



## Exploration Of Plant Microbiome Diversity And Its Implications For Agriculture

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### Abstract

Organisms and plants co-developed and interface normally. Plant microbiota are crucial for vegetation. Contingent upon have wellbeing, plant-microorganism (PM) communications are fortunate or unfortunate. Microbiota are known to advance plant development and protect against pressure. Ongoing advances in plant microbiome local area arrangement and driving factors have expanded our comprehension. In this manner, plant microbiome is a dependable strategy for another green unrest and satisfying worldwide food need in supportable and eco-accommodating horticulture. Shotgun metagenomics was utilized to portray tomato, spinach, tenderized olive, and dried fg microorganisms. Metagenome-gathered genomes of new lactic corrosive microorganisms from green olives and impressive intra-and between species variety of *Pseudomonas* in tomatoes were found. *Pseudomonas* colonized all examples, supporting earlier perceptions of various local area structure. Compounds for nutrient and short-chain unsaturated fat digestion and sugar corruption, including plant strands, were found. Disconnecting, sequencing, and planning the ruling microorganisms to its metagenome affirmed their personality and showed the microbiota is culturable. We tracked down significant hereditary variety, crude genera, and explicit capabilities, recommending a plant have association. This study proposes that plant microorganisms in our eating regimens might add to the stomach microbiome for a brief time.

**Keywords:** Soil, Plants, Animals, Phyllosphere, Endosphere, Rhizosphere, Enzymes, Vitamin Metabolism, Short-chain Fatty Acid Metabolism, Carbohydrate Substrate Degradation

### 1. INTRODUCTION

With regards to the normal world, plants and creatures are continually collaborating with a wide assortment of microbial species all through the sum of their life cycles. People have been presented to a different microbial climate starting from the start of their transformative history, which has stretched out their ability to adjust to a sound way of life. Likewise, plants coincide with microorganisms, which are aggregately alluded to as microbiota. These organisms incorporate archaea, protists, microorganisms, and growths. With the beginning of microbial life tracing all the way back to the beginning of life (more than 3.5 billion years), it is feasible to induce that connections between microorganisms have created and become more different over the span of time. This happened a lot of time before plants adjusted to the land life, or, in other words, before 450 million years. Over the span of advancement, higher plants and photosynthetic green growth integrated cyanobacterial endosymbionts. These endosymbionts are today known as chloroplasts or plastids. Accordingly, the transformative history of plants and microorganisms share normal starting points, and the endurance of both depends on an associated relationship. As a result of this, the "plant microbiota" that is found inside or in nearness to the surfaces of the plant parts has earned some further consideration. To acquire a superior comprehension of the plant-organism (PM) connections, a quickly creating thought is the profiling of the plant-related microbiome, which comprises of the genomic gatherings, everything being equal. Through various cycles, microbiota builds the limit of plants to adjust to changing natural circumstances. Plant development advancement (PGP), insurance against biotic and abiotic stresses through the preparing of plant invulnerable framework or enlistment of plant guard pathways, variation to a variable climate, mycorrhizal advantageous interaction, supplement take-up, and change of inaccessible supplement structures into plant-open structure are instances of valuable communications with PM. Reference gives an outline of these cooperations. The communications among PM and the host plants are two-way, and microorganisms likewise secure supplements from the plants that they are living on. The connection between a plant and a microorganism can form into particular organizations relying upon the effect it has on the wellbeing of the plant. These associations can be mutualistic, and that implies that they are helpful to the two accomplices (advantageous), nonpartisan, and that implies that they are valuable to only one accomplice (commensalistic), or unsafe, and that implies that they are impeding to the host plant (pathogenic). These connections between PM are a fundamental part of supportable agribusiness and the climate, especially concerning the administration of wellbeing and food creation, separately.

As indicated by the discoveries of an investigation into the host plant and the related microbiome, which is in some cases alluded to as a holobiont, apparently plant-microorganism, plant, and organism microorganism collaborations occurred at the same time. Current advances, for example, cutting edge sequencing (NGS), omics methods (metagenomics,

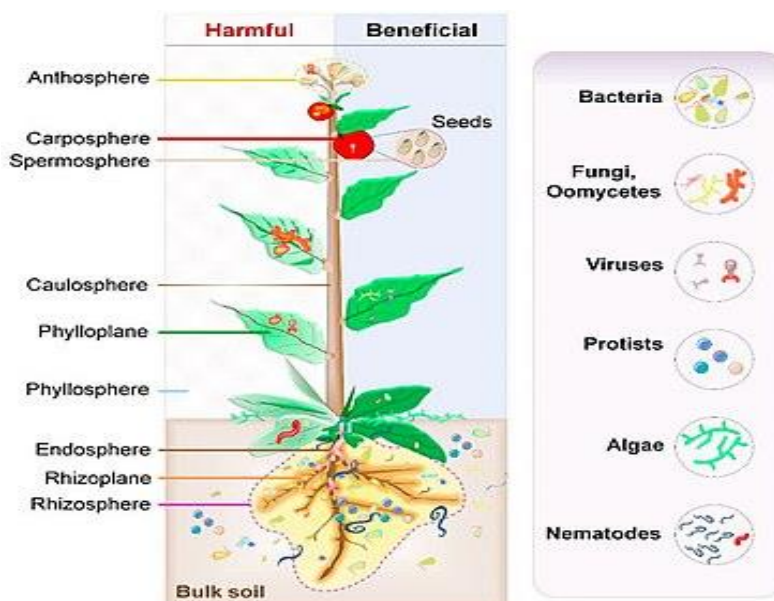
transcriptomics, proteomics, and metabolomics), and computational devices make it conceivable to understand the sub-atomic components of the PM communications that impact the qualities of plants at the local area level. There have been various distributions that have been distributed as of late that investigate the a huge number of plant microbiota as well as the impact of host genotype on different pieces of the microbiome (Table 1).

**Table 1:** Host Sampling in Rhizosphere Microbiota Research

Host	Sampling	Key Findings
Agave	Rhizosphere, whole plant	The plant compartment significantly influenced the microbial makeup, whereas the plant host biogeography primarily determined the fungal community composition..
Arabidopsis	Root, rhizosphere	It has been discovered that the environment, not the host species, determines the composition of the rhizospheric microbiota.
Barley	Root, rhizosphere	Root and rhizospheric bacteria have an impact on plant growth. Differentiated microbiota are driven by interactions between microbes and plant microbes.
Citrus	Root, rhizosphere	Numerous potentially helpful plant microbial species and identified over-represented microbial functional features make up the core rhizosphere microbiome.
Grapevine	Grape must	The distinct microbiota associated with grapevines is determined by environmental conditions, variation, and regional origins. These elements are essential to the wine's distinct flavor and caliber.
Maize	Roots, rhizosphere	Significant field-specific heritable variation was seen in the associated microbiota, along with heritable variation in the community makeup of the rhizosphere.
Petunia, Arabidopsis	Root, rhizosphere	The composition and reactions of the root microbiota differ significantly depending on the amount of phosphorus (P) applied.

**1.1 Composition and Driving Factors of the Plant–Microbe (PM) Interactions**

**Composition:** The rhizosphere, which is the dirt that is near the root surface, the rhizoplane, which is the root surface, and the endosphere, which is the root inside, make up the subterranean microbial territory. The over the ground home of microorganisms is known as the phyllosphere, and it is comprised of the accompanying parts: leaves (phylloplane), stem (caulosphere), blossoms (anthosphere), seeds (spermosphere), and natural products (carposphere) (Figure 1). Microorganisms from the general climate are effectively enrolled by plants, either through the dirt or the air. The transmission of specific microorganisms, for example, endophytes, can happen either on a level plane (by getting from the climate with each new age) or in an upward direction (by moving from parental seeds). Endophytes can dwell inside the plant tissues without incurring any mischief to the host plants. The NGS-intervened profiling of microbial arrangement living underneath or more ground territories of a few plants, including agave, Arabidopsis, wild and developed grain, citrus, grapevine, maize, petunia, potato, rice, soybean, sugar beet, sugarcane, tomato, wheat, cucumber, wild mustard, and lettuce, has given extensive insights concerning the design of the local area as to these plants.



**Figure 1:** Microbiome in plant ecosystem

Other microorganisms, including as viruses, protozoa, fungi, oomycetes, nematodes, and algae, are also important contributors to the composition of the microbiota, despite the fact that several metagenomic studies suggest that the bacterial population is the most abundant in the microbiota composition (Table 1). Comparison of the data obtained from these research is not possible because of the different sampling procedures, primers, and sequencing techniques that were utilized in each of the studies. Actinobacteria, Proteobacteria, Firmicutes, and Bacteroidetes are the four phyla that are considered to take the lead in the makeup of bacterial communities, according to all of these studies. It was discovered that the leaf- and root-associated microbiomes of *A. thaliana*, agave, grapevine, and wild mustard all have a number of microbial species in common. Host plants have the ability to genetically regulate the composition of the leaf microbiome, but not the root microbiome. Furthermore, numerous bacterial species that are found in leaf microbiomes are also found in root microbiomes, which suggests that these microbiomes were acquired from the soil. In general, a number of research suggest that the structure of the microbiota is reliant on the context in which it is found. This structure is comprised of highly conserved microbial taxa that reside in a specific plant component across a variety of host species and conditions. Nevertheless, additional research is required to grasp the impact that driving variables have on the interactions between microbes and other microbes, plants and other plants, and PM throughout the growth and development of plants.

### 1.2 Factors Influencing Microbial Communities and PM Interactions

Rather of being the outcome of irregular choice, the microbial structure of a plant's microbiota is directed by gathering rules. This is on the grounds that arbitrary determination doesn't happen. The variety of microorganisms lessens in an ever-evolving way from the mass soil to the rhizosphere. One gathering of microorganisms is urged to thrive in a better way by plant-related substances, while the other gathering is repressed. Ongoing improvements in the planning of plant microbiota utilizing cutting edge sequencing (NGS) have given significant experiences into the biotic (plant-related factors, microbial variables, and anthropogenic exercises) and abiotic (soil properties, natural elements) factors that impact the arrangement and construction of the microbial local area (Figure 2). The significant impacts of various factors that impact the PM associations have been thoroughly revealed in the model plant *Arabidopsis*, as well as in trees and harvests (Table 1).

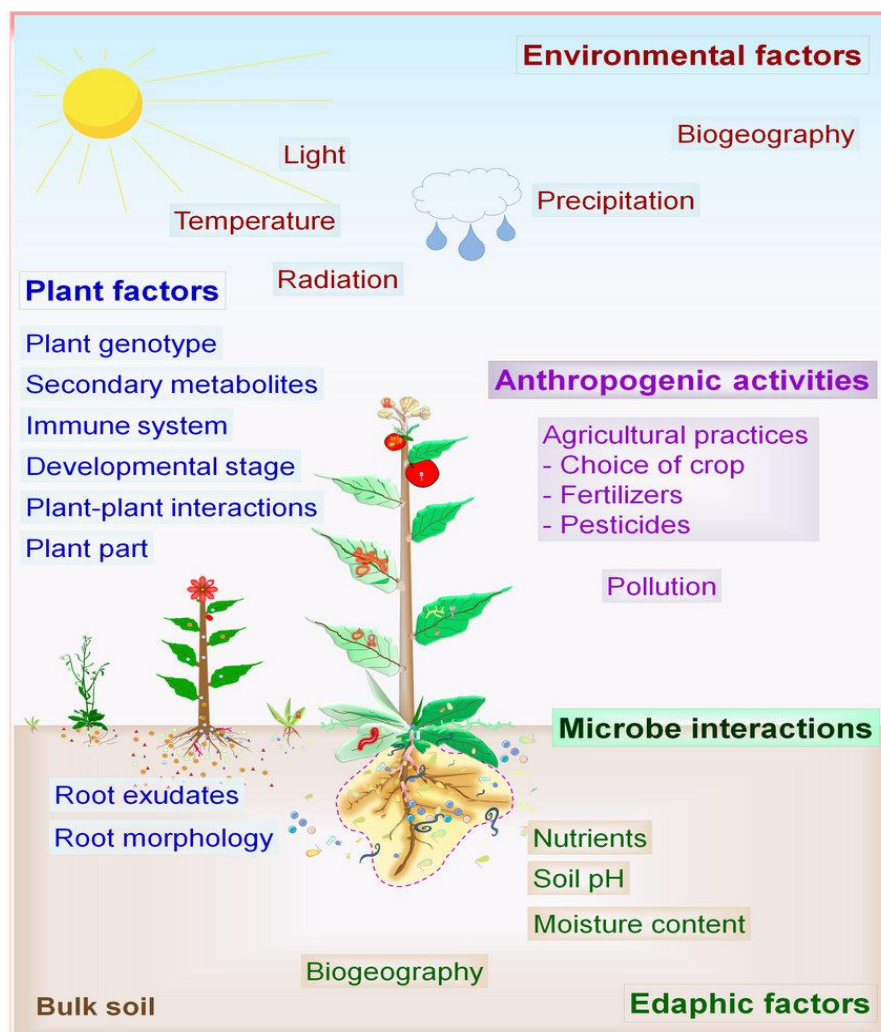


Figure 2: Driving factors of plant-microbe interactions

### 1.2.1 Biotic Factors

A couple of instances of plant factors are the host genotype, the resistant framework, the compartment of the plant, the discharges of metabolites, the age of the plant, the communications between plants, the root morphology, and the root exudates. Among these, the plant genotype is the main driving component that decides the organization and construction of the microbial local area that is found in the rhizosphere. There is an extensive variety of variety in the rhizosphere and phyllosphere networks of many plant species. Consequently, this shouldn't come as a shock given that the genotype of the plant decides the qualities of the root and leaf surface, the sort of exudates that are created by the roots, the substance flagging pathways, and the amount and nature of supplements that are accessible to microorganisms. Plant metabolites, for example, coumarins, meaningfully affect the microbiota of the host, a job in the development of the root microbiome, and a semiochemical job in the cooperations among PM and the host. The structure of the microbiota and the communications that they have with plants are likewise impacted by the sorts of microorganisms that are accessible specifically topographical districts. This is on the grounds that the different microbiome not entirely set in stone by the consolidated activity of the plant, microorganism organism, and PM associations. The presence of harmonious microbial species in the specialties of the rhizosphere and the phyllosphere is huge due to the presence of positive and specific plant pressure. Plant-pathogenic microorganisms, then again, are liable for a tremendous change in the number of inhabitants in organisms that are hostile to them, as well as in the resistant reactions of plants, which eventually brings about the control of microbes. The nature of soil, air, and water is harmed by anthropogenic factors, for example, horticultural strategies, which incorporate expanding portions of manures and pesticide showers, cultivating rehearses contamination, and various other human exercises. This hence meaningfully affects the designs of microorganisms and the PM associations they have with each other. In particular, the organization of the root microbiota of petunia and Arabidopsis adjusted decisively in light of the organization of phosphorus (P), and different plant species answered distinctively to states of low phosphate. This was seen comparable to the usage of manure. As an extra focal point, the leaf microbiome of maize and soybean were found to show practically identical impacts in light of nitrogen (N) treatment. It will be exceptionally fascinating to examine the effect that escalated cultivating strategies have on the progressions that happen in the PM affiliations and the design of plant microbiota later on.

### 1.2.2 Abiotic Factors

The qualities of the dirt affect the bacterial and contagious networks that are pervasive in the rhizosphere at some random time. Considering the way that the dirt is the normal stockpile of supplements, it fills in as a microbial seed bank for the local area that is found in the rhizosphere. The development of the microbial local area is driven by the qualities of the dirt, which incorporate the dirt's pH, soil type, dissemination of macronutrients, soil natural matter, levels of saltiness, soil design, and dampness content. Regardless of whether they are filled in similar soil climate, different plant species will enroll different microbial networks in the rhizosphere, rhizoplane (epiphytes, which colonize plant surfaces), and endosphere (endophytes, which colonize inward plant segments). Then again, certain plant species or genotypes can enroll the center plant microbiota, which is a bunch of microorganisms that are viable with the plant no matter what the ecological and soil conditions. There are various natural components that considerably affect the phyllosphere microorganisms. These variables incorporate environment, light, water, bright (UV) radiation, and geographic area. The aggregate of a plant, as a rule, is the consequence of collaborations between the genotype of the plant, the microbiota related with the plant, and ecological factors. As a general rule, plant microbiota can be obtained either upward (by means of seed or spread material) or evenly (through soil or air) and lives on or inside the tissues of the plant. This is where the components that have been all referenced above add to the development of the microbial local area by impacting its construction.

## 2. LITERATURE REVIEW

**Santos and Olivares (2021)** investigates the complex structure of the plant microbiome as well as the defining role it plays in the development of environmentally responsible agriculture methods. The microbiome, which is comprised of a wide variety of microorganisms including bacteria, fungus, archaea, and viruses, is present in both the internal and external tissues of plants. It has a significant impact on the health of plants as well as the environmental dynamics of ecosystems. An investigation into the elements that influence the composition of the plant microbiome is going to be the primary focus of this conversation. These factors include the type of soil, the genotype of the plant, the environmental conditions, and the agricultural techniques. A detailed analysis is used in this study to shed light on the symbiotic interactions that exist between plants and the microbiota that are connected with them. This review also highlights the numerous benefits that are bestowed onto the plants that serve as hosts. In addition to improved nutritional uptake, stress tolerance, disease suppression, and general resilience to environmental perturbations, these benefits also include increased disease suppression. The research highlights the possibility for harnessing microbial variety to maximize agricultural productivity while simultaneously avoiding environmental impacts. This is accomplished by deciphering the complex relationship that exists between plants and their microbiome. In the end, a more in-depth understanding of the plant microbiome holds tremendous potential for the advancement of sustainable agriculture practices that are tailored to address the difficulties of a fast changing global climate and growing need for food.

**Andreote et.al. (2014)** work investigates the complex interactions that occur within plant microbiomes, providing vital insights into the ecological significance of these interactions as well as potential uses in agricultural systems. In the beginning of the review, the dynamic nature of plant-associated microbial communities is explained, with an emphasis placed on the crucial role that these communities play in determining the health, growth, and productivity of plants. The

purpose of this review is to investigate the complex interactions that take place within the plant microbiome. These interactions include microbial diversity, community structure, and functional dynamics. This assessment is accomplished by conducting a thorough examination of the findings of recent research. Some of the most important subjects that are discussed are the mechanisms that are responsible for the colonization of plant tissues by microorganisms, such as root exudates, and the influence that environmental conditions have on the composition and function of the microbiome. In addition, the analysis sheds light on the wide variety of microbial interactions that are taking place inside the plant microbiome. These interactions include symbiotic, pathogenic, and commensal partnerships, as well as the consequences these relationships have for the cohabitation of plant-microbes and microbes with one another. The review highlights the potential of harnessing plant microbiomes to increase agricultural sustainability through tactics such as biofertilization, biocontrol of plant diseases, and reduction of environmental stresses. This potential is shown by synthesizing the existing body of information. This review, in its entirety, offers a complete account of the intricate interactions that occur within plant microbiomes. It also gives significant insights into the ecological functions that these interactions play and the practical implications that they have for sustainable agriculture methods.

**Andreote and e Silva's (2017)** study offers a complete analysis of the microbial communities that are connected with plants, building on the knowledge gained from natural systems to inform the use of these communities in agricultural settings. The first part of the paper focuses on the significant part that plant-associated microbial communities play in enhancing the health of plants and increasing their output. This review examines the variety and composition of these microbial communities for the purpose of illustrating the intricate interactions that occur between plants and the microbiota that are associated with them. This is accomplished through a synthesis of the most recent studies. Among the most important themes that are discussed are the mechanisms that are responsible for the colonization of plant surfaces and interior tissues by microorganisms, as well as the factors that influence the structure and function of microbial communities. Furthermore, the paper highlights the potential of plant-associated microorganisms to improve stress tolerance, promote nutrient uptake, and inhibit plant diseases, all of which contribute to the implementation of sustainable agricultural methods. The review highlights the significance of effectively utilizing microbial diversity in order to maximize agricultural output and resilience. This is accomplished by providing an explanation of the principles that regulate the interactions between plants and microbes in natural ecosystems. In general, the review offers insightful information regarding the possible applications of plant-associated microbial communities in agricultural settings. It also draws attention to the possibilities for novel methods to crop management and environmental sustainability.

### 3. RESEARCH METHODOLOGY

The information that has been supplied provides insights that are extremely helpful in understanding the frequency and percentage distribution of different bacterial species within a variety of samples or populations. The following is a summarization of the findings:

- **The earliest Girl Tomatoes**

With 32 observations, *Lelliottia* emerges as the most abundant species, accounting for approximately 17.77% of the total population of bacteria. Following closely behind are the bacteria *Enterobacter* and *Klebsiella*, which have frequencies of 25 and 19, respectively, which correspond to approximately 13.88% and 10.55% of the total bacteria that were found. Other species that are considered to be significant are *Rahnella*, *Erwinia*, and *Citrobacter*. These three species were identified with frequencies ranging from 13 to 17, and they contributed from 7.22 percent to 9.44 percent of the total bacterial population. Particularly noteworthy are the bacterial species *Serratia* and *Pantoea*, which are found in the population of bacteria at rates of 12 and 10, respectively, and contribute approximately 6.66% and 5.55% to the overall makeup.

*Pseudomonas* and *Tatumella* are each seen with a frequency of nine and seven, respectively, which corresponds to approximately five percent and three point eight percent of the total bacteria that have been discovered. The term "Others" refers to a category that includes a variety of bacterial species that were found 22 times, which accounts for approximately 12.22% of the total overall population.

- **The Baby Spinach**

The species *Erwinia* stands out as the one that is observed the most frequently, with a total of 22 occurrences and representing around 12.22% of the comprehensive bacterial population. *Pantoea* and *Escherichia* come in a close second and third, respectively, with rates of 21 and 20, which correspond to approximately 11.66% and 11.11% of the total bacteria that were found.

With frequencies ranging from 18 to 21, *Enterobacter*, *Lelliottia*, and *Serratia* each contribute around 10% to the overall bacterial mix. These three bacterial species demonstrate significant frequencies. *Aeromonas*, *Klebsiella*, and *Kluyvera* are found with frequencies ranging from 10 to 15, and they are responsible for around 5.55% to 8.33% of the total population. The frequencies of *Kosakonia* and *Others* are eight and twelve, respectively, and they contribute approximately 4.44% and 6.66% to the total composition of the overall bacterial population.

- **Green olives are**

*Pseudomonas* is the species that is recognized the most frequently, as it has been spotted a total of 26 times and accounts for around 14.44% of the total bacterial population.

With rates of 25 and 22, respectively, representing approximately 13.88% and 12.22% of the total bacteria that were found, *Oenococcus* and *Acid Propionibacterium* come in a close second and third, respectively.

*Proteus* and *Ralstonia* make significant contributions to the overall bacterial composition, with 16 and 20 occurrences respectively, which accounts for approximately 8.88% and 11.11% of the total contributions.

There is a presence of *Lactobacillus*, *Streptomyces*, and *Pediococcus*, with frequencies ranging from 13 to 19, which accounts for around 7.22% to 10.55% of the total population.

Both *Bacillus* and *Weissella* are found with frequencies of 10 and 13, respectively, which accounts for approximately 5.55% and 7.22% of the total bacterial composition, respectively.

- **Some Black Mission Figures**

There were 32 instances of the species *Pasteurella*, which accounts for roughly 17.77% of the total bacterial population. *Pasteurella* is the species that is observed the most frequently.

*Pantoea* and *Stenotrophomonas* come in a close second and third, respectively, contributing around 16.66% and 12.77% of the total bacteria that were found, with frequencies of 30 and 23, respectively.

There are 19 and 17 instances of *Rahnella* and *Pseudomonas*, respectively, which contribute around 10.55% and 9.44% to the overall bacterial composition. These two bacterial species demonstrate significant frequencies.

There is a presence of *Cupriavidus*, *Herbaspirillum*, and *Bradyrhizobium*, with frequencies ranging from 10 to 15, which accounts for around 5.55% to 8.33% of the total population.

A total of twenty different bacterial species were found to be included in the category of "others," which accounts for about 11.11% of the total bacterial composition.

#### 4. DATA ANALYSIS

A detailed overview of the frequency and percentage distribution of numerous bacterial species within a specific sample or population is provided by the data that has been presented. *Lelliottia* emerges as the most abundant species among the detected species, having been spotted 32 times and accounting for about 17.77% of the overall population of bacteria. Following closely behind are the bacteria known as *Enterobacter* and *Klebsiella*, which have frequencies of 25 and 19, respectively. These frequencies represent approximately 13.88% and 10.55% of the total bacteria that have been recognised. Among the other significant species are *Citrobacter*, *Erwinia*, and *Rahnella*. Each of these species was observed with frequencies ranging from 13 to 17, and they accounted for around 7.22% to 9.44% of the overall population of bacteria. *Serratia* and *Pantoea*, which are found in the bacterial population at rates of 12 and 10, respectively, contribute approximately 6.66% and 5.55% to the overall bacterial composition. Furthermore, *Pseudomonas* and *Tatumella* are observed with frequencies of 9 and 7, respectively, which correspond to roughly 5% and 3.88% of the total bacteria that have been identified. In conclusion, a category that is referred to as "Others" includes a variety of bacterial species that are not specifically specified, those that have been detected 22 times, and that constitute around 12.22% of the entire population. In addition to providing significant insights about the relative abundance and diversity of bacterial species that are present in the sample, this precise breakdown also serves as a platform for future investigation into the composition of the microbial community and the dynamics that occur within the given environment.

**Table 2: Microbial Frequency Distribution**

Bacteria	Frequency	Percentage
<i>Citrobacter</i>	17	9.44
<i>Enterobacter</i>	25	13.88
<i>Erwinia</i>	14	7.77
<i>Klebsiella</i>	19	10.55
<i>Lelliottia</i>	32	17.77
Others	22	12.22
<i>Pantoea</i>	10	5.55
<i>Pseudomonas</i>	09	5
<i>Rahnella</i>	13	7.22
<i>Serratia</i>	12	6.66
<i>Tatumella</i>	07	3.88

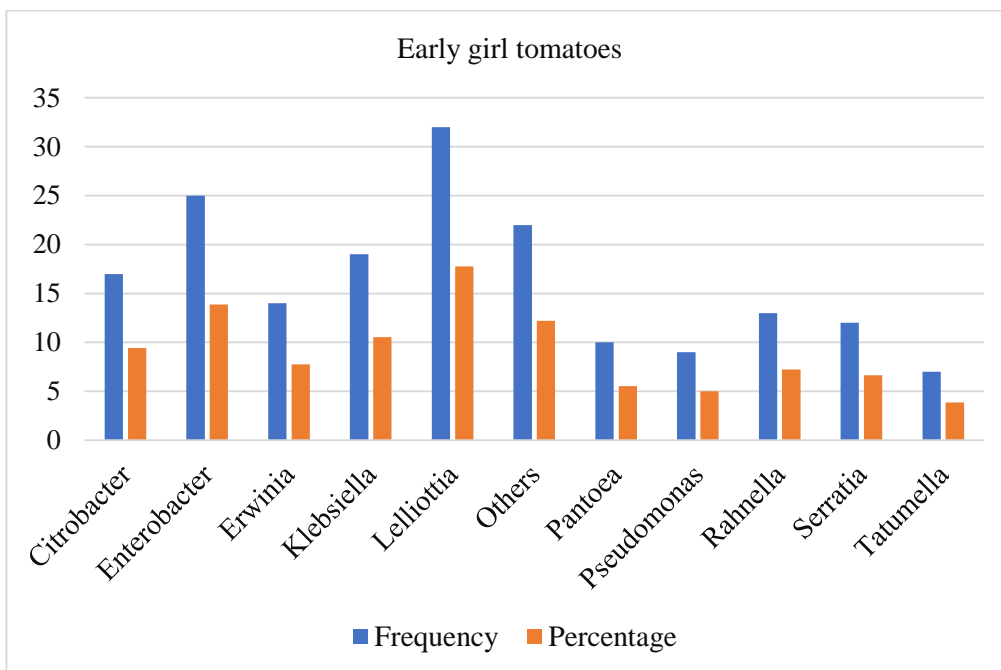


Figure 3: Graphical Representation on Percentage and frequency of Early girl tomatoes

Table 3: Bacterial Species Distribution

Species	Frequency	Percentage
Aeromonas	14	7.77
Enterobacter	18	10
Erwinia	22	12.22
Escherichia	21	11.66
Klebsiella	15	8.33
Kluyvera	10	5.55
Kosakonia	8	4.44
Lelliottia	19	10.55
Others	12	6.66
Pantoea	20	11.11
Serratia	21	11.66

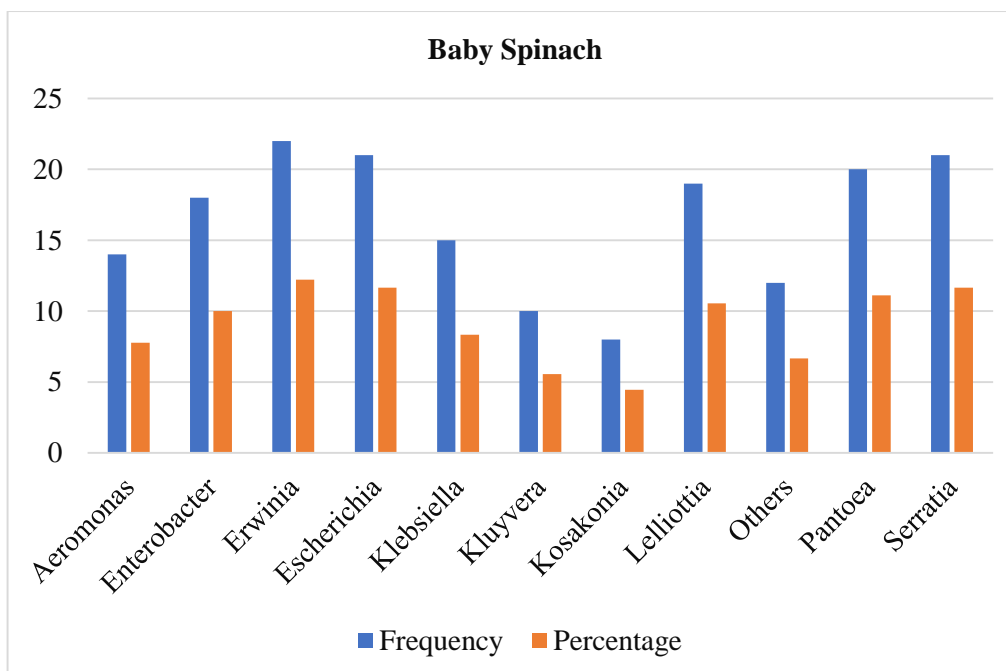
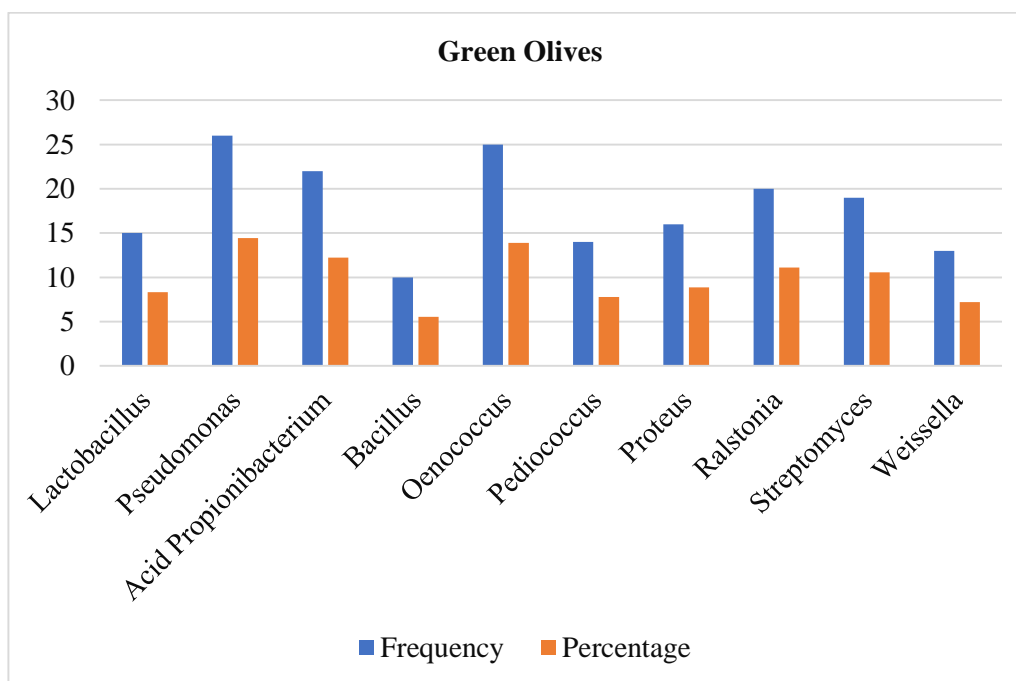


Figure 4: Graphical Representation on Percentage and frequency of Baby Spinach

The data that has been supplied illustrates the frequency of various bacterial species within a sample or population, as well as the percentage distribution of those species. Particularly noteworthy is the fact that *Erwinia* emerges as the species that occurs the most frequently, as it has been observed 22 times and accounts for around 12.22% of the total bacterial population. *Escherichia* and *Pantoea* come in a close second and third, respectively, with rates of 21 and 20, which correspond to approximately 11.66% and 11.11% of the total bacteria that have been found. In addition, the bacterial species *Enterobacter*, *Lelliottia*, and *Serratia* exhibit considerable frequencies, which range from 18 to 21, and each contribute around 10% to the overall bacterial composition. There are observations of *Aeromonas*, *Klebsiella*, and *Kluyvera* with frequencies ranging from 10 to 15, which accounts for around 5.55% to 8.33% of the overall population of bacteria. Furthermore, *Kosakonia* and *Others*, which have frequencies of 8 and 12, respectively, contribute approximately 4.44% and 6.66% to the overall bacterial composition, respectively. This detailed breakdown offers vital insights on the relative abundance and variety of bacterial species that are present in the sample. It also provides a platform for future exploration into the composition of the microbial community and the dynamics that occur within the environment that is being studied.

**Table 4:** Bacterial Frequency Distribution

Bacteria	Frequency	Percentage
Lactobacillus	15	8.33
Pseudomonas	26	14.44
Acid Propionibacterium	22	12.22
Bacillus	10	5.55
Oenococcus	25	13.88
Pediococcus	14	7.77
Proteus	16	8.88
Ralstonia	20	11.11
Streptomyces	19	10.55
Weissella	13	7.22



**Figure 5:** Graphical Representation on Percentage and frequency of Green Olives

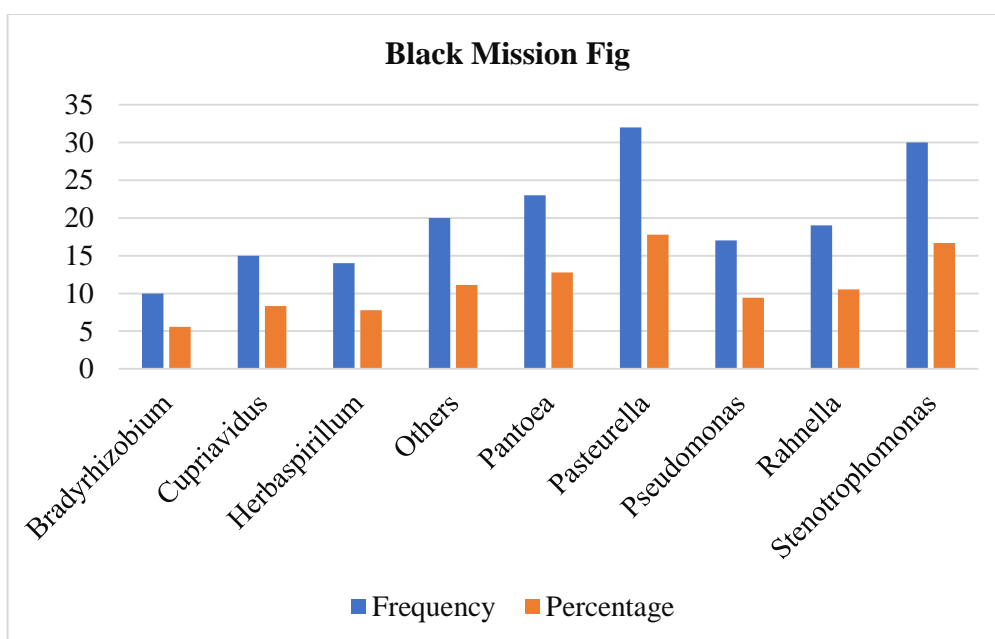
The data that has been presented makes it possible to gain an understanding of the frequency and percentage distribution of different bacterial species within a particular sample or population. In comparison to the other species that have been found, *Pseudomonas* is the one that has been observed the most frequently. It has been observed 26 times and accounts for roughly 14.44% of the overall bacterial population. Immediately following closely after are the bacteria *Oenococcus* and *Acid Propionibacterium*, which have frequencies of 25 and 22, respectively. These frequencies represent approximately 13.88% and 12.22% of the total bacteria that have been found. Additionally, *Proteus* and *Ralstonia* exhibit substantial frequencies, with 16 and 20 occurrences, respectively, contributing roughly 8.88% and 11.11% to the entire bacterial makeup. *Ralstonia* is composed of around 11.11% of the total bacteria. It has been shown that *Lactobacillus*, *Streptomyces*, and *Pediococcus* are present with frequencies ranging from 13 to 19, which accounts for around 7.22% to 10.55% of the overall population of bacteria. Furthermore, *Bacillus* and *Weissella* are discovered with frequencies of 10 and 13, respectively, which constitute approximately 5.55% and 7.22% of the overall bacterial composition, respectively.



In addition to providing significant insights about the relative abundance and diversity of bacterial species that are present in the sample, this precise breakdown also serves as a platform for future investigation into the composition of the microbial community and the dynamics that occur within the given environment.

**Table 4: Bacterial Species Distribution**

Bacteria	Frequency	Percentage
Bradyrhizobium	10	5.55
Cupriavidus	15	8.33
Herbaspirillum	14	7.77
Others	20	11.11
Pantoea	23	12.77
Pasteurella	32	17.77
Pseudomonas	17	9.44
Rahnella	19	10.55
Stenotrophomonas	30	16.66



**Figure 6:** Graphical Representation on Percentage and frequency of Black Mission Figs

The information that has been supplied illustrates the frequency and percentage distribution of a number of different bacterial species within a particular sample or population. Particularly noteworthy is the fact that Pasteurella is the species that is observed the most frequently, with a total of 32 observations and accounting for approximately 17.77% of the overall bacterial population. Stenotrophomonas and Pantoea come in a close second and third, respectively, accounting for around 16.66% and 12.77% of the total bacteria that have been found. Their respective frequencies are 30 and 23, respectively. Both Rahnella and Pseudomonas exhibit considerable frequency, with 19 and 17 occurrences, respectively, contributing around 10.55% and 9.44% to the overall bacterial composition. Rahnella is the more common of the two. A total of around 5.55% to 8.33% of the overall bacterial population is comprised of Cupriavidus, Herbaspirillum, and Brabyrhizobium, which are seen with frequencies ranging from 10 to 15. Furthermore, the category that is labeled as "Others" includes a variety of bacterial species that are not expressly identified, which have been detected twenty times and account for approximately 11.11% of the total bacterial composition. This detailed breakdown offers vital insights on the relative abundance and variety of bacterial species that are present in the sample. It also provides a platform for future exploration into the composition of the microbial community and the dynamics that occur within the environment that is being studied.

**5. CONCLUSION**

A full comprehension of the frequency and percentage distribution of diverse bacterial species within distinct samples or populations emerges as a result of the data that has been presented. A wide variety of bacterial species can be seen in the samples of Early Girl Tomatoes, Baby Spinach, Green Olives, and Black Mission Figs. Each of these bacterial species contributes in a unique way to the overall microbial composition of the samples. It is important to note that certain species, such as Lelliottia, Erwinia, and Pasteurella, have greater frequencies, which indicates that they are highly prevalent in the settings that were investigated. Pseudomonas is also one of the species that sticks out frequently, as it is one of the species that is observed the most frequently across a variety of samples. The comprehensive analysis of bacterial frequencies

offers essential insights into the microbial ecosystems that are associated with various food products. Not only does this knowledge contribute to a deeper comprehension of the diversity of microorganisms, but it also sets the groundwork for further research into the dynamics and interactions that occur within these communities of microorganisms. Furthermore, the graphical representations that accompany the data bolster the visualization of the data and make it simpler to grasp the frequency and percentage distributions. This assists researchers in conducting an in-depth analysis and investigation of the microbial communities that are present inside these food samples. The findings, taken as a whole, highlight the significance of researching the microbial communities that are present within food products. This research can provide significant insights for the purposes of ensuring the quality, safety, and preservation of food.

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