

Supplementary Information:

# Moderate Phosphorus Addition to Field-Grown Bananas Enhanced Soil Microbial Enzyme Activities but Had Negligible Impacts on Bacterial, Fungal, and Nematode Diversity

Anna-Belle C. Clarke <sup>1</sup>, Hazel R. Lapis-Gaza <sup>2</sup>, Stuart Irvine-Brown <sup>3</sup>, Rebecca Lyons <sup>1</sup>, Jiarui Sun <sup>1</sup>, Anthony B. Pattison <sup>1,2</sup> and Paul G. Dennis <sup>1,\*</sup>

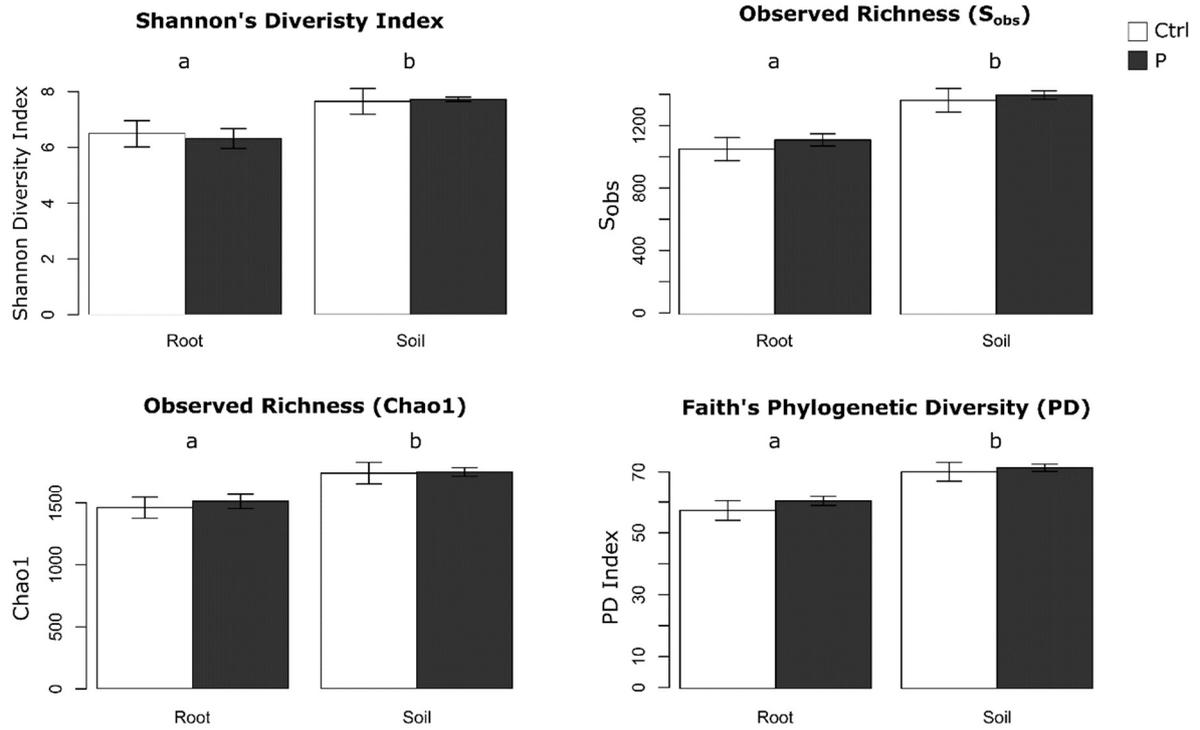
- <sup>1</sup> School of Environment, The University of Queensland, Turrbal Country, Brisbane, QLD 4072, Australia; tony.pattison@daff.qld.gov.au (A.B.P.)
- <sup>2</sup> Department of Agriculture and Fisheries, Centre for Wet Tropics Agriculture, 24 Experimental Station Road, South Johnstone, QLD 4859, Australia; hazel.gaza@daf.qld.gov.au
- <sup>3</sup> Department of Agriculture and Fisheries, Maroochy Research Facility, 47 Mayers Road, Nambour, QLD 4560 Australia; stuart.irvinebrown@daf.qld.gov.au
- \* Correspondence: p.dennis@uq.edu.au

Content:

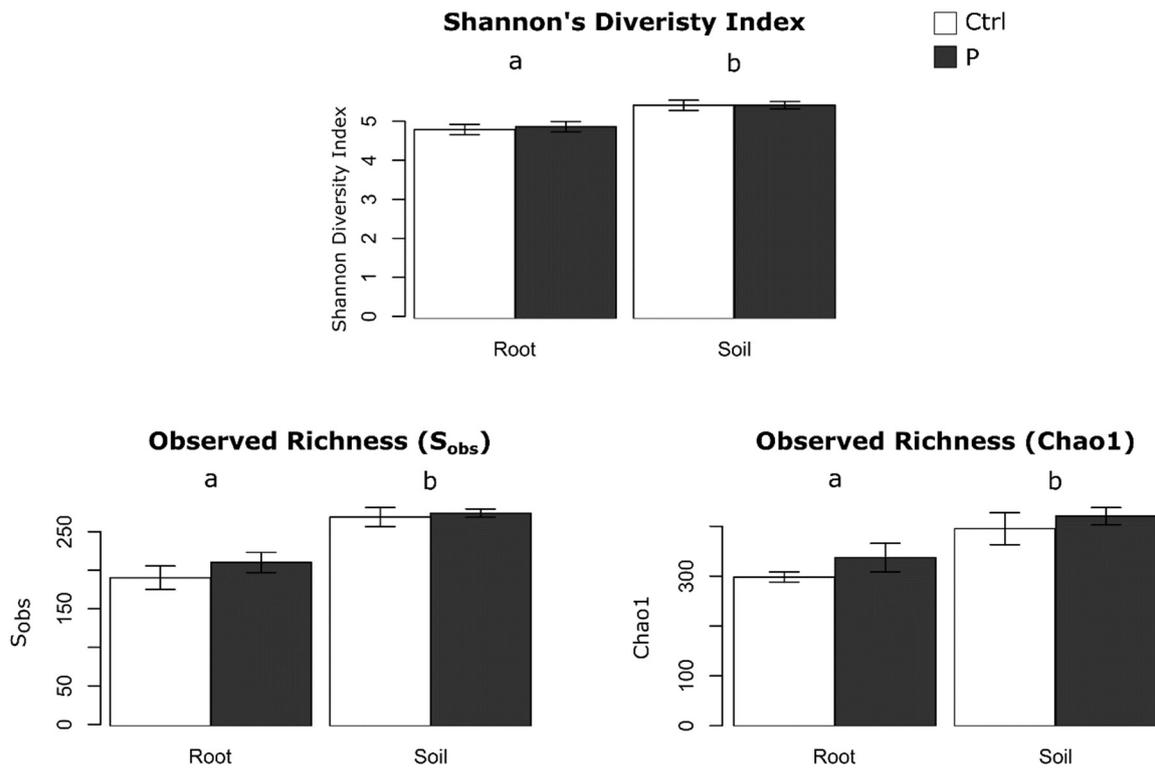
<b>Table S1</b> ANOVA results for microbial alpha diversity.....	2
<b>Figure S1</b> Barcharts of bacterial alpha diversity .....	3
<b>Figure S2</b> Barcharts of fungal alpha diversity.....	4
<b>Figure S3</b> RDAs of bacterial and fungal communities.....	5
<b>Table S2</b> Similarity of 16S OTUs with core bacteria in Birt et al. (2022).....	6
<b>Table S3</b> Similarity of ITS2 OTUs with core fungi in Birt et al. (2023).....	7
<b>Figure S4</b> Foliar P.....	8

**Table S1** ANOVA results summarising the main and interactive effects of compartment (soil and root) and treatment (control and elevated P) on the alpha diversity of bacterial and fungal communities, and of rate for nematode taxonomic groups in bulk soil.

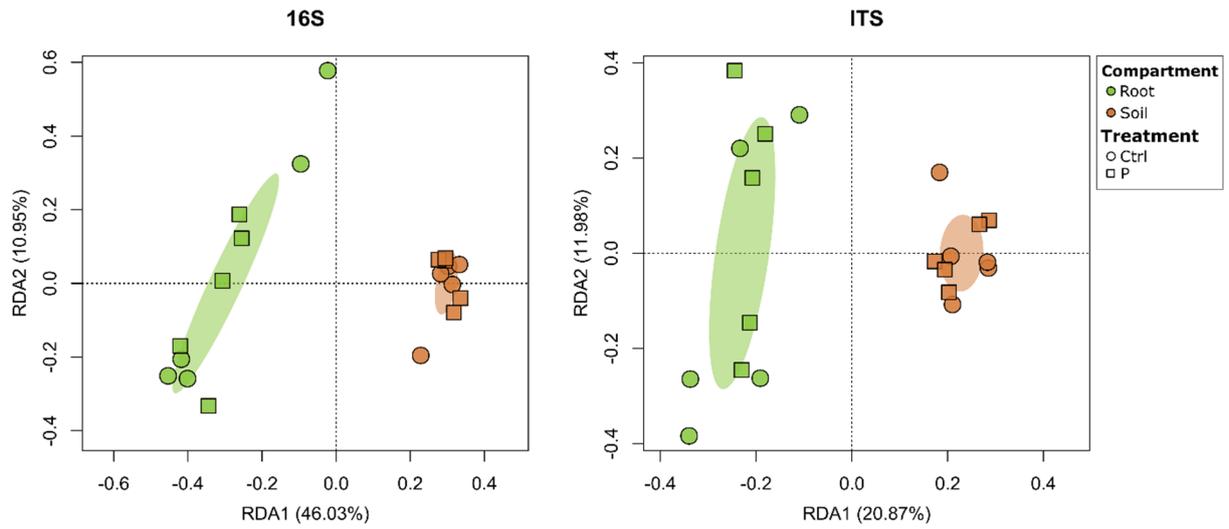
<b>Target</b>	<b>Response variable</b>	<b>Predictor variable</b>	<b>F value</b>	<b>P value</b>
<b>Bacteria</b>	Observed OTUs	Compartment	26.67	<0.001 ***
		Treatment	0.63	0.438
		Compartment : Treatment	0.05	0.834
	Predicted OTUs (Chao 1)	Compartment	14.55	0.002 **
		Treatment	0.19	0.670
		Compartment : Treatment	0.09	0.771
	Phylogenetic Diversity	Compartment	25.01	<0.001 ***
		Treatment	0.86	0.369
		Compartment : Treatment	0.13	0.722
<b>Fungi</b>	Observed OTUs	Compartment	34.74	<0.001 ***
		Treatment	1.07	0.317
		Compartment : Treatment	0.36	0.555
	Predicted OTUs (Chao 1)	Compartment	14.54	0.002 **
		Treatment	1.85	0.193
		Compartment : Treatment	0.08	0.776
<b>Nematodes</b>	Observed taxonomic groups	Treatment	3.27	0.108



**Figure S1** The influence of compartment and P addition on bacterial alpha diversity. Letters indicate Tukey *post hoc* analysis on the effect of compartment.



**Figure S2** The influence of compartment and P addition on fungal alpha diversity. Letters indicate Tukey *post hoc* analysis on the effect of compartment.



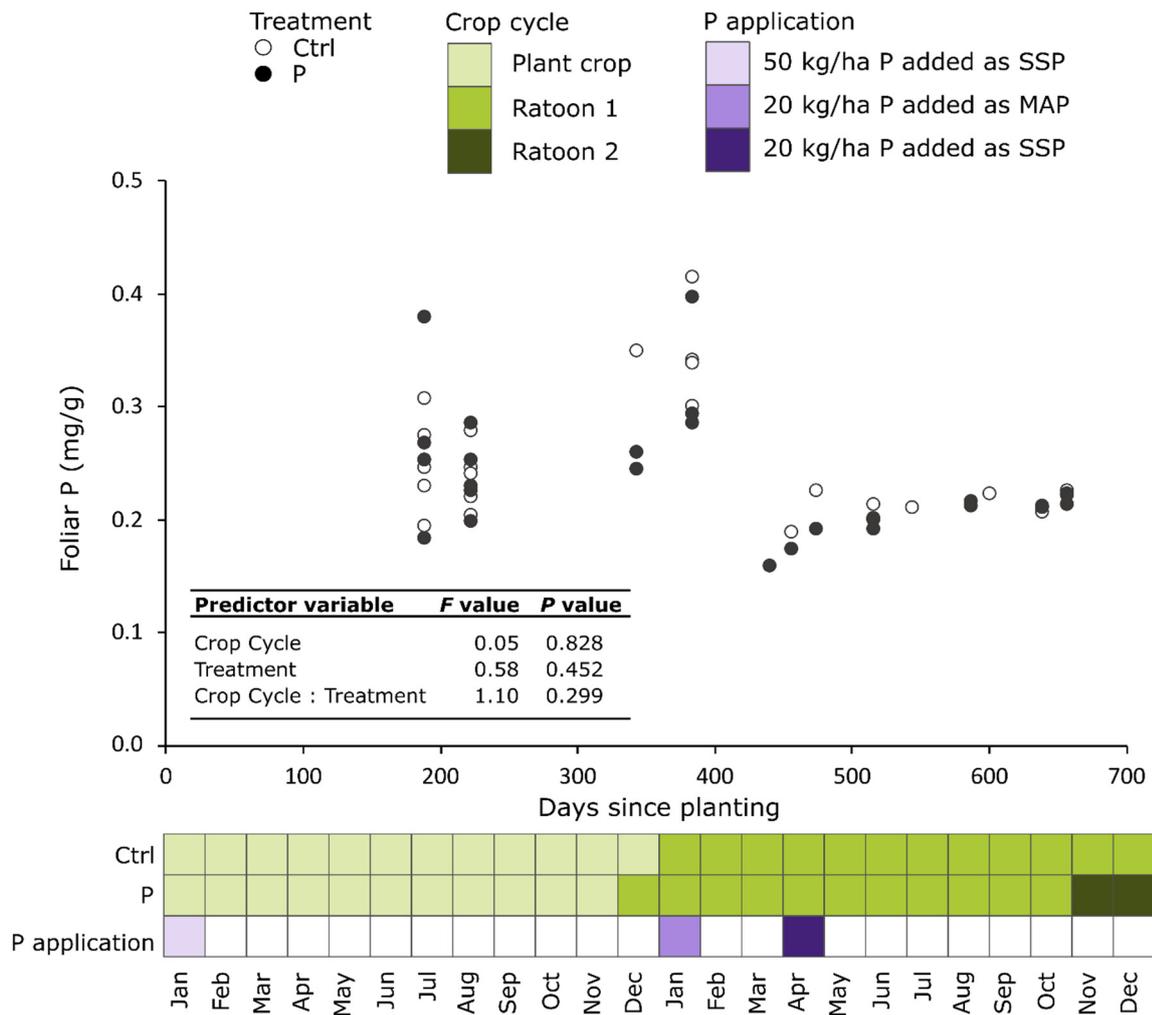
**Figure S3** Redundancy analysis (RDA) highlighting differences in the composition of bacterial (16S) and fungal (ITS) communities as represented by the Hellinger transformed relative abundances of OTUs between compartment (root = green, soil = brown) and treatment (control = circles; elevated P = squares).

**Table S2** USEARCH results comparing the 16S OTU sequences of this study with the core bacterial sequences in Birt *et al.* (2022). OTUs that were  $\geq 97\%$  similar are listed with the corresponding OTU number in Birt *et al.* (2022). Also shown are ANOVA results summarising the main and interactive effects of compartment (soil and root) and treatment (control and elevated P) on the relative abundance of bacterial OTUs identified as members of the core bacterial microbiome of banana ( $P \leq 0.001^{***}$ ;  $P \leq 0.01^{**}$ ;  $P \leq 0.05^*$ ;  $P \leq 0.1^{\cdot}$ ).

OTU ID (this study)	Compartment	Treatment	Compartment : Treatment	Similarity (%)	Core OTU (Birt et al., 2022)
[16] Variovorax	**			100	[18] Acidovorax
[4] Neobacillus	**			100	[17] Bacillus
[17] Priestia	**			100	[3] Bacillus
[79] Bacillus				100	[35] Bacillus
[9] Bradyrhizobium	*			100	[9] Bradyrhizobium
[459] Duganella	***			99	[170] Duganella
[2124] Telluria	***			97	[170] Duganella
[50] Dyella	**			100	[20] Dyella
[1] Pantoea	**			100	[8] Enterobacter
[146] Palsa-739	***			100	[40] Gaiella
[99] Unc.	***			99	[40] Gaiella
[27] Unc.	***			97	[40] Gaiella
[56] Palsa-739	**			97	[40] Gaiella
[48] JADJOM01	**			100	[23] Gemmatimonadaceae
[43] Oxalicibacterium	***	.	.	98	[5] Herbaspirillum
[1163] Methylobacteriu	.			98	[104] Methylobacterium
[72] Microbacterium	*			100	[73] Microbacterium
[38] Mycobacterium	.			100	[16] Mycobacterium
[29] Nitrospira_C	***			100	[28] Nitrospira
[21] Pseudolabrys	***			100	[24] Pseudolabrys
[629] VAZQ01	***			98	[41] Pseudolabrys
[1272] VAZQ01	**			97	[41] Pseudolabrys
[26] VAZQ01	***			97	[41] Pseudolabrys
[2] Pseudomonas_E	**			100	[42] Pseudomonas
[8] Ralstonia	.			100	[10] Ralstonia
[7] Agrobacterium	***			100	[2] Rhizobium
[61] Rhizobium	**			100	[99] Rhizobium
[20] Rhizobium	**			98	[11] Rhizobium
[13] Unc.	***			100	[13] SC-I-84
[159] VBCG01	***			98	[108] SC-I-84
[1767] VBCG01	***			97	[108] SC-I-84
[6] Sphingobium	**			100	[21] Sphingobium
[111] Sphingomicrobium				100	[169] Sphingomonas
[318] Sphingomonas_N				100	[98] Sphingomonas
[28] Sphingomicrobiurr	**			99	[12] Sphingomonas
[100] Sphingomonas	***			98	[4] Sphingomonas
[40] Streptomyces				100	[25] Streptomyces
[2276] Pseudolabrys	**			98	[131] Xanthobacteraceae

**Table S3** USEARCH results comparing the ITS2 OTU sequences of this study with the core Fungal sequences in Birt *et al.* (2023). OTUs that were  $\geq 97\%$  similar are listed with the corresponding OTU number in Birt *et al.* (2023). Also shown are ANOVA results summarising the main and interactive effects of compartment (soil and root) and treatment (control and elevated P) on the relative abundance of fungal OTUs identified as members of the core fungal microbiome of banana ( $P \leq 0.001^{***}$ ;  $P \leq 0.01^{**}$ ;  $P \leq 0.05^*$ ;  $P \leq 0.1^{\cdot}$ ).

OTU_ID (this study)	Compartment	Treatment	Compartment : Treatment	Similarity (%)	Core OTU (Birt et al., 2023)
[2469] Dothideomycetes				97	[74] Chaetosphaeriaceae
[32] Cyphellophoraceae	.			100	[29] Chaetothyriales
[61] Cladosporiaceae				100	[63] Cladosporium
[939] Cladosporiaceae	*			97	[63] Cladosporium
[73] Didymellaceae			.	100	[22] Didymellaceae
[123] Dothideomycetes	**			100	[37] Dothideomycetes
[816] Dothideomycetes	.			98	[37] Dothideomycetes
[3] Nectriaceae	*			100	[1] <i>F. oxysporum</i>
[1776] Nectriaceae				100	[1] <i>F. oxysporum</i>
[24] Nectriaceae	**			97	[15] <i>F. solani</i>
[30] Nectriaceae				100	[2] <i>Fusarium</i>
[10] Nectriaceae		.	*	100	[5] <i>Fusarium</i>
[2130] Nectriaceae				100	[5] <i>Fusarium</i>
[480] Chaetosphaeriaceae				100	[69] <i>Fusarium</i>
[6] Nectriaceae				100	[9] <i>Fusarium</i>
[2715] Nectriaceae				97	[9] <i>Fusarium</i>
[17] Sordariomycetes	*			100	[25] <i>M. theobromae</i>
[335] Plectosphaerellaceae				97	[25] <i>M. theobromae</i>
[1018] Plectosphaerellaceae				97	[25] <i>M. theobromae</i>
[3027] Mortierellaceae				98	[88] <i>Mortierella</i>
[2801] Nectriaceae				97	[6783] Nectriaceae
[4] Trichosphaeriaceae	***			100	[4] <i>Nigrospora</i>
[568] Trichosphaeriaceae				100	[4] <i>Nigrospora</i>
[1] Pleosporales				100	[3] <i>P. tabarestanensis</i>
[103] Pleosporales				100	[3] <i>P. tabarestanensis</i>
[751] Pleosporales				100	[3] <i>P. tabarestanensis</i>
[23] Pleosporales				98	[3] <i>P. tabarestanensis</i>
[2750] Pleosporales				98	[3] <i>P. tabarestanensis</i>
[1618] Pleosporales				97	[3] <i>P. tabarestanensis</i>
[3156] Pleosporales				97	[3] <i>P. tabarestanensis</i>
[130] Nectriaceae		.		100	[33] <i>Paracremonium</i>
[64] Phaeosphaeriaceae				100	[59] <i>Phaeosphaeria</i>



**Figure S4** Foliar P ( $\text{mg P g}^{-1}$  leaf dry mass) of plants during the plant crop and first ratoon of elevated P (black) and control (white) plots. An ANOVA in the bottom left hand corner indicates no differences between crop cycles or treatments. An accompanying timeline depicting ratoon duration (shades of green) and fertiliser treatments (shades of purple) is below.