

CUSTOMER INFORMATION			
Name:		Grower Name:	
Address:		Field ID:	
Phone:		Crop Type:	
Bill To:		Crop Variety:	N/A

Sample ID	Field 1	
Microbe Populations		
Number of Genera	2,565	
Diversity	100%	Very High
Evenness	15%	Very Low
Mycorrhizae Abundance	76%	High
Fungi to Bacteria Ratio	1 to 2.14	
Ectomycorrhizal to Arbuscular Ratio	3.41 to 1	

Crop Functions of Interest		
Anoxic Environment	61%	High
High Oxygen Environment	31%	Low
Low Oxygen Environment	33%	Low
Carbon Fixation	54%	Medium
Organic Carbon Breakdown	40%	Medium
Methanogenesis	44%	Medium
Denitrification	88%	Very High
Nitrification	51%	Medium
Nitrogen Fixation	29%	Low
Organic Nitrogen Breakdown	46%	Medium
Phosphorus Mobilization	58%	Medium
Potassium Solubilization	46%	Medium
Nodulating Bacteria	45%	Medium
Sulfur Oxidation	58%	Medium
Sulfur Reduction	75%	High
Calcium Transport	72%	High
Iron Acquisition	44%	Medium
Plant Stress Adaptation	50%	Medium

Community structure and function ratings were calculated by comparing the relative abundance of species or genes in the rhizosphere to a large data set of other agricultural samples to generate a percentile, which represents the value in a normal distribution that has a specific percentage of observations below it. For research purposes only, the information in this report is not advice, and should not be treated as such. No part of this report may be reproduced without permission in writing from RhizeBio.

Contact RhizeBio:

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Taxonomic Profile					
Top 20 Bacterial Genera			Top 20 Fungal Genera		
Pseudomonas	9.50%	AE	Fusarium	4.1%	F
Streptomyces	8.04%	AE	Penicillium	0.7%	AE
Pantoea	6.16%	F	Aspergillus	0.6%	AE
Enterobacter	5.05%	AE	Cladosporium	0.6%	
Nocardioides	4.85%	OA	Alternaria	0.5%	
Arthrobacter	3.98%	OA	Furcasterigmium	0.3%	
Bradyrhizobium	2.98%	AE	Solicoccozyma	0.3%	
Rhodococcus	2.52%	AE	Clonostachys	0.2%	
Salmonella	2.21%	F	Epicoccum	0.2%	
Microbacterium	1.57%	AE	Mucor	0.2%	
Mesorhizobium	1.21%	OA	Microdochium	0.1%	
Mycobacterium	1.11%	AE	Trichoderma	0.1%	AE
Pseudarthrobacter	1.01%	AE	Acremonium	0.1%	
Variovorax	0.99%	AE	Graphiopsis	0.1%	
Curtobacterium	0.98%	AE	Preussia	0.1%	
Terrabacter	0.96%	OA	Phyllachora	0.1%	
Phycococcus	0.93%	OA	Pochonia	0.1%	AE
Kribbella	0.90%	OA	Bipolaris	0.1%	
Mycolicibacterium	0.79%		Pleurotus	0.1%	
Rhizobium	0.74%	AE	Purpureocillium	0.1%	F
AE = Aerobic AN = Anaerobic OA = Obligate Aerobic ON = Obligate Anaerobic F = Facultative MA = Microaerophilic ECM = Ecyomycorrhizal Fungi AMF = Arbuscular Mycorrhizal Fungi					

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Sample ID	Field #1	Report Date	4/30/2025
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Detected Pathogens

<u>Pathogen Disease and Species</u>	Pathogen Presence Detected	Abundant Pathogen Presence	High Pathogen Pressure	Pathogen Pressure Score
Common Smut <i>Ustilago maydis</i>				125%
Souther Corn Rust <i>Puccinia polysora</i>				101%
Pythium Root Rot <i>Pythium inflatum</i>				91%
Pythium Root Rot <i>Pythium pyrilobum</i>				89%
Pythium Root Rot <i>Pythium torulosum</i>				51%
Graminicola Downy Mildew <i>Sclerospora graminicola</i>				Minimal

Undetected Pathogens

Pathogens not found in the sample or found in such low abundance they can be considered insignificant

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Report Date	5/1/2025
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Top 100 Bacteria Species Identified

AE = Aerobic AN = Anaerobic OA = Obligate Aerobic ON = Obligate Anaerobic F = Facultative MA = Microaerophilic					
1	Mycobacterium tuberculosis	3.34% AE	51	Afpia carboxidovorans	0.17% AE
2	Arthrobacter sp.	3.30% OA	52	Oerskovia sp.	0.17% AE
3	Parvibaculum sp.	2.91% AE	53	Brevundimonas sp.	0.16% AE
4	Mycobacterium paragordoniae	2.35% AE	54	Rhodoplanes sp.	0.16% AE
5	Reyranella sp.	1.66% MA	55	Acidovorax facilis	0.16% AE
6	Bacillus sp.	1.18% AE	56	Pseudolabrys sp.	0.16%
7	Cellulosimicrobium cellulans	1.04% AE	57	Nitrosomonas sp.	0.15% AE
8	Parvibaculum lavamentivorans	1.01% AE	58	Simplicispira lacusdiani	0.15% AE
9	Salmonella enterica	0.94% F	59	Pseudolabrys sp.	0.15%
10	Leucobacter denitrificans	0.90% AE	60	Rhodopseudomonas palustris	0.15% F
11	Pseudomonas aeruginosa	0.80% AE	61	Enhydrobacter sp.	0.15% F
12	Reyranella aquatilis	0.68% MA	62	Devosia sp.	0.15% OA
13	Acinetobacter lwoffii	0.64% AE	63	Oerskovia rustica	0.15% AE
14	Mycolicibacter arupensis	0.62%	64	Hyphomicrobium sp.	0.14% AE
15	Escherichia coli	0.57% F	65	Hydrogenophaga sp.	0.14% AE
16	Hydrogenophaga pseudoflava	0.50% AE	66	Enhydrobacter aerosaccus	0.14% F
17	Neobacillus niacini	0.48%	67	Cellulosimicrobium sp.	0.14% AE
18	Bacillus thuringiensis	0.47% AE	68	Kaistia adipata	0.14% OA
19	Mesorhizobium sp.	0.45% OA	69	Enterobacter hormaechei	0.14% AE
20	Hydrogenophaga sp.	0.45% AE	70	Microbacterium sp.	0.13% AE
21	Klebsiella pneumoniae	0.44% AE	71	Methylibium petroleiphilum	0.13% F
22	Ensifer sp.	0.41% AE	72	Phenylobacterium sp.	0.13% AE
23	Limnobacter sp.	0.41% AE	73	Rhizobium leguminosarum	0.12% AE
24	Metabacillus sp.	0.40%	74	Pseudorhodoplanes sinuspersici	0.12%
25	Cellulosimicrobium sp.	0.38% AE	75	Pseudomonas sp.	0.12% AE
26	Pseudolabrys taiwanensis	0.38%	76	Arthrobacter sp.	0.11% OA
27	Staphylococcus aureus	0.37% AE	77	Erythrobacter sp.	0.10% AE
28	Bosea sp.	0.36% AE	78	Rhodococcus rhodochrous	0.10% AE
29	Mycobacterium gordonae	0.36% AE	79	Metabacillus halosaccharovorans	0.10%
30	Mycobacterium sp.	0.36% AE	80	Bacillus sp.	0.10% AE
31	Reyranella massiliensis	0.35% MA	81	Phenylobacterium sp.	0.10% AE
32	Aquabacterium sp.	0.35% AE	82	Rhodoplanes serenus	0.10% AE
33	Bradyrhizobium sp.	0.33% AE	83	Achromobacter xylooxidans	0.10% AE
34	Metabacillus sp.	0.32%	84	Stenotrophomonas maltophilia	0.09% AE
35	Metabacillus idriensis	0.31%	85	Acidovorax sp.	0.09% AE
36	Bradyrhizobium japonicum	0.30% AE	86	Acidovorax sp.	0.09% AE
37	Acinetobacter baumannii	0.29% AE	87	Pseudoroseomonas aerophila	0.09%
38	Microbacterium sp.	0.26% AE	88	Mycobacterium paraintracellulare	0.09% AE
39	Limnobacter sp.	0.25% AE	89	Cellulosimicrobium sp.	0.09% AE
40	Aquabacterium sp.	0.25% AE	90	Niallia taxi	0.09%
41	Tabrizicola piscis	0.25%	91	Microbacterium gallinarum	0.09% AE
42	Mycobacterium intracellulare	0.25% AE	92	Luteitalea sp.	0.09%
43	Mycolicibacterium vanbaalenii	0.22%	93	Enterococcus faecium	0.09% MA
44	Pseudomonas kielensis	0.22% AE	94	Acidovorax sp.	0.09% AE
45	Bacillus tuaregi	0.20% AE	95	Agrobacterium tumefaciens	0.08% AE
46	Azohydromonas sp.	0.20% AE	96	Rhodoplanes roseus	0.08% AE
47	Pseudomonas putida	0.19% AE	97	Luteitalea sp.	0.08%
48	Bradyrhizobium diazoefficiens	0.19% AE	98	Ferrovibrio sp.	0.08%
49	Solimonas sp.	0.18% OA	99	Rhodoplanes elegans	0.08% AE
50	Ensifer adhaerens	0.18% AE	100	Ottowia sp.	0.08% F

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Top 100 Fungi Species Identified

AE = Aerobic AN = Anaerobic F = Facultative AMF= Arbuscular Mycorrhizal ECM = Ectomycorrhizal			
1	Saccharomyces pastorianus	0.07% F	
2	Aspergillus sojae	0.04% AE	
3	Cutaneotrichosporon dermatis	0.04%	
4	Rhizopus microsporus	0.04%	
5	Geosiphon pyriformis	0.03% AMF	
6	Alternaria alternata	0.03%	
7	Candida albicans	0.03% AE	
8	Saccharomyces cerevisiae	0.02% F	
9	Fusarium oxysporum	0.02% F	
10	Schizophyllum commune	0.02%	
11	Fusarium solani	0.02% F	
12	Cantharellus lutescens	0.02% ECM	
13	Botryosphaeria dothidea	0.02%	
14	Puccinia striiformis	0.02% AE	
15	Clavaria fumosa	0.02%	
16	Aspergillus unguis	0.02% AE	
17	Podosphaera leucotricha	0.01%	
18	Fusarium subglutinans	0.01% F	
19	Melampsora pinitortica	0.01%	
20	Cetranspora pellucida	0.01% AMF	
21	Lasiodiplodia theobromae	0.01%	
22	Gigaspora margarita	0.01% AMF	
23	Clarireedia jacksonii	0.01%	
24	Acaulospora colombiana	0.01% AMF	
25	Rhizopus arrhizus	0.01%	
26	Fusarium proliferatum	0.01% F	
27	Pleurotus eryngii	0.01%	
28	Phenoliferia glacialis	0.01%	
29	Niveomyces insectorum	0.01%	
30	Morchella esculenta	0.01%	
31	Cantharellus cibarius	0.01% ECM	
32	Beauveria bassiana	0.01%	
33	Austropuccinia psidii	0.01%	
34	Rhodotorula graminis	0.01%	
35	Rhizophagus irregularis	0.01% AMF	
36	Rhizoctonia solani	0.01% AE	
37	Puccinia trititica	0.01% AE	
38	Metschnikowia pulcherrima	0.01%	
39	Gyromitra ancilis	0.01%	
40	Diaporthe helianthi	0.01%	
41	Coemansia sp.	0.01%	
42	Auricularia cornea	0.01%	
43	Rhodotorula babjevae	0.01%	
44	Pyricularia oryzae	0.01%	
45	Penicillium catenulatum	0.01% AE	
46	Neurospora sp.	0.01% AE	
47	Massospora cicadina	0.01%	
48	Lentinus polychrous	0.01%	
49	Friedmanniomyces endolithicus	0.01%	
50	Escovopsis sp.	0.01%	
51	Colletotrichum gloeosporioides	0.007% AE	
52	Ambrosiozyma kamigamensis	0.007%	
53	Trichoderma asperellum	0.006% AE	
54	Saitozyma podzolica	0.006%	
55	Pseudozyma flocculosa	0.006%	
56	Neurospora sp.	0.006% AE	
57	Mycena olivaceomarginata	0.006%	
58	Hortaea werneckii	0.006%	
59	Hemileia vastatrix	0.006%	
60	Golovinomyces magnicellulatus	0.006%	
61	Fusarium circinatum	0.006% F	
62	Exophiala xenobiotica	0.006%	
63	Cyathus pygmaeus	0.006%	
64	Cantharellus appalachiensis	0.006% ECM	
65	Sordaria brevicollis	0.005%	
66	Rhodotorula toruloides	0.005%	
67	Pseudogymnoascus destructans	0.005%	
68	Pestalotiopsis kenya	0.005%	
69	Penicillium sumatrense	0.005% AE	
70	Ophiostoma populinum	0.005%	
71	Mycena leptoccephala	0.005%	
72	Ganoderma lucidum	0.005%	
73	Gaeumannomyces tritici	0.005%	
74	Exophiala oligosperma	0.005%	
75	Entomophthora muscae	0.005%	
76	Corynespora cassicola	0.005%	
77	Colletotrichum siamense	0.005% AE	
78	Clarireedia paspali	0.005%	
79	Ceratocystis fimbriata	0.005%	
80	Blastocladiella emersonii	0.005%	
81	Anncaliia algerae	0.005%	
82	Ambispora leptoticha	0.005% AMF	
83	Verticillium zaregamsianum	0.004%	
84	Vanrija albidia	0.004%	
85	Trichothecium roseum	0.004%	
86	Trichoglossum hirsutum	0.004%	
87	Tremella fuciformis	0.004%	
88	Trametes sp.	0.004%	
89	Tolypocladium nubicola	0.004%	
90	Tolypocladium album	0.004%	
91	Tilletiopsis washingtonensis	0.004%	
92	Termitomyces sp.	0.004%	
93	Termitomyces sp.	0.004%	
94	Sporothrix cf.	0.004%	
95	Rhodotorula kratochvilovae	0.004%	
96	Rhizophagus clarus	0.004% AMF	
97	Racocetra fulgida	0.004% AMF	
98	Puccinia polysora	0.004% AE	
99	Puccinia arachidis	0.004% AE	
100	Parastagonospora avenae	0.004%	