

Microbiome Analysis Report

LONG PILE

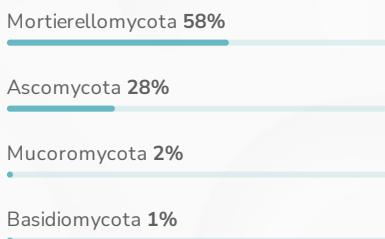
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DATE
14-Mar-2023

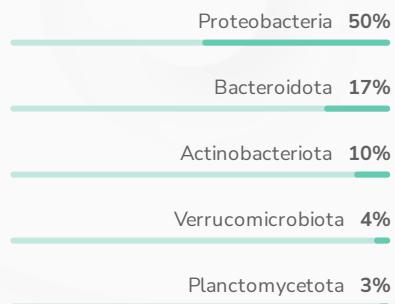
Microbial Population

All the information shown in this microbial report is based on the detected presence of 873 different species.

FUNGAL PHYLUM DISTRIBUTION



BACTERIAL PHYLUM DISTRIBUTION



Conclusions

STRENGTHS

- Carbon fixation 2%
- Inorganic nitrogen release 2%

Biosustainability

BIODIVERSITY

1.75

0 Richness, evenness and 10
equilibrium of microbial species

FUNCTIONALITY

3.37

0 Capability of soil microbial 10
communities to perform
multiple functions

Plant health improvement

Biocontrol agents, plant growth promoting organisms

BIOCONTROL

Microbial species grouped according to the type of pest they encounter, capable of preventing pathogenic species from taking hold or proliferation

Fungicide agents

< 1%

Bactericide agents

NOT DETECTED

Insecticide agents

< 1%

Nematicide agents

< 1%



HORMONE PRODUCTION

Microbial species grouped according to the type of phytohormone they generate

Auxin production (IAA)

CELL DIVISION, STEM ELONGATION

14%

Cytokinin production (CK)

CELL PROLIFERATION, CELL DIFFERENTIATION

5%

Gibberellin production (GA)

STEM ELONGATION, GERMINATION, FLOWERING

2%



STRESS ADAPTATION

Microbial species grouped according to their relationship with the metabolisms linked to the capability to withstand stress conditions

Exopolysaccharide production

NUTRIENT TRAP, SALINITY PROTECT., DROUGHT PROTECT.

5%

ACC deaminase (ACC-d)

PATHOGEN PROTECT., SALINITY PROTECT., DROUGHT PROTECT.

6%

Heavy metal solubilization

BIOREMEDIATION, DETOXIFICATION, ALLEViate HEAVY METAL STRESS

3%

Salicylic acid (SA)

DROUGHT PROTECT., SALINITY PROTECT., ALLEViate HEAVY METAL STRESS

< 1%

Salt tolerance

SALINITY PROTECT., ROOT GROWTH PROMOTION

4%

Abscisic acid (ABA)

GROWTH REGULATION, PLANT RESISTANCE, INCREASE YIELDS

< 1%



Siderophore production

IRON AVAILABILITY, BIOFERTILIZER

3%

Nutrition

Nutritional status based on the microbial mobilization of certain compounds

MAJOR COMPOUNDS



GAIN

Carbon fixation

LOSS

Aerobic respiration 7%
Fermentation 1%
Methanogenesis 3%

INDIRECT BENEFITS

Organic matter release



NUTRIENT SUPPLY

Inorganic nitrogen release

NUTRIENT COMPETITION

Inorganic nitrogen consumption 3%

INDIRECT BENEFITS

Nitrogen cycle



NUTRIENT SUPPLY

Inorganic P solubilization

NUTRIENT COMPETITION

Inorganic P consumption

INDIRECT BENEFITS

Organic P assimilation



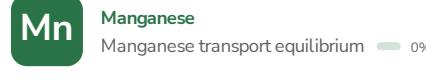
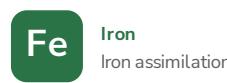
NUTRIENT SUPPLY

Potassium solubilization

NUTRIENT COMPETITION

Potassium consumption

MINOR COMPOUNDS



APPENDIX

Bacterial Quantification 2.0

Methodology

The Next-Gen sequencing in combination with the addition of a known quantity spike-in enables the knowledge of the total microbial load in a sample.

The present analysis relies on the application of a spike-in of our synthetic proprietary DNA sequence in known quantities into crude samples. After the sequencing and data processing, the relative abundance of the exogenous spike-in allows us to extrapolate the original absolute quantity of the 16S copies of the sample species, while knowledge of the number of gene copies per genome in the species allows us to calculate the number of Cells.

Results are expressed in 'cells per gram' or 'cells per milliliter', depending on the sample being a solid or liquid.

1	Rhodanobacter sp.	1.25e+8	16	Dongia sp.	3.18e+7
2	Nitrosocosmicus oleophilus	1.13e+8	17	Bryobacter sp.	3.18e+7
3	Pseudolabrys sp.	8.81e+7	18	Luteolibacter sp.	3.04e+7
4	Altererythrobacter sp.	8.81e+7	19	Povalibacter uvarum	2.75e+7
5	Acidibacter sp.	6.65e+7	20	Lysobacter sp.	2.57e+7
6	Hyphomicrobium sp.	5.15e+7	21	Gaiella sp.	2.40e+7
7	Devosia insulae	4.94e+7	22	Rhodoplanes sp.	2.39e+7
8	Pirellula sp.	4.94e+7	23	Parafilimonas sp.	2.34e+7
9	Pedomicrobium sp.	4.03e+7	24	Bauldia sp.	2.33e+7
10	Gemmamimonas sp.	3.96e+7	25	Mycobacterium brisbanense	2.27e+7
11	Lysobacter pocheonensis	3.79e+7	26	Asticcacaulis sp.	2.21e+7
12	Devosia sp.	3.68e+7	27	Pedobacter sp.	2.21e+7
13	Reyranella sp.	3.64e+7	28	Bradyrhizobium sp.	2.14e+7
14	Mycobacterium sp.	3.36e+7	29	Phenylobacterium sp.	1.97e+7
15	Stenotrophobacter sp.	3.26e+7	30	Taibaiella sp.	1.87e+7

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31	<i>Micropeltis sp.</i>	1.87e+7	53	<i>Cellvibrio sp.</i>	1.09e+7
32	<i>Mucilaginibacter sp.</i>	1.87e+7	54	<i>Arachidicoccus ginsenosidivorans</i>	1.02e+7
33	<i>Hirschia sp.</i>	1.70e+7	55	<i>Solibacter sp.</i>	9.81e+6
34	<i>Mycobacterium tusciae</i>	1.57e+7	56	<i>Planctomicrobium sp.</i>	9.62e+6
35	<i>Parvibaculum sp.</i>	1.47e+7	57	<i>Solirubrobacter sp.</i>	9.48e+6
36	<i>Luteitalea pratensis</i>	1.39e+7	58	<i>Abditibacterium sp.</i>	9.34e+6
37	<i>Dokdonella sp.</i>	1.36e+7	59	<i>Steroidobacter sp.</i>	9.20e+6
38	<i>Flavobacterium sp.</i>	1.35e+7	60	<i>Bradyrhizobium cytisi</i>	9.20e+6
39	<i>Opitutus sp.</i>	1.35e+7	61	<i>Terrimonas sp.</i>	8.98e+6
40	<i>Solimonas terrae</i>	1.34e+7	62	<i>Sphingopyxis sp.</i>	8.53e+6
41	<i>Ramlibacter sp.</i>	1.31e+7	63	<i>Hassallia sp.</i>	8.52e+6
42	<i>Terrimicrobium sp.</i>	1.29e+7	64	<i>Wandonia sp.</i>	8.34e+6
43	<i>Aquicella sp.</i>	1.26e+7	65	<i>Ohtaekwangia sp.</i>	8.22e+6
44	<i>Luteimonas lutimaris</i>	1.25e+7	66	<i>Edaphobaculum sp.</i>	8.04e+6
45	<i>Puia sp.</i>	1.25e+7	67	<i>Ilumatobacter sp.</i>	7.76e+6
46	<i>Nocardioides sp.</i>	1.22e+7	68	<i>Rhizobium sp.</i>	7.72e+6
47	<i>Ferruginibacter sp.</i>	1.21e+7	69	<i>Phenylbacterium mobile</i>	7.70e+6
48	<i>Lacunisphaera sp.</i>	1.21e+7	70	<i>Pseudorhodoplanes sp.</i>	7.59e+6
49	<i>Microbacterium paraoxydans</i>	1.19e+7	71	<i>Pseudoxanthomonas suwonensis</i>	7.54e+6
50	<i>Brevundimonas basaltis</i>	1.16e+7	72	<i>Bythopirellula sp.</i>	7.48e+6
51	<i>Pseudoxanthomonas humi</i>	1.14e+7	73	<i>Sphingomonas sp.</i>	7.43e+6
52	<i>Mesorhizobium sp.</i>	1.14e+7	74	<i>Pseudomonas putida</i>	7.29e+6

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75	Luteitalea sp.	7.15e+6	97	Micromonospora sp.	5.15e+6
76	Bdellovibrio sp.	6.87e+6	98	Hephaestia sp.	5.15e+6
77	Blastopirellula sp.	6.76e+6	99	Moheibacter sp.	5.11e+6
78	Coxiella sp.	6.65e+6	100	Iamia sp.	4.96e+6
79	Aminobacter sp.	6.56e+6	101	Novosphingobium sp.	4.95e+6
80	Solirubrobacter soli	6.32e+6	102	Nordella sp.	4.93e+6
81	Nitrospira japonica	6.26e+6	103	Neochlamydia sp.	4.78e+6
82	Aquisphaera sp.	6.06e+6	104	Achromobacter xylosoxidans	4.69e+6
83	Sphingomonas hengshuiensis	6.04e+6	105	Nitrosocosmicus sp.	4.63e+6
84	Nitrosotenuis sp.	5.99e+6	106	Mucilaginibacter polysaccharaeus	4.60e+6
85	Conexibacter sp.	5.93e+6	107	Pseudohongiella sp.	4.57e+6
86	Prosthecobacter sp.	5.82e+6	108	Shinella sp.	4.53e+6
87	Pseudaminobacter sp.	5.78e+6	109	Pedobacter boryungensis	4.41e+6
88	Chthoniobacter sp.	5.71e+6	110	Aeromicrobium marinum	4.38e+6
89	Arenimonas sp.	5.65e+6	111	Legionella sp.	4.38e+6
90	Sphingomonas daechungensis	5.65e+6	112	Galbitalea sp.	4.35e+6
91	Luteimonas mephitis	5.65e+6	113	Cellvibrio mixtus	4.34e+6
92	Nakamurella sp.	5.63e+6	114	Xenophilus aerolatus	4.29e+6
93	Novosphingobium ginsenosidimutans	5.54e+6	115	Haliangium sp.	4.21e+6
94	Luedemannella sp.	5.45e+6	116	Planctopirus sp.	4.18e+6
95	Luminiphilus sp.	5.29e+6	117	Pedobacter bauzanensis	4.17e+6
96	Nitrosospira lacus	5.21e+6	118	Brevundimonas sp.	4.13e+6

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119	Demequina sp.	4.12e+6	141	Sphingopyxis macrogoltabida	3.21e+6
120	Taibaiella yonginensis	4.05e+6	142	Paludisphaera borealis	3.18e+6
121	Nitrospira sp.	4.05e+6	143	Dyella ginsengisoli	3.13e+6
122	Arenimonas daechungensis	3.96e+6	144	Saccharimonas sp.	3.10e+6
123	Cellulomonas sp.	3.93e+6	145	Phenylobacterium koreense	3.10e+6
124	Methylobacillus sp.	3.91e+6	146	Fluvicola riflensis	3.08e+6
125	Caulobacter sp.	3.91e+6	147	Vampirovibrio sp.	3.08e+6
126	Solimonas sp.	3.82e+6	148	Hyphomicrobium facile	3.05e+6
127	Pseudoxanthomonas wuyuanensis	3.80e+6	149	Altererythrobacter mangrovi	2.99e+6
128	Adhaeribacter terreus	3.74e+6	150	Massilia sp.	2.98e+6
129	Diaphorobacter sp.	3.70e+6	151	Sphingopyxis taejonensis	2.94e+6
130	Nitrobacter vulgaris	3.60e+6	152	Nitrosovibrio tenuis	2.88e+6
131	Herminiiimonas glaciei	3.55e+6	153	Chryseolinea sp.	2.83e+6
132	Dyella sp.	3.55e+6	154	Granulicella sp.	2.83e+6
133	Klebsiella pneumoniae	3.49e+6	155	Streptomyces sp.	2.80e+6
134	Singulisphaera sp.	3.42e+6	156	Sumerlaea sp.	2.77e+6
135	Cephaloticoccus sp.	3.38e+6	157	Lysobacter soli	2.74e+6
136	Microbacterium kitamiense	3.38e+6	158	Labrys sp.	2.72e+6
137	Methanobacterium sp.	3.38e+6	159	Nitrososphaera sp.	2.72e+6
138	Porphyrobacter tepidarius	3.35e+6	160	Reyranella aquatilis	2.60e+6
139	Cytophaga sp.	3.27e+6	161	Luteolibacter gellanilyticus	2.60e+6
140	Flavitalea sp.	3.25e+6	162	Mucilaginibacter yixingensis	2.60e+6

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163	Pedobacter metabolipauper	2.59e+6	185	Microbacterium pumilum	1.83e+6
164	Roseimicrobium sp.	2.51e+6	186	Pseudomonas alcaligenes	1.83e+6
165	Luteibacter sp.	2.44e+6	187	Mitsuaria chitosanitabida	1.79e+6
166	Methyloceanibacter sp.	2.38e+6	188	Jatrophihabitans sp.	1.77e+6
167	Afipia felis	2.36e+6	189	Paludisphaera sp.	1.75e+6
168	Pseudomonas sp.	2.34e+6	190	Fontimonas sp.	1.75e+6
169	Rhodoferax sp.	2.33e+6	191	Leptothrix sp.	1.66e+6
170	Peredibacter sp.	2.30e+6	192	Methylophilus sp.	1.66e+6
171	Pedobacter composti	2.26e+6	193	Frankia sp.	1.63e+6
172	Massilia timonae	2.16e+6	194	Rhizobium giardinii	1.63e+6
173	Rhodopirellula sp.	2.16e+6	195	Legionella tucsonensis	1.63e+6
174	Hyphomicrobium denitrificans	2.16e+6	196	Nitrolancea sp.	1.61e+6
175	Niastella sp.	2.11e+6	197	Gemmata sp.	1.57e+6
176	Paenibacillus sp.	2.07e+6	198	Pseudonocardia sp.	1.57e+6
177	Pseudarthrobacter oxydans	2.05e+6	199	Rhizobium leguminosarum	1.55e+6
178	Amaricoccus sp.	2.02e+6	200	Amphiphilicatus sp.	1.50e+6
179	Sphingosinicella vermicomposti	2.00e+6	201	Arachidicoccus sp.	1.50e+6
180	Lysinimonas soli	1.91e+6	202	Nocardioides islandensis	1.50e+6
181	Pseudoxanthomonas sp.	1.91e+6	203	Berkella sp.	1.50e+6
182	Afipia sp.	1.88e+6	204	Hydrogenispora sp.	1.50e+6
183	Streptomyces thermophilaceus	1.88e+6	205	Phaselicystis sp.	1.46e+6
184	Candidimonas bauzanensis	1.85e+6	206	Pelobium sp.	1.45e+6

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207	Rhodovastum sp.	1.45e+6	229	Bosea thiooxidans	1.16e+6
208	Sphingobium sp.	1.44e+6	230	Rhizobium arenae	1.13e+6
209	Geminisphaera sp.	1.44e+6	231	Peredibacter starrii	1.11e+6
210	Alysiosphaera sp.	1.43e+6	232	Sphingopyxis alaskensis	1.11e+6
211	Microterricola viridarii	1.42e+6	233	Microvirga lotononis	1.09e+6
212	Bacillus megaterium	1.42e+6	234	Vicinamibacter sp.	1.05e+6
213	Sphingomonas changbaiensis	1.41e+6	235	Kaistia sp.	1.05e+6
214	Mucilaginibacter kameinonensis	1.40e+6	236	Phenylbacterium haematophilum	1.05e+6
215	Pajaroellobacter sp.	1.40e+6	237	Oxalicibacterium sp.	1.03e+6
216	Microbispora rosea	1.37e+6	238	Sphingomonas oligoaromativorans	1.03e+6
217	Sphingomonas wittichii	1.33e+6	239	Devosia riboflavina	9.98e+5
218	Patulibacter minatonensis	1.33e+6	240	Paenarthrobacter sp.	9.79e+5
219	Mycobacterium conspicuum	1.33e+6	241	Pusillimonas sp.	9.79e+5
220	Bordetella bronchialis	1.29e+6	242	Lysinibacillus massiliensis	9.65e+5
221	Parafilimonas rhizosphaerae	1.27e+6	243	Agromyces aureus	9.61e+5
222	Luteibacter yeoujensis	1.25e+6	244	Flavitalea gansuensis	9.61e+5
223	Dongia soli	1.22e+6	245	Arachidicoccus rhizosphaerae	9.61e+5
224	Mucilaginibacter carri	1.22e+6	246	Rhodomicrobium sp.	9.42e+5
225	Paracoccus sp.	1.22e+6	247	Aridibacter sp.	9.42e+5
226	Edaphobacter sp.	1.22e+6	248	Flavobacterium saccharophilum	9.18e+5
227	Flavisolibacter sp.	1.19e+6	249	Streptomyces avermitilis	9.05e+5
228	Lysobacter dokdonensis	1.19e+6	250	Terrimonas lutea	9.05e+5

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251	 <i>Agromyces ulmi</i>	9.05e+5		
252	 <i>Flavobacterium hauense</i>	8.87e+5		
253	 <i>Nitrosomonas oligotropha</i>	8.87e+5		
254	 <i>Algoriphagus sp.</i>	8.68e+5		
255	 <i>Lysinimonas sp.</i>	8.59e+5		
256	 <i>Pedosphaera sp.</i>	8.59e+5		
257	 <i>Sphaerisporangium sp.</i>	8.41e+5		
258	 <i>Bacillus cereus</i>	8.35e+5		
259	 <i>Aeromicrobium panaciterrae</i>	8.31e+5		
260	 <i>Xiphinema bacter sp.</i>	8.31e+5		
261	 <i>Sphingopyxis ginsengisoli</i>	8.31e+5		
262	 <i>Brevundimonas diminuta</i>	8.31e+5		
263	 <i>Streptomyces albidoflavus</i>	8.31e+5		
264	 <i>Acidicaldus sp.</i>	8.17e+5		
265	 <i>Ferrovibrio sp.</i>	8.04e+5		
266	 <i>Shinella kummerowiae</i>	7.94e+5		
267	 <i>Rhodoblastus acidophilus</i>	7.94e+5		
268	 <i>Rhodopseudomonas palustris</i>	7.76e+5		
269	 <i>Chitinophaga sp.</i>	7.76e+5		
270	 <i>Rhizobacter sp.</i>	7.76e+5		
271	 <i>Alterococcus sp.</i>	7.76e+5		
272	 <i>Noviherbaspirillum sp.</i>	7.57e+5		
273	 <i>Dokdonella ginsengisoli</i>	7.48e+5		
274	 <i>Pseudoxanthomonas helianthi</i>	7.48e+5		
275	 <i>Spirilliplanes yamanashiensis</i>	7.39e+5		
276	 <i>Dactylosporangium sp.</i>	7.39e+5		
277	 <i>Steroidobacter flavus</i>	7.20e+5		
278	 <i>Udaeobacter copiosus</i>	7.20e+5		
279	 <i>Novosphingobium barchamii</i>	7.20e+5		
280	 <i>Rhizobium etli</i>	7.20e+5		
281	 <i>Solimonas soli</i>	7.20e+5		
282	 <i>Alkalihalobacillus clausii</i>	7.05e+5		
283	 <i>Pantoea cypripedii</i>	7.05e+5		
284	 <i>Comamonas sp.</i>	6.98e+5		
285	 <i>Nocardioides daedukensis</i>	6.93e+5		
286	 <i>Leifsonia sp.</i>	6.65e+5		
287	 <i>Conexibacter woeselii</i>	6.65e+5		
288	 <i>Leifsonia lichenia</i>	6.65e+5		
289	 <i>Microlunatus sp.</i>	6.65e+5		
290	 <i>Raoultella planticola</i>	6.44e+5		
291	 <i>Luteimonas aestuarii</i>	6.37e+5		
292	 <i>Dongia rigui</i>	6.37e+5		
293	 <i>Thermomonas haemolytica</i>	6.37e+5		
294	 <i>Brevundimonas subvibrioides</i>	6.37e+5		

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295	Aeromonas hydrophila	6.32e+5	317	Udaeobacter sp.	4.99e+5
296	Micromonospora echinospora	6.28e+5	318	Sporichthya polymorpha	4.99e+5
297	Cellvibrio fulvus	6.28e+5	319	Devosia limi	4.99e+5
298	Streptomyces thermocarboxydus	6.28e+5	320	Pantoea agglomerans	4.99e+5
299	Longispora sp.	6.10e+5	321	Phytohabitans sp.	4.99e+5
300	Brevundimonas bullata	6.10e+5	322	Ensifer adhaerens	4.99e+5
301	Paeniglutamicibacter kerguelensis	5.96e+5	323	Sediminibacterium salmonicum	4.99e+5
302	Variovorax sp.	5.82e+5	324	Paludibaculum sp.	4.99e+5
303	Ancyllobacter sp.	5.82e+5	325	Terrimonas crocea	4.80e+5
304	Mesorhizobium amorphae	5.82e+5	326	Bacillus pumilus	4.78e+5
305	Paraburkholderia caribensis	5.73e+5	327	Acinetobacter johnsonii	4.75e+5
306	Shinella fusca	5.54e+5	328	Brevundimonas variabilis	4.71e+5
307	Stenotrophomonas rhizophila	5.54e+5	329	Lysobacter ginsengisoli	4.71e+5
308	Kaistia granuli	5.54e+5	330	Pseudoxanthobacter sp.	4.71e+5
309	Pseudoxanthomonas indica	5.54e+5	331	Rhodoplanes piscinae	4.71e+5
310	Oerskovia sp.	5.54e+5	332	Virgibacillus halodenitrificans	4.64e+5
311	Niabella sp.	5.54e+5	333	Pusillimonas noertemannii	4.62e+5
312	Neobacillus drentensis	5.36e+5	334	Parasegetibacter sp.	4.62e+5
313	Frateuria terrea	5.26e+5	335	Cellvibrio gandavensis	4.62e+5
314	Defluviicoccus sp.	5.26e+5	336	Adhaeribacter sp.	4.43e+5
315	Agromyces sp.	5.17e+5	337	Stenotrophobacter terrae	4.43e+5
316	Dyadobacter sp.	5.13e+5	338	Methanomassiliicoccus sp.	4.43e+5

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339	Sediminibacterium sp.	4.43e+5	361	Steroidobacter denitrificans	3.88e+5
340	Occallatibacter sp.	4.43e+5	362	Nitrospira nitrificans	3.88e+5
341	Chitinophaga taiwanensis	4.43e+5	363	Phenylbacterium conjunctum	3.88e+5
342	Cellulosimicrobium cellulans	4.43e+5	364	Glycomyces mongolensis	3.88e+5
343	Dokdonella fugitiva	4.43e+5	365	Streptomyces xishensis	3.88e+5
344	Methylocystis sp.	4.43e+5	366	Stella sp.	3.88e+5
345	Thermomonas sp.	4.43e+5	367	Advenella incenata	3.88e+5
346	Cerasicoccus sp.	4.43e+5	368	Cohnella sp.	3.81e+5
347	Reyranella massiliensis	4.43e+5	369	Bacillus acidiceler	3.77e+5
348	Salinibacterium amurskyense	4.43e+5	370	Luteolibacter flavesiens	3.69e+5
349	Olivibacter sp.	4.30e+5	371	Nocardia aciditolerans	3.69e+5
350	Paracoccus koreensis	4.25e+5	372	Bordetella petrii	3.69e+5
351	Protochlamydia sp.	4.25e+5	373	Captivus acidiprotistae	3.60e+5
352	Salinispora sp.	4.25e+5	374	Fluviicola sp.	3.60e+5
353	Roseomonas sp.	4.21e+5	375	Fluviicola hefeinensis	3.60e+5
354	Rhodococcus erythropolis	4.21e+5	376	Leucobacter sp.	3.60e+5
355	Alkanibacter sp.	4.16e+5	377	Nitrosoarchaeum limnia	3.60e+5
356	Luteimonas sp.	4.16e+5	378	Herminiimonas fonticola	3.60e+5
357	Caballeronia glathei	4.16e+5	379	Dinghuibacter sp.	3.51e+5
358	Microbacterium oxydans	4.16e+5	380	Algiphagus terrigena	3.51e+5
359	Nitrosotenuis aquarius	3.88e+5	381	Asanoa sp.	3.51e+5
360	Ovatusbacter sp.	3.88e+5	382	Nonomuraea kuesteri	3.51e+5

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383	Cytophaga hutchinsonii	3.51e+5	405	Longispora albida	3.14e+5
384	Actinoallomorus oryzae	3.33e+5	406	Roseomonas lacus	3.10e+5
385	Cupriavidus necator	3.33e+5	407	Castellaniella sp.	3.05e+5
386	Nocardiopsis dassonvillei	3.33e+5	408	Brevundimonas vesicularis	3.05e+5
387	Sphingomonas jaspisi	3.33e+5	409	Aquicella siphonis	3.05e+5
388	Leifsonia poae	3.33e+5	410	Nocardoides kribbensis	3.05e+5
389	Nitrobacter sp.	3.33e+5	411	Aquihabitans daechungensis	3.05e+5
390	Mucilaginibacter psychrotolerans	3.33e+5	412	Methylotenera sp.	3.05e+5
391	Starkeya novella	3.33e+5	413	Microbacterium thalassium	3.05e+5
392	Nitrosomonas sp.	3.33e+5	414	Shinella zooglooides	2.96e+5
393	Legionella pneumophila	3.33e+5	415	Taibaiella smilacinae	2.96e+5
394	Pedomicrobium manganicum	3.33e+5	416	Rhodococcus opacus	2.91e+5
395	Rhodococcus globerulus	3.33e+5	417	Koribacter sp.	2.77e+5
396	Rhizorhabdus argentea	3.33e+5	418	Phenylbacterium deserti	2.77e+5
397	Mesorhizobium camelthorni	3.33e+5	419	Mycobacterium frederiksbergense	2.77e+5
398	Jatrophihabitans endophyticus	3.33e+5	420	Bacillus circulans	2.77e+5
399	Schlesneria sp.	3.33e+5	421	Rugosimonospora sp.	2.77e+5
400	Pusillimonas ginsengisoli	3.14e+5	422	Frigidibacter albus	2.77e+5
401	Candidimonas sp.	3.14e+5	423	Mesorhizobium alhagi	2.77e+5
402	Streptosporangium roseum	3.14e+5	424	Bradyrhizobium japonicum	2.77e+5
403	Glutamicibacter nicotianae	3.14e+5	425	Microvirga sp.	2.77e+5
404	Nitrotoga fabula	3.14e+5	426	Actinotalea caeni	2.77e+5

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427	Sphingomonas echinoides	2.77e+5	449	Gellertiella hungarica	2.22e+5
428	Caballeronia zhejiangensis	2.63e+5	450	Jidaibacter sp.	2.22e+5
429	Aquisphaera giovannonii	2.59e+5	451	Flavimarincola sp.	2.22e+5
430	Sporocytophaga sp.	2.59e+5	452	Camelimonas lactis	2.22e+5
431	Brevibacillus borstelensis	2.52e+5	453	Microbacterium humi	2.22e+5
432	Marmoricola ginsengisoli	2.49e+5	454	Rubrobacter sp.	2.22e+5
433	Variovorax paradoxus	2.49e+5	455	Solirubrobacter phytolaccae	2.22e+5
434	Marmoricola sp.	2.49e+5	456	Terrimicrobium sacchariphilum	2.22e+5
435	Actinoplanes tereljensis	2.49e+5	457	Bosea sp.	2.22e+5
436	Microvirga ossetica	2.49e+5	458	Acidothermus sp.	2.22e+5
437	Bacillus horikoshii	2.42e+5	459	Janibacter melonis	2.22e+5
438	Isosphaera sp.	2.40e+5	460	Cellulomonas cellasea	2.22e+5
439	Tumebacillus sp.	2.40e+5	461	Vulgatibacter sp.	2.22e+5
440	Stenotrophomonas maltophilia	2.36e+5	462	Lysobacter erysipheiresistens	2.22e+5
441	Sphingobacterium faecium	2.36e+5	463	Paraburkholderia xenovorans	2.12e+5
442	Acrocarpospora sp.	2.31e+5	464	Paenibacillus glycanilyticus	2.11e+5
443	Terribacillus sp.	2.29e+5	465	Cupriavidus metallidurans	2.08e+5
444	Metabacillus niabensis	2.22e+5	466	Fimbriiglobus sp.	2.08e+5
445	Pseudoxanthomonas yeongjuensis	2.22e+5	467	Ochrobactrum intermedium	2.08e+5
446	Inquilinus sp.	2.22e+5	468	Roseomonas wooponensis	2.00e+5
447	Parviterribacter sp.	2.22e+5	469	Kitasatospora aureofaciens	1.97e+5
448	Roseiarcus sp.	2.22e+5	470	Microbacterium sp.	1.94e+5

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471	Lysobacter concretionis	1.94e+5	493	Erythrobacter sp.	1.66e+5
472	Anaeromyxobacter sp.	1.94e+5	494	Micavibrio sp.	1.66e+5
473	Niabella terrae	1.94e+5	495	Megaira polyxenophila	1.66e+5
474	Oligoflexus sp.	1.94e+5	496	Williamsia sp.	1.66e+5
475	Arsenicitalea sp.	1.94e+5	497	Pseudonocardia dioxanivorans	1.66e+5
476	Bacteriovorax sp.	1.94e+5	498	Kinneretia sp.	1.66e+5
477	Kribbella sp.	1.94e+5	499	Emticicia soli	1.66e+5
478	Luteimonas composti	1.94e+5	500	Sphingomonas soli	1.66e+5
479	Tropicimonas sp.	1.94e+5	501	Brevundimonas olei	1.66e+5
480	Nocardioides hankookensis	1.94e+5	502	Paraburkholderia susongensis	1.66e+5
481	Dyella japonica	1.94e+5	503	Pseudoxanthomonas taiwanensis	1.66e+5
482	Franconibacter sp.	1.94e+5	504	Luteibacter jiangsuensis	1.66e+5
483	Amycolatopsis albispora	1.94e+5	505	Shimazuella sp.	1.66e+5
484	Myxococcus fulvus	1.94e+5	506	Microbacterium pseudoresistens	1.66e+5
485	Bacillus oleronius	1.88e+5	507	Rhodopila sp.	1.66e+5
486	Eoetvoesia caeni	1.85e+5	508	Sphingomonas psychrolutea	1.66e+5
487	Leadbetterella sp.	1.85e+5	509	Geobacter sp.	1.66e+5
488	Stenotrophomonas panacihumi	1.80e+5	510	Labedella gwakjiensis	1.66e+5
489	Rhodococcus maanshanensis	1.80e+5	511	Microbacterium esteraromaticum	1.66e+5
490	Legionella fallonii	1.80e+5	512	Actinomadura sp.	1.66e+5
491	Sphingopyxis granuli	1.66e+5	513	Cupriavidus gilardii	1.66e+5
492	Rickettsia sp.	1.66e+5	514	Acinetobacter bohemicus	1.57e+5

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515	<i>Actinocorallia libanotica</i>	1.55e+5	537	<i>Brevibacillus sp.</i>	1.45e+5
516	<i>Sphingobacterium multivorum</i>	1.52e+5	538	<i>Actinomadura keratinilytica</i>	1.44e+5
517	<i>Pedobacter lignilitoris</i>	1.52e+5	539	<i>Comamonas jiangduensis</i>	1.44e+5
518	<i>Microvirga flocculans</i>	1.52e+5	540	<i>Thermomonas brevis</i>	1.39e+5
519	<i>Thauera sp.</i>	1.52e+5	541	<i>Pseudoxanthomonas mexicana</i>	1.39e+5
520	<i>Rhodococcus sp.</i>	1.52e+5	542	<i>Sphingomonas polyaromaticivorans</i>	1.39e+5
521	<i>Sanguibacter suarezii</i>	1.52e+5	543	<i>Microbacterium aoyamense</i>	1.39e+5
522	<i>Stenotrophomonas sp.</i>	1.52e+5	544	<i>Omnitrophus sp.</i>	1.39e+5
523	<i>Paenibacillus pectinilyticus</i>	1.50e+5	545	<i>Sphingomonas mali</i>	1.39e+5
524	<i>Methanobacterium paludis</i>	1.48e+5	546	<i>Panacagrimonas sp.</i>	1.39e+5
525	<i>Rhodococcus triatomae</i>	1.48e+5	547	<i>Pseudoxanthomonas daejeonensis</i>	1.39e+5
526	<i>Legionella anisa</i>	1.48e+5	548	<i>Profundibacterium mesophilum</i>	1.39e+5
527	<i>Segetibacter sp.</i>	1.48e+5	549	<i>Taonella sp.</i>	1.39e+5
528	<i>Metachlamydia lacustris</i>	1.48e+5	550	<i>Bacillus sp.</i>	1.39e+5
529	<i>Streptomyces albus</i>	1.48e+5	551	<i>Paraburkholderia kururiensis</i>	1.39e+5
530	<i>Mucilaginibacter pineti</i>	1.48e+5	552	<i>Halyseosphaera europeae</i>	1.39e+5
531	<i>Aurantisolimonas sp.</i>	1.48e+5	553	<i>Pedobacter insulae</i>	1.39e+5
532	<i>Nitratireductor sp.</i>	1.48e+5	554	<i>Sphingobacterium sp.</i>	1.39e+5
533	<i>Agromyces cerinus</i>	1.48e+5	555	<i>Methylotenera versatilis</i>	1.29e+5
534	<i>Rhizobium puerariae</i>	1.48e+5	556	<i>Pelomonas saccharophila</i>	1.29e+5
535	<i>Novosphingobium lindaniclasticum</i>	1.48e+5	557	<i>Georgfuchsia toluolica</i>	1.29e+5
536	<i>Protochlamydia amoebophila</i>	1.48e+5	558	<i>Pseudonocardia zijingensis</i>	1.29e+5

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559	Chelativorans sp.	1.29e+5	581	Paenibacillus sacheonensis	1.11e+5
560	Actinoplanes sp.	1.29e+5	582	Nannocystis exedens	1.11e+5
561	Streptomyces lannensis	1.29e+5	583	Nocardoides hungaricus	1.11e+5
562	Sorangium sp.	1.25e+5	584	Acinetobacter junii	1.11e+5
563	Sphingobacterium nematocida	1.25e+5	585	Pedobacter oryzae	1.11e+5
564	Tundrisphaera sp.	1.25e+5	586	Parapedobacter sp.	1.11e+5
565	Chryseobacterium sp.	1.20e+5	587	Brevundimonas balnearis	1.11e+5
566	Cohnella plantaginis	1.18e+5	588	Micromonospora chokoriensis	1.11e+5
567	Blastomonas aquatica	1.11e+5	589	Acidovorax facilis	1.11e+5
568	Oligoflexus tunisiensis	1.11e+5	590	Tepidisphaera mucosa	1.11e+5
569	Flavobacterium succinicans	1.11e+5	591	Pseudoflavitalea sp.	1.11e+5
570	Nordella oligomobilis	1.11e+5	592	Saccharomonospora azurea	1.11e+5
571	Aeromicrobium tamlense	1.11e+5	593	Mucilaginibacter soli	1.11e+5
572	Caulobacter henricii	1.11e+5	594	Marmoricola terrae	1.11e+5
573	Microvirga guangxiensis	1.11e+5	595	Labrenzia suaedae	1.11e+5
574	Chitinophaga cymbidii	1.11e+5	596	Novosphingobium tardaugens	1.11e+5
575	Aquamicrobium aestuarii	1.11e+5	597	Bacillus funiculus	1.05e+5
576	Flavihumibacter sp.	1.11e+5	598	Thermoactinomyces daquus	1.03e+5
577	Clostridium algidixylanolyticum	1.11e+5	599	Actinoplanes cibodasensis	1.02e+5
578	Cupriavidus sp.	1.11e+5	600	Laceyella sacchari	1.02e+5
579	Paracaedibacter sp.	1.11e+5	601	Parapedobacter defluvii	9.70e+4
580	Actinopolymorpha singaporense	1.11e+5	602	Rhodococcus tukisamuensis	9.70e+4

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603	Flavobacterium granuli	9.50e+4
604	Paenibacillus barengoltzii	9.42e+4
605	Paenibacillus rhizoryzae	9.42e+4
606	Sphingomonas colocasiae	9.24e+4
607	Pseudoduganella sp.	9.24e+4
608	Sediminibacterium goheungense	9.24e+4
609	Duganella radicis	9.24e+4
610	Actinoplanes globisporus	9.24e+4
611	Flavobacterium arsenitoxidans	8.71e+4
612	Fictibacillus nanhaiensis	8.71e+4
613	Brevundimonas aveniformis	8.31e+4
614	Microbacterium sorbitolivorans	8.31e+4
615	Rathayibacter oskolensis	8.31e+4
616	Hydrogenophaga intermedia	8.31e+4
617	Methylobacillus rhizosphaerae	8.31e+4
618	Estrella lausannensis	8.31e+4
619	Nocardoides aromaticivorans	8.31e+4
620	Mycetocola sp.	8.31e+4
621	Nakamurella multipartita	8.31e+4
622	Oceanicella actignis	8.31e+4
623	Leucobacter denitrificans	8.31e+4
624	Mesorhizobium olivaresii	8.31e+4
625	Aeromicrobium sp.	8.31e+4
626	Advenella mimigardefordensis	8.31e+4
627	Parapedobacter lycopersici	8.31e+4
628	Adhaeribacter terrae	8.31e+4
629	Bacillus simplex	8.31e+4
630	Angustibacter luteus	8.31e+4
631	Microvirga aerilata	8.31e+4
632	Psychrobacillus psychrodurans	7.76e+4
633	Brachybacterium tyrofermentans	7.39e+4
634	Legionella dresdenensis	7.39e+4
635	Curtobacterium flaccumfaciens	7.39e+4
636	Chryseolinea serpens	7.39e+4
637	Anaerocolumna xylanovorans	7.39e+4
638	Sporocytophaga myxococcoides	7.39e+4
639	Gordonia malaquae	7.39e+4
640	Tumebacillus avium	7.39e+4
641	Isoptericola variabilis	7.39e+4
642	Methanosaarcina mazei	7.39e+4
643	Chelativorans multitrophicus	7.39e+4
644	Agromyces atrinae	7.39e+4
645	Paenibacillus pueri	7.20e+4
646	Paenibacillus lactis	7.20e+4

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647	<i>Thermoactinomyces vulgaris</i>	7.13e+4	669	<i>Plantactinospora sp.</i>	5.54e+4
648	<i>Brevibacterium aurantiacum</i>	6.93e+4	670	<i>Nocardia sp.</i>	5.54e+4
649	<i>Microvirga vignae</i>	6.93e+4	671	<i>Verticella sp.</i>	5.54e+4
650	<i>Flavobacterium anhuiense</i>	6.93e+4	672	<i>Thermobifida alba</i>	5.54e+4
651	<i>Dyadobacter fermentans</i>	6.93e+4	673	<i>Eoetvoesia sp.</i>	5.54e+4
652	<i>Hungateiclostridium sp.</i>	6.93e+4	674	<i>Lysinimicrobium sp.</i>	5.54e+4
653	<i>Agrobacterium tumefaciens</i>	6.93e+4	675	<i>Aureimonas populi</i>	5.54e+4
654	<i>Amycolatopsis sp.</i>	6.93e+4	676	<i>Pseudonocardia carboxydovorans</i>	5.54e+4
655	<i>Mobilitalea sp.</i>	6.65e+4	677	<i>Virgisporangium sp.</i>	5.54e+4
656	<i>Domibacillus sp.</i>	6.65e+4	678	<i>Legionella bozemanae</i>	5.54e+4
657	<i>Flavobacterium nitrogenifigens</i>	6.47e+4	679	<i>Bacillus borbori</i>	5.54e+4
658	<i>Lysinibacillus sphaericus</i>	6.47e+4	680	<i>Pantoea ananatis</i>	5.54e+4
659	<i>Flavobacterium aquicola</i>	6.33e+4	681	<i>Bacillus licheniformis</i>	5.54e+4
660	<i>Ureibacillus thermosphaericus</i>	6.16e+4	682	<i>Streptomyces atratus</i>	5.54e+4
661	<i>Myroides sp.</i>	6.16e+4	683	<i>Actinomadura rubrobrunea</i>	5.54e+4
662	<i>Paenibacillus cineris</i>	6.10e+4	684	<i>Actinocorallia sp.</i>	5.54e+4
663	<i>Micromonospora echinaurantiaca</i>	5.54e+4	685	<i>Cohnella xylinolytica</i>	5.54e+4
664	<i>Methylosinus trichosporium</i>	5.54e+4	686	<i>Paenibacillus odorifer</i>	5.54e+4
665	<i>Luteolibacter luojensis</i>	5.54e+4	687	<i>Cupriavidus taiwanensis</i>	5.54e+4
666	<i>Uliginosibacterium sp.</i>	5.54e+4	688	<i>Pseudomonas koreensis</i>	5.54e+4
667	<i>Rhodobacter maris</i>	5.54e+4	689	<i>Ochrobactrum pseudogrignonense</i>	5.54e+4
668	<i>Bordetella sp.</i>	5.54e+4	690	<i>Gordonia alkanivorans</i>	5.54e+4

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691	Arcticibacter sp.	5.54e+4	713	Paenibacillus mendelii	3.88e+4
692	Angustibacter sp.	5.54e+4	714	Herbidospora cretacea	3.69e+4
693	Amycolatopsis rhabdoformis	5.54e+4	715	Streptomyces sulfonofaciens	3.69e+4
694	Kineococcus sp.	5.54e+4	716	Paenibacillus laetus	3.46e+4
695	Sphingobacterium shayense	5.54e+4	717	Pedobacter ginsengisoli	3.33e+4
696	Singulisphaera acidiphila	4.85e+4	718	Pseudomonas marincola	3.33e+4
697	Thermoactinomyces khenchelensis	4.75e+4	719	Anaerosporobacter sp.	3.33e+4
698	Flavobacterium banpakuense	4.75e+4	720	Bacillus pichinotyi	3.33e+4
699	Chryseobacterium indologenes	4.62e+4	721	Caenibacillus caldisaponilyticus	3.17e+4
700	Actinoplanes digitatis	4.62e+4	722	Clostridium sp.	3.08e+4
701	Lysinibacillus sp.	4.62e+4	723	Bacillus fordii	2.77e+4
702	Paenibacillus thailandensis	4.43e+4	724	Streptomyces turgidiscabies	2.77e+4
703	Roseomonas oryzicola	4.43e+4	725	Seinonella sp.	2.77e+4
704	Sporosarcina psychrophila	4.43e+4	726	Streptomyces bluensis	2.77e+4
705	Paenibacillus kobensis	4.43e+4	727	Acinetobacter albensis	2.77e+4
706	Streptacidiphilus sp.	4.16e+4	728	Ruminiclostridium sp.	2.77e+4
707	Paraburkholderia denitrificans	4.16e+4	729	Solibacillus silvestris	2.77e+4
708	Thermobispora bispora	4.16e+4	730	Shewanella morhuae	2.46e+4
709	Buttauxella gaviniae	4.16e+4	731	Oceanobacillus profundus	2.38e+4
710	Parapedobacter pyrenivorans	4.16e+4	732	Tuberibacillus calidus	2.38e+4
711	Kineosporia rhamnosa	4.16e+4	733	Oceanobacillus luteolus	2.38e+4
712	Oceanobacillus sojae	3.96e+4	734	Flavobacterium suncheonense	2.38e+4

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735	Flavobacterium hercynium	2.38e+4
736	Bacillus andreesenii	2.22e+4
737	Bacillus timonensis	2.22e+4
738	Bacillus gottheilii	2.22e+4
739	Geobacillus sp.	2.22e+4
740	Paenibacillus hareniae	2.22e+4
741	Cohnella laeviribosi	2.08e+4
742	Cohnella yongneupensis	2.08e+4
743	Bacillus thermoamylovorans	2.08e+4
744	Paenibacillus stellifer	2.02e+4
745	Pelosinus sp.	1.85e+4
746	Desulfosporosinus sp.	1.85e+4
747	Paenibacillus sepulcri	1.66e+4
748	Paenibacillus alginolyticus	1.66e+4
749	Paenibacillus typhae	1.66e+4
750	Paenibacillus polymyxa	1.28e+4
751	Clostridium beijerinckii	1.19e+4

Notes

Species belonging to a genus present in the CDFA Approved Microorganisms List

Species present in the CDFA Approved Microorganisms List

APPENDIX

Fungi Quantification 2.0

The Next-Gen sequencing in combination with the addition of a known quantity spike-in enables the knowledge of the total microbial load in a sample. The present analysis relies on the application of a spike-in of our synthetic proprietary DNA sequence in known quantities into crude samples. After the sequencing and data processing, the relative abundance of the exogenous spike-in allows us to extrapolate the original absolute quantity of the ITS copies of the sample species. NOTE: number of cells cannot be provided for Fungi due to many factors including very limited knowledge of ITS copies per genome, ploidy variations, pluricellularity, etc.

Results are expressed in 'ITS copies per gram' or 'ITS copies per milliliter', depending on the sample being a solid or liquid.

#	Genus & Species	Percentage	Copies	#	Genus & Species	Percentage	Copies
1	Mortierella hyalina	34.06%	~ 12 Mill.	18	Sebacina sp.	0.9178%	334,971
2	Pythium sp.	9.55%	~ 3 Mill.	19	Mortierella elongatula	0.7584%	276,806
3	Mortierella alpina	6.24%	~ 2 Mill.	20	Talaromyces marneffei	0.7277%	265,594
4	Mortierella sp.	5.61%	~ 2 Mill.	21	Mortierella gamsii	0.6662%	243,171
5	Aspergillus fumigatus	4.16%	~ 1 Mill.	22	Talaromyces columbinus	0.6451%	235,459
6	Mortierella ambigua	3.95%	~ 1 Mill.	23	Talaromyces sp.	0.6298%	229,853
7	Mortierella elongata	3.08%	~ 1 Mill.	24	Talaromyces piceae	0.5587%	203,924
8	Ochroconis sp.	2.98%	~ 1 Mill.	25	Pseudogymnoascus sp.	0.5453%	199,024
9	Chrysosporium pseudomerdari...	2.89%	~ 1 Mill.	26	Talaromyces radicus	0.5165%	188,512
10	Mortierella amoeboides	2.67%	974,082	27	Penicillium melinii	0.5126%	187,106
11	Humicola nigrescens	2.02%	735,818	28	Penicillium variratense	0.4301%	156,976
12	Penicillium citreonigrum	1.62%	591,459	29	Coniochaeta fasciculata	0.3802%	138,753
13	Penicillium solitum	1.54%	561,324	30	Penicillium amphipolaria	0.2765%	100,912
14	Mucor circinelloides	1.31%	476,529	31	Penicillium aeris	0.2746%	100,212
15	Mortierella zychae	1.16%	424,671	32	Volutella sp.	0.2669%	97,406
16	Cercophora samala	1.14%	417,665	33	Mucor racemosus	0.2515%	91,800
17	Aspergillus ustus	1.14%	415,559	34	Penicillium sp.	0.2458%	89,700

Relative Fungal Abundance

Results are expressed in 'ITS copies per gram' or 'ITS copies per milliliter', depending on the sample being a solid or liquid.

#	Genus & Species	Percentage	Copies	#	Genus & Species	Percentage	Copies
35	Aspergillus sp.	0.2438%	89,000	55	Humicola olivacea	0.0979%	35,741
36	Penicillium pinophilum	0.2381%	86,894	56	Globisporangium irregularare	0.0864%	31,535
37	Podospora sp.	0.2362%	86,194	57	Thermothielavioides terrestris	0.0864%	31,535
38	Lophiostoma sp.	0.2170%	79,188	58	Globisporangium heterothallic...	0.0845%	30,835
39	Globisporangium hypogynum	0.2074%	75,682	59	Talaromyces verruculosus	0.0845%	30,835
40	Trichoderma harzianum	0.1958%	71,476	60	Lophiostoma corticola	0.0826%	30,135
41	Pseudogymnoascus roseus	0.1882%	68,676	61	Mortierella wolffii	0.0768%	28,029
42	Globisporangium rostratifingens	0.1728%	63,071	62	Papiliotrema laurentii	0.0749%	27,329
43	Aspergillus inflatus	0.1728%	63,071	63	Chaetomium globosum	0.0730%	26,629
44	Oidiodendron truncatum	0.1709%	62,371	64	Chrysosporium merdarium	0.0710%	25,929
45	Mortierella indohii	0.1536%	56,065	65	Coniochaeta sp.	0.0672%	24,529
46	Thraustotheca sp.	0.1459%	53,259	66	Chaetomium acropullum	0.0672%	24,529
47	Penicillium griseofulvum	0.1402%	51,159	67	Tolypocladium inegoense	0.0672%	24,529
48	Pseudogymnoascus pannorum	0.1344%	49,053	68	Phialophora americana	0.0653%	23,824
49	Oidiodendron griseum	0.1325%	48,353	69	Talaromyces subtropicalis	0.0634%	23,124
50	Aspergillus versicolor	0.1286%	46,953	70	Physioprinus pouzarii	0.0634%	23,124
51	Cladosporium herbarum	0.1229%	44,847	71	Tauonia pullulans	0.0614%	22,424
52	Penicillium brevicompactum	0.1210%	44,147	72	Penicillium dierckxii	0.0614%	22,424
53	Aspergillus niger	0.1171%	42,747	73	Venturia sp.	0.0595%	21,724
54	Trichoderma asperellum	0.1037%	37,841	74	Trichoderma atroviride	0.0595%	21,724

Relative Fungal Abundance

Results are expressed in 'ITS copies per gram' or 'ITS copies per milliliter', depending on the sample being a solid or liquid.

#	Genus & Species	Percentage	Copies	#	Genus & Species	Percentage	Copies
75	 <i>Trichoderma virens</i>	0.0557%	20,324	95	 <i>Tylospora asterophora</i>	0.0288%	10,512
76	 <i>Mucor hiemalis</i>	0.0518%	18,924	96	 <i>Rhizopus oryzae</i>	0.0288%	10,512
77	 <i>Purpureocillium lilacinum</i>	0.0499%	18,218	97	 <i>Penicillium sumatraense</i>	0.0288%	10,512
78	 <i>Talaromyces rugulosus</i>	0.0461%	16,818	98	 <i>Mariannaea sp.</i>	0.0288%	10,512
79	 <i>Rasamsonia emersonii</i>	0.0461%	16,818	99	 <i>Fusarium solani</i>	0.0288%	10,512
80	 <i>Aspergillus nidulans</i>	0.0461%	16,818	100	 <i>Zopfiella marina</i>	0.0269%	9,812
81	 <i>Barnettozyma californica</i>	0.0442%	16,118	101	 <i>Aspergillus subversicolor</i>	0.0269%	9,812
82	 <i>Talaromyces neofusicolor</i>	0.0442%	16,118	102	 <i>Thermomyces lanuginosus</i>	0.0250%	9,112
83	 <i>Chaetomium sp.</i>	0.0422%	15,418	103	 <i>Penicillium lagenae</i>	0.0250%	9,112
84	 <i>Mortierella exigua</i>	0.0422%	15,418	104	 <i>Gymnopus luxurians</i>	0.0250%	9,112
85	 <i>Chrysosporium lobatum</i>	0.0403%	14,718	105	 <i>Meliomyces sp.</i>	0.0250%	9,112
86	 <i>Oidiodendron setiferum</i>	0.0403%	14,718	106	 <i>Fusicolla aquaeductuum</i>	0.0230%	8,412
87	 <i>Acremonium sp.</i>	0.0384%	14,018	107	 <i>Cercophora coprophila</i>	0.0230%	8,412
88	 <i>Oidiodendron sp.</i>	0.0384%	14,018	108	 <i>Subulicystidium brachysporum</i>	0.0230%	8,412
89	 <i>Penicillium polonicum</i>	0.0384%	14,018	109	 <i>Pyrenophaetopsis leptospora</i>	0.0230%	8,412
90	 <i>Wallemia canadensis</i>	0.0365%	13,318	110	 <i>Chaetomium homopilatum</i>	0.0211%	7,706
91	 <i>Hypomyces sp.</i>	0.0365%	13,318	111	 <i>Metarhizium marquandii</i>	0.0211%	7,706
92	 <i>Furcasterigium furcatum</i>	0.0346%	12,612	112	 <i>Neosetophoma sp.</i>	0.0211%	7,706
93	 <i>Parascedosporium putredinis</i>	0.0326%	11,912	113	 <i>Trichoderma citrinoviride</i>	0.0211%	7,706
94	 <i>Penicillium citrinum</i>	0.0307%	11,212	114	 <i>Gymnopus sp.</i>	0.0211%	7,706

Relative Fungal Abundance

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#	Genus & Species	Percentage	Copies	#	Genus & Species	Percentage	Copies
115	<i>Alternaria eichhorniae</i>	0.0211%	7,706				
116	<i>Apiotrichum gracile</i>	0.0211%	7,706				
117	<i>Cladophialophora immunda</i>	0.0211%	7,706				
118	<i>Lasionectriopsis spinosa</i>	0.0211%	7,706				
119	<i>Scedosporium boydii</i>	0.0192%	7,006				
120	<i>Trichoderma hamatum</i>	0.0192%	7,006				
121	<i>Saitozyma podzolica</i>	0.0192%	7,006				
122	<i>Orbilia luteorubella</i>	0.0192%	7,006				

Notes

Species belonging to a genus present in the CDFA Approved Microorganisms List

Species present in the CDFA Approved Microorganisms List

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