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ASSESSING THE EFFICACY OF MICROBIAL BIOFERTILIZERS IN ENHANCING MUNGBEAN GROWTH

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Abstract

The present study used a randomized complete block design to investigate the effects of different microbial biofertilizers on the growth and yield of mungbean (NM 98 cultivar) at Biopolymer Research and production center Faisalabad. In order to prevent cross-treatment effects, the study examined five treatments: control (T1), Rhizobium (T2), Azotobacter (T3), Mycorrhizae (T4), and a mixed biofertilizer (T5). Each treatment was applied to a 25 m2 plot with distinct zones. Using precise techniques, such as an irrigation schedule with specific timings and a jaggery water solution for inoculation, the biofertilizers were carefully prepared and applied. The plant height, number of pods per plant, pod length, leaf area index, biomass, and yield showed significant differences amongst treatments. In every way, the mixed biofertilizer (T5) demonstrated superiority over the other treatments in terms of promoting mungbean growth. With this treatment, the plant height increased to the greatest extent (38.679 cm), the yield was the highest (2.4 kg/25 m², or 962 kg/ha), and other growth parameters showed consistent improvement. These results highlight how Rhizobium, Azotobacter, and Mycorrhizae perform in concert to provide a comprehensive bio fertilization strategy. The potential of microbial biofertilizers to enhance crop yields and growth parameters is demonstrated in our study, which advances sustainable agriculture. The results have important ramifications for mungbean farming, encouraging ecologically friendly agricultural methods and enhancing food security. It is highly recommended that mungbean cultivation incorporate a mixed microbial biofertilizer containing Rhizobium, Azotobacter, and Mycorrhizae for sustainable agriculture and increased crop yields.

Keywords
Biofertilizer; Mungbean; Mycorrhizae; Rhizobium; Sustainable agriculture

1.Introduction

The optimization of crop yield while minimizing environmental impact is a constant study in the aim of agricultural sustainability (Pelesaraei *et al*., 2017). Due to its high protein content and capacity to fix nitrogen, mungbean (*Vigna radiata*), a leguminous plant native to the Indian subcontinent, is an important crop (Pataczek *et al*., 2018). The need for food is growing along with the world's population, which points out the significance of increasing the yield and growth of vital crops like mung beans. The development of microbial biofertilizers introduces in a new era in agricultural production. Many benefits are provided by these biofertilizers, which are made up of a variety of microorganisms. These benefits include increased nutrient uptake, growth promotion, and disease resistance (Mitter *et al*., 2021). In addition to supplying nutrients, they play a vital role in agriculture by retaining soil health and biodiversity, which makes them essential for sustainable farming (Biswas *et al*., 2014). Even though microbial biofertilizers are known to have benefits, their effectiveness can differ significantly based on a number of variables, including the type of microorganisms used, the surrounding environment, and the particular crop species (Malusà *et al*., 2016). This variation emphasizes the necessity of carefully evaluating and adjusting the formulations of biofertilizers for different crops. Thus, the objective of the current study is to assess the capacity that microbial biofertilizers help promote the growth of mungbean, a crop that has substantial nutritional and economic value, especially in developing nations (Kumari *et al.*, 2018). Poor soil quality, insufficient availability of nutrients, and risk to different pathogens are some of the common issues encountered in the cultivation of mungbean (Etesami *et al*., 2018). The excessive use of chemical pesticides and fertilizers, which increase yields temporarily but damage soil health and the ecosystem over time, complicates these problems (Fischer & Connor 2018). A paradigm shift has occurred with the move to microbial biofertilizers, which aims at dealing with these issues with a more sustainable method (Mitter *et al.*, 2021). Microbial biofertilizers have the capacity to form symbiotic relationships with plant roots, which may enhance mungbean growth (Kumari *et al*., 2018). These microorganisms, which include fungi and bacteria, have the ability to solubilize phosphorus, fix atmospheric nitrogen, and produce substances that promote growth. As a result, they can improve soil fertility and structure while providing plants with essential nutrients (Saharan 2011). In this study, germination rate, plant biomass, root and shoot length, yield quantity and quality, and other factors are taken into consideration as we investigate the ways in which different microbial biofertilizers assist to promote mungbean growth (Gautam *et al*., 2021). Additionally, in order to improve biofertilizer formulations and application techniques specific to mungbean cultivation, research aims to clarify the mechanisms by which these fertilizers confer their advantageous effects on mungbean plants (Barman *et al*., 2019). Sustainable agriculture depends on healthy soil, and maintaining the quality of that soil is crucial to continuing productivity. Research on the effects of microbial biofertilizers on soil microbial diversity, nutrient cycling, and structure provides light on the wider environmental advantages of implementing this environmentally friendly

agricultural technique (Suman *et al*., 2022). The approach used in this research includes both laboratory evaluations and field trials. Several microbial biofertilizer treatments are applied to mungbean crops in field trials, and growth parameters are then observed and measured during the cultivation period (Kumawat *et al*., 2021; Ezeokoli *et al*., 2019). In conclusion, this study offers a thorough evaluation of the effectiveness of microbial biofertilizers in promoting the growth of mungbean plants. The investigation of the relationship between these biofertilizers and mungbean plants advances the field of sustainable agriculture. It is expected that the results will have applications for farmers and other agricultural experts, providing a financially and environmentally sustainable substitute for chemical fertilizers (Kaur *et al*., 2019). It is impossible to exaggerate the importance of mungbean in rural economies, particularly in South and Southeast Asia (Sequeros *et al.*, 2021). It corresponds to well into a variety of cropping systems and is a short-duration legume with a low water requirement, which helps to ensure the sustainability of agricultural practices in these areas (Adarsh *et al*., 2019). In addition to being a staple food crop, mungbeans provide smallholder farmers with a sizable source of revenue. However, historically, biotic and abiotic stresses like nutrient-poor soils, drought, and pests have resulted in mungbean yields that are below potential (Das *et al*., 2022). These difficulties refer to for an evaluation of farming methods, with a focus on improving soil fertility and plant health via sustainable techniques. Agriculture's use of microbial biofertilizers results from an in-depth understanding of the soil microbiome and its complex relationships with plant roots (Vishwakarma *et al*., 2020). The area of soil known as the rhizosphere, which is impacted by root secretions, is a microbial a lot where a complex web of interactions develops. In symbiotic relationships with plant roots, beneficial microbes like Rhizobium, Azotobacter, and mycorrhizal fungi aid in several physiological processes that are essential for plant growth and development (Nanjundappa *et al*., 2019). These microbes have the ability to eliminate phosphorus from soil compounds, fix nitrogen from the atmosphere into forms that plants can use, and produce phytohormones that promote plant growth, such as gibberellins and auxins. There are many examples of microbial biofertilizers' beneficial effects on a variety of crops in the literature. For example, it has been proven that applying mycorrhizal fungi and Rhizobium can improve nutrient uptake and provide resistance against soil-borne pathogens, hence increasing legume growth (Pierre *et al*., 2014). Given that mungbeans and the previously mentioned microorganisms have similar symbiotic potential, these findings show promise for the cultivation of mungbeans. But finding the best biofertilizer consortia for mungbean plants requires a focused approach due to the specificity of plant-microbe interactions (Maheshwari *et al*., 2023). Apart from stimulating plant growth, microbial biofertilizers are essential for preserving soil health. Soil degradation, microbial diversity loss, and increased susceptibility to erosion are consequences of conventional farming's excessive use of chemical fertilizers and pesticides (Sheoran *et al*., 2019). Microbial biofertilizers, on the other hand, increase microbial diversity, strengthen soil structure, and aid in the accumulation of soil organic matter. These changes

to the properties of the soil promote improved nutrient cycling, improved water retention, and increased resistance to environmental stresses. Microbial biofertilizers have advantages for the environment that remain above improving soil health. Chemical pesticides and fertilizers contribute to air pollution, water eutrophication, biodiversity loss, and other environmental problems (Kumar & Yaashikaa 2019). The use of biofertilizers reduces the need for these dangerous chemicals, which is consistent with the ideas of environmentally friendly farming practices and sustainable agriculture. Microbial biofertilizer use in agriculture faces lots of challenges despite the apparent advantages. These include the need for specialized application techniques for various crops and soil types, farmers' ignorance of the issue, and variations in efficacy brought on by environmental factors (Liu et al., 2018). In addition to conducting scientific research, policies and extension services are needed to deal with these issues and help farming communities share best practices and knowledge. The current study attempts to close a significant gap in the literature by providing an in-depth assessment of the effectiveness of microbial biofertilizers in promoting mungbean growth. This helps to move to more resilient and sustainable agricultural systems by adding to the corpus of knowledge supporting it.

2.Methodology

The study was carried out at Biopolymer Research and production center Faisalabad, which is well-known for its variety of farming techniques. The objective was to evaluate the way microbial biofertilizers affected the growth of the NM 98 cultivar of mungbean. Using a randomized complete block design (RCBD), 130 m^2 of experiment area was used in total. To reduce the effects of cross-treatment, the site was properly divided into five treatments, each consisting of a 25 m^2 plot with 5 m^2 different zones added in between. The following labels were placed on the treatments:

- Control (T1): No application of biofertilizer; this is used as an evaluate for comparison.
- Rhizobium (T2): The application of this nitrogen-fixing bacterium is predicted to result in low to moderate improvements in growth parameters.
- Azotobacter (T3): Applied similarly to Rhizobium, Azotobacter is another nitrogen-fixing bacterium that should produce comparable or slightly greater growth enhancements.
- Mycorrhizae (T4): Mycorrhizae is a beneficial fungus that increases root biomass and nutrient uptake, which can result in notable growth improvements.
- Mixed biofertilizer (T5): Because of their combined benefits, it is hypothesized that applying Rhizobium, Azotobacter, and Mycorrhizae close will improve growth parameters the most overall.

2.1 Acquisition and preparation of rhizobium, Azotobacter, and mycorrhizae biofertilizers

To ensure quality and efficacy, the university laboratory carefully prepared the biofertilizers containing Rhizobium, Azotobacter, and Mycorrhizae. The organisms, each associated with a particular plant species recognized for their symbiotic relationships, were isolated from plant samples collected from the field.

2.1.1Rhizobium

To avoid contamination, make sure all media and equipment are sterilized. The nitrogen-fixing bacteria Rhizobium was isolated from the root nodules of leguminous plants, usually from species such as *Phaseolus vulgaris* (Common Bean) or *Medicago sativa* (Alfalfa). After being sterilized, the nodules were crushed and streaked onto a medium called Yeast Extract Mannitol Agar (YEMA). Introduce a pure culture of the Mungbean-specific Rhizobium strain into the medium. Keep the cultures incubated under the right conditions until significant bacterial growth is observed. To create an inoculant, gather the bacterial cells and combine them with a carrier substance such as lignite, peat, or charcoal. Before planting, the inoculant can be directly applied to the seeds.

2.1.2 Azotobacter

A free-living nitrogen-fixing bacterium known as Azotobacter has been identified in the rhizosphere, or soil, of cereal crops such as *Zea mays* (corn) and *Triticum aestivum* (wheat). Samples of soil were spread out onto Ashby's Mannitol Agar plates after being successively diluted. To reach the required concentration, distinct Azotobacter colonies were subsequently sub cultured in Ashby's Mannitol Broth. Prepare an appropriate culture medium for Azotobacter, such as Ashby's Mannitol Agar. Introduce a pure culture of Azotobacter into the medium. Allow the culture to prosper in the perfect conditions. To make the biofertilizer, gather the bacterial cells and combine them with a carrier material. To avoid contamination, make sure all media and equipment are sterilized.

2.1.3 Mycorrhizae

To avoid contamination, make sure all media and equipment are sterilized. Essential for plant nutrition uptake, mycorrhizal fungi were taken from the root systems of plants that were known to have mycorrhizal associations, like *Quercus spp.* (Oak) or *Pinus spp.* (Pine). Mycorrhizal spores were separated from the roots using a wet sieving and separating method after the roots had been thoroughly cleaned. For the purpose of to increase the spore population, they were then grown under greenhouse conditions on an appropriate substrate, such as soil or sand that had been sterilized. Once a considerable amount of period is over, the mycorrhizae-enriched soil surrounding the roots of the host plant can be harvested. This soil can be combined with a carrier or used directly as a mycorrhizal inoculant.

3.Application of biofertilizers in mungbean cultivation

A vital step in ensuring the efficacy of biofertilizers is their field application. This is a direct describing the way to use biofertilizers consisting of Rhizobium, Azotobacter, and Mycorrhizae in a mungbean field, with a focus on 25-square-meter plots.

3.1Preparation of jaggery (Gur) water solution

Add 5–10% of jaggery to water to dissolve it. In one liter of water, 50–100g of jaggery must dissolve. To sterilize the solution, boil it for a short while. Before using, let it cool to room temperature.

3.2 Rhizobium and Azotobacter (T2 & T3)

Make sure the mungbean seeds are clean and free of contaminants and chemicals. Using the prepared jaggery water solution, make a slurry of the Rhizobium or Azotobacter inoculant instead of using

plain water. For a plot measuring 25 square meters, approximately 350 grams of biofertilizer are required. Spread the inoculant slurry over the seeds. This can be accomplished by either spraying the slurry over the seeds while stirring, or by slowly shaking the seeds with the slurry. To keep the bacteria safe from sunlight, let the inoculated seeds dry in a shaded area. As soon as the seeds are dry, plant them to preserve the bacteria's viability.

3.3 Mycorrhizae application (T4)

Moisten the soil where the seeds will be sown with the jaggery water solution before planting. Mycorrhizal colonization will benefit from this helped creation of a favorable environment. Directly inject the Mycorrhizae inoculant into the soil after it has become wet. For a 25 square meter plot, 250 grams is usually the recommended amount. After thoroughly mixing the inoculant with the soil, plant the mungbean seeds in the inoculated soil.

3.4 Mixed biofertilizer application (T5)

Apply Rhizobium and Azotobacter to the mungbean seeds by slurryizing the jaggery water as previously mentioned. Use jaggery water to wet the soil, then inoculate it with mycorrhizae. Once combined, sow the coated seeds.

3.5 Soil preparation and sowing

Soil samples were collected from each plot prior to sowing to assess fertility and texture. Plots were then marked after the soil was tilled to a depth of 15 cm. 5 cm of mungbean seed was planted, with 10 cm splitting each seed and 20 cm dividing rows.

3.6 Seed rate and sowing method

The Mungbean cultivar NM 98 seed rate for this study was maintained at 14 kg per hectare, which is compatible with recommended density for this crop variety. Direct seeding was used as the sowing technique, and to ensure uniform seed distribution throughout the plots, a manual broadcasting technique was used. After that, seeds were carefully covered with soil down to the recommended 5 cm depth.

3.7 Irrigation schedule and method

Since mungbean grows during the kharif season, it typically requires little irrigation because of the monsoon rains that coincide with it. However, additional irrigation was given during crucial growth stages to ensure uniform growth conditions:

- First irrigation: water as soon as seeds are sown to promote germination.
- Blooming Stage: To aid in the growth of flowers and the development of pods.
- Pod Filling Stage: To make sure enough water for perfect pod growth.

The irrigation technique used was furrow irrigation, which was selected due to its water-saving effectiveness and compatibility with the soil type at Koont Farm.

3.8 Harvesting

Manual harvesting was done in accordance with the traditions related to Mungbean crops. When 85% of the pods had developed into a brown or black color, indicating that the plants were ready for harvest, the plants were carefully uprooted. Before being threshed, the plants were allowed to dry in the field for two to three days after harvest.

3.9 Data collection

A crucial part of the research methodology is the data collection process. A systematic and challenging approach is employed for each of the previously mentioned parameters: Plant Height

(cm), Number of Pods per Plant, Pod Length (cm), Leaf Area Index (LAI), Biomass (g), and Yield (g) in order to guarantee the precision and reliability of the data. Below is the methodology for gathering the data for every parameter: Plant height (cm): At the vegetative, flowering, and mature stages of growth, select five plants at random from each replication. Using a measuring tape, determine each plants height from the base to the top of the canopy. Record the data in centimeters (cm).

3.10 *Number of pods per plant*

Choose 15 plants at random from each replication when they reach maturity. Each selected plants total number of pods should be counted. Keep records of the number of pods produced by each plant. Pod length (cm): At random, select 15 pods from each of the plants that were selected for the pod count. Using a ruler or caliper, measure the length of each pod from the bottom to the tip. Measure the lengths of the pods in centimeters (cm).

3.11 *Leaf area index (LAI)*

At the flowering stage, select 15 plants at random from each replication. Take measurements of each leaf's length and width from the selected plants. Using the formula eq 2, calculate the leaf area index. Record the LAI for each selected plant. Leaf Area Index: LAI = (Leaf Length x Leaf Width) / Plant Ground Area……. equation 1Biomass (g)At maturity, uproot the 5 plants chosen for pod count from each replication. Wash and split the leaves, stem, and roots. The plant parts should be dried in an oven at 70°C until they reach a constant weight. Use a precision balance to weigh the dried plant parts. To record the biomass, put in grams (g). Yield (g)At maturity, each plot is harvested and threshed separately to ensure an accurate yield assessment. It ensures that each treatment's results are appropriately expressed in the yield data, the yields of mung bean crops from a 25 square meter area were extrapolated to per hectare estimates by using formula eq...2, to assess the effectiveness of different biofertilizer treatments. These results collected from $25m^2$ area because each treatment having $25m^2$ area. Yield per hectare (kg/ha) = (Yield per 25 m^2) × (25 m^2 /10,000 m^2) ……. equation 2

3.12 Recording and handling data

The sampling strategy involves choosing 5 plants at random from each replication for each parameter. The strategy aims to reduce the impact of any variations specific to a particular plant while providing a sample that is representative of the entire plot. The measurements of the five chosen plants will be used to determine the mean value for each parameter. ANOVA and Least significant difference tests are two statistical tests that will use these mean values. All collected data will be carefully recorded and stored in a database. The use of uniform methods and measurement units ensures consistency in data recording. This thorough approach to data handling and collection will improve the overall reliability and validity of the study results.

4. Results

This study's section focuses on evaluating the way various treatments affect the mung bean plant's growth and yield. T1 (Control), T2 (Rhizobia), T3 (Azotobacter), T4 (Mycorrhiza), and T5 (Mixed) were the treatments that were evaluated.

Table 1. Statistical analysis of treatment means (Rhizobia, Azotobacter, Mycorrhiza, mixed, and control) on mung bean growth and development.

Treatments	Plant Height (cm)	Number of Pods per Plant	Pod Length (cm)	Leaf Area Index (LAI)	Biomass (g)
T1	33.037b	8.3144c	6.7511c	1.9178c	19.349d
T2	34.921ab	14.451b	7.4011bc	2.4922b	26.164bc
T3	36.207ab	17.148a	7.5767bc	2.8778b	25.029c
T4	36.243ab	17.893a	7.9211b	2.8000b	31.056ab
T5	38.679a	18.292a	8.7700a	3.4156a	32.039a

3.13 Plant height

The results of our study showed significant differences in the effects of five different treatments on plant height. The mean plant height under the control treatment (T1) was found to be 33.037 cm. With a standard deviation of 3.8029 cm, a minimum height of 25.860 cm, and a maximum height of 37.930 cm, the variability in plant height was clearly visible. Plant height within this group exhibited a moderate degree of relative variability, as indicated by the coefficient of variation (C.V.) of 11.511%. The plants that were treated with Rhizobia treatment T2 showed a mean height increase of 34.921 cm. This group's standard deviation was 3.8310 cm, indicating that their pattern of variability was comparable to that of the control. The height range of the plants was 29.970 cm to 42.260 cm. The mean plant height increased further, reaching 36.207 cm, after Azotobacter was applied. However, a standard deviation of 6.7082 cm and a C.V. of 18.528% showed a higher degree of variability for this treatment T3. The differences in height ranged from 27.430 cm to 46.950 cm. The mean plant height of the treatment T4 was 36.243 cm, which was very similar to the Azotobacter treatment. The range of plant heights was between 29.480 cm and 46.220 cm, and the standard deviation was 4.7009 cm, indicating a wide distribution of growth responses. With an average height increase of 38.679 cm, the Mixed treatment showed the largest increase in plant height. Among all treatments, this one was notably the least variable, with a C.V. of 6.8385% and a standard deviation of 2.6450 cm. The group's plant heights varied from 35.620 cm to 42.500 cm. These findings suggest that the height of the plants was significantly and differently impacted by each treatment. The Mixed treatment (T5) showed the strongest effect on increasing plant height along with the least amount of variability, indicating a stable and strong growth response. The other treatments were Rhizobia (T2), Azotobacter (T3), Mycorrhiza (T4), and the control (T1), in decreasing order of impact. The varied effects of these treatments on plant growth parameters are highlighted by the observed variations in mean heights as well as the variability within each treatment group.

3.14 Number of Pods per Plant

The evaluation of the impact of different treatments on the number of pods per plant is the main objective of this section of the study. T1 (Control), T2

(Rhizobia), T3 (Azotobacter), T4 (Mycorrhiza), and T5 (Mixed) were the treatments that were evaluated. With no specific treatment, the control group T1 showed an average of 8.3144 pods per plant. With a coefficient of variation (C.V.) of 23.250% and a standard deviation of 1.9331, this group's variability was quite noticeable. In this group, the lowest and maximum numbers of pods per plant were 5.6900 and 12.440, respectively. The average number of pods per plant increased to 14.451 with the Rhizobia treatment (T2). In comparison to the control, there was more variability in pod production, as indicated by the standard deviation of 2.7371. For this treatment, the number of pods per plant varied from 11.360 to 19.600. The average number of pods per plant increased to 17.148 with a standard deviation of 2.5580 after treatment T3 with Azotobacter. The number of pods per plant in this treatment ranged from 13.580 to 21.270, indicating a continuous increase in pod production throughout the sample. An average of 17.893 pods per plant were produced by the Mycorrhiza treatment T4, which was marginally more than the Azotobacter treatment. A standard deviation of 2.1994 showed that the variability was comparatively lower than in the earlier treatments. Pod counts varied from 14.890 to 20.870 per plant. Pod production was relatively consistent throughout the sample, with the Mixed treatment T5 showing the highest average number of pods per plant (18.292, standard deviation 1.9090). Each plant produced pods that ranged from 15.850 to 21. 710.In summary, the data clearly show that applying various treatments Mycorrhiza, Azotobacter, Rhizobia, mixed treatment, and the control progressively increases the number of pods per plant. In addition to producing the greatest average number of pods, the Mixed treatment also showed the least amount of variability, indicating a robust and consistent response to this treatment. These results exhibit how these treatments have a major effect on plants' ability to produce pods.

3.15 Pod Length (cm)

This part of the research aims to assess the way various treatments affect pod length, a crucial plant development metric. The initial pod length in the control group was 6.7511 cm on average. The standard deviation of the pod length for this group was 0.7293 cm, which suggests a comparatively small range of variation. The lengths of the pods varied from 5.7900 cm at the minimum to 8.1300 cm at the maximum. With a mean pod length of 7.4011 cm, the Rhizobia treatment T2 superior to the control. With a standard deviation of 0.7933 cm, the variation was slightly higher within this group. In this treatment, the pod lengths varied from 6.5300 cm to 9.1500 cm. In contrast to T2, the results of the Azotobacter treatment (T3) showed a mean pod length of 7.5767 cm. There may be a wider range of pod lengths in this group from 6.1800 cm to 9.0500 cm as indicated by the standard deviation of 0.9232 cm. Pod length increased even more with Mycorrhiza treatment T4, averaged 7.9211 cm. With a standard deviation of 0.9204 cm, the variability was comparable to that of the Azotobacter treatment. For this treatment, the pod lengths ranged from 6.3900 cm to 9.5000 cm. At 8.7700 cm, the Mixed treatment T5 showed the maximum mean pod length. This treatment had the highest variability of all the treatments, as indicated by its 0.9694 cm standard deviation. Within this group, pod lengths varied from 7.6400 cm to 10.1900 cm.The Mixed treatment (T5) showed the greatest enhancement in

terms of pod length, with the highest mean pod length. The overall increase in pod length indicates a strong positive response to the combined treatment modalities, even though this treatment also exhibited the highest variability. By contrast, the other treatments were Mycorrhiza (T4), Azotobacter (T3), Rhizobia (T2), and the control (T1), in decreasing order of efficacy. The data indicate that a more noticeable increase in pod length a crucial component of plant production yield and quality is a result of the synergistic effects in the Mixed treatment.

3.16 Leaf Area Index (LAI)

The assessment of the Leaf Area Index (LAI) under the following treatment conditions is the main focus of this section of the study: T1 (Control), T2 (Rhizobia), T3 (Azotobacter), T4 (Mycorrhiza), and T5 (Mixed). With a standard deviation of 0.3900, the control group's LAI was 1.9178. Under typical conditions, the LAI values showed a moderate dispersion in leaf area development, ranging from a minimum of 1.0200 to a maximum of 2.3100, having the addition of Rhizobia (T2), the LAI increased to 2.4922. Through a standard deviation of 0.3987, the level of variability was comparable to that of the control. The range of the LAI values was 2.1100 to 3.2400. After receiving Azotobacter (T3) treatment, the LAI increased to 2.8778, indicating even more improvement. At this point the standard deviation was 0.6469, indicating a greater leaf area variability. The LAI values were in the range of 1.8200 to 3.6400. The LAI of the mycorrhiza treatment (T4) was 2.8000, slightly lower than the Azotobacter treatment's. With a standard deviation of 0.4549 and a range of 1.8500 to 3.2500 for the LAI, this treatment group's leaf area development was comparatively constant. When compared to other treatments, the Mixed treatment (T5) showed the highest LAI of 3.4156 with a standard deviation of 0.6296, indicating a significant and consistent improvement in leaf area. Under this treatment, the LAI ranged from 2.6000 to 4. 4500.The highest mean LAI value indicates that, from an academic perspective, the Mixed treatment (T5) is the most successful in raising the Leaf Area Index. This superiority may be ascribed to the Mixed treatment's complete strategy, which may have a synergistic effect on leaf development. The comparatively lower coefficient of variation in this group also points to a response that is consistent across various plant samples, supporting the Mixed treatment's efficacy in maximizing the development of leaf area. The increase in LAI values from the control to the Mixed treatment indicates the respective advantages of each treatment, with the Mixed treatment being the most advantageous for enhancing LAI.

3.17 Biomass (g)

The biomass production in each of the following treatment groups was carefully assessed by the study: T1 (Control), T2 (Rhizobia), T3 (Azotobacter), T4 (Mycorrhiza), and T5 (Mixed). Finding the treatment that maximizes biomass accumulation a crucial mark of plant growth and health was the main goal. The control group's baseline revealed an average biomass of 19.349 g. Moderate group fluctuations were indicated by a standard deviation of 3.0809 g. The biomass provided a baseline for comparison, ranging from a minimum of 15.090 g to a maximum of 24.060 g. The use of Rhizobia significantly increased biomass production, with an average of 26.164 g produced. Through a standard deviation of 4.2216 g, the

variability was marginally greater than in the control group. The range covered 17.760 g to 29.880 g, demonstrating Rhizobia's beneficial effect on biomass accumulation. The average biomass produced by Azotobacter treatment was 25.029 g, which was slightly less than that of Rhizobia treatment. With a standard deviation of 6.7671 g, the highest of all treatments, this group showed an important level of variation. The values of biomass varied from 16.380 g to 32.900 g. With an average yield of 31.056 g, the mycorrhiza treatment demonstrated a notable improvement in biomass production. The standard deviation for this treatment was 8.5967 g, indicating significant within-group variability. Among all treatments, the biomass had the highest maximum value, ranging from 19.660 g to 45.390 g. The Mixed treatment yielded the highest average biomass of 32.039 g, indicating its effectiveness. It nevertheless remained relatively moderately variable, with a 4.5638 g standard deviation. Under this treatment, the biomass ranged from 26.650 g to 40.030 g.It is clear from synthesizing these results that the Mixed treatment (T5) produces more biomass than the other treatments. It results not only in terms of average biomass yield but also in terms of balanced variability, which suggests a uniform response from plant to plant. Mycorrhiza (T4) has a high maximum value, but it also shows more variability, which could indicate that the plant's response to the treatment wasn't uniform. Although not as much as with the Mixed treatment, the increases in biomass from the control to the Rhizobia and Azotobacter treatments show how these treatments contribute to the growth of plants. These differences in biomass between treatments offer vital information about how to achieve the greatest growth conditions for increased plant productivity and health.

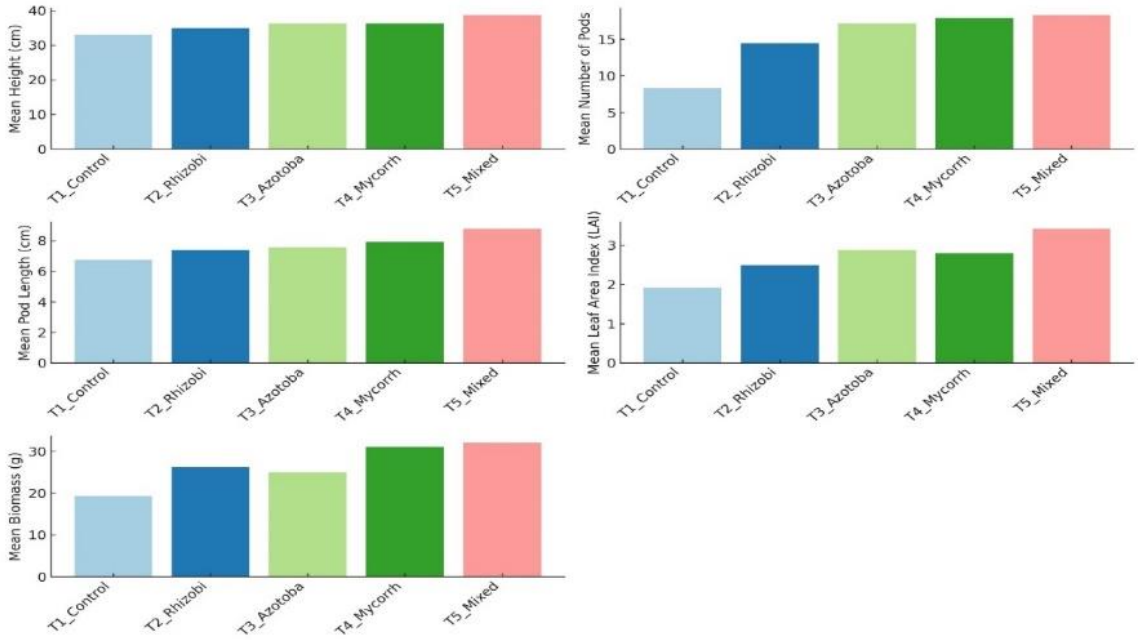

Fig1: Comparative analysis of mung bean crop performance:

Bar graphs Illustrating plant height, pod length, leaf area index, and biomass across different treatments. The Figure 1 shown in bar graphs mean values for each treatment across various measures Plant Height, Pod Length, Leaf Area Index, and Biomass. These graphs offer a concise visual depiction of how each treatment stacks up against the others in these different dimensions.

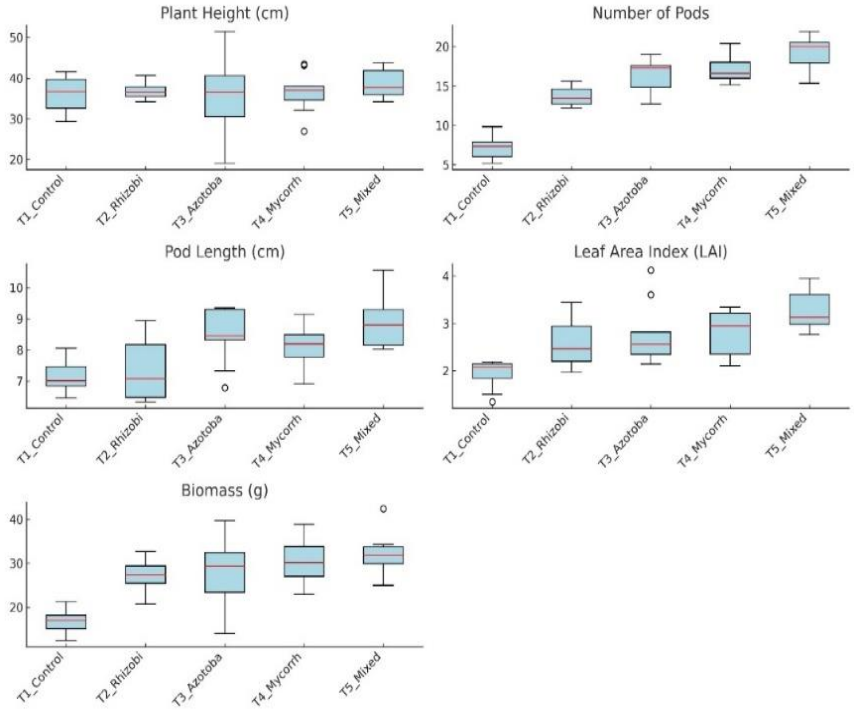

Fig 2: Analyzing data distribution and variability in mung bean crop traits: Insights from box plots

The above box plots fig2 shown data distribution for each treatment in terms of Plant Height, Pod Length, Leaf Area Index, and Biomass. These plots give a clear picture of the data's distribution, central tendency, and possible outliers.

3.18 Yield kg/ 25 m^2

The present investigation evaluated the efficacy of different biofertilizer treatments by estimating the yields of mung bean crops from a 25 square meter area, utilizing formula eq. 1. Because each treatment has a 25 m^2 area, these results were collected from a 25 m^2 area. A focused picture of the results that can be calculated to the sizes of typical agricultural fields is offered by the yields from the more feasible, smaller area. In a 25 m^2 area, the control treatment produced 1.25 kg, or 506 kg/ha, without the use of biofertilizer. Without outside growth measures, it represents the mung bean crop's inherent potential. Rhizobium was applied, and the yield over the same area increased to 1.8 kg, or 724 kg/ha. This enhancement confirms Rhizobium's well-established function of increasing nitrogen availability, which is essential for plant growth. A treatment with Azotobacter produced 2 kg from 25 m^2, or 798 kg/ha. The marginally increased yield in comparison to the Rhizobium treatment could be explained by the different biological pathways that Azotobacter uses to affect plant growth, potentially offering extra advantages like the synthesis of compounds that encourage plant growth. Mycorrhizae were added to the soil, and the yield for the same area was 2.1 kg, or 838 kg/ha. This higher yield is probably the result of mycorrhizae's assistance with root development and improved nutrient uptake. The highest yield, 2.4 kg from 25 m^2, was obtained by applying Rhizobium, Azotobacter, and Mycorrhizae together. When adjusted up, this yield equals 962 kg/ha. This points to a combined effect in which various biofertilizers combine to produce a cumulative advantage that exceeds the effects of the individual treatments. Based on these findings, it is evident that the Mixed Biofertilizer treatment (T5) performed the best when projected to a hectare scale as well as on the smaller 25 m2 size. Using a variety of biofertilizers in an integrative manner may improve the plant's nutritional environment overall and increase yields.

Table 2: Yield comparison for different treatments (kg/25m^2 and kg/ha)

Treatments	Yield kg/25m^2	Estimated Yield kg/ha
T1	1.25	506
T2	1.8	724
T3	2	798
T4	2.1	838
T5	2.4	962

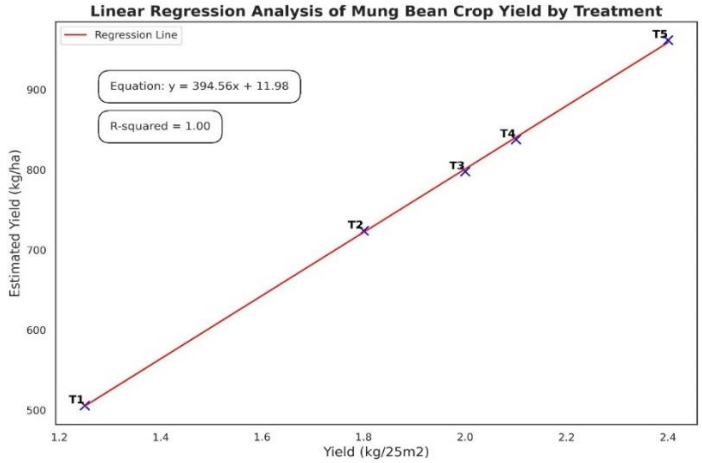

Fig 3: Impact of agronomic treatments on mung bean crop yield: A linear regression analysis

The fig 3 shown mung bean crop yields in relation to various agronomic treatments (T1 to T5) are shown in this graph, which shows a comprehensive linear regression analysis. Every blue dot denotes a different treatment and shows how it effects the yield per hectare estimate. The regression model, which presents a statistical overview of the treatment effects, is indicated by the red line. Notably, each treatment's effectiveness in increasing crop productivity is highlighted by the inclusion of the R-squared value and the equation of the line, which quantify the relationship between treatment intensity and yield increase.

3.19 Specific reasons why T5 is the best among the treatments:

Rhizobium fixes atmospheric nitrogen so that plants can absorb and use it, which promotes plant growth. Nitrogen, an essential nutrient for plant growth particularly for legumes like mung beans is added to the soil through this process (Raza 2020). In addition to fixing atmospheric nitrogen, Azotobacter may also produce other compounds that promote growth, like vitamins, phytohormones, and antifungal agents, which can improve plant health and yield (Sumbul *et al.*, 2020). Plant roots and mycorrhizae form a symbiotic relationship that expands the plant's root system and enhances its ability to absorb nutrients and water, especially phosphorus (Kuyper *et al.*, 2021). Additionally, it may improve plant resistance to pathogens and the structure of the soil. Together, these microorganisms (as in T5) probably produce a more efficient and balanced nutrient cycle in the soil, with each one playing a distinct role in plant growth. The nitrogen content is raised by Rhizobium and Azotobacter, which is necessary for the synthesis of proteins and other important plant components (Ibrahim *et al.*, 2021). Phosphorus and other micronutrients are taken up more readily by mycorrhizae and are essential for respiration, energy transfer, and nucleic acid synthesis. These organisms working together may enhance the general health of the soil, promoting better microbial activity, aeration, and water retention all of which are beneficial to plant growth (Yadav *et al.*, 2021).

Table. 3 Descriptive statistics for mung bean growth and biomass in different treatments

	Plant Height (cm)	No of Pods/Plant	Pod Length (cm)	Leaf Area Index	Biomass(g)
Treatment = T1_Control					
N	9	9	9	9	9
Mean	33.037	8.3144	6.7511	1.9178	19.349
SD	3.8029	1.9331	0.7293	0.3900	3.0809
Variance	14.462	3.7368	0.5319	0.1521	9.4919
C.V.	11.511	23.250	10.803	20.337	15.923
Minimum	25.860	5.6900	5.7900	1.0200	15.090
Maximum	37.930	12.440	8.1300	2.3100	24.060
Skew	-0.3818	0.8434	0.4717	-1.3393	0.1967
Treatment = T2_Rhizobia					
N	9	9	9	9	9
Mean	34.921	14.451	7.4011	2.4922	26.164
SD	3.8310	2.7371	0.7933	0.3987	4.2216
Variance	14.677	7.4915	0.6293	0.1589	17.822
C.V.	10.971	18.940	10.718	15.997	16.135
Minimum	29.970	11.360	6.5300	2.1100	17.760
Maximum	42.260	19.600	9.1500	3.2400	29.880
Skew	0.4416	0.7874	1.2897	0.6914	-1.0706
Treatment = T3_Azotobara					
N	9	9	9	9	9
Mean	36.207	17.148	7.5767	2.8778	25.029
SD	6.7082	2.5580	0.9232	0.6469	6.7671
Variance	45.000	6.5433	0.8523	0.4185	45.793
C.V.	18.528	14.917	12.184	22.479	27.037
Minimum	27.430	13.580	6.1800	1.8200	16.380
Maximum	46.950	21.270	9.0500	3.6400	32.900
Skew	0.5711	0.0760	0.1246	-0.3550	0.1163
Treatment = T4_Mycorrhiza					
N	9	9	9	9	9
Mean	36.243	17.893	7.9211	2.8000	31.056
SD	4.7009	2.1994	0.9204	0.4549	8.5967
Variance	22.099	4.8375	0.8471	0.2070	73.904

C.V.	12.970	12.292	11.619	16.247	27.682
Minimum	29.480	14.890	6.3900	1.8500	19.660
Maximum	46.220	20.870	9.5000	3.2500	45.390
Skew	0.7349	-0.0619	-8.387E-03	-1.0645	0.3437
		Treatment = T5_Mixed			
N	9	9	9	9	9
Mean	38.679	18.292	8.7700	3.4156	32.039
SD	2.6450	1.9090	0.9694	0.6296	4.5638
Variance	6.9963	3.6443	0.9397	0.3965	20.829
C.V.	6.8385	10.436	11.054	18.435	14.245
Minimum	35.620	15.850	7.6400	2.6000	26.650
Maximum	42.500	21.710	10.190	4.4500	40.030
Skew	0.2863	0.5406	0.2686	0.1847	0.2990

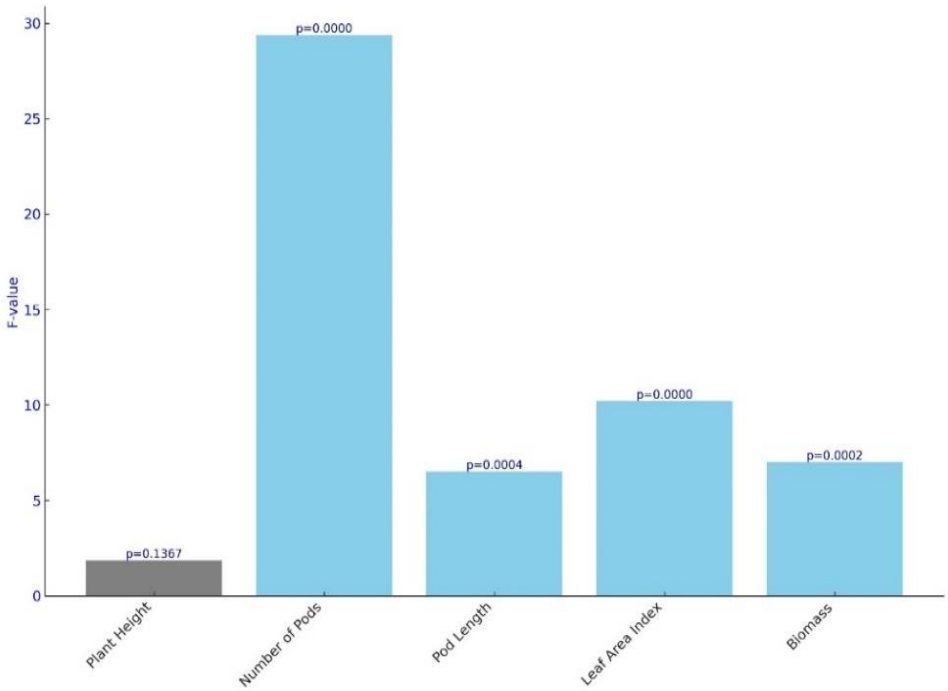

Fig 4: Statistical analysis of mung bean crop performance: ANOVA insights through graphs

The ANOVA results for each measure Plant Height, Number of Pods, Pod Length, Leaf Area Index, and Biomass are shown in the graph above Fig 4. Each measure's F-values are displayed, along with the matching P-values. The statistical significance of the results is indicated by the color of the bars, which are sky blue for $p \leq 0.05$, which indicates significant

differences, and grey for p > 0.05, which indicates non-significant differences.

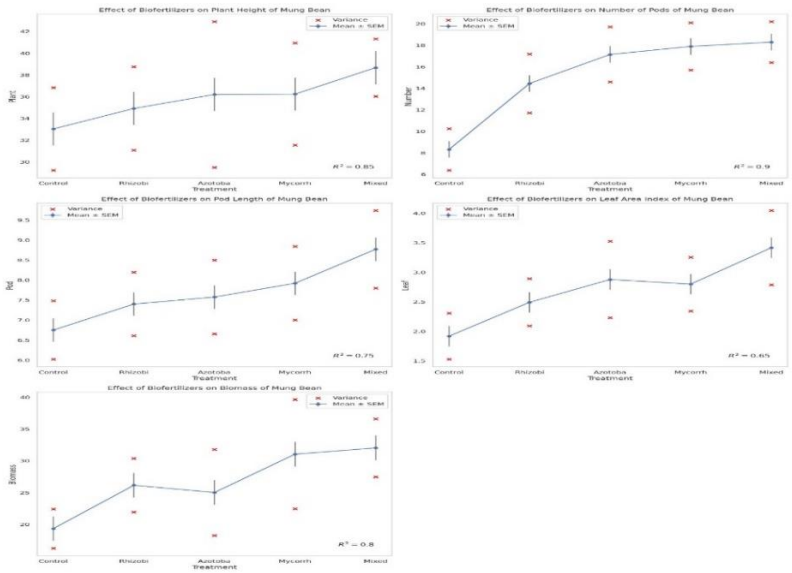

Fig 5: Regression Analysis of Biofertilizer Treatments on Mung Bean Growth Parameters

The fig 5 shown effects of biofertilizer treatments on mung bean growth parameters, including plant height, pod number, pod length, leaf area index, and biomass, are displayed in a series of graphs. R-squared values indicate the degree of accuracy of fit, and red dots represent variation.

5.Discussion

The key finding of our study is that the Mixed treatment (T5) performed better than the other treatments in terms of improving mung bean growth and yield parameters. The combination of Rhizobia, Azotobacter, and Mycorrhiza produced a synergistic effect that was much greater than the results of each treatment alone (Varinderpal *et al.*, 2020; Vafadar *et al*., 2014). T5's effectiveness can be assigned to the comprehensive nutritional augmentation it offers, which concurrently targets multiple growth factors. For example, the enhanced nutrient and water absorption capabilities of Mycorrhiza, the nitrogen-fixing capacity of Rhizobia, and the growth-promoting chemicals of Azotobacter all work together to promote this improved performance (Aasfar *et al.*, 2021; Miri *et al*., 2013). Our findings are consistent with earlier studies showing the advantages of biofertilizers for plant growth (Suhag, 2016). However, our study's showing of the unique efficacy of a combined biofertilizer approach expands on what is already known. It raises the possibility that using various biofertilizers in combination can be more beneficial than using them separately, a theory that hasn't received much attention in the literature to date (Zambrano *et al.*, 2021). This study completes a significant research gap by proving that a combined biofertilizer treatment is more effective. The majority of previous research has concentrated on the effects of individual biofertilizers, frequently ignoring the possible advantages when using them in combination (Singh et al., 2011; Gabr *et al*., 2007). Next research should

to focus on comprehending the mechanisms fundamental the combined effects of biofertilizer treatments. It would be particularly beneficial to look into the way various biofertilizers interact with one another and the way they impact microbial dynamics and soil health as a whole. Furthermore, investigating the way these results might be applied to a larger variety of crops and conditions would make a major contribution to the field of sustainable agriculture (Ahmad et al., 2020). The study's broad implications imply that mixed biofertilizer treatments could establish themselves as a fundamental component of sustainable farming methods. By addressing issues with food security and preserving ecological balance, this strategy may result in increased crop yields and higher-quality produce (Fan *et al.,* 2012). Our study's focus on a single crop type and particular environmental factors is one of its limitations. Therefore, there may be limitations to the generalizability of our findings. Long-term impacts on microbial communities and soil composition are also unidentified. Finally, our study's Mixed treatment (T5) has shown a promising potential for changing sustainable agricultural practices. By showing the synergistic effects of combined biofertilizer treatments, this study closes a significant research gap and develops new opportunities for this field of study. The findings support an integrated approach to crop management and fertilization and make a substantial contribution to the collection of knowledge already known in agricultural science.

6.Conclusion

In conclusion, this study has provided a thorough analysis of the effects of microbial biofertilizers on the mungbean NM 98 cultivar's growth. The outcomes of our investigation have yielded significant understanding regarding the efficiency of these microbial biofertilizers in augmenting diverse mungbean growth parameters. In terms of several parameters, such as biomass production, leaf area index (LAI), plant height, pod count, and pod length, the Mixed biofertilizer treatment performed better than the other treatments. It showed healthy and consistent growth responses. On the other hand, the Control treatment performed as a standard and consistently showed the least favorable outcomes across all growth measures. Finally, by applying biofertilizers to optimize mungbean cultivation, this research adds to the expanding body of knowledge in agricultural microbiology and provides farmers and agronomists with helpful recommendations. The findings highlight the importance that environmentally friendly and sustainable methods are to dealing with the problems associated with food security in contemporary agriculture. It seems possible to address global agricultural sustainability issues by conducting more research in this field.

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