Table 1. Alpha diversity indices of bacterial communities of bulk soil and rhizosphere collected at two sampling times from a small plot replicated field trial with azoxystrobin and *Rhizoctonia solani* inoculation treatments in Geneva, NY in 2021.

Sampling Time, Type	Treatment	ASV[1] Richness	H[2]	D[3]	J[4]
28 DAP[5], Bulk soil	Nontreated	1,007	6.13	0.004	0.89
	Azoxystrobin	1,159	6.32	0.004	0.90
	Inoculum	1,209	6.34	0.004	0.90
	Azoxystrobin + Inoculum	1,055	6.18	0.005	0.89
	P =	0.477	0.446	0.455	0.514
28 DAP, Rhizosphere	Nontreated	1,003	6.21	0.004	0.90
	Azoxystrobin	1,149	6.38	0.003	0.91
	Inoculum	1,095	6.37	0.003	0.91
	Azoxystrobin + Inoculum	1,161	6.41	0.003	0.91
	P =	0.513	0.444	0.370	0.559
70 DAP, Bulk soil	Nontreated	1,118	6.47	0.003	0.92
	Azoxystrobin	1,423	6.73	0.002	0.93
	Inoculum	1,253	6.56	0.002	0.92
	Azoxystrobin + Inoculum	1,694	6.79	0.002	0.92
	P =	0.260	0.175	0.101	0.069
70 DAP, Rhizosphere	Nontreated	1,256	6.57	0.003	0.92
	Azoxystrobin	1,203	6.58	0.002	0.93
	Inoculum	1,131	6.31	0.009	0.90
	Azoxystrobin + Inoculum	1, 239	6.63	0.002	0.93
	P =	0.735	0.227	0.279	0.140

[1]ASV = Amplicon sequence variant.
[2]Shannon diversity, *H*, incorporates richness and abundance data. Greater values indicate higher diversity.
[3]Simpson diversity, *D*. Higher values indicate greater dominance from a small number of ASVs.
[4]Pielou evenness, *J*, depicts the distribution of ASVs. Values approaching 1 indicate a similar abundance of all taxa.
[5]DAP = days after planting.

Table 2. Alpha diversity indices of bacterial communities of bulk soil and rhizosphere samples collected at two sampling times from a small plot replicated field trial with azoxystrobin and *Rhizoctonia solani* inoculation treatments in Geneva, New York in 2022.

Sampling Time, Type	Treatment	ASV[1] Richness	H[2]	D[3]	J[4]
34 DAP[5], Bulk soil	Nontreated	1,119	6.48	0.002	0.92
	Azoxystrobin	1,185	6.52	0.002	0.92
	Inoculum	1,037	6.39	0.003	0.92
	Azoxystrobin + Inoculum	1,202	6.53	0.002	0.92
	$P =$	0.394	0.353	0.416	0.818
34 DAP, Rhizosphere	Nontreated	1,056	6.21	0.005	0.89
	Azoxystrobin	1,039	6.24	0.004	0.90
	Inoculum	1,073	6.23	0.010	0.89
	Azoxystrobin + Inoculum	1,202	6.14	0.021	0.87
	$P =$	0.483	0.981	0.597	0.749
75 DAP, Bulk soil	Nontreated	1,282	6.55	0.002	0.92
	Azoxystrobin	1,192	6.51	0.002	0.92
	Inoculum	1,294	6.56	0.002	0.92
	Azoxystrobin + Inoculum	1,253	6.53	0.002	0.92
	$P =$	0.653	0.883	0.990	0.864
75 DAP, Rhizosphere	Nontreated	1,099	6.41	0.003	0.92
	Azoxystrobin	1,182	6.47	0.003	0.92
	Inoculum	1,160	6.29	0.005	0.89
	Azoxystrobin + Inoculum	1,056	6.36	0.004	0.90
	$P =$	0.872	0.857	0.701	0.653

[1]ASV = Amplicon sequence variant.
[2]Shannon diversity, *H*, incorporates richness and abundance data. Greater values indicate higher diversity.
[3]Simpson diversity, *D*. Higher values indicate greater dominance from a small number of ASVs.
[4]Pielou evenness, *J*, depicts the distribution of ASVs. Values approaching 1 indicate a similar abundance of all taxa.
[5]DAP = days after planting.

Table 3. Alpha diversity indices of fungal communities from rhizosphere and bulk soil samples collected at two sampling times from a small plot replicated field trial with azoxystrobin and *Rhizoctonia solani* inoculation treatments in Geneva, New York in 2021.

Sampling Time, Type	Treatment	ASV[1] Richness	H[2]	D[3]	J[4]
28 DAP[5], Bulk soil	Nontreated	154.3	3.40	0.07	0.68
	Azoxystrobin	127.3	3.11	0.10	0.65
	Inoculum	127.0	2.96	0.15	0.61
	Azoxystrobin + Inoculum	176.3	3.37	0.09	0.65
	P =	0.359	0.648	0.601	0.740
28 DAP, Rhizosphere	Nontreated	149.5	2.87	0.18	0.58
	Azoxystrobin	117.5	2.60	0.22	0.55
	Inoculum	134.8	2.59	0.21	0.53
	Azoxystrobin + Inoculum	87.3	1.97	0.38	0.44
	P =	0.098	0.117	0.089	0.354
70 DAP, Bulk soil	Nontreated	162.8	3.52	0.07	0.69
	Azoxystrobin	147.3	3.43	0.09	0.69
	Inoculum	172.0	3.45	0.07	0.67
	Azoxystrobin + Inoculum	171.0	3.39	0.09	0.66
	P =	0.532	0.931	0.762	0.676
70 DAP, Rhizosphere	Nontreated	158.5	3.30	0.12	0.65
	Azoxystrobin	149.8	2.67	0.26	0.54
	Inoculum	166.0	3.22	0.10	0.63
	Azoxystrobin + Inoculum	161.5	2.73	0.21	0.54
	P =	0.920	0.449	0.296	0.547

[1]ASV = Amplicon sequence variant.
[2]Shannon diversity, *H*, incorporates richness and abundance data. Greater values indicate higher diversity.
[3]Simpson diversity, *D*. Higher values indicate greater dominance from a small number of ASVs.
[4]Pielou evenness, *J*, depicts the distribution of ASVs. Values approaching 1 indicate a similar abundance of all taxa.
[5]DAP = days after planting.

Table 4. Alpha diversity indices of fungal communities from rhizosphere and bulk soil samples collected on two occasions from a small plot replicated field trial with azoxystrobin and *Rhizoctonia solani* inoculation treatments in Geneva, New York in 2022.

Sampling Time, Type	Treatment	ASV[1] Richness	H[2]	D[3]	J[4]
34 DAP[5], Bulk soil	Nontreated	146.8	1.84 a	0.42 a[6]	0.37 a
	Azoxystrobin	181.0	2.55 b	0.25 b	0.49 b
	Inoculum	161.5	2.18 ab	0.31 ab	0.43 ab
	Azoxystrobin + Inoculum	160.0	2.70 b	0.21 b	0.53 b
	$P =$	0.602	0.037	0.035	0.029
	LSD	-	0.602	0.142	0.107
34 DAP, Rhizosphere	Nontreated	143.3	2.25	0.31	0.45
	Azoxystrobin	129.3	2.48	0.23	0.51
	Inoculum	182.3	2.71	0.20	0.52
	Azoxystrobin + Inoculum	146.0	2.53	0.23	0.51
	$P =$	0.220	0.634	0.524	0.706
75 DAP, Bulk soil	Nontreated	228.8	2.81	0.15	0.52
	Azoxystrobin	168.3	2.79	0.15	0.55
	Inoculum	203.3	2.77	0.16	0.52
	Azoxystrobin + Inoculum	190.2	2.65	0.19	0.51
	$P =$	0.462	0.707	0.567	0.746
75 DAP, Rhizosphere	Nontreated	246.0	2.94	0.16	0.53
	Azoxystrobin	237.8	3.06	0.13	0.57
	Inoculum	229.8	2.60	0.21	0.48
	Azoxystrobin + Inoculum	162.3	2.65	0.19	0.52
	$P =$	0.263	0.171	0.319	0.275

[1]ASV = Amplicon sequence variant.

[2]Shannon diversity, *H*, incorporates richness and abundance data. Greater values indicate higher diversity.

[3]Simpson diversity, *D*. Higher values indicate greater dominance from a small number of ASVs.

[4]Pielou evenness, *J*, depicts the distribution of ASVs. Values approaching 1 indicate a similar abundance of all taxa.

[5]DAP = days after planting.

[6]Means followed by the different letters within a column are significantly different at the 0.05 level (Fishers protected least significant difference (LSD), *P* = 0.05).

Table 5. Table beet crop stand on selected dates, root weight, average shoulder diameter, root disease incidence, and average root disease severity following in-furrow azoxystrobin application and post-emergent inoculation with *Rhizoctonia solani* AG 2-2 in a small plot replicated trial in Geneva, New York, in 2021 and 2022.

2021

Treatment	Crop Stand (plants/m)			Root weight[4] (kg)	Average Root Shoulder Diameter[4] (mm)	Root disease incidence (%)	Average disease severity per root[4] (%)
	Early[1]	Middle[2]	Late[3]				
Nontreated	46.1	35.1	26.6	3.6	32.6	24.5 a[5]	1.28
Inoculum	52.0	40.4	28.7	3.1	31.5	40.7 b	2.37
Azoxystrobin	56.7	37.2	36.9	4.1	33.3	18.6 a	0.61
Azoxystrobin + Inoculum	54.1	33.7	36.4	4.1	36.3	24.2 a	1.01
LSD	-	-	-	-	-	15.4	-
P =	0.507	0.727	0.192	0.226	0.43	0.048	0.155

2022

Treatment	Early	Middle	Late	Root weight	Root Shoulder Diameter	Root disease incidence	Average disease severity
Nontreated	50.1	43.8	28.5	3.5	38.2	32.1	1.03
Inoculum	35.7	50.5	35.4	4.6	37.9	33.7	1.77
Azoxystrobin	56.9	44.0	33.0	3.4	43.7	16.5	0.54
Azoxystrobin + Inoculum	58.0	49.5	39.2	4.4	39.2	25.4	0.52
P =	0.311	0.535	0.142	0.073	0.986	0.153	0.1514

[1]Early crop stands on 14 June (25 DAP) in 2021 and 13 June (26 DAP) in 2022.
[2]Mid-season crop stands on 13 July (54 DAP) in 2021 and 5 July (48 DAP) in 2022.
[3]Late-season crop stands on 4 August (77 DAP) in 2021 and 1 August (75 DAP) in 2022.
[4]Root weight, average root shoulder diameter, and average disease severity per root were calculated from all plants within a 1-m transect from each plot.
[5]Means followed by the same letter within a column are not significantly different (Fishers protected least significant difference (LSD), $P = 0.05$).
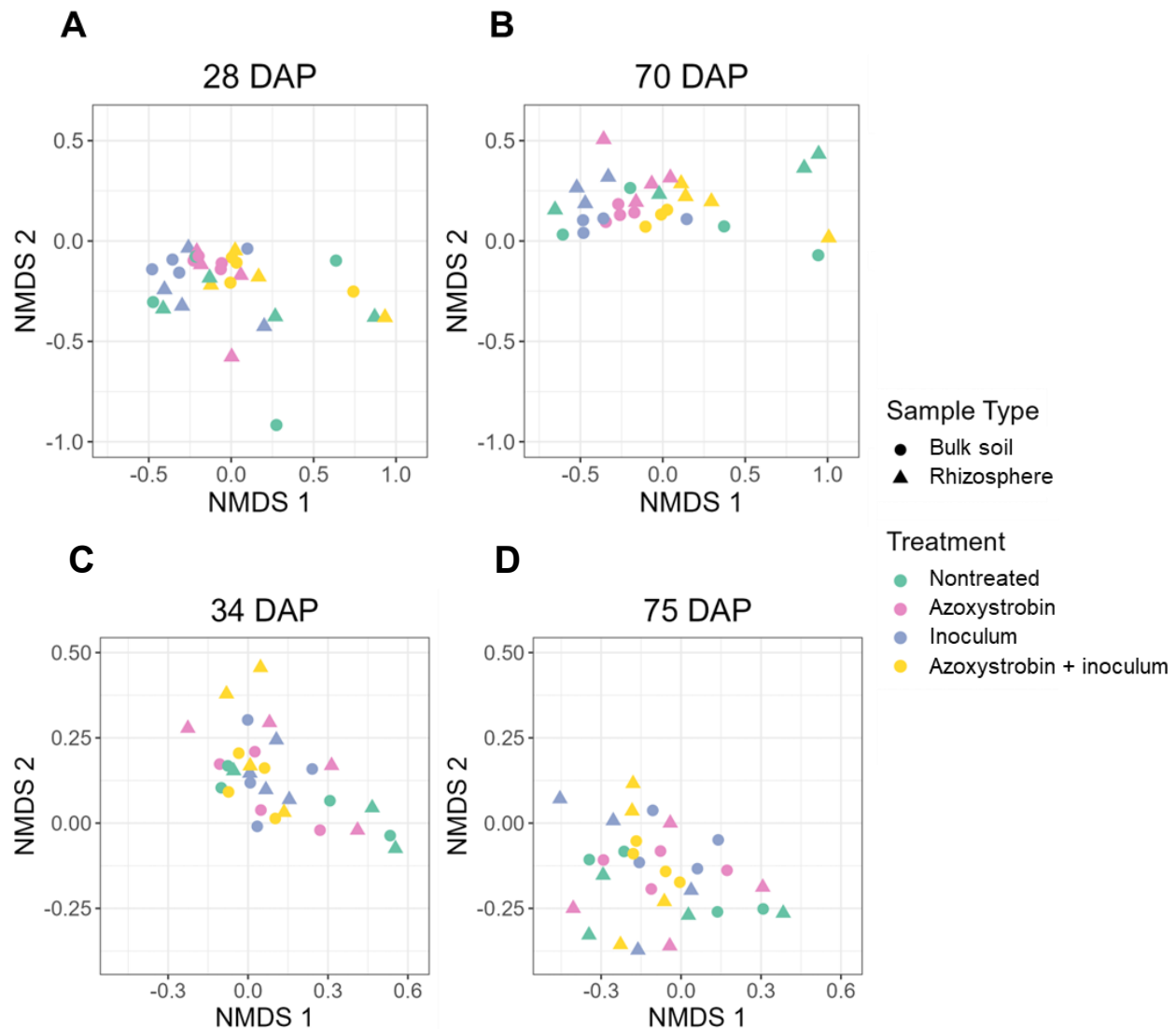
Fig. 1. Bacterial community composition quantified with non-metric multidimensional scaling (NMDS) plots of Bray-Curtis distances and the effect of sample type and treatment from replicated small plot trials of table beet in Geneva, New York. **A,** 28 days after planting (DAP), and **B,** 70 DAP in 2021 (stress = 0.16). In 2021, the effect of treatment was not significant at 28 DAP ($R^2 = 0.11$, $P = 0.06$) but was significant at 70 DAP ($R^2 = 0.14$, $P = 0.03$). The effect of sample type on community composition was significant at both times in 2021 (28 DAP: $R^2 = 0.16$, $P = 0.001$; 70 DAP: $R^2 = 0.12$, $P = 0.001$). **C,** 34 DAP and **D,** 75 DAP in 2022 (stress = 0.19). In 2022, the effect of treatment was not significant at 34 or 75 DAP (34 DAP: $R^2 = 0.09$, $P = 0.36$; 75 DAP: $R^2 = 0.07$, $P = 0.91$). The effect of sample type on community composition was significant at both times in 2022 (34 DAP: $R^2 = 0.12$, $P = 0.001$ and 75 DAP: $R^2 = 0.13$, $P = 0.001$).
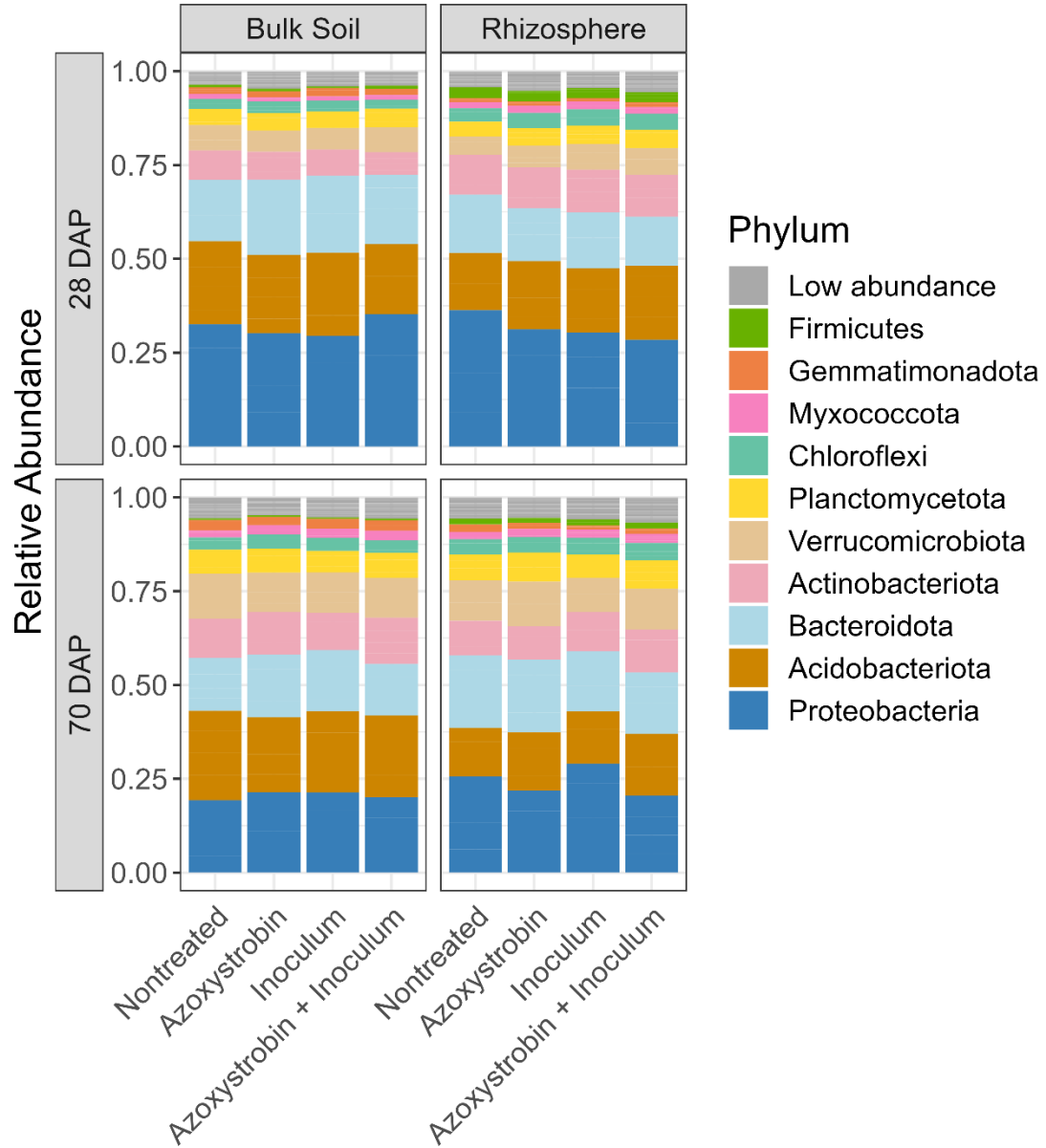
Fig. 2. Relative abundance of phyla that each constitute at least 1% of the total bacterial community based on 16S rRNA gene sequences from bulk soil and table beet rhizosphere samples collected in small plot replicated field trial in Geneva, New York in 2021.
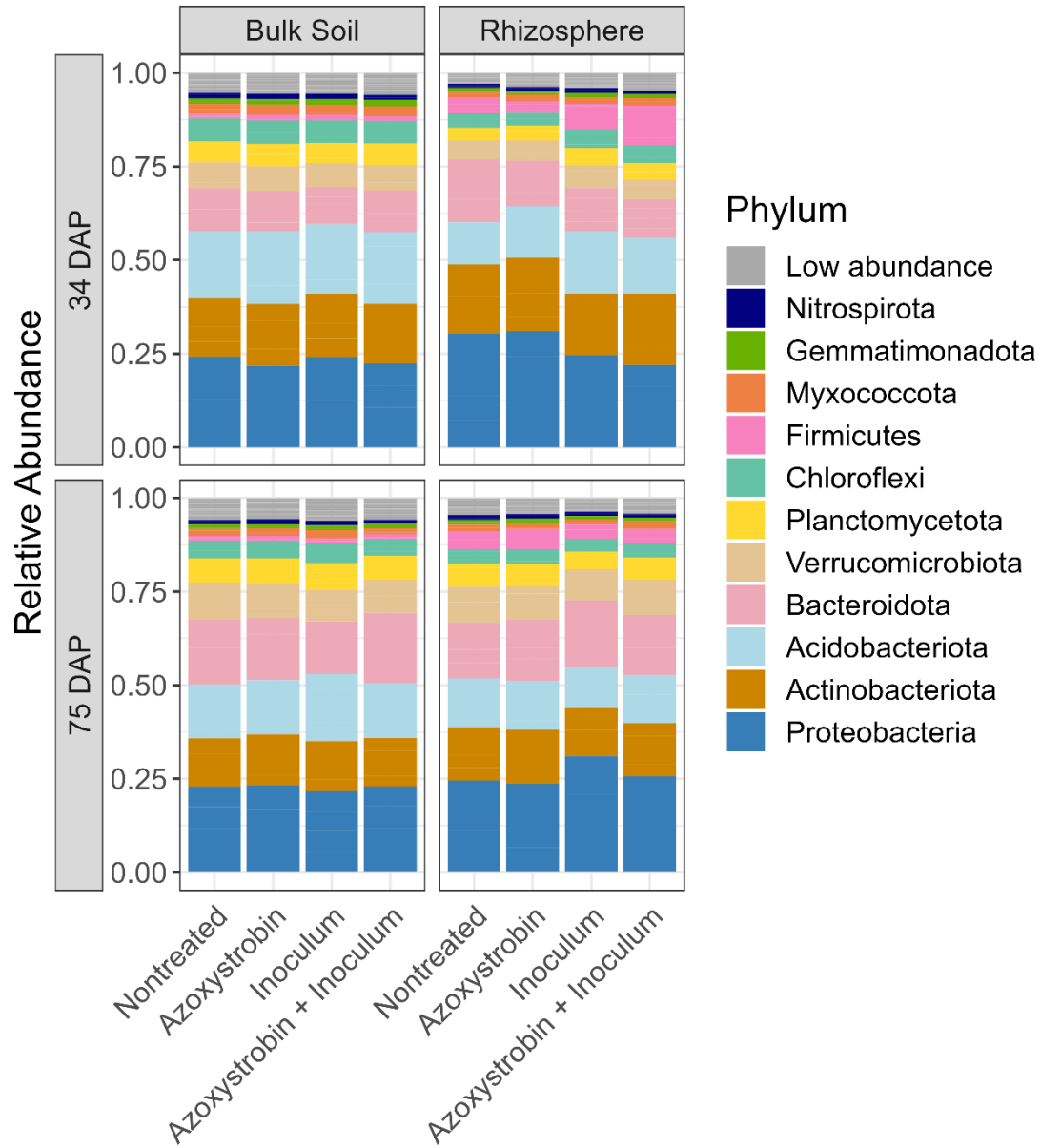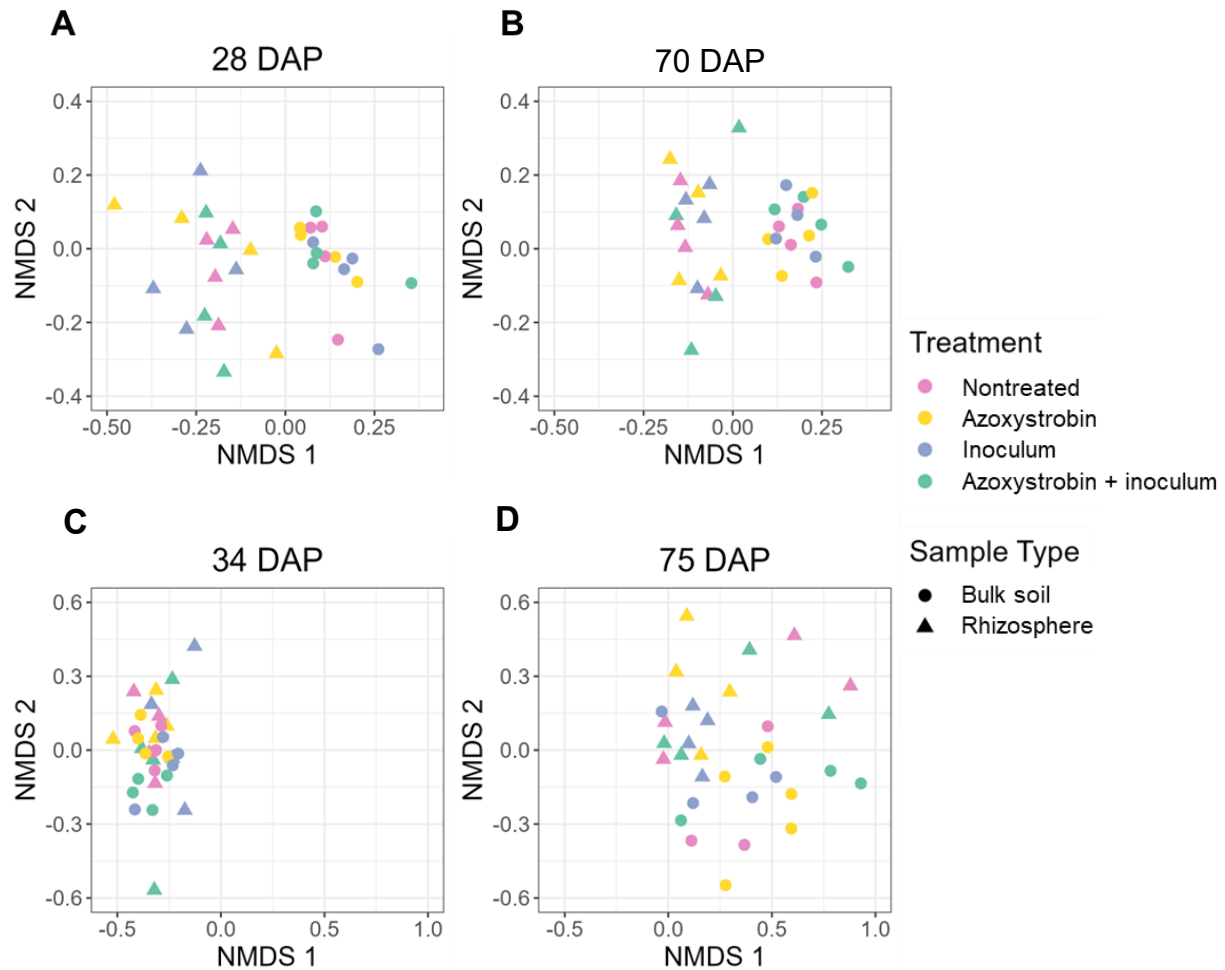
Fig. 3. Relative abundance of phyla that each constitutes at least 1% of the total bacterial community based on 16S rRNA gene sequences from bulk soil and table beet rhizosphere samples collected in small plot replicated field trial in Geneva, New York in 2022.

Fig. 4. Fungal community composition shown with non-metric multidimensional scaling (NMDS) plots of Bray-Curtis distances and the effect of sample type and treatment from replicated small plot trials of table beet in Geneva, New York. **A,** 28 days after planting (DAP) and **B,** 70 DAP in 2021 (stress = 0.21). In 2021, The effect of treatment on community composition was not significant at 28 DAP ($R^2 = 0.05$, $P = 0.69$) or 70 DAP ($R^2 = 0.07$, $P = 0.41$). The effect of sample type on significant at both times in 2021 (28 DAP: $R^2 = 0.35$, $P = 0.001$ and 70 DAP: $R^2 = 0.28$, $P = 0.001$). **C,** 34 DAP and **D,** 75 DAP in 2022 (stress = 0.21). In 2022, the effect of treatment on community composition was not significant at 28 DAP ($R^2 = 0.09$, $P = 0.45$) or 70 DAP ($R^2 = 0.08$, $P = 0.51$). The effect of sample type was significant at both times in 2022 (28 DAP: $R^2 = 0.17$, $P = 0.001$ and 70 DAP: $R^2 = 0.24$, $P = 0.001$).
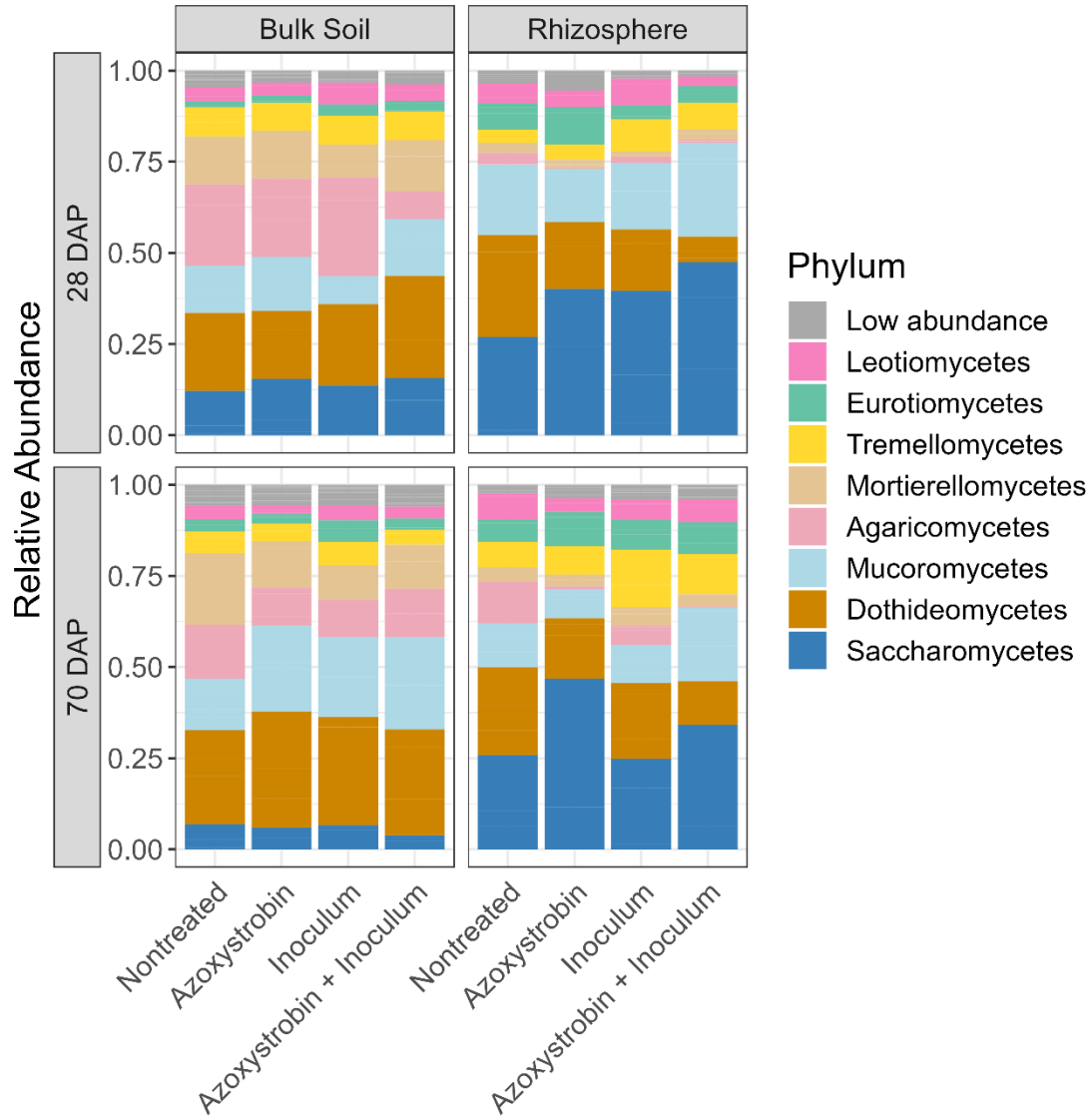
Fig. 5. Relative abundance of classes that each constitute at least 1% of the total fungal community based on internal transcribed spacer (ITS) region sequences from bulk soil and table beet rhizosphere samples collected in small plot replicated field trial in Geneva, New York in 2021.
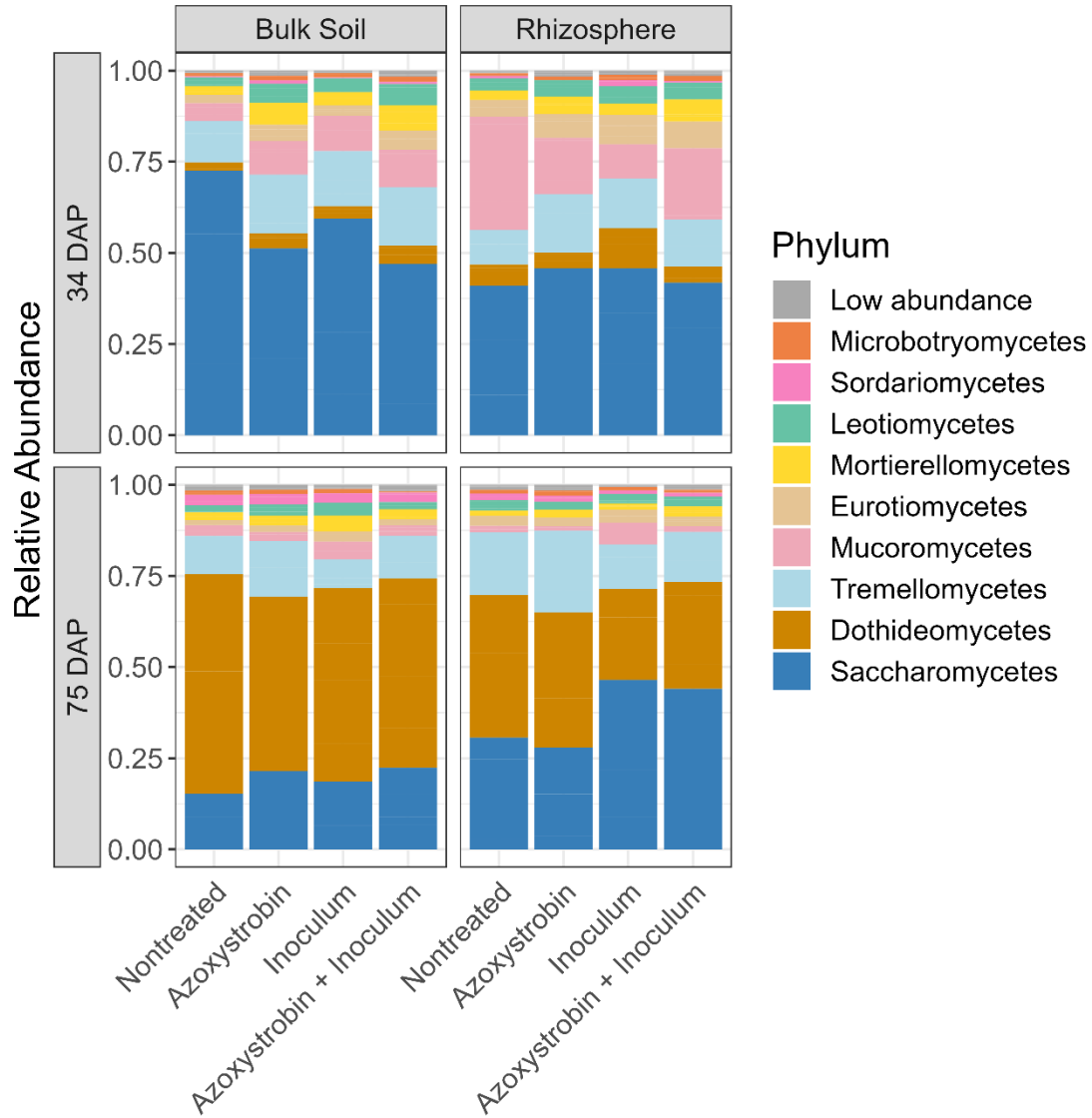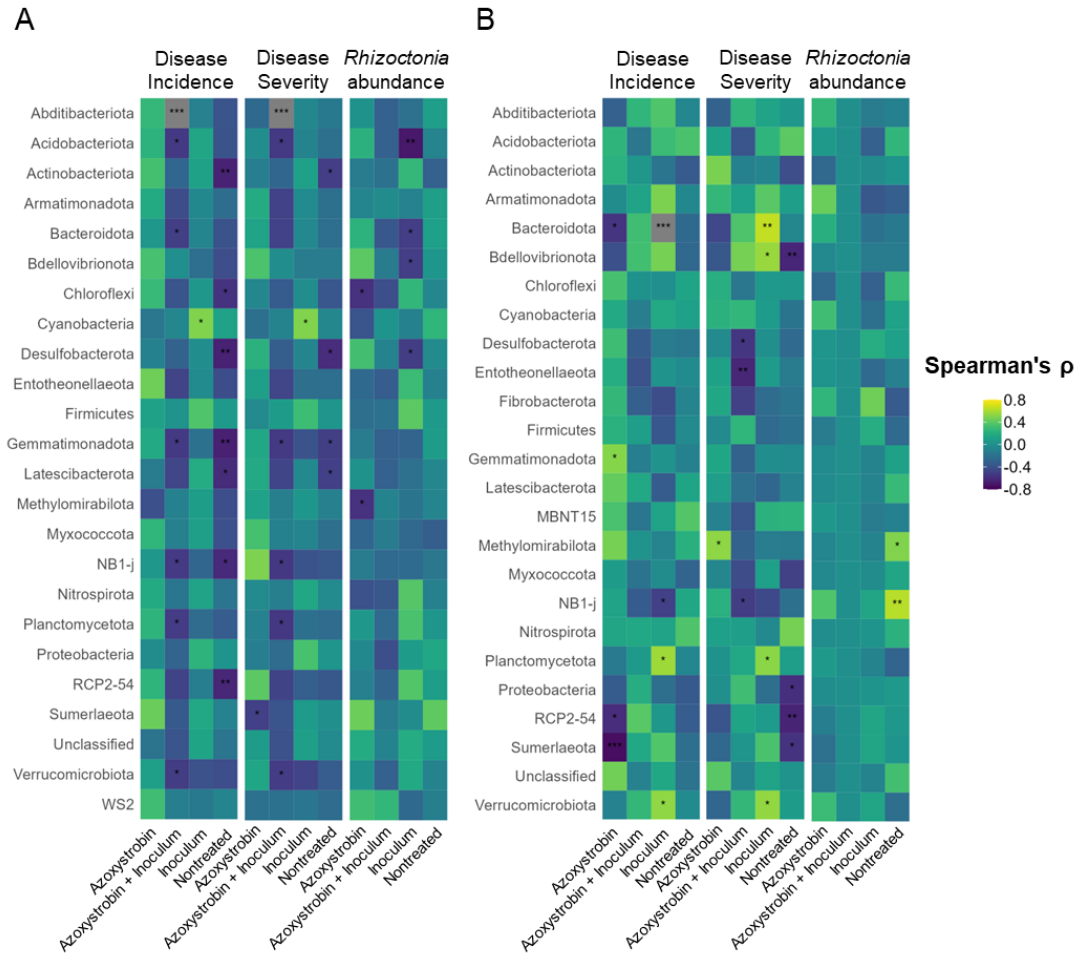
Fig. 6. Relative abundance of phyla that each constitute at least 1% of the total fungal community based on internal transcribed spacer (ITS) region sequences from bulk soil and table beet rhizosphere samples collected in small plot replicated field trial in Geneva, New York in 2022.

Fig. 7. Correlation heatmaps between disease incidence (left), disease severity (center), abundance of *Rhizoctonia solani* sequences (right), and the relative abundance of bacterial phyla present in the soil and rhizosphere microbiome of table beet in **A,** 2021, and **B,** 2022. Asterisks indicate probability values for Spearman's rank correlation: *, $P > 0.05$; **, $P > 0.01$, ***, $P > 0.001$.
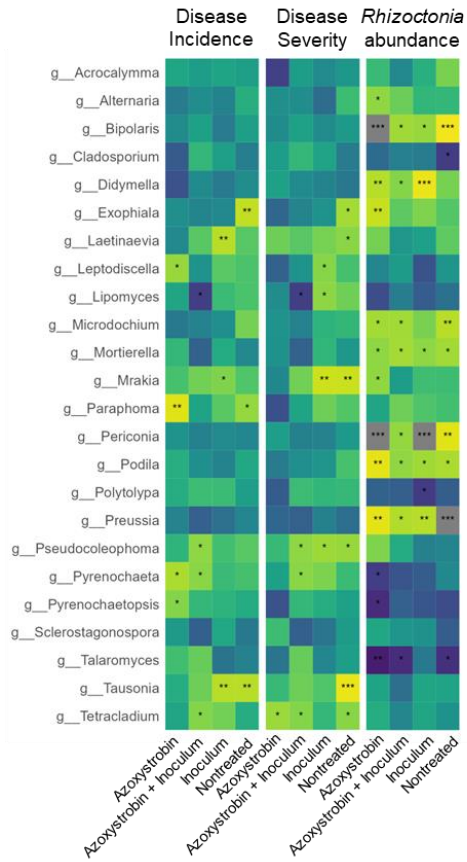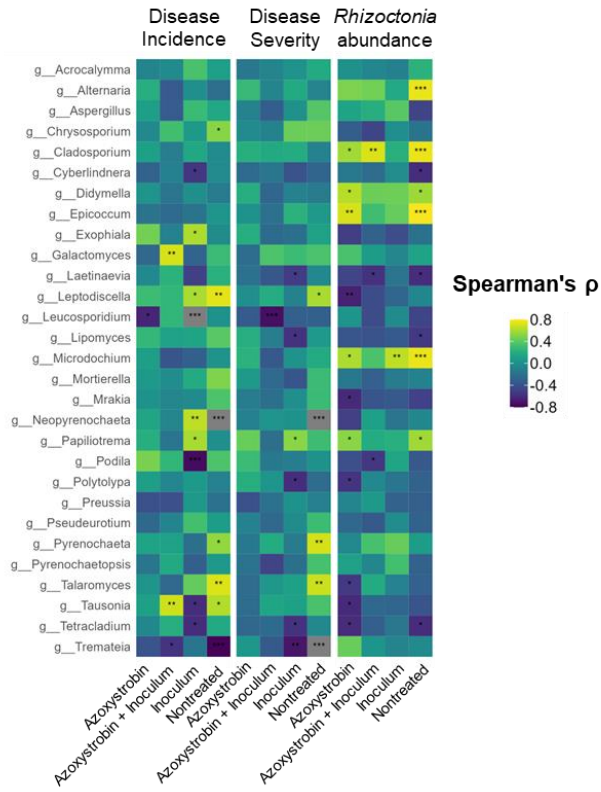
Fig. 8. Correlation heatmaps between disease incidence (left), disease severity (center), abundance of *Rhizoctonia solani* sequences (right), and the relative abundance of fungal genera present in the soil and rhizosphere microbiome of table beet in **A,** 2021 and **B,** 2022. Asterisks indicate probability values for Spearman's rank correlation: *, $P > 0.05$; **, $P > 0.01$, ***, $P > 0.001$.