

Arbor True

21456 W Knox

Porter, TX 77365

Date Processed: 5/4/2018 Sample(s) from Harris County

Bio-Solid Analysis Report

Soil, Water and Forage Testing Laboratory Department of Soil and Crop Sciences 2478 TAMU College Station, TX 77843-2478 979/845-4816

Visit our website: http://soiltesting.tamu.edu

Section 1:	Based on analysis of over	en dried sa	mple(s)						
Laboratory #	Customer Sample Identification	Total Nitrogen %	Total Phosphorus %	Total Potassium %	Total Calcium %	Total Magnesium %	Total Sodium %	Total Zinc ppm	Total Iron ppm
45017417		0.3494	0.0549	0.2634	1.1218	0.1349	0.0445	298.81	12942.40
45017418	53	0.3315	0.0751	0.2175	1.0642	0.1334	0.0491	580.05	18923.90
45017419	52	0.9982	0.1287	0.4994	1.7214	0.1822	0.0361	68.02	5138.49
45017420	51	1.0305	0.1989	0.4853	2.0915	1.0110	0.3305	79.82	11758.00
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Cheap compost is often made with toxic materials like treated pallets and railroad ties. Toxic levels of heavy metal will result.

Laboratory #	Total Copper ppm	Total Manganese ppm	Total Sulfur ppm	Total Boron ppm	% Dry Matter	pH	Cond. Umhos/cm
45017417	175.65	193.46	754.97	4.25	64.6	7.5	1069
45017418	329.28	179.79	892.87	11.99	62.6	7.4	779
45017419	28.37	172.64	1140.43	10.23	55.4	7.3	1270
45017420	32.09	497.26	1652.48	23.84	53.2	7.6	1033

Pounds of nutrient per ton on an as received bas

Laboratory #	Customer Sample Identification	Nitrogen Ibs/wet ton	P ₂ O ₅ lbs/wet ton	K₂O Ibs/wet ton	Calcium lbs/wet ton	Magnesium lbs/wet ton	Sodium lbs/wet ton	Zinc lbs/wet ton	Iron Ibs/wet ton
45017417	200	4.52	1.63	4.09	14.50	1.74	0.57	0.386	16.730
45017418	5 3	4.15	2.15	3.27	13.32	1.67	0.62	0.726	23.694
45017419	52	11.05	3.26	6.64	19.06	2.02	0.40	0.075	5.690
45017420	51	10.96	4.85	6.20	22.25	10.76	3.52	0.085	12.510

Laboratory #	Copper lbs/wet ton	Manganese Ibs/wet ton	Sulfur lbs/wet ton	Boron Ibs/wet ton	
45017417	0.227	0.250	0.976	0.005	
45017418	0.412	0.225	1.118	0.015	
45017419	0.031	0.191	1.263	0.011	
45017420	0.034	0.529	1.758	0.025	
			A 10000	DANIE C	



Client: AT Field Tests

PCR Pathogen Panel ArborTrue Labs 21456 W. Knox Drive Porter, TX 77365 ArborTrue.com

Processed: 5-1-2018

Properly aged compost will have time to "cook" out the pathogens

Sample 2 NEG Sample 2 POS Sample 4 POS

> All but one compost yard tested positive for common disease causing pathogens

Soil Foodweb Report

1. 1



Environment Celebration Institute Inc. 13193 Oroville Quincy Highway Berry Creek, CA 95916 530-589-9947 info@environmentcelebration.com

Arbor True En Brad Phillips 21456 W. Knox Dr. Porter, TX 77365 (832)803-8950 388arborist@gmail.com April 13, 2018

"Dedicated to promote peace, harmony, and dignity amongst all living things

Beneficial Microorganisms	Minimum Reauirements	Sample Results	Sample Name: Sample L Sample Type: Compost Plants Present/Desired: Turf = Standard Devlation
Bacteria (um/g)	300	4,304	High: The bacterial biomass is above the recommended range.
		583	Needs to be reduced.
Actinobacteria (um/g)	1-4	0.5	Low: The actinobacteria is lower than what is normally found in
		0.3	healthy soils with similar plants.
Fungi (um/g)	300	77	Low: The beneficial fungal biomass does not meet the minimum
		114	recommendations. Need to replenish and enhance.
F:B Ratio	0.8:1 - 1:1	0.02	Low: The bacterial biomass needs to be reduced and the fungal
			biomass needs to be replenished. Once this is achieved, then the F:B ratio will be closer to the desired range for your types of plants.
Protozoa (Total)	>50000		Good: The beneficial protozoa numbers observed met the minimum
Flagellate (#/g)	(See Total)	16,304	requirements for your types of plants.
		36,457	
Amoebae (#/g)	(See Total)	65,216	
		36,457	
Nematodes			
Bacterial-feeding (#/g)	200	0	None detected: Bacteria-feeding nematodes help keep bacteria
			populations in balance. Need to replenish. None detected: Fungal-feeding nematodes help to release nutrients
Fungal-feeding (#/g)	20	0	from fungal hyphae to the plants. Need to replenish.
Predatory (#/g)	2	0	None detected: Need to replenish.
Detrimental Microorganisms			
Disease-Causing Fungi			
Oomycetes (um/g)	0	0	None detected. No disease-causing fungi were observed in the
		0	sample. Great!
Anaerobic Protozoa			
Ciliate (#/g)	0	0	None detected: No ciliates were observed in the sample. Great!
		0	
<u>Nematode</u>	40-1		
Root-feeding (#/g)	0	0	None detected. No root-feeding nematodes were detected. Great!

Soil Foodweb Report



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Were any anaerobic indicating bacteria observed in the sample? Were any pathogenic bacteria observed in the sample?

Sample Name. Sample 7 Sample 7 Sample 7 Sample 7 Plants Present/Desired: = Standard Deviation Beneficial Microorganisms Okay: The results were within range but very high compared to beneficial fungi biomass. Reducing bacteria is recommended. Bacteria (um/g) 300 1.663 213 ow: The actinobacteria is lower than what is normally found in Actinobacteria (um/g) 1-4 0.6 healthy soils with similar plants. 0.4 w: The beneficial fungal biomass does not meet the minimum commendations. Need to replenish and enhance. 300 27 Fungi (um/g) 40 Low: The bacterial biomass needs to be reduced and the fungal biomass needs to be replenished. Once this is achieved, then the F:B ratio will be closer to the desired range for your types of plants. F:B Ratio 0.8:1 – 1:1 0.02 Low: Bacteria is the main source of food for protozoa. Protozoa help to keep the bacterial biomass in range and release nutrients into plant available form by consuming the bacteria. Need to replenish. Protozoa (Total) >50000 (See Total) Flagellate (#/g) 0 (See Total) 8,152 18,228 Nematodes e detected: Bacteria-feeding nematodes help keep bacteri Bacterial-feeding (#/g) 200 oppulations in balance. Need to replenish.

None detected: Fungal-feeding nematodes help to release r 20 Fungal-feeding (#/g) om fungal hyphae to the plants. Need to replenish None detected: Need to replenish. Predatory (#/g) **Detrimental Microorganisms** Disease-Causing Fungi None detected. No disease-causing fungi were observed in the Oomycetes (um/g) sample, Great! 0 Anaerobic Protozoa one detected: No ciliates were observed in the sample. Great! one detected. No root-feeding nematodes were detected. Great! Root-feeding (#/g) 0 0

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April 13, 2018

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Sample Name:	4	Samo	le3
Sample Type: Com	pos	t ¹	

Beneficial Microorganisms	Minimum Reauirements	Sample Results	
	300	4 500	Standard Deviation Okay: The results were within range but very high compared to
Bacteria (um/g)	300	1,500	beneficial fungi biomass. Reducing bacteria is recommended.
		136	
Actinobacteria (um/g)	1-4	0.7	Low: The actinobacteria is lower than what is normally found in healthy soils with similar plants.
		0.5	
Fungi (um/g)	300	37	Low: The beneficial fungal biomass does not meet the minimum
		58	recommendations. Need to replenish and enhance.
F:B Ratio	0.8:1 - 1:1	0.02	Low: The bacterial biomass needs to be reduced and the fungal biomass needs to be replenished. Once this is achieved, then the F:B
			ratio will be closer to the desired range for your types of plants.
Protozoa (Total)	>50000		None detected: Bacteria is the main source of food for protozoa.
Flagellate (#/g)	(See Total)	(See Total) 0 Protozoa help to keep the bacterial bioma	
		0	nutrients into plant available form by consuming the bacteria. Need to replenish.
Amoebae (#/g)	(See Total)	0	CO CONCINOTO
,,,,,,		0	
Nematodes			
Bacterial-feeding (#/g)	200	0	None detected: Bacteria-feeding nematodes help keep bacteria populations in balance. Need to replenish. None detected: Fungal-feeding nematodes help to release nutrients
Fungal-feeding (#/g)	20	0	None detected: Fungal-feeding nematodes help to release nutrients from fungal hyphae to the plants. Need to replenish.
Predatory (#/g)	2	0	None detected: Need to replenish.
Detrimental Microorganisms	75.55		
Disease-Causing Fungi			
Oomycetes (um/g)	0	0	None detected. No disease-causing fungi were observed in the
	7.17	0	sample. Great!
Anaerobic Protozoa			
Ciliate (#/g)	0	0	None detected: No ciliates were observed in the sample. Great!
	200	0	
Nematode			
Root-feeding (#/g)	0	0	None detected. No root-feeding nematodes were detected. Great!

Were any anaerobic indicating bacteria observed in the sample? Were any pathogenic bacteria observed in the sample?