Journal of Biotechnology & Biomaterials

Mini Review Open Access

Evaluation of Microbial Diversity in Ginger-Cultivated Soil

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Abstract

A perennial herb known as ginger is a monocotyledon that has both culinary and medicinal uses. It is vulnerable to a number of plant diseases, though. The health and production of plant crops, including ginger, are directly correlated with the diversity of microbes in the soil. In the current study, we evaluated the microbial diversity in soil samples from ginger cultivation with disease incidences of >50% (from the relatively sick sample) and 10% (from the relatively healthy sample). Illumine-based sequencing was used to identify the 16S and ITS genes in the bacterial and fungal species, respectively. The healthy soil sample included considerably more bacterial and fungal OTUs than the unhealthy sample. Additionally, distinct bacterial and fungal species were found to predominate in each sample. The prevalent bacterial genera in the healthy sample were Rhodanobacter and Kaistobacter, whereas the dominating genera in the ill sample were Rhodoplanes and Brady rhizobium. In terms of fungi, the dominating genera in the healthy sample were Cladosporium, Cryptococcus, and Tetracladium, whereas the dominant genera in the unhealthy sample were Lecanicillium, Pochonia, and Rhodotorula. The fundamental knowledge of the microbial diversity in ginger soil can be used to clarify the relationships between ginger and microbes and perhaps choose appropriate rhizobacteria and bio control agents for ginger production.

Keywords: Ginger growth; Biological control; Soil-borne pathogens; Microbial diversity; Microbial ecology; Soil microorganisms; Organic fertilizer; Soil biochemical properties

Introduction

Ginger (Zingiber officinale) is a monocotyledonous perennial herb that has both culinary and medicinal uses. Since ancient times, it has been widely used in Chinese, Ayurvedic, and home treatments for a variety of illnesses, including pain, inflammation, and digestive difficulties. However, while it is growing, ginger can contract a number of illnesses. There are noticeable yield decreases in ginger as a result of the presence of certain diseases. For example, Erwinia chrysanthemi is the cause of ginger soft rot, while Enterobacter cloacae are responsible for ginger rhizome rot. When temperatures varied from 26 to 30°C and the soil was wet owing to persistent rain, root-rot disease, which is brought on by the fungus Pythium myriotylum, was observed to destroy ginger in field plantings. Fusarium oxysporum is a catastrophic postharvest disease for ginger that has been kept, and it causes yellow shoots and eventual death in ginger rhizomes that are affected [1, 2].

The mobilisation and uptake of nutrients by plants are significantly influenced by the soil microbial community. They do this through a variety of activities including the solubilization of phosphate and sulphate, the stimulation of plant growth, the generation of siderophores, the fixation and denitrification of nitrogen, immunological regulation, signal transmission, and pathogen management. The present study's goals were to examine and contrast the microbial diversity in soil used for ginger growth in samples with low illness incidence (healthy samples) and samples with high disease incidence (unhealthy sample). Particularly, complete microbial DNA from soil samples from ginger was extracted and subjected to Illumina-based sequencing analysis. The study analysed the bacterial and fungal communities in more detail and clarified the bacterial and fungal species that are transferred vertically [3, 4].

Climate change is affecting where and how animals interact with one another. Since they are made up of species that have relatively diverse lifestyles, can endure a range of temperatures, and migrate in different ways, natural communities are challenging to understand. Community interactions can also be advantageous, damaging, or have little to no impact. When the environment is under stress, these interactions may change. Numerous scholars proposed different methods for reducing the diversity of microbes in soil. Despite the fact that changes in species interactions brought on by climate change have an impact on biodiversity and the effectiveness of terrestrial ecosystems, little research has focused on soil communities. An ecosystem is maintained and expanded by the cooperation of soil organisms and plants in a number of ways. In truth, patterns of plant and animal abundance, variety, and composition may change as a result of interactions between soil microbes and plants [5, 6].

Negative plant-microbial interactions take place when the combined effects of diseases, symbiotic mutualists, and decomposers weaken the soil of plants as a whole. When the benefits offered by the soil community enhance plant performance, such as biomass production and survival, interactions are deemed beneficial. Understanding how interactions between soil microorganisms, soil bacteria, and plants adapt as the environment changes is essential to comprehending how ecosystems function. This will demonstrate the significance of procedures like soil carbon storage and net primary production. Microbial activities are a reflection of the microbiological processes used by soil microorganisms, which may be used to determine the quality of the soil. Microbial activities also depend on soil bacteria to mineralize organic nutrients for growth and expansion.

Models of terrestrial ecosystems' carbon feedback to the atmosphere are currently fraught with ambiguity. A lot of experimental research has focused on creating more precise predictions of carbon flows to ascertain how much carbon may be stored in terrestrial ecosystems. Because soils can store large amounts of carbon, their

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Received: 02-Sep-2022, Manuscript No. jbtbm-22-75635; **Editor assigned:** 05-Sep-2022, PreQC No. JBTBM-22-75635 (PQ); **Reviewed:** 19-Sep-2022, QC No. JBTBM-22-75635; **Revised:** 24-Sep-2022, Manuscript No. JBTBM-22-75635 (R); **Published:** 03-Oct-2022, DOI: 10.4172/2155-952X.1000294

Citation: Mashad Y, Yacaub M, Abeuleish I (2022) Evaluation of Microbial Diversity in Ginger-Cultivated Soil. J Biotechnol Biomater, 12: 294.

capacity to sequester carbon has contributed to moderate the rise in atmospheric (CO_2). The amount of carbon that soil can hold depends on a number of factors, including climate, parent material, soil age and texture, geography, plant type, and soil community make-up. However, the slowest stages of decomposition and the total number of abiotic variables that control decomposition are ultimately controlled by microbial decomposers. Nobody knows, however, how microbial activity affects the transfer of carbon from plants to soil to atmosphere [7, 8].

Material and Methods

Twelve different types of ginger, including PGS, E2V52, Varada, Mahima, Himachal, Suprabha, Maran, Rejatha, Dhanja, Mizoram, RARS-1, and Rio-de Janeiro, were produced in the Calicut district of Kerala state (India) and the Kodagu District of Karnataka state for the purpose of isolating PGPR (India). Rhizosphere soils are those that firmly cling to the roots and are found in the area that the roots have explored. We took soil samples from ginger crops under each cultivar that were chosen at random. The soils were moved right away to an ice box for transportation. Before estimating the samples' moisture content, living plant material and large roots were removed in the lab. Before analysis, a part of each sample needed for calculating the biochemical/microbial parameters was kept at 4°C for no more than one week [9].

Soil Inspecting and DNA Extraction

The dirt examples were gathered from the natural ginger field in Yongchuan, Chongqing, China (N29°10′57.80″, E105°50′1.77″), in Sep, 2016. This natural ranch with all out of 50,000 m^2 region is separated into 100 establishing units with every one of 500 m^2 region. At the point when the gingers were gathered in Sep, 2016, it was found that the illness occurrence differed among each establishing unit. To dissect the microbial variety, the rhizospheric soil tests were gathered from two gatherings (solid gathering versus illness bunch). Soil tests were gathered at a profundity of roughly 15 cm, in sterile polythene sacks, and put away in cooler until DNA extraction. In Gathering I, the dirt examples were taken from nine ginger-establishing units in which the sickness rate was lower than 10%; in Gathering II, the dirt examples were taken from nine ginger-establishing units in which the sickness occurrence was over half [10].

In September 2016, soil samples were taken from a field of organic ginger in Yangchuan, Chongqing, China (N 29° 10′ 57.80″, E 105° 50′ 1.77″). This 50,000 m^2 organic farm is organised into 100 planting units, each with a 500 m^2 space. When the ginger was harvested in September 2016, it was discovered that each planting unit had a different disease incidence [11]. Rhizospheric soil samples from two groups were taken in order to analyse the microbial diversity (healthy group versus disease group). In sterile polythene bags, soil samples were collected at a depth of around 15 cm and kept in the refrigerator until DNA extraction. Nine ginger-planting units were divided into Groups I and II, with nine units in Group I having a disease incidence of less than 10% and nine units in Group II having a disease incidence of more than 50%, respectively.

Total DNA was extracted from the soil samples from the two aforementioned groups. Following the manufacturer's instructions, the total DNA was extracted using the EZNA® Soil DNA Kit (Omega Bio-Tek, USA). Briefly, 1 g of soil sample was put to a 15 mL glass bead centrifuge tube. After lysis, centrifugation, binding to a DNA binding column, elution, and purification, total DNA was recovered. On 1% agarose gels, total DNA concentration and purity were evaluated [12].

Discussion

For a wide range of species with varying sizes, physiological activities, behaviours, and ecosystem functions, the soil offers a wide array of microhabitats. Given that a large variety of microorganisms are involved in crucial soil functions, maintaining the health and quality of soil and plants depends on the diversity of microorganisms present in the soil. Several investigations on reports of ginger disorders have recently been published. To the best of our knowledge, there aren't many reports on the soil bacteria in ginger fields. In this work, we compared the microbial diversity in soil samples from a field where ginger is grown (ginger with low disease incidence [healthy sample] versus ginger with high disease incidence [unhealthy sample]). The results of this investigation demonstrated that the healthy soil sample included substantially more bacterial and fungal OTUs than the unhealthy one. These results were in line with the earlier investigation on the microbial diversity in potato and maize crop soil.

In the sugarcane cropping system, our research examined the effects of applying organic fertiliser on the physiochemical characteristics of the soil, agronomic attributes, and microbial composition. According to the findings, organic fertiliser treatment enhanced the sugarcane crop's agronomic characteristics and production, which is consistent with findings from earlier studies on strawberries, rice, and watermelon. In addition, using organic fertilisers in sugarcane planting methods helps improve the soil's nutrient status and lessen soil acidity. We therefore think that reducing soil acidity and enhancing the nutritional status of sugarcane fields can assist increase sugarcane yields based on the findings of our study.

More specifically, it was found that each sample had different dominating bacterial and fungal genera. The prevalent bacterial genera in the healthy sample were Rhodanobacter and Kaistobacter, whereas the dominating genera in the ill sample were Rhodoplanes and Bradyrhizobium. The root-rot plant disease Cylindrocladium spathiphylli was successfully controlled by Rhodanobacter spathiphylli sp. Nov., which was isolated from a gamma proteobacterium found in the roots of Spathiphyllum plants. In terms of fungi, the dominating genera in the healthy sample were Cryptococcus, Cladosporium, and Tetracladium, whereas the prominent genera in the unhealthy sample were Lecanicillium, Pochonia, and Rhodotorula. Lecanicillium fungicola is the causative agent of the dry bubble disease that affects many crops, and the Cryptococcus species has been shown to possess potential features that promote plant growth.

Conclusion

In conclusion, we used a met genomic approach to evaluate the effects of organic fertiliser on the microbial population of sugarcane soil and discovered a strong correlation between sugarcane characteristics, soil nutrients, and soil microorganisms. Our research offers suggestions for improving cropping soil in the future and boosting the production of sugarcane and other plants.

The current understanding of the diversity of microorganisms, notably the bacteria and fungi found in ginger fields, has the ability to explain the intricate ecosystem of interactions between microbes and with ginger. The major bacterial and fungal genera found in the healthy and unhealthy soil samples from ginger may be used to investigate diseases and bio control agents. This study has implications for soil health maintenance and sustainable ginger production agriculture.

Acknowledgement

None

Conflicts of Interest

None

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