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Comparison of soil microbial composition and fertility in rhizosphere of healthy and *Fusarium* wilt-affected sweet potato plants

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Abstract. *Nafi'ah HH, Fajarfika R, Fatimah R, Maulana H, Yoel A. 2025. Comparison of soil microbial composition and fertility in rhizosphere of healthy and* Fusarium *wilt-affected sweet potato plants. Biodiversitas 26: 941-950. Fusarium* wilt is a significant disease impacting sweet potato plants, primarily affecting the stem and inhibiting optimal growth. The severity of the disease is hypothesized to be influenced by soil microbial composition and fertility. Therefore, this research aimed to compare the microbial composition and soil fertility parameters in the rhizosphere of healthy sweet potato plants and those infected with *Fusarium* wilt. The hypothesis posited that these two plant groups had significant differences in microbial composition and soil fertility. The method used was a Cross-Sectional Survey, a robust approach that involved data collection obtained through observation and soil sampling. Soil samples were obtained from Kuningan and Garut Regencies. Microbial diversity and abundance were analyzed using targeted quantification techniques, including the Total Plate Count method on selective media. Parameters of soil fertility, such as pH, organic matter content, and nutrient concentrations, were also evaluated. The results showed significant distinctions in microbial composition, with diseased plants exhibiting a higher microbial population dominated by beneficial microbes, such as Phosphate-Solubilizing Bacteria (PSB) and nitrogen-fixing bacteria. A negative correlation was observed between *Fusarium* fungi and PSB. Additionally, differences in soil fertility characteristics were evident between the two locations. This research provided a better understanding of the microbial population in sweet potato plants and a foundation for developing more effective strategies to manage *Fusarium* wilt.

Keywords: *Fusarium*, microbial composition, pathogen, rhizosphere, sweet potato

INTRODUCTION

The demand for sweet potato (*Ipomoea batatas* L.) is stable in both local and international markets. The plant's diverse varieties with unique colors and flavors open up opportunities for the development of more varied processed products, such as chips, flour, and drinks (Truong et al. 2018; Carey et al. 2021). Sweet potatoes can be the main raw material in the food industry (Bach et al. 2021; Histifarina et al. 2023). The starch from sweet potato plants is used as a substitute for wheat flour in various food products (Dereje et al. 2020; Ayo-Omogie 2021). Essential nutrients in sweet potatoes include carbohydrates act as the main source of energy and fiber to aid digestion and maintain gut health. Additionally, it contains vitamins, particularly vitamin A (beta-carotene), C, and various B complex vitamins, minerals such as potassium, calcium, iron, and zinc, and antioxidants that help protect cells from damage caused by free radicals (Tegeye et al. 2019; Kumalasari et al. 2020; Senthilkumar et al. 2020; Muhammad et al. 2022; Ranteallo et al. 2023). Several countries have successfully exported sweet potatoes in fresh or processed form, showing high demand in the global market (George et al. 2024; Laurie et al. 2024).

The wilt disease is one of the serious threats to sweet potato production. This disease is caused by pathogenic fungi from the genus *Fusarium*, which attacks the plant's vascular system (Rahman et al. 2021; Srivastava et al. 2024). The impact of this fungus includes a decrease in the quantity and quality of sweet potato production (Paul et al. 2020; Nie et al. 2023; Ogero and van der Vlugt 2023). *Fusarium* fungus infects all parts of the plant, from the roots to the stems, causing the death of the entire plant (Ekwomadu and Mwanza 2023). The spores can survive in soil for a long time, making them difficult to eradicate (Shabeer et al. 2021). Transmission occurs through agricultural equipment contaminated with fungal spores, which spread the disease to other plants.

Soil microbes play a crucial role in maintaining plant health. Beneficial soil microbes compete with pathogens for nutrients and space around plant roots (Liu et al. 2021; Wang et al. 2021a). Antibiotic compounds produced by soil microbes have a broad spectrum of activity, making them effective against various pathogens (Das et al. 2022). Phosphorus is an essential nutrient for plant growth and increases disease resistance. Phosphate-Solubilizing Bacteria (PSB) help plants to absorb phosphorus bound in soil (Tian et al. 2021).

The differences in soil microbial composition between healthy and diseased plants are an interesting and expanding field. Despite extensive research, several gaps still need to be explored to gain a more comprehensive understanding. The intricate interactions between microbial species and pathogens pose significant challenges in identifying one or two species as definitive biomarkers (Mougin and Joyce 2023). The mechanisms behind the interactions between beneficial soil microbes, pathogens, and plants are still not fully understood. Soil microbial composition is strongly influenced by environmental factors such as climate, soil type, and land management practices. This spatial and temporal variability makes it difficult to generalize research results. Therefore, the primary objective of this research is to understand in depth the relationship between soil microbial composition and the health condition of sweet potato plants, particularly plants infected with *Fusarium* wilt disease. This research aimed to determine how differences in soil microbial composition in the rhizosphere of healthy and diseased sweet potato plants related to the soil fertility levels and the presence of *Fusarium* wilt disease. This provides insights that could inform sustainable agricultural practices and disease management strategies.

MATERIALS AND METHODS

Research location

The study was conducted in Garut and Kuningan Regencies, West Java, Indonesia, which are large sweet potato centers in West Java (Dinas Tanaman Pangan dan Hortikultura 2023). The location in Garut District was in Margalaksana Village, Cilawu Sub-district (coordinates -7.259022, 107.900624), while the location in Kuningan District was in Linggarjati Village, Cilimus Sub-district (coordinates -6.877570, 108.473493).

Sampling

The method used was a Cross-Sectional Survey, with data obtained through observation and soil sampling. Samples were taken from the soil and rhizosphere of both healthy and diseased plants. Soil samples were obtained 30 cm below the surface using a soil drill. The samples taken were composite from 10 randomly selected points. Rhizosphere samples were taken from 3 healthy and 3 *Fusarium* wilt-affected sweet potato plants. The sample codes are shown in Table 1.

Table 1. Sample code

Sample code	Description
s1l1	soil from healthy plant location 1
s1l2	soil from healthy plant location 2
s2l1	soil from diseased plant location 1
s2l2	soil from diseased plant location 2
r1l1(1)	the rhizosphere of healthy plant location 1 sample 1
r1l2(1)	the rhizosphere of healthy plant location 2 sample 1
r1l1(2)	the rhizosphere of healthy plant location 1 sample 2
r1l2(2)	the rhizosphere of healthy plant location 2 sample 2
r1l1(3)	the rhizosphere of healthy plant location 1 sample 3
r1l2(3)	the rhizosphere of healthy plant location 2 sample 3
r2l1(1)	the rhizosphere of diseased plant location 1 sample 1
r2l2(1)	the rhizosphere of diseased plant location 2 sample 1
r2l1(2)	the rhizosphere of diseased plant location 1 sample 2
r2l2(2)	the rhizosphere of diseased plant location 2 sample 2
r2l1(3)	the rhizosphere of diseased plant location 1 sample 3
r2l2(3)	the rhizosphere of diseased plant location 2 sample 3

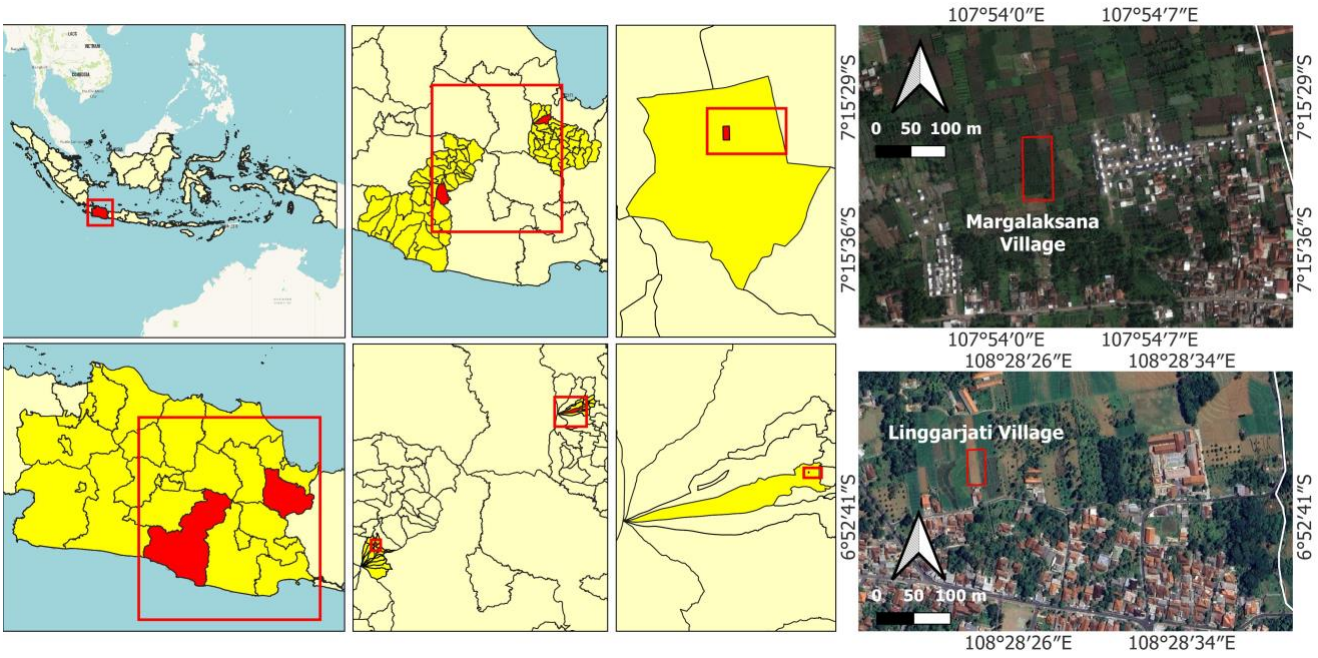

Figure 1. Location sampling point in Margalaksana Village, Cilawu Sub-district, Garut District, and Linggarjati Village, Cilimus Sub-district, Kuningan District, West Java, Indonesia

Laboratory analysis

Microbial composition analysis

Microbial tests were conducted at the Soil Biology Laboratory, Faculty of Agriculture, Universitas Padjadjaran. The target microbes in this research included *Azotobacter*, *Azospirillum*, Phosphate-Solubilizing Bacteria (PSB), *Penicillium*, and *Fusarium*. Each microorganism was cultured using a specific medium. *Azotobacter* was isolated using Ashby's medium, which contains sucrose, K_2HPO_4, $MgSO_4 \cdot 7H_2O$, NaCl, $CaCO_3$, and agar, maintaining a pH of 7.0-7.2. *Azospirillum* was grown on Okon's medium, which includes malic acid, K_2HPO_4, $MgSO_4 \cdot 7H_2O$, NaCl, $FeSO_4 \cdot 7H_2O$, and agar, with a pH of 6.8-7.0. Phosphate-Solubilizing Bacteria (PSB) were cultured using *Pikovskaya's* medium, which contains glucose, $Ca_3(PO_4)^2$, $(NH_4)2SO_4$, NaCl, $MgSO_4 \cdot 7H_2O$, $MnSO4 \cdot H_2O$, $FeSO_4 \cdot 7H_2O$, and agar, with a pH of 7.0. *Penicillium* and *Fusarium* were isolated using Potato Dextrose Agar (PDA), prepared from peeled potato infusion, dextrose, and agar, with a pH of 5.6. This protocol provides a standardized approach for isolating and identifying key microbial groups in soil samples using selective media.

Soil fertility analysis

Soil fertility analysis was conducted at the Soil Fertility and Plant Nutrition Laboratory, Faculty of Agriculture, Padjajaran University. Soil analysis was conducted to determine several physicochemical properties using standardized analytical methods. pH was measured in a 1:2.5 soil-to-water suspension using a pH meter following ISO 10390:2005. C-Organic content was analyzed using the Walkley-Black wet oxidation method (Nelson and Sommers 1982). N-Total was determined via the Kjeldahl method (Bremner 1960). The C/N ratio was calculated as the ratio of C-Organic to N-Total. Available phosphorus (P_2O_5) was measured using spectrophotometry after extraction with Bray I or Olsen method, depending on soil pH (Koralage et al. 2015). Exchangeable potassium (K_2O) was extracted using ammonium acetate (1N, pH 7) and measured by flame photometry (Knudsen et al. 1982). Basic cations (K, Na, Ca, Mg) were extracted using 1N ammonium acetate and analyzed by Atomic Absorption Spectrophotometry (AAS). Cation Exchange Capacity (CEC) was determined using the ammonium acetate titration method. Finally, soil texture was analyzed using the hydrometer method, which measures particle size distribution of sand, silt, and clay after dispersion with sodium hexametaphosphate. All analyses followed standardized procedures to ensure the accuracy and comparability of results.

Data analysis

The data analysis involved descriptive statistical methods to assess microbial population distribution. Spider plots were employed to represent the variation in microbial populations across different samples visually. Next, to explore relationships between microbial populations, correlation analysis was performed using heatmaps, providing insights into potential associations among different microbes. Additionally, Principal Component Analysis (PCA) with angle vectors was applied to identify patterns and groupings within the microbial communities. To further analyze and quantify the Multi-trait Genotype-Ideotype Distance Index (MGIDI), the "metan" package in R Studio was utilized, allowing for a comprehensive evaluation of microbial traits in relation to plant health and environmental conditions.

RESULTS AND DISCUSSION

Number of microbial populations

Microbial population analysis using spider web showed that data located on the outermost web had the highest population. The microbial population analysis revealed variations in the abundance of different microbial groups across the collected samples. *Azotobacter* had the highest population in the r1l2 (1) sample, with 238,700,000 CFU.g^{-1}, followed by s1l2 with 180,183,333 CFU.g^{-1} (Figure 2). *Azospirillum* was most abundant in s2l2 with 515,000,000 CFU.g^{-1}, followed by r2l2 (1) with 475,000,000 CFU.g^{-1} (Figure 3). The phosphate-solubilizing bacteria (PSB) population was most abundant in r1l2 (1) with 161,416,666.7 CFU.g^{-1}, followed by r2l1 (3) with 116,100,000 CFU.g^{-1} (Figure 4). In contrast, *Penicillium* populations were highest in s2l2 and r2l1 (2), each with 7,000 CFU.g^{-1} (Figure 5). Furthermore, *Fusarium* was most abundant in r2l1 (1) with 9,000 CFU.g^{-1}, followed by r2l2 (2) with 8,000 CFU.g^{-1} (Figure 6).

The analysis of microbial populations revealed distinct distribution patterns between healthy and diseased sweet potatoes across both study locations (Garut and Kuningan). *Azotobacter* populations were higher in the rhizosphere of healthy plants compared to diseased plants, indicating a possible correlation between its presence and plant health. In contrast, *Azospirillum* exhibited greater abundance in diseased plants than in healthy ones in both soil and rhizosphere samples. The distribution of Phosphate-Solubilizing Bacteria (PSB) was notably uneven between healthy and diseased plants, suggesting variability in their colonization patterns. Similarly, *Penicillium* populations were more prevalent in diseased plants at both locations, indicating a potential association with plant stress conditions. Furthermore, *Fusarium*, a known pathogenic fungus, was found in higher concentrations in diseased plants compared to healthy plants, with a greater presence in the rhizosphere than in bulk soil at both locations. These findings suggest that microbial composition is influenced by plant health status, with potential implications for plant growth and disease dynamics.

Relationships between microbes using Pearson Correlation and Principal Component Analysis (PCA)

Figures 8 and 9 show microbial correlation using a heatmap and PCA angle vector. The results of Pearson correlation analysis (Figure 7) show that *Fusarium* fungus was significantly and positively correlated with *Azospirillum* (0.61). *Penicillium* also had a positive and significant correlation with *Azospirillum* (0.51). The correlation analysis showed that no fungi were significantly correlated with PSB. However, PCA angle vector analysis showed that PSB had a strong relationship with *Azotobacter* (Figure

8). It was also observed that *Azospirillum*, *Fusarium*, and *Penicillium* had a strong relationship, while *Penicillium* had the opposite relationship with PSB.

Treatment selection using Multi-Index analysis

The five microbes tested were grouped into Factors (FA), as shown in Table 2. In FA1, the associated microbes were *Azospirillum*, *Penicillium*, and *Fusarium*, while in FA2, the associated microbes were *Azotobacter* and PSB. The grouping of microbes in MGIDI was consistent with that of PCA angle vector analysis. This grouping was then followed by an analysis of each sample's strengths and weaknesses.

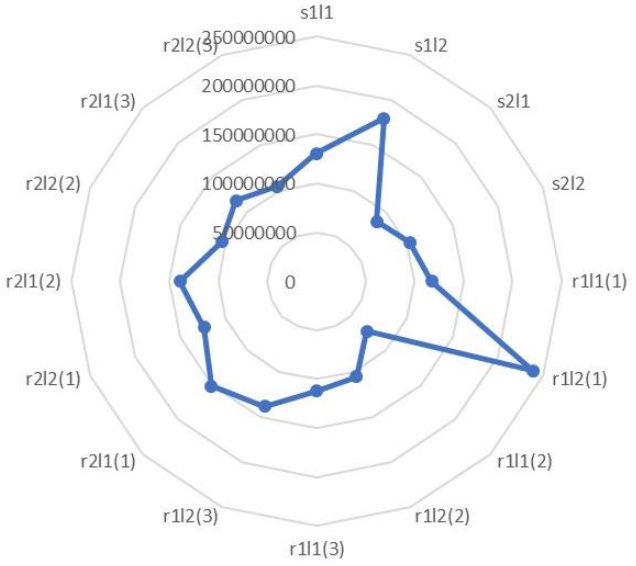

Figure 2. *Azotobacter* population (CFU.g^{-1}) on sample codes at two locations

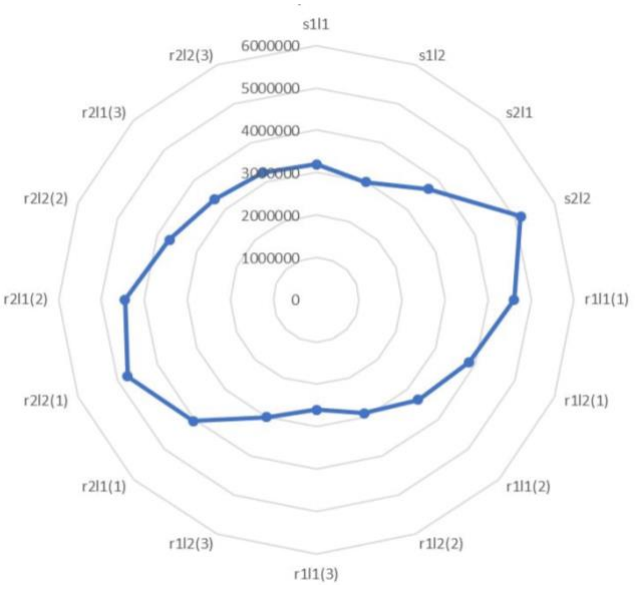

Figure 3. *Azospirillum* population (CFU.g^{-1}) on sample codes at two locations

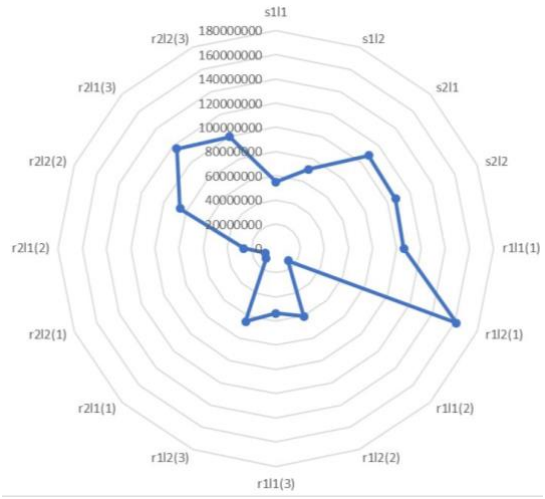

Figure 4. PSB Population (CFU.g^{-1}) on sample codes at two locations

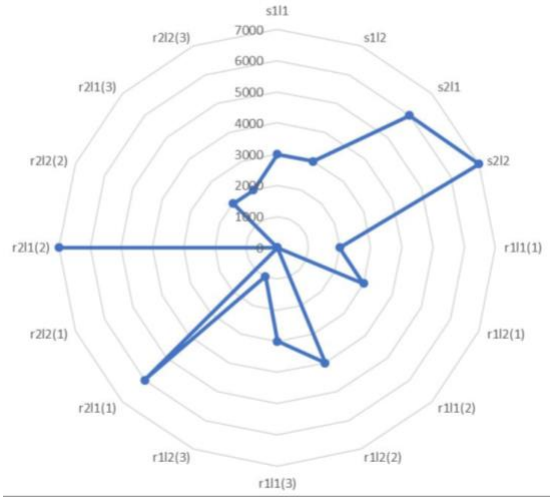

Figure 5. *Penicillium* Population (CFU.g^{-1}) on sample codes at two locations

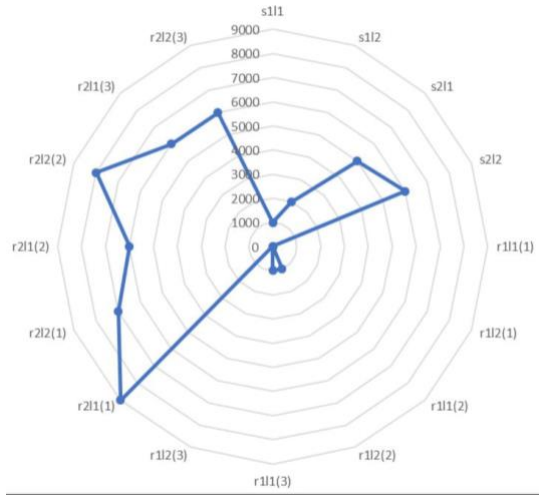

Figure 6. *Fusarium* population (CFU.g^{-1}) on sample codes at two locations

Table 2. Analysis factors on MGIDI

Bacteria	Sense	Factor	FA1	FA2	Communal	Uniqueness
Azospirillum	Decrease	FA1	0.81	-0.01	0.65	0.35
Penicillium	Increase	FA1	-0.69	0.24	0.53	0.47
Fusarium	Increase	FA1	-0.74	-0.37	0.69	0.31
Azotobacter	Decrease	FA2	0.02	-0.79	0.62	0.38
PSB	Decrease	FA2	0.00	-0.77	0.59	0.41

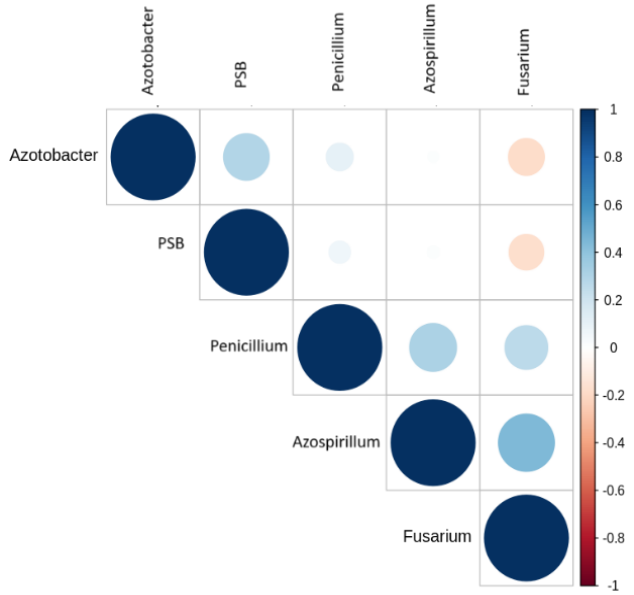

Figure 7. Microbial correlation using the heatmap

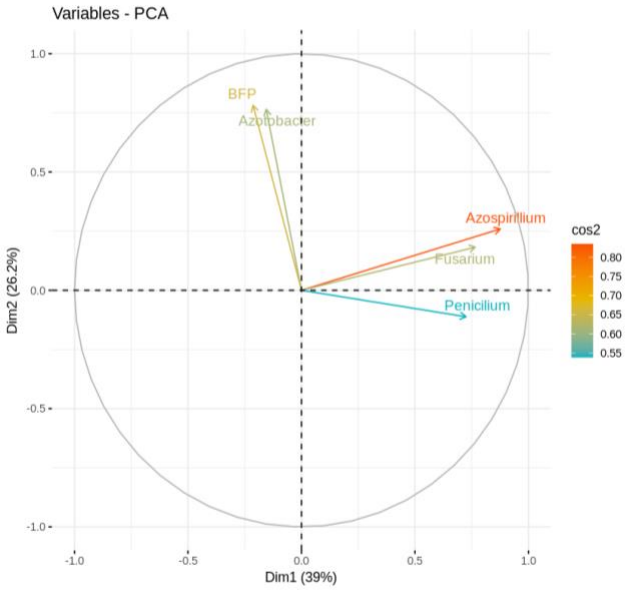

Figure 8. Microbial correlation using Vector Angle PCA

Figure 9 shows the strengths and weaknesses of each treatment calculated using the proportion of each factor to MGIDI. FA1 had the smallest contribution to r2l2(1), s2l1, r1l1(1), r1l2(1), and r2l2(3), showing that among all treatments, these produced the highest value for FAI-associated microbes. FA1 had the highest MGIDI contribution to r1l1(2), suggesting lower productivity for the related traits in this sample. The same interpretation can be extended to other factors identified in Figure 9. Sample r1l1(2) had the most strength related to microbes in FA2. Since all microbes in FA2 desire a positive increase, this sample should have the same high value/amount for *Azotobacter* and PSB (see Table 2 for traits in FA1 and FA2). However, if this is contradictory, then selection should be based on the respective criteria.

In Figure 10, MGIDI analysis identified the best sample based on the five microbes tested. The samples selected based on MGIDI were s2l1 and r2l1(3). Sample s2l1 was above the cutoff point (the red line showing the selected treatment according to selection pressure), while r2l1 was at the cutoff point. This shows that the two samples have the best values/amounts for all microbes tested. Sample r1l1(1) was almost at the cutoff point, which is interesting and necessitates attention to investigate what factors contribute to the closeness. Meanwhile, sample r2l2(1) was at the center point, showing the lowest value for all microbes tested.

Soil fertility

Soil fertility at the same location with diseased and healthy plants did not significantly differ. However, there were differences in values at different locations, where Garut District (l1) had high fertility compared to Kuningan District (l2). Data from the results of soil fertility analysis can be seen in Table 3.

Discussion

Differences in microbial composition in healthy and diseased sweet potatoes

Soil microbes play both beneficial and detrimental roles for plants. *Azotobacter*, *Azospirillum*, Phosphate-Solubilizing Bacteria (PSB), and *Penicillium* are identified as beneficial microbes that are commonly found in sweet potato fields (Nafi'ah et al. 2021; Prawan and Kumar 2023). In contrast, *Fusarium* is identified as a detrimental microbe due to its ability to cause diseases in sweet potato plants. The presence of both beneficial and detrimental microbes influences the growth and yield of sweet potatoes.

The analysis revealed that microbial populations varied across different bulk soil and rhizosphere samples, underscoring the importance of understanding these variations. Beyond the environmental variations between niches, the primary distinction between bulk soil and the rhizosphere played a crucial role in microbiota composition (Ling et al. 2022). *Azotobacter* (Figure 2) was more abundant in the rhizosphere of healthy plants, whereas *Azospirillum* (Figure 3) and *Penicillium* (Figure 5) were more prevalent in diseased plants. PSB showed an uneven distribution between healthy and diseased plants (Figure 4). *Fusarium*, a known pathogen, had a higher population in diseased plants and was more concentrated in the rhizosphere than in the soil (Figure 6). These findings suggest variations in microbial composition, where diseased plants have a higher microbial population, primarily

consisting of beneficial microbes like Phosphate-Solubilizing Bacterias (PSBs) and nitrogen-fixing bacteria. This research is crucial in understanding the complex dynamics of microbial populations in soil and their role in plant health.

Azotobacter can improve soil fertility and support plant growth (Gao et al. 2020; Sumbul et al. 2020; Aasfar et al. 2021). *Azospirillum* population is higher in diseased plants and inversely proportional to *Azotobacter*. Based on the results, samples with high *Azotobacter* populations had low *Azospirillum* populations. This may imply that plants experiencing stress or disease may produce certain bacteria-attracting compounds (Chieb and Gachomo 2023) or that *Azospirillum* is a response to unfavorable conditions (Gureeva and Gureev 2023). These bacteria are highly essential to increasing soil fertility and supporting plant growth by providing phosphate to plants (da Silva et al. 2023). Several factors can influence the uneven distribution of PSB populations, including soil biochemical conditions, the availability of available phosphate in soil, and rhizosphere conditions (Dey et al. 2021; Timofeeva et al. 2022). Diseased plants may produce certain compounds that attract PSB (Febriyanti et al. 2023). This can increase the bacterial population around the diseased plant, even though the health of the plant is compromised. During certain growth phases, the plant may produce more root exudates that support bacterial growth, causing population fluctuations (Zhao et al. 2021; Ma et al. 2022; Upadhyay et al. 2022). *Penicillium* populations increase along with the high amount of organic matter that decomposes due to root death or diseased plant tissue (Oses-Pedraza et al. 2020). Populations may be higher in the rhizosphere of diseased plants due to the abundance of root exudates (Wang et al. 2021b). Increased *Fusarium* population in diseased plants is often associated with damage to plant tissue. Infection spreads through the roots, causing serious vascular damage and wilting of the plant, which leads to cell death (Syed Nabi et al. 2021). The fungus is more common in monoculture cultivation, where the soil is diseased even when crop rotation has been implemented (Xu et al. 2022; Hong et al. 2023). Land with a history of being attacked by *Fusarium* tends to cause disease if there is no treatment.

Correlation between soil microbes, Fusarium *pathogens, and sweet potato plants*

Soil microbes can enhance sweet potato growth by increasing nutrient availability, stimulating the plant's immune system, and protecting plants from pathogens. *Fusarium* is commonly found in soil and causes a variety of diseases in plants, including sweet potatoes. Species such as *Fusarium solani* and *Fusarium oxysporum* are known to be important pathogens that cause root rot and wilt (El-Kazzaz et al. 2022; Yan and Nelson Jr 2022). This fungus can cause sweet potato plants to wilt, become soft, stunted, and turn yellow, resulting in decreased yields and quality, making the produce unmarketable (Rimada et al. 2020; Nanaware et al. 2024).

Soil microbes compete with *Fusarium* pathogens for resources and space. These microbes can trigger plant immune system responses, increasing sweet potato resistance to *Fusarium* infection. For instance, root exudates produced by plants attract beneficial microbes that protect the plants. Some microbes also improve plant health, such as *Azotobacter* and *Azospirillum* (Gao et al. 2020; Ilyas et al. 2020), which increase resistance to *Fusarium* infection. Several microbes, including PSB and certain species of *Penicillium*, act as biocontrol agents that help inhibit *Fusarium* growth (Adedayo and Babalola 2023; Guo et al. 2024). Ecosystem-based methods that integrate the use of soil microbes in agricultural management improve sustainability. Methods such as crop rotation, use of organic fertilizers, and inoculation with beneficial microbes can help minimize the negative impacts of pathogens.

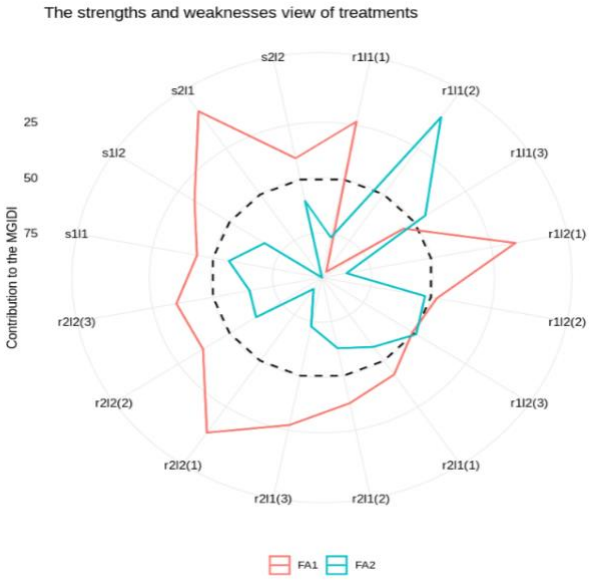

Figure 9. The strengths and weaknesses of treatments

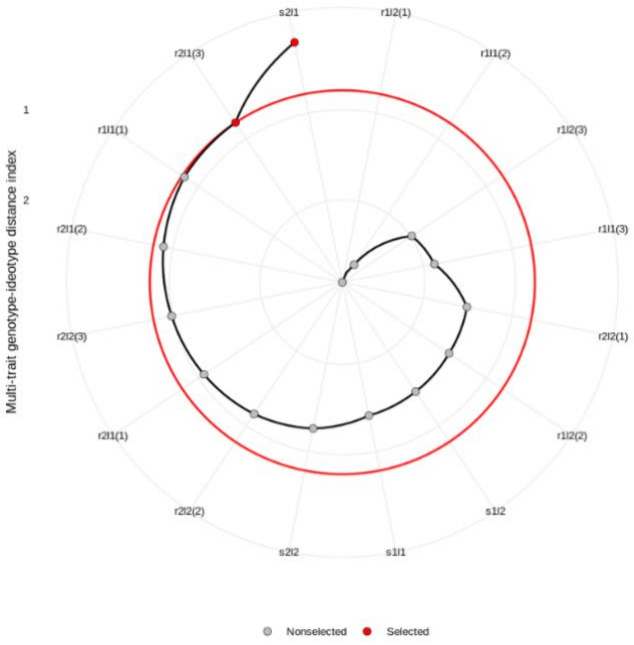

Figure 10. Multi-trait genotype-ideotype distance index

Table 3. Results of soil fertility analysis

Sample	pH	C-Organic	Total N	C/N	P available	K_2O	Exch. K	Exch. Na	Exch. Ca	Exch. Mg	CEC
s1l1	5.5	1.27	0.17	8	99.13	46.21	4.54	0.29	13.56	3.39	28.93
s1l2	5.8	1.18	0.15	8	93.3	14.41	0.52	0.15	4.94	1.21	27.19
s2l1	5.5	1.76	0.24	7	99.34	41.65	4.02	0.27	13.02	3.48	32.25
s2l2	5.6	1.35	0.17	8	98.27	18	0.63	0.19	5.26	1.36	25.64

Notes: s1l1 soil from healthy plants location 1, s1l2 soil from healthy plants location 2, s2l1 soil from diseased plant location 1, s2l2 soil from diseased plant location 2

The correlation analysis of all tested microbes showed that *Fusarium* fungus correlates significantly and positively with *Azospirillum* (0.61), as does *Penicillium* (0.51) (Figure 7). This shows that each correlated microbe had a linear influence on the other (Maulana et al. 2023). The results of PCA angle vector analysis showed that PSB had a strong relationship with *Azotobacter* (Figure 8). It was also observed that *Azospirillum*, *Fusarium*, and *Penicillium* had a strong relationship, while *Penicillium* had an opposite relationship with PSB. Additionally, PCA angle vector analysis can assess the relationship between the tested traits (Maulana et al. 2023; Maxiselly et al. 2023), with acute angles having a strong relationship and obtuse angles having the opposite relationship (Jolliffe 2002; Maxiselly et al. 2024).

In previous research, the best treatment was determined based on careful consideration of the proximity of the selection index cutoff points such as MGIDI (Olivoto et al. 2022; Jalalifar et al. 2023). In this research, s2l1 and r2l1(3) were identified at and above the cutoff point, implying better performance for all tested microbes. MGIDI analysis shows how samples relate to known factors by specifying the contribution of each trait. This provides insights into the strengths and weaknesses across traits (Olivoto et al. 2022). For example, r1l1(2) shows weakness in FA1, but has strength in FA2 (Figure 9). The strengths and weaknesses identified by MGIDI help in targeting the development of selection models with samples for specific microbes of interest. Therefore, the use of MGIDI is very effective in evaluating the strengths and weaknesses of samples by analyzing different microbes using factor analysis.

Microbial composition impacts soil

Soil microbes play an essential role in soil ecosystem, influencing the physical, chemical, and biological properties of soil. The analysis showed that soil and rhizosphere of diseased plants had the most diverse microbial populations compared to healthy plants. Microbial diversity in soil can have a significant impact on soil fertility and nutrient availability for plants. Soil's physical properties, such as texture, structure, and water-holding capacity, are greatly influenced by microbial activity (Sakin et al. 2024). Microbes contribute to the formation of soil aggregates, which improves aeration and water infiltration, decomposition of organic matter, and nutrient cycling (Zhang et al. 2024). The biological properties of soil are related to the biodiversity of microbes present in it.

Microbial diversity can influence biological activities, including organic matter decomposition, nitrogen fixation, and pest control. Soils rich in microbes generally have more biological activity, which has a positive impact on plant health because they tend to be more resistant to disease and have better growth (Mataranyika et al. 2022). Microbes can synthesize phytohormones, antibiotic siderophores, and many other secondary metabolites that act on the plant immune system (Bertola et al. 2021). Diverse microbes can stimulate sweet potato growth and yield.

The potential of beneficial soil microbes as biological control agents to control Fusarium *wilt disease*

Fusarium wilt disease, caused by the pathogenic fungus *Fusarium oxysporum*, is a serious threat to the growth and production of sweet potatoes. Control of this disease is generally carried out through the use of chemical pesticides, which can have negative impacts on the environment and human health. Therefore, the use of beneficial soil microbes as biological control agents is a promising alternative. Some genera that are known to be effective in controlling *Fusarium* wilt include *Pseudomonas, Bacillus, Rhizobacter*, *Trichoderma* spp., *Myrothecium* spp., and *Streptomyces* spp. (Assena et al. 2024; Lu et al. 2024). Soil microbes can control *Fusarium* wilt disease through various mechanisms, including i) Control microbes can compete with *Fusarium* for space and nutrients, thereby reducing the chance of infection (Pellan et al. 2021); ii) Some microbes produce antifungal secondary metabolites, which can inhibit the growth of pathogenic fungi (El-Saadony et al. 2022); and iii) Microbes play a role in increasing plant resistance to stress by increasing nutrient absorption and regulating growth hormones (Kang et al. 2022; Koza et al. 2022). Beneficial soil microbes have great potential as biological control agents to control *Fusarium* wilt disease in sweet potato plants.

In conclusion, the soil and rhizosphere of diseased plants had the most diverse microbial populations compared to healthy plants, and the microbial composition was related to soil fertility levels and the presence of *Fusarium* wilt disease. Further research is required to understand the complex interactions in the soil ecosystem before microbes are implemented as control agents in the field on a large scale. The research should also investigate microbial interactions and environmental factors that affect effectiveness. Additionally, microbe-based inoculant products should be developed for use in sweet potato cultivation.

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