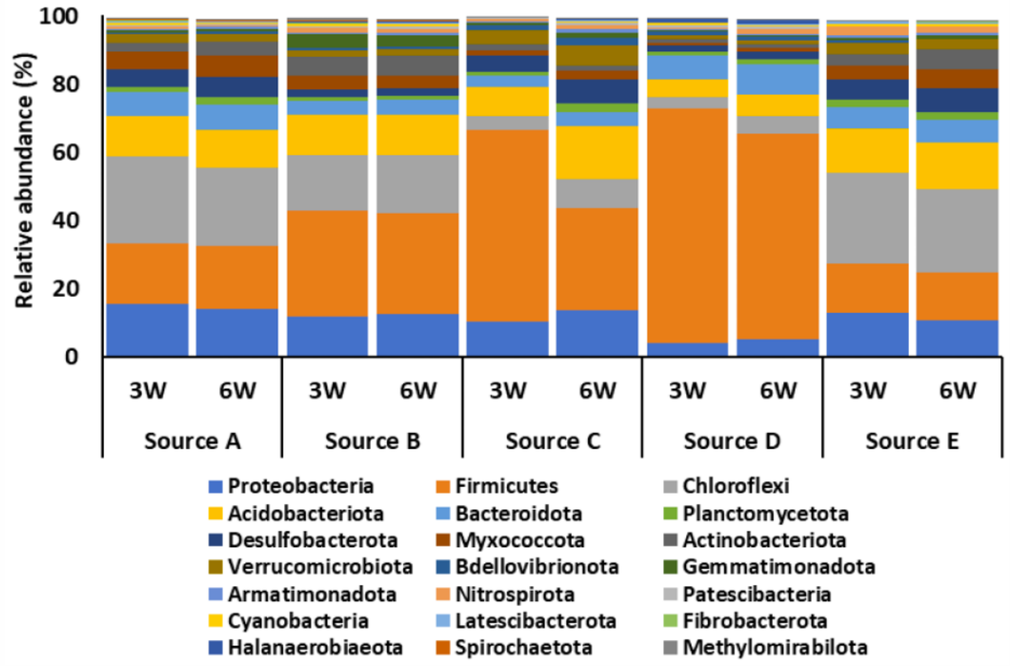

Fig. 3: Relative abundance of endophytic bacteria at phylum level

Table 2: Summary of the diversity and richness of bacterial endophytes after 3 and 6 weeks, respectively

		Microbial source	Time	Microbial source X Time
α - diversity	Shannon	$F_{(4, 20)} = 42.34$***	$F_{(1, 20)} = 17.04$***	$F_{(4, 20)} = 12.26$***
	Faith	$F_{(4, 20)} = 59.61$***	$F_{(1, 20)} = 31.61$***	$F_{(4, 20)} = 24.81$***
	Evenness	$F_{(4, 20)} = 22.76$***	$F_{(1, 20)} = 16.41$***	$F_{(4, 20)} = 12.84$***
β - diversity	Weighted UniFrac	$F_{(4, 20)} = 12.75$***	$F_{(1, 20)} = 24.13$***	$F_{(4, 20)} = 9.85$***

Significance level: *p<0.05, **p<0.01, ***p<0.001

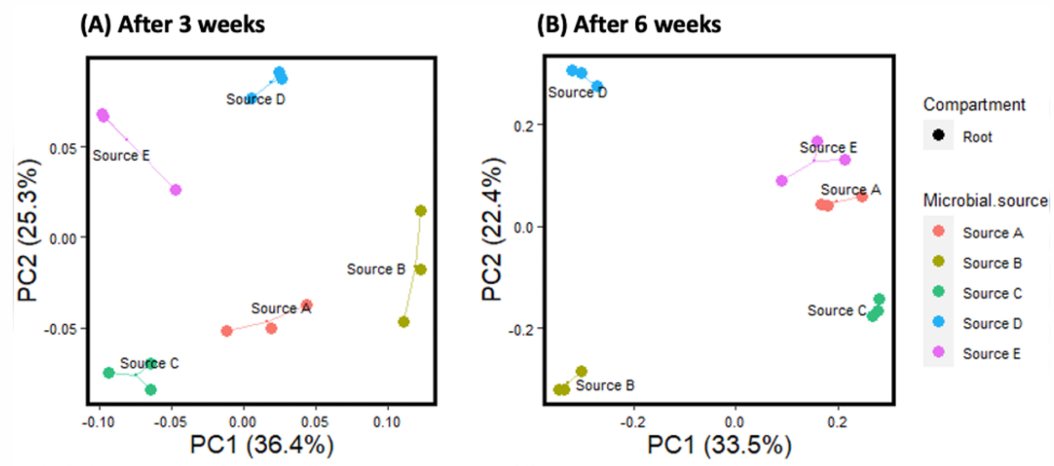

Fig. 4: Beta diversity - Principal Coordinate Analysis(PCoA) based on weighted UniFrac distances

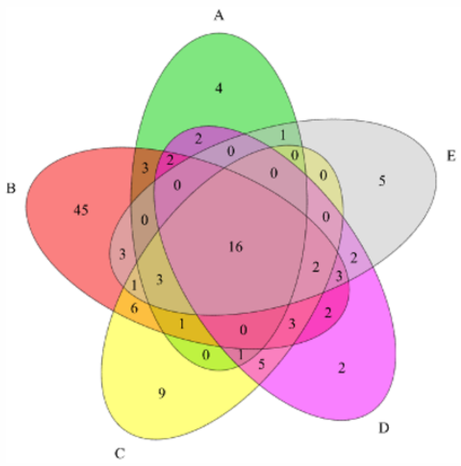

Table 3: Summary of shared and unique endophytic bacterial taxa (genus)

	Total	Unique	Shared	Unique
			Relative abundance (%)	
Source_A	57	4	79.24	1.72
Source_B	128	45	47.00	27.68
Source_C	73	9	78.18	4.70
Source_D	64	2	73.12	0.62
Source_E	70	5	76.99	2.94

Fig. 5: Venn diagram of shared and unique bacterial taxa – genus level

Conclusion

Overall, the findings of this study show sufficiently that the microbial source is a key determinant factor of the formation of endophytic bacterial communities, thereby confirming our hypothesis.

References

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