



# Bacterial Microbiome Report

**Sample Name:**PEG00001  
**Prepared For:** Permaculture Gardens  
**Prepared On:** 11/05/2023

DNA concentration post extraction:	36.9 ng/ul
Total high quality 16S bacterial sequences:	97522
Total Unique Sequences:	2312
Shannon Diversity:	6.89
Potential plant growth promoting organisms:	34.6%
Anaerobic indicator organisms:	5%
Pathogen Indicator organisms:	0.01%

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# Alpha Diversity

Alpha Diversity is a measurement of species “richness” or number of species in a sample and “evenness” or how proportionally they are distributed in the population.

We provide two alpha diversity measurements “total unique sequences” which is a species estimate and the Shannon diversity index which takes into account both species richness and evenness.

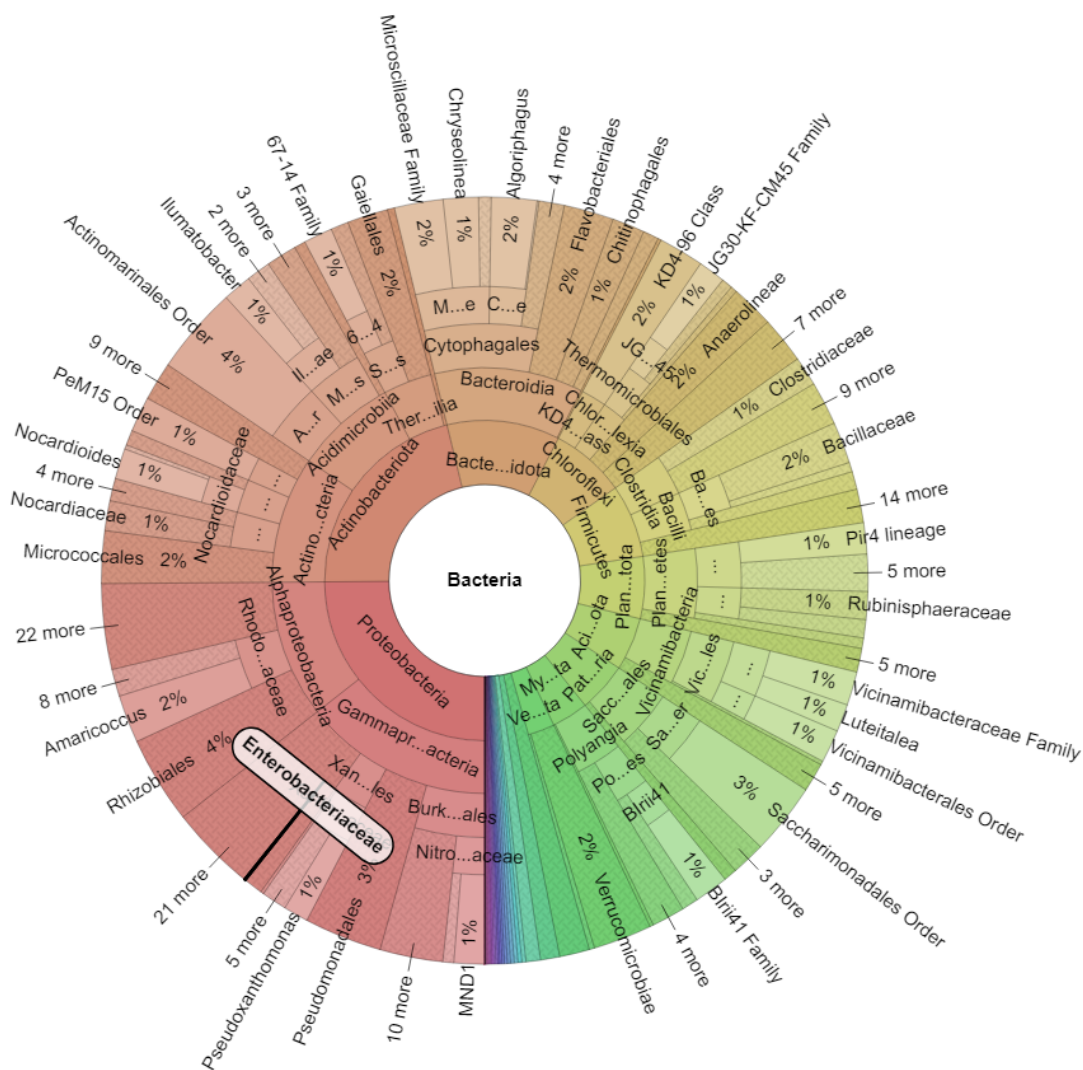
Total Unique Sequences: 2312

Total Observed Genera: 630

Shannon Diversity: 6.89

# Krona Plots

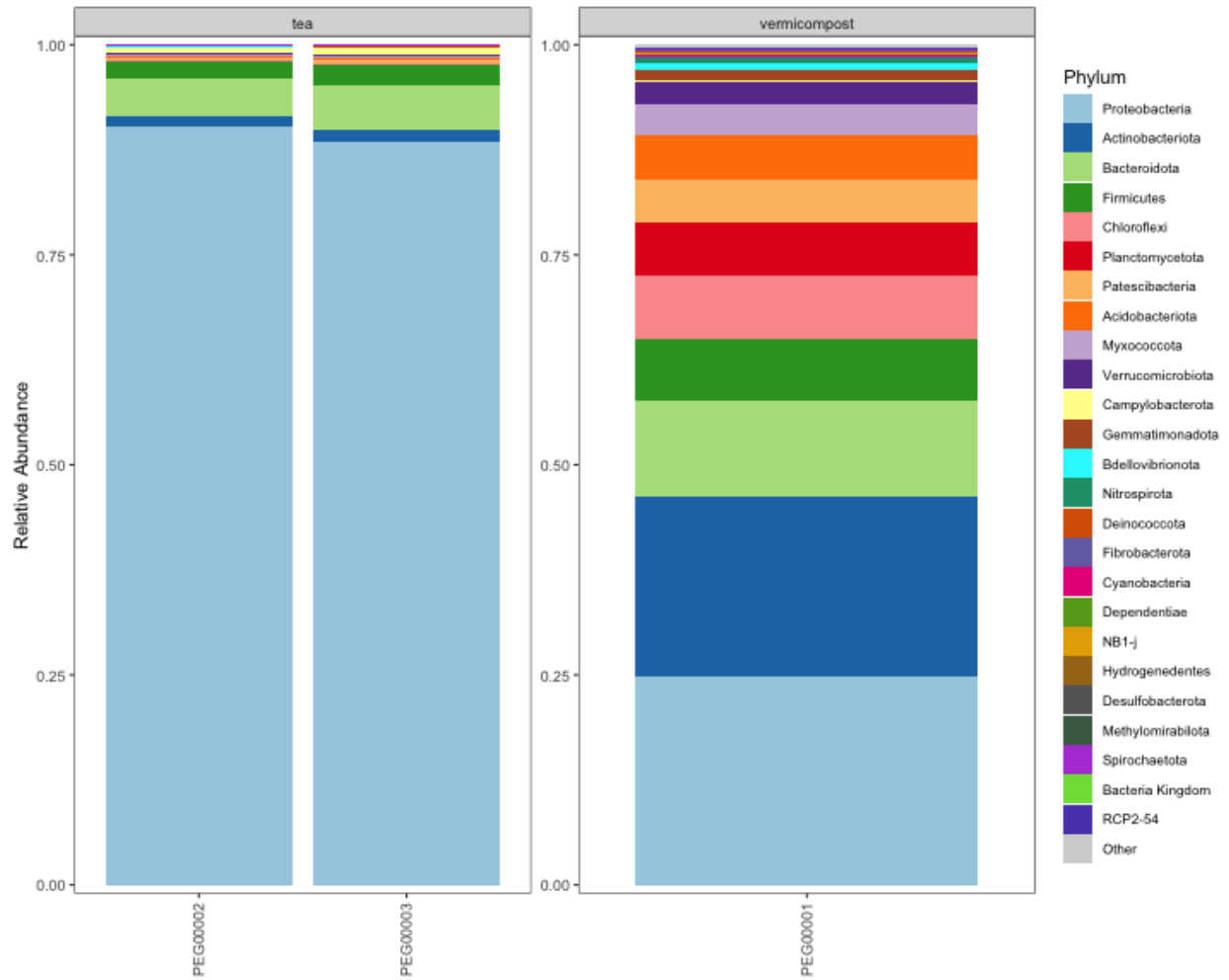
These plots are our preferred way to view sample data as it is an interactive way to explore your sample(s) microbiome from Phylum down to the genus level. Open the files directly from the folder with a web browser. Each sample is listed in the top left and can be individually selected. Double click on any sections of the graph to zoom in. Zoom back out by clicking in the middle of the plot. Statistics about the selected organisms are shown in the top right. Please contact Zack for any help with the plots.



# Taxonomy Bar Plots

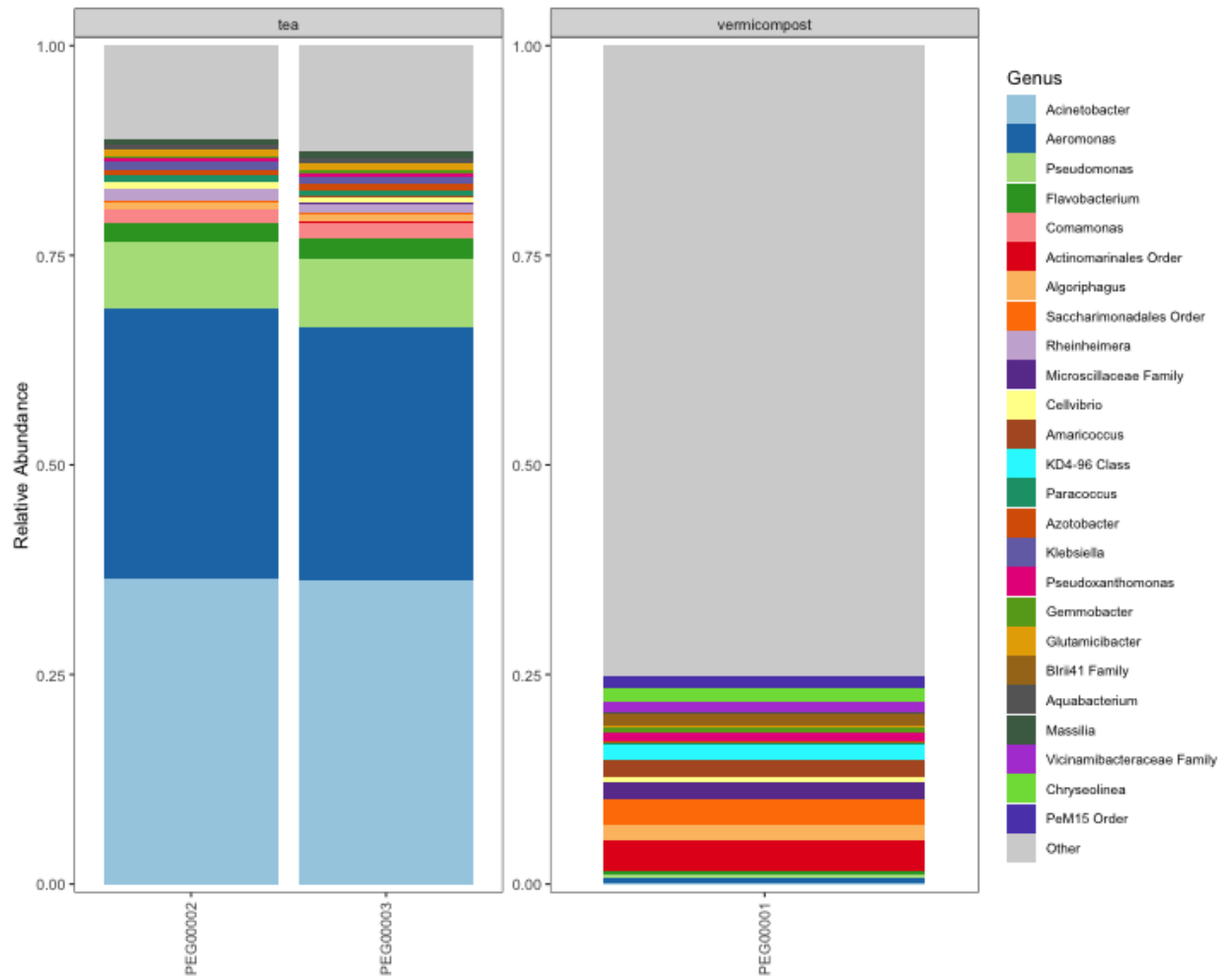
## Phylum Level

The top 25 Phyla are shown. This is the highest level of classification.



# Genus level

The top 25 genus (one level above species). Large gray “other” bar is due to the high diversity of the sample and represents all organisms outside of the top 25 most abundant.



# Beneficial Organism Analysis

Aggrego Data performs a screening for potential beneficial organisms using a proprietary database based on published literature. For vermicompost, the three main groups of beneficial bacteria are Rhizobiales (Order), Actinobacteria (Class), and Bacillales (Class). Other potentially beneficial organisms are also included.

## Order: Rhizobiales (4%)

This order of organisms are well-known beneficial partners in plant-microbe interactions. They commonly exert beneficial functions for their hosts by providing various nutrients, phytohormones as well as precursors for essential plant metabolites. The order contains many Genus of nitrogen-fixing, methanotrophic, legume-nodulating, microsymbiotic bacteria. (Garrido-Oter et al. 2018)

### Family: Hyphomicrobiaceae (1%)

#### Genus: Hyphomicrobium (0.3%)

Budding, methanol utilizing microorganisms. They have been seen in the rhizosphere of wheat and pea plants (Macey et al. 2020) and increased in the presence of earthworms and AMF (Cao, Ji, and Wang 2015). Some species are known nitrogen (N<sub>2</sub>) fixers (Fesefeldt et al. 1998)

#### Genus: Pedomicrobium (0.4%)

- Positively correlated with plant growth in long term organic fertilizer agriculture study (Shi et al. 2021)
- Iron and manganese oxidizers with some strains. Similar to Hyphomicrobium in that they both form filamentous hyphae. (Gebbers 1981)
- Seen to be increased in abundance of sugar beet rhizosphere (Szymańska et al. 2021)

### Family Xanthobacteraceae (0.5%)

Mainly nitrogen fixers (Oren 2014)

### Family: Devosiaceae (0.3%)

#### Genus: Devosia (0.2%)

Contains several species of plant growth promoting organisms which produce siderophores and plant growth hormones- auxin (Chhetri et al. 2022).



They also produce flavonoids which have been shown to significantly increase seed germination of canola and soy under ideal and salt stressed conditions (Shah, Subramanian, and Smith 2022).

Long term organism fertilization increased the abundance of devosia in kiwi fruit rhizosphere and was correlated to increase in crop yield (Liu et al. 2020).

Some species of devosia have also been shown to fix nitrogen in legume nodules (Rivas et al. 2003; "Devosia Yakushimensis Sp. Nov., Isolated from Root Nodules of Pueraria Lobata (Willd.) Ohwi | Microbiology Society" n.d.).

#### Family: Rhizobiaceae (0.8%)

Contains genera associated with soil and plant hosts. Bacteria in this family are predominantly aerobic and contain large plasmids which harbor a large proportion of their genome including genes involved in interactions with specific hosts including nitrogen fixation (Alves et al. 2014).

##### Genus: Mesorhizobium(0.2%)

- Contains species widely known as nitrogen fixing bacteria for legumes
- In a paper studying 24 strains 100% produced indole acetic acid (IAA) an auxin, 46% solubilize potassium, 33% solubilize phosphate, and 17% produce siderophores which make iron available. (Menéndez et al. 2020)
- Has the ability to colonize roots of different plants and demonstrated increased growth/macro nutrient uptake of tomato seedlings when inoculated (Menéndez et al. 2020)
- Increased growth and phosphorus content of chickpeas and barely when inoculated into soils with insoluble forms of phosphorus. (Peix et al. 2001)
- Indigenous Mesorhizobium increased nutrient uptake growth and yield of chickpea plants.

#### Family: Sphingomonadaceae (0.3%)

Sphingomonadaceae family promotes plant growth by producing phytohormones such as auxin and gibberellin, alleviating heavy metal and drought stress, and protecting against pathogens. (Nakayasu et al. 2021; Khan et al. 2014)

## Gammaproteobacteria (14%)

#### Order: Burkholderiales (4%)

##### Family: Nitrosomonadaceae (2%)

All organisms in this family are ammonia oxidizers. In an agricultural context they can cause a loss of ammonium based fertilizers through nitrous oxide off gassing and nitrate leaching (Prosser, Head, and Stein 2014).

Family: Comamonadaceae (1%)

Genus Rhizobacter

Possible plant pathogen that causes root gall in carrots (Kawarazaki et al. 2012).

Order: Pseudomonadales (3%)

Family: Pseudomonadaceae (0.8%)

Genus: Pseudomonas (0.6%)

- One of the most highly studied PGPB as they produce any antifungal molecules for disease suppression. They also can produce phytohormones auxin and gibberellin as well as siderophores. (Dorjey, Dolkar, and Sharma 2017)
- Same species of pseudomonas can be both plant pathogens and beneficial organisms to plants (Preston 2004).
- Found to be key PGPB in garlic with six different beneficial strains isolated (Zhuang et al. 2021) .

Genus: Azotobacter (0.2%)

“Two strains *A. chroococcum* 67B and 76A were selected for their multiple plant growth promotion activities (N<sub>2</sub>-fixing activity, synthesis of siderophores and indole-3-acetic acid) as well as antimicrobial activity against *Sclerotinia minor*. The two *Azotobacter chroococcum* strains exhibited high tolerance to salt and drought stresses and could alleviate the negative effects exerted by abiotic stress on tomato plants. Overall results showed that the strains *Azotobacter chroococcum* 67B and *Azotobacter chroococcum* 76A could be interesting candidates to be employed as bio-effector in sustainable agricultural systems also under stressful conditions leading to improved economic and environmental benefits.” (Viscardi et al. 2016)

Seed bacterization with Azb19 [*Azotobacter chroococcum*] resulted in increased plant height, shoot height, root volume, leaf area and total plant dry mass. Further, bacterial inoculation also significantly increased macro-and micronutrient uptake by sorghum plants. (Sultana, Desai, and Reddy, n.d.)

Family: Cellvibrionaceae (1%)

Genus: Cellvibrio (0.5%)

Nitrogen fixer and positively associated with wheat yield (Anderson and Habiger 2012; Suarez et al. 2014)

Part of core microbiome of Mexican teosinte seeds. (De-la-Vega-Camarillo et al. 2023)

Stimulated by biochar amendments and known to fix N

Family: Moraxellaceae(0.2%)

Genus: Acinetobacter (0.03%)

- Some isolates were able to produce auxin, while nearly all were able to solubilize phosphorus, and all produced siderophores. Also evidence for fungal pathogen inhibition. Significantly enhanced the shoot height, root length, and root dry weights of pearl millet seedlings in pot experiments when compared with controls, underscoring the plant-growth-promoting potential of these isolates (Rokhbakhsh-Zamin et al. 2011).
- Acinetobacter is a Gram-negative bacterium present everywhere in nature and is usually found in the rhizosphere of many plants. It plays a significant role as plant growth-promoting bacteria (PGPR) and has gained importance in agriculture worldwide. Acinetobacter is known to produce IAA, siderophore, gibberellin, antibiotic, biosurfactants/bioemulsifiers and solubilize phosphate, potassium, and zinc, which make it an important PGPR (Mujumdar et al. 2023).

Order: Xanthomonadales (2%)

Strictly aerobic organisms with diverse metabolisms especially that of hydrocarbons. Contains Xanthomonas genus (within the Xanthomonadaceae family below) which is known for many phytopathogens. However, this order also contains species known to be beneficial to plants and provide disease resistance.(Stewart et al. 2021)

Family: Xanthomonadaceae (2%)

Genus: Pseudoxanthomonas

Isolate seen to solubilize phosphorous, fix N, solubilize iron (siderophore production), reduce plant stress (ACC deminase), and produce auxin (IAA). (Castellano-Hinojosa et al. 2016)

Isolate shown to be arsenic resistant, HCN production, auxin production, and N fixation. Reduced harmful effects of arsenic on plant growth and stimulated plant growth of mung beans. (Huda et al. 2022)

Genus: Arenimonas (0.5%)

- Found in early growth stages of corn and seedlings of tomatoes suggesting plant growth promoting properties but more study is needed (Hu et al. 2020; Li et al. 2014)
- Bioremediation Generalist (Brereton et al. 2020)

## Order: Enterobacterales (0.8)

### Family: Aeromonadaceae (0.6%)

#### Genus: Aeromonas (0.6%)

- This genus contains potential human pathogens as well as plant growth promoting organisms. It is unclear which type of organisms are present.
- Can degrade fungicide MBC and contains plant growth promoting properties include phosphorus and zinc solubilization, auxin production, and HCN production (Silambarasan and Abraham 2020)
- “The species *Aeromonas salmonicida* N264 promoted the largest number of tillers [sugarcane] 30 and 45 DAI [days after inoculation], with 30.26 total indoles and 14.83  $\mu\text{g mL}^{-1}$  phosphate solubilization.” (Morgado González et al. 2015)
- “The data reveal that plants inoculated with the bacterial consortium (SAL-21 + SAL-17) [both *Aeromonas* isolates] showed a maximum increase in leaf proline content, nitrate reductase activity, chlorophyll a/b, stomatal conductance, transpiration rate, root length, shoot length, and grain weight over non-inoculated plants grown in saline soil. Also produces auxins, plant salt tolerance hormones, and ACC deaminase. (Nawaz et al. 2020)
- Under suboptimal root zone temperature nodule number and dry weight of plants receiving *Aeromonas hydrophila* P73 they were increased by 72 and 31% at  $17\pm 5$  °C RZT when coinoculated with *Bradyrhizobium*. (Zhang 1997)
- “*Aeromonas caviae* strain A1-2 showed positive results in in vitro tests for plant growth-promoting traits such as indole-3-acetic acid production (7), nitrogen fixation (5), phosphate production (8), 1-aminocyclopropane-1-carboxylate (ACC) deaminase production (9), ammonia production (10), and siderophore production (5).”

### Family: Rhodanobacteraceae (0.2%)

Members from this family contain several genera have been reported as terrestrial PGPB; *Rhodanobacter* sp. MTR-45B as an efficient PGPB for quailbush and buffalo grass, *Dyella* spp. for *Lespedeza* sp., *Luteibacter rhizovincinus* MIMR1 for barley, *Frateuria aurantia* for tobacco, and *Dokdonella* spp. for wheat. These data indicate that this family tends to contain multiple PGPB strains (Makino et al. 2022).

## Class: Bacilli (3%)

Aerobic spore formers

Family: Bacillaceae (2%)

Genus: Ureibacillus (0.0.6%)

Associated with composts with disease suppression properties(Mayerhofer et al. 2021)Mayer

Genus: Bacillus (0.7%)

- Bacillus Subtilis is one of the most studied PGPB and one of the most commonly isolated Genus from the soil. It has been shown to fix nitrogen, solubilize phosphorus, produce phytohormones, as well as reduce drought and salt stress. It has also been shown to inhibit fungal and bacterial plant pathogens. (Blake, Christensen, and Kovács 2021).
- Several other species of this genus have also been identified as PGPB and share properties of B.Subtilis. (Sansinenea 2019)

Genus: Geobacillus

- “ The Geobacillus thermodenitrificans PS41 secondary metabolites showed potential antifungal activity against plant pathogenic fungi. However, no toxic effect was exerted upon earthworm (*Perionyx excavatus*) when treated with PS41 bacterial metabolites. The potential PS41 strain was also found supporting the plant growth. The potential bacterial strain PS41 did not show antagonistic activity against soil bacteria. The potential test organism, Geobacillus thermodenitrificans PS41, possessing biopesticide and biofertilizer properties can be a suitable ecofriendly organic applicant in agricultural field for enhancing crop production.”(Siddharthan et al. 2023)
- Isolate seen to be Arsenic resistant, produce auxin, siderophores, and AAC deaminase. (Das et al. 2014)

Family: Paenibacillaceae (0.1%)

Genus: Paenibacillus (0.05%)

Plant growth promoting organisms known to fix nitrogen, produce antimicrobial compounds, increase nutrient availability through hydrolytic enzymes, and produce auxins, gibberellins and AAC deaminase. (Jeong et al. 2011; Verma et al. 2016).

Family: Planococcaceae (0.2%)

Species within this family are seen to solubilize phosphorus, magnesium and zinc, as well as produce auxins(Verma et al. 2016).

## Class: Actinobacteria (10%)

One of the most promising classes of organisms for plant growth promotion as some species show nearly all capabilities of plant growth promotion. (Boukhatem, Merabet, and Tsaki 2022)

### Order: Micrococcales (2%)

Family: Demequinaceae (0.9%)

Genus: Demequina (0.9%)

Strongly correlated with plant growth in apple orchards (Peruzzi et al. 2017)

Family: Microbacteriaceae (0.5%)

Isolate from wild rice was the highest producer of phytohormone out of >200 isolates (Borah et al. 2018).

Genus: Leucobacter (0.2%)

Has plant growth promoting properties including ACC deaminase (Kadioglu et al. 2018) and auxin production (Yoo, Ji-Yeong et al. 2017).

Genus: Agromyces

ACC deaminase and Auxin production (Bal et al. 2013)

Genus: Microbacterium (0.2%)

- Volatiles from root-associated bacteria of the genus *Microbacterium* can enhance the growth of different plant species and can prime plants for growth promotion without direct and prolonged contact between the bacterium and the plant (Cordovez et al. 2018).
- "Strain AI-S262T exhibited ACC deaminase activity, phosphate solubilization and sulfur oxidation when examined through plate assays but was negative for siderophore production. Strain AI-S262T produced IAA and ACC deaminase activity at a concentration of 12.3  $\mu\text{g ml}^{-1}$  and a rate of 20.2  $\text{nmol } \alpha\text{-ketobutyrate min}^{-1}$  ( $\text{mg protein}^{-1}$ ), respectively. From the gnotobiotic growth pouches assay, the root lengths of the AI-S262T-treated tomato (16.2% increase over control) and canola (45.7% increase over control) seeds were comparatively greater when compared with the uninoculated control (data not shown)." (Madhaiyan et al. 2010)

- “ Microbacterium sp. P27 showed positive result for Indole-3-acetic acid production, ammonia production, and 1-aminocyclopropane-1-carboxylate deaminase activity.(Singh and Singh 2019)”

Genus: Frondihabitans (0.3%)

Isolate shown to produce auxin, fix nitrogen, and wide range and antimicrobial activity (Vega-Celedón et al. 2021)

Genus: Agromyces (0.03)

ACC deaminase and Auxin production

Family: Micrococcaceae (0.1%)

Genus: Pseudarthrobacter (0.05%)

An in vitro test revealed that the strain could fix nitrogen, solubilize phosphate and potassium, and synthesize indole acetic acid. The bacterial strain was identified and characterized as a kind of Pseudarthrobacter chlorophenolicus. tomato plants treated with strain BF2P4-5 showed little to no variation with NPK fertilizer treatment, including plant height, stem length, girth, leaf number per plant, and chlorophyll content. (Issifu et al. 2022)

Gram-positive, aerobic, rod-shaped, auxin-producing bacterium. The strain contains genes related to auxin biosynthesis and heavy metal resistance (Park et al. 2020).

Order: Propionibacteriales (2%)

Family: Nocardioidaceae (1%)

Genus: Nocardioides (1%)

Have been isolates from Grapevine roots and capable of siderophore production, nitrogen fixation and antifungal properties (Nafis et al. 2019).

Identified as PGPB in sugar beets (Okazaki et al. 2021).

## Order: Streptosporangiales (0.22%)

### Family: Streptosporangiaceae (0.06%)

Members of the family are mainly found in soil and a few species were isolated from seashore including sand or sediments, and plant materials including roots and leaves (Otoguro, Yamamura, and Quintana 2014)

This family contains many isolates of plant growth promoting bacteria (Hamedi and Mohammadipanah 2015).

### Genus: Thermopolyspora (0.03%)

Significantly associated with highly disease suppressing composts (Marasco et al. 2022).

## Order: Micromonosporales (0.5%)

### Family: Micromonosporaceae (0.5%)

Several members of this family are known as PGPB. They have been found to fix nitrogen and produce auxins and gibberellins (Hamedi and Mohammadipanah 2015).

### Genus: Longispora (0.7%)

Isolate of this genus is found to produce HCN, antifungal properties, and solubilize phosphorus. (Boukaya et al. 2018)

## Family: Streptomycetaceae (0.4%)

### Genus: Streptomyces (0.4%)

One of the most promising Genus of organisms for both biocontrol and biofertilizer. They produce a range of antimicrobial compounds accounting for nearly 60% of production of agriculturally important antibiotics. They also have nearly all plant growth promoting abilities including auxin production, nitrogen fixation, phosphate solubilization, and siderophore production (Boukhatem, Merabet, and Tsaki 2022; Sousa and Olivares 2016).

## Order: Flavobacteriales (2%)

### Flavobacteriaceae (0.8%)

#### Genus: Flavobacterium (0.3%)

Represent a significant fraction of root- and leaf-associated microbiomes in a broad range of plant species. (Kolton et al. 2016)



34/44 flavobacterium isolates were able to solubilize inorganic phosphorus and all isolates were able to produce auxin (Soltani et al. 2010)  
Strain showed highest beneficial effects on plant growth parameters for maize inoculum due to nitrogen fixation, auxin production, and siderophore production.(Youseif 2018)  
Increased wheat yield by 15% compared to control (Rahmani et al. 2016).  
SHown to increased drought and salt stress tolerance (Kim et al. 2020)  
Suppressed wilt in tomato plants (Kwak et al. 2018)

## Phylum: Acidobacteria (5%)

Relatively unknown phylum due to difficulty in culturing but very commonly found in soil. There is genetic evidence for nitrogen fixation, auxin production, siderophore formation, antifungals, antibiotics, antivirals, antitumor agents, and antinematodal agents . There are also studies suggesting that these are “keystone” organisms in soil environments and ecosystem engineers due to their ability to drive various nutrient cycles and plant growth promotion. (Kalam et al. 2020)

### Class: Vicinamibacteria (4%)

Order: Vicinamibacterales (4%)

Family: Vicinamibacteraceae (3%)

Members of the Vicinamibacteraceae are aerobic, neutrophilic, psychrotolerant to mesophilic chemoheterotrophs. Their cells stain Gram-negative, do not form capsules or spores, and are non-motile. (Huber and Overmann 2018)

Genus:Luteitalea

## Phylum: Patescibacteria (5%)

Order:Saccharimonadales (3%)

Our results suggest that addition of sugars selected for indigenous soil Saccharimonadales, enhancing alkaline phosphatase activity in the rhizosphere. These rare microbial taxa may be a key species in soil phosphorus cycling.(Wang et al. 2022)

# Anaerobic Indicator Organisms:

These groups of organisms are commonly found in vermicompost (ideally at low abundances) and include all anaerobic organisms

## Class: Clostridia (3%)

All organisms in this class lack aerobic respiration and are known to ferment decaying plant material. Unlikely to contain any plant growth promoting properties.

## Class: Anaerolineae (2%)

Cells are non-spore-forming, nonmotile, and filamentous. Known described species are fermentative and grow under strictly anaerobic conditions (Yamada and Sekiguchi 2018).

Comment: These are fairly low abundances for anaerobic organisms. Nearly all vermicompost has some amount of anaerobic organisms. They are not “bad” but a large population of them might indicate your composting or storage conditions are not suitable for aerobic beneficial organisms.

# Pathogenic Indicator Organisms

These organisms are *potential* human pathogens. We are currently only screening for the family Enterobacteriaceae as it includes human pathogens such as Salmonella, Escherichia coli, Klebsiella, Shigella, Enterobacter and Citrobacter . Members of the Enterobacteriaceae can be referred to as enterobacteria or "enteric bacteria" as several members live in the intestines of animals.

Family: Enterobacteriaceae (0.1%)

All organisms of this family in this sample are undefined past this level and unlikely to be pathogenic as all human pathogens are heavily studied and identified.

Comment: This is a really low percentage and nothing to be concerned about. No vermicompost is 100% free of these types of organisms and are unlikely to be pathogenic to humans.

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