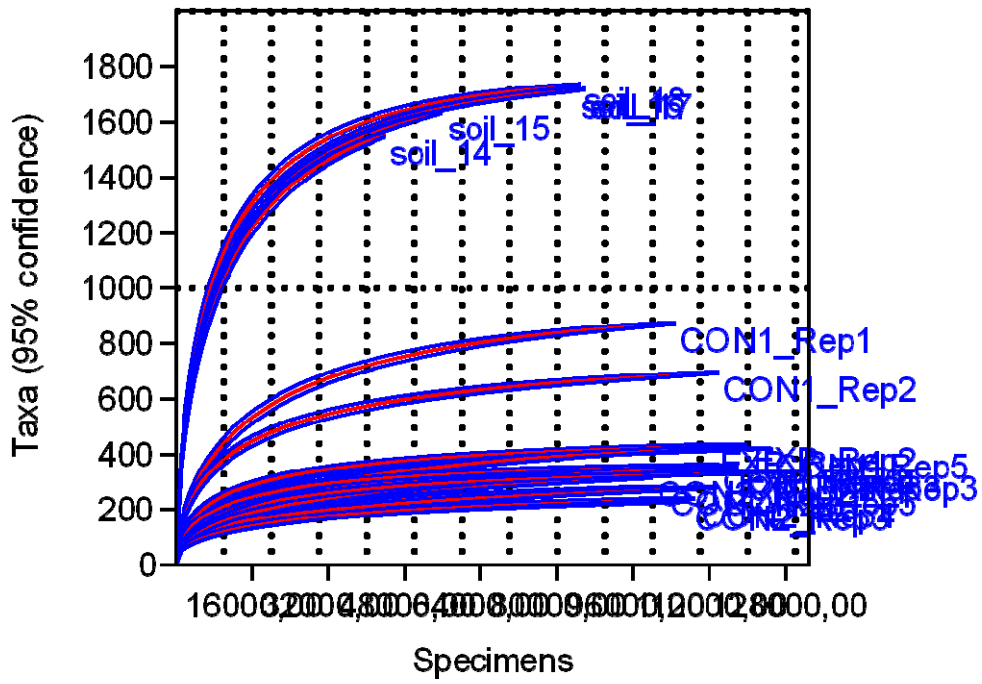
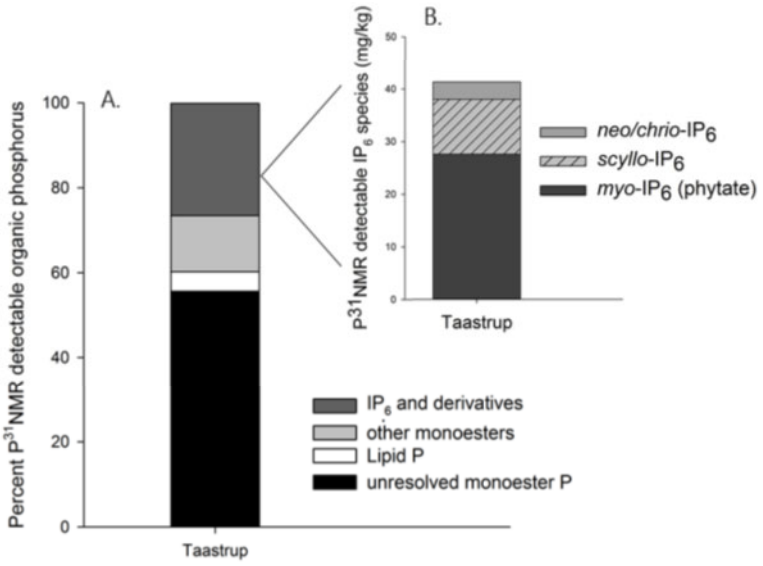
Supplementary material

Sup. Table S1. primers used in this study

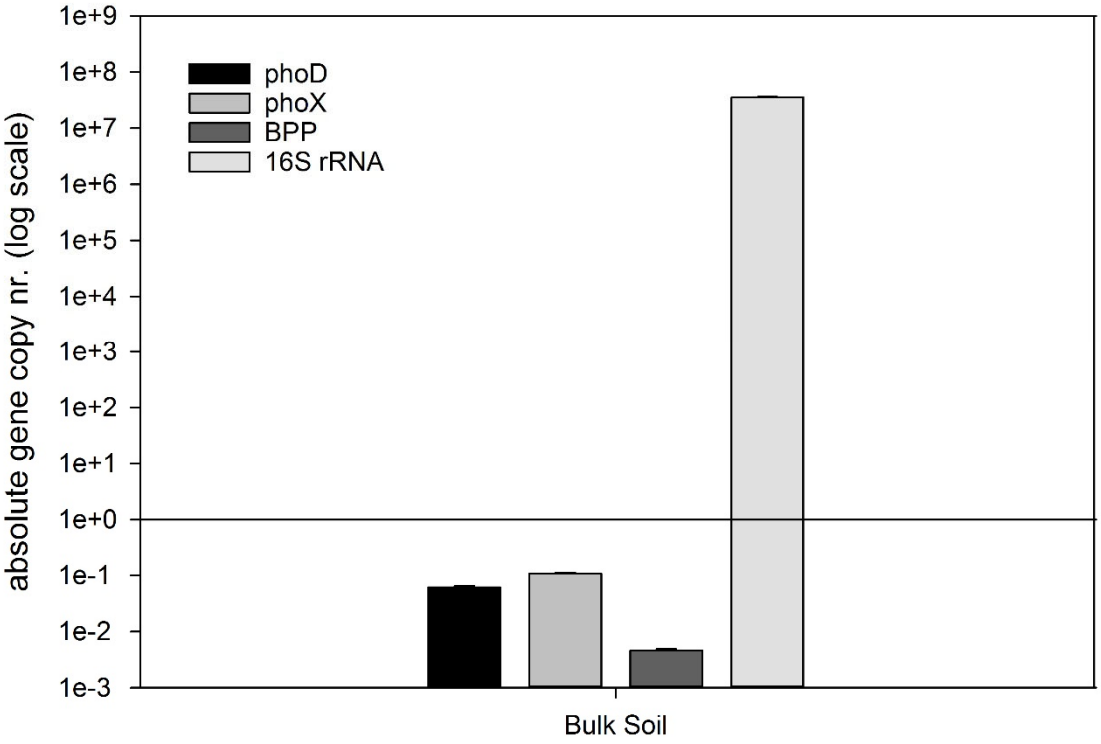
Target genes	primers	Sequences (5'-3')	references
16S rRNA gene	341F	CCTAYGGGRBGCASCAG	(Yu, Lee, Kim, & Hwang, 2005)
	806R	GGACTACNNGGGTATCTAAT	
phoD	ALPS-F730	CAGTGGGACGACCACGAGGT	(Sakurai, Wasaki, Tomizawa, Shinano, & Osaki, 2008)
	ALPS-R1101	GAGGCCGATCGGCATGTCG	
phoX	phoX2-F	GARGAGAACWTCCACGGYTA	(Valdespino-Castillo et al., 2014)
	phoX2-R	GATCTCGATGATRTGRCCRAAG	
BPP	BPP-F	GACGCAGCCGAYGAYCCNGCNITNTGG	(Huang et al., 2009)
	BPP-R	CAGGSCGCANRTCIACRTTRTT	



Sup. Figure S1. Rarefaction curve generated by the CLC program. Microcosms treatments are CON = Ca-phytate (Ca-IP_6), CON2 = root-exudate alone (RE), EXP = Ca- phytate combined with root-exudate (Ca-IP_6 + RE), and Soil = bulk soil. Five replicates per treatment were analyzed using 16S amplicon sequencing.



Sup. Figure S2. P^{31}NMR-extractable organic phosphorus and total inositol phosphate stereoisomers found in LTNDT, N_1K_1 soil.



Sup. Figure S3. Absolute abundance of marked genes found per gram bulk soil. A. *phoX* = alkaline phosphatase, B. *phoD* = alkaline phosphatase, C. *BPP* = beta propeller phytase, *16S rRNA* = small ribosomal subunit gene. Error is shown in SEM.