Table S1. Plant nutrient contents, N:P, and plant P utilization efficiency index (PPEI).

Plant species	Abbreviation	Plant nutrient contents (mg/g)					N:P	PPEI
		C	N	P	K	Ca		
Nandina domestica Thunb.	ND	454.0 ± 13.0	37.0 ± 0.5	2.8 ± 0.1	4.1 ± 0.6	5.9 ± 0.5	13.21 ± 0.4	0.075 ± 0.005
Mahonia bodinieri Gagnep.	MB	391.6 ± 16.6	12.6 ± 0.6	0.8 ± 0.1	3.8 ± 0.8	6.4 ± 0.2	15.75 ± 0.73	0.078 ± 0.003
Pyracantha fortuneana (Maxim.) Li	PF	410.2 ± 17.5	13.5 ± 0.8	0.8 ± 0.1	2.4 ± 0.5	17.4 ± 0.6	16.88 ± 0.73	0.073 ± 0.003
Rhus chinensis Mill.	RC	485.4 ± 15.0	15.7 ± 0.8	0.8 ± 0.1	4.0 ± 1.2	15.8 ± 0.7	17.44 ± 0.60	0.057 ± 0.002
Zanthoxylum armatum DC.	ZA	467.0 ± 18.7	26.7 ± 1.4	1.4 ± 0.1	5.2 ± 0.4	12.8 ± 0.8	17.80 ± 0.81	0.056 ± 0.006
Loropetalum chinense (R. Br.) Oliver	LC	471.8 ± 14.8	13.9 ± 0.4	0.7 ± 0.1	2.6 ± 0.6	14.7 ± 0.3	19.86 ± 0.21	0.050 ± 0.005
Diospyros dumetorum W. W. Sm.	DD	463.6 ± 13.9	12.3 ± 0.5	0.6 ± 0.1	5.7 ± 0.6	11.0 ± 0.4	20.50 ± 1.41	0.049 ± 0.004
Lindera communis Hemsl.	LC	565.3 ± 24.5	15.5 ± 0.5	0.8 ± 0.01	2.6 ± 0.3	8.5 ± 0.5	19.38 ± 0.73	0.052 ± 0.003
Liquidambar formosana Hance	LF	460.6 ± 23.7	23.2 ± 1.2	1.1 ± 0.1	3.4 ± 0.7	12.1 ± 0.3	21.09 ± 1.92	0.047 ± 0.005
Viburnum brachybotryum Hemsl.	VB	498.6 ± 17.0	15.9 ± 0.8	0.7 ± 0.2	5.1 ± 0.6	14.8 ± 1.0	22.71 ± 0.4	0.044 ± 0.006
Cinnamomum glanduliferum (Wall.) Nees	CG	443.3 ± 18.2	16.7 ± 0.8	0.8 ± 0.1	3.0 ± 0.1	11.3 ± 1.2	20.88 ± 0.28	0.048 ± 0.003
Phoebe crassipedicella S. K. Lee & F. N. Wei	PC	453.7 ± 16.1	15.2 ± 0.4	0.7 ± 0.2	3.1 ± 0.1	9.0 ± 1.0	21.71 ± 1.25	0.046 ± 0.003
Hydrangea aspera D. Don	HA	478.5 ± 16.4	19.3 ± 0.6	0.8 ± 0.1	2.9 ± 0.2	11.3 ± 0.9	24.12 ± 0.24	0.041 ± 0.011
Euonymus japonicus Thunb.	EJ	406.3 ± 13.9	13.0 ± 0.2	0.5 ± 0.02	2.7 ± 0.04	7.7 ± 0.6	26.00 ± 0.40	0.038 ± 0.005
Camellia ilicifolia Y. K. Li ex Huang T. Chang	CI	468.2 ± 24.8	12.1 ± 0.5	0.5 ± 0.1	2.7 ± 0.1	21.6 ± 1.8	24.20 ± 0.7	0.041 ± 0.005
Pteroceltis tatarinowii Maxim.	PT	448.4 ± 12.5	17.9 ± 1.0	0.7 ± 0.1	3.5 ± 0.2	21.3 ± 2.8	25.57 ± 0.86	0.039 ± 0.003
Gardenia jasminoides J. Ellis	GJ	428.7 ± 14.0	20.3 ± 1.0	0.8 ± 0.04	5.3 ± 0.3	11.2 ± 1.3	25.38 ± 0.96	0.039 ± 0.002
Tirpitzia sinensis (Hemsl.) Hallier f.	TS	476.9 ± 19.5	27.4 ± 0.9	1.0 ± 0.04	3.4 ± 0.3	19.0 ± 1.1	27.40 ± 1.5	0.037 ± 0.004
Albizia kalkora (Roxb.) Prain	AK	507.5 ± 23.9	37.2 ± 0.8	1.2 ± 0.1	2.6 ± 0.1	8.8 ± 1.3	31.00 ± 1.91	0.032 ± 0.004
Morella rubra Lour.	MR	511.5 ± 15.0	16.1 ± 0.8	0.4 ± 0.04	2.4 ± 0.1	9.5 ± 1.2	40.25 ± 3.27	0.025 ± 0.004
Average		464.6 ± 41.8	19.1 ± 7.5	0.9 ± 0.5	3.5 ± 1.1	12.5 ± 4.7	22.73 ± 5.98	0.047 ± 0.012

*Data are expressed as means ± SD by one-way ANOVA.

Table S2. Rhizosphere soil properties of the 20 investigated plants.

Plant species	Abbreviation	pH	Total nutrients (%)			Available nutrients (mg/kg)			
			TN	TP	TCa	SOC	AN	AP	ACa
Nandina domestica Thunb.	ND	6.03	0.66	1.42	0.78	62.8	360.7	13.9	30.41
Mahonia bodinieri Gagnep.	MB	5.68	0.43	1.53	0.40	43.4	257.6	6.0	17.05
Pyracantha fortuneana (Maxim.) Li	PF	5.53	0.36	1.27	0.35	39.3	240.8	6.6	15.57
Rhus chinensis Mill.	RC	6.09	0.33	1.56	0.40	34.3	193.2	17.6	18.96
Zanthoxylum armatum DC.	ZA	6.02	0.46	1.91	0.51	44.4	270.2	5.8	22.02
Loropetalum chinense (R. Br.) Oliver	LC	5.83	0.34	1.20	0.35	31.4	223.3	4.5	15.94
Diospyros dumetorum W. W. Sm.	DD	5.91	0.31	1.63	0.35	29.7	180.6	5.1	15.10
Lindera communis Hemsl.	LC	5.95	0.38	1.47	0.30	40.6	217.9	6.8	15.19
Liquidambar formosana Hance	LF	5.72	0.42	2.75	0.44	41.4	260.4	6.1	19.49
Viburnum brachybotryum Hemsl.	VB	6.30	0.42	1.41	0.59	40.3	212.8	11.2	26.51
Cinnamomum glanduliferum (Wall.) Nees	CG	6.12	0.56	1.41	0.79	56.2	330.9	17.2	32.50
Phoebe crassipedicella S. K. Lee & F. N. Wei	PC	6.01	0.74	1.52	0.89	70.7	391.1	9.1	34.38
Hydrangea aspera D. Don	HA	6.11	0.47	3.41	0.65	44.9	262.3	5.2	26.39
Euonymus japonicus Thunb.	EJ	5.78	0.28	0.95	0.24	25.2	163.8	5.1	10.33
Camellia ilicifolia Y. K. Li ex Huang T. Chang	CI	6.19	0.55	1.45	0.62	50.8	304.7	6.1	24.32
Pteroceltis tatarinowii Maxim.	PT	6.03	0.51	2.13	0.62	51.2	293.1	6.5	26.41
Gardenia jasminoides J. Ellis	GJ	5.68	0.28	1.22	0.38	25.9	162.9	23.6	15.55
Tirpitzia sinensis (Hemsl.) Hallier f.	TS	6.13	0.94	2.05	1.25	93.3	478.3	14.2	45.86
Albizia kalkora (Roxb.) Prain	AK	5.85	0.26	1.48	0.38	21.4	122.3	3.7	16.02
Morella rubra Lour.	MR	6.29	0.58	1.59	0.87	59.4	295.9	8.0	37.42
Average		5.96	0.46	1.67	0.56	45.3	261.1	9.12	23.27

Table S3. The average relative abundance (%) of genes involved in the four P cycling groups for plants with high and low PPEI.

P cycling groups	PPEI		Independent *T*-test
	High	Low	
Inorganic P solubilization	3.77 ± 0.36	3.42 ± 0.30	*
Organic P mineralization	6.88 ± 0.73	5.97 ± 0.40	**
P uptake and transport system	3.14 ± 0.26	2.71 ± 0.24	**
P starvation response regulation	1.01 ± 0.17	0.86 ± 0.10	*

[*]PPEI, plant P utilization efficiency index; Data are expressed as means ± SD ($n = 9$) by one-way ANOVA; [*] and [**] indicate significant differences at $p < 0.05$ and $p < 0.01$ between the two groups of plants based on an independent *T*-test.

Table S4. The average relative abundance (%) of genes involved in the six organic P mineralization groups for plants with high and low PPEI.

Organic P mineralization groups	PPEI		Independent *T*-test
	High	Low	
Phosphomonoesterase	2.69 ± 0.27	2.32 ± 0.14	**
Phosphodiesterase	2.71 ± 0.45	2.36 ± 0.30	*ns*
Organic pyrophosphatase	0.72 ± 0.09	0.61 ± 0.04	**
C-P lyase	0.46 ± 0.12	0.41 ± 0.07	*ns*
Phosphonatase	0.20 ± 0.05	0.18 ± 0.03	*ns*
Phosphotriesterase	0.10 ± 0.02	0.10 ± 0.01	*ns*

[*]PPEI, plant P utilization efficiency index; Data are expressed as means ± SD ($n = 9$) by one-way ANOVA; [*] and [**] indicate significant differences at $p < 0.05$ and $p < 0.01$ between the two groups of plants based on an independent *T*-test.

Table S5. The average relative abundance (%) of genes involved in the four P uptake and transport system groups for plants with high and low PPEI.

P uptake and transport system	PPEI		Independent T-test
	High	Low	
Phosphate transport system	1.92 ± 0.23	1.64 ± 0.12	**
Phosphonate transport system	0.76 ± 0.21	0.68 ± 0.11	ns
GP phosphate transport system	0.44 ± 0.06	0.37 ± 0.05	*
IP phosphate transport system	0.01 ± 0.002	0.01 ± 0.004	ns

[*]PPEI, plant P utilization efficiency index; Data are expressed as means $\pm$ SD ($n = 9$) by one-way ANOVA; [*] and [**] indicate significant differences at $p < 0.05$ and $p < 0.01$ between the two groups of plants based on an independent T-test.

Table S6. The average relative abundance (%) of genes involved in the four P uptake and transport system groups for plants with high and low PPEI.

Phosphate transport system	PPEI		Independent T-test
	High	Low	
High-affinity phosphate-specific transporters ($pstS + pstA + pstB + pstC$)	0.017 ± 0.002	0.015 ± 0.001	**
Low-affinity phosphate-specific transporters (pit)	0.0018 ± 0.0006	0.0016 ± 0.0006	ns

[*]PPEI, plant P utilization efficiency index; Data are expressed as means $\pm$ SD ($n = 9$) by one-way ANOVA; [*] and [**] indicate significant differences at $p < 0.05$ and $p < 0.01$ between the two groups of plants based on an independent T-test.

Table S7. The relative abundance (%) of top 10 predominant microbial species involved in P cycling.

Microbial species	Microbial phyla	ND	MB	PF	TS	AK	MR
Actinobacteria_bacterium	Actinobacteria	0.108 ± 0.109a	0.053 ± 0.001a	0.029 ± 0.006a	0.060 ± 0.011a	0.050 ± 0.027a	0.033 ± 0.006a
Alphaproteobacteria_bacterium	Proteobacteria	0.045 ± 0.029a	0.071 ± 0.038a	0.058± 0.022a	0.034 ± 0.008a	0.066 ± 0.024a	0.059 ± 0.036a
Candidatus_Rokubacteria_bacterium	Candidatus_Rokubacteria	0.060 ± 0.031a	0.061 ± 0.020a	0.057 ± 0.009a	0.046 ± 0.008a	0.061 ± 0.014a	0.049 ± 0.015a
Deltaproteobacteria_bacterium	Proteobacteria	0.061 ± 0.024a	0.054 ± 0.028a	0.048 ± 0.009a	0.046 ± 0.012a	0.072 ± 0.014a	0.052 ± 0.007a
Acidobacteria_bacterium	Acidobacteria	0.048 ± 0.006a	0.060 ± 0.027a	0.070 ± 0.034a	0.032 ± 0.006a	0.072 ± 0.025a	0.051 ± 0.021a
Betaproteobacteria_bacterium	Proteobacteria	0.036 ± 0.016c	0.053 ± 0.015ab	0.087 ± 0.026a	0.034 ± 0.007c	0.079 ± 0.029ab	0.044 ± 0.013bc
Rhizobiales_bacterium	Proteobacteria	0.080 ± 0.054a	0.067 ± 0.032a	0.045 ± 0.009a	0.056 ± 0.016a	0.034 ± 0.006a	0.051 ± 0.013a
Verrucomicrobia_bacterium	Verrucomicrobia	0.042 ± 0.028a	0.063 ± 0.037a	0.064 ± 0.027a	0.032 ± 0.006a	0.076 ± 0.020a	0.055 ± 0.036a
Alphaproteobacteria_bacterium_13_2_20CM_2_64_7	Proteobacteria	0.050 ± 0.031a	0.076 ± 0.042a	0.056 ± 0.016a	0.032 ± 0.008a	0.064 ± 0.018a	0.055 ± 0.028a
Bradyrhizobium_erythrophlei	Proteobacteria	0.056 ± 0.035a	0.065 ± 0.032a	0.052 ± 0.017a	0.044 ± 0.007a	0.055 ± 0.011a	0.061 ± 0.025a

*In each line, means ± SD followed by different small letters indicate a significant difference ($p < 0.05$) between the six studied plants based on a one-way ANOVA followed by an LSD test.
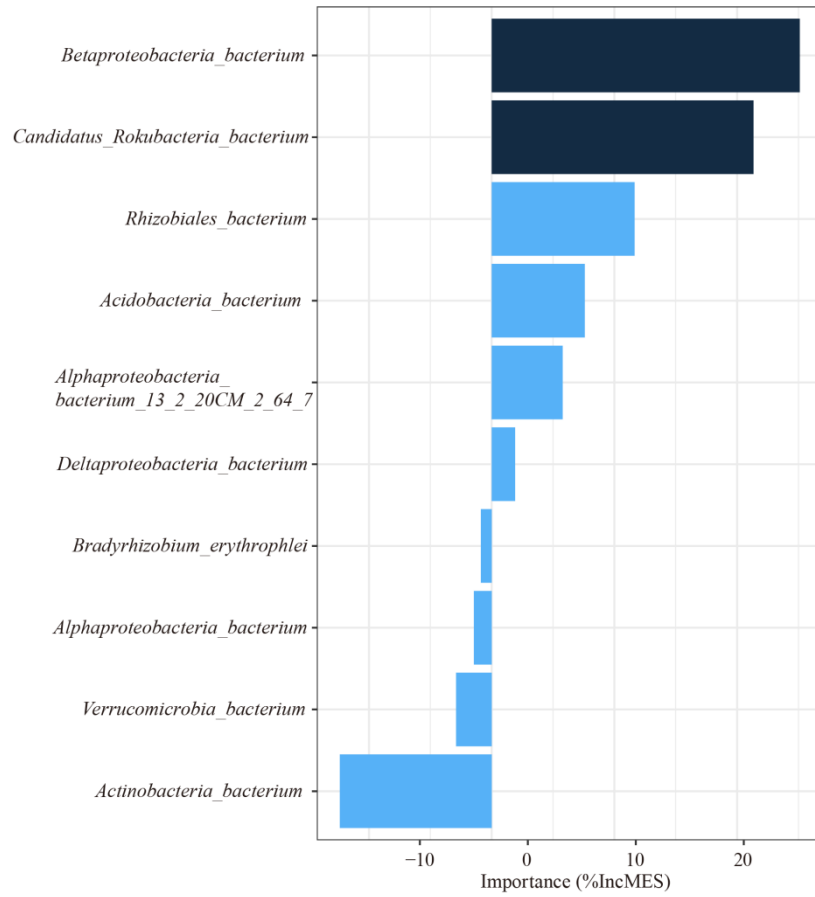
Figure S1. Relative importance of the relative abundance of the top 10 microbial species to the PPEI. The dark blue color

indicates a significant effect ($p < 0.05$) and the light blue indicates not significant. The higher the %IncMSE value, the more

important the variable. PPEI, plant P utilization efficiency index.