Characterization of plant growth promoting rhizobacteria of maize

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Abstract. Isolation and characterization of rhizobacteria are an effort to determine the ability of root colony bacteria to produce various compounds that can be used for various purposes of bio-fertilizer formulations and microbial-based industrial interests. This study aims to characterize biochemically, morphologically and physiologically as well as the ability of root bacteria in maize to produce hormones that can stimulate plant growth. There is a wide variety of isolates morphologically and biochemically, besides that there is the ability of bacterial isolates to physiologically dissolve phosphate, fix nitrogen, produce ACC-deaminase, IAA and GA enzymes.

1. Introduction
The microorganisms in the soil are very diverse including as a bacteria, archaea, yeast, fungi, algae and protozoa. Microorganisms can live in the environment with humans and are also found in extreme conditions such as in hot springs, in oceans for miles away, in rocks and can live in very cold weather and temperatures.

Bacterial populations in the soil play an important role in the nutrient cycle including Nitrosomonas and Nitrobacter (nitrification), Thiobacillus (sulfur and iron oxidation), Rhizobium and Frankia (N2 fixation), Bacillus and Clostridium (carbon cycle) and Caulobacter and Pseudomonas (manganese oxidation). In addition, large numbers of bacteria have been found to produce various types of chemicals that are exploited in the biotechnology industry. Bacteria have been found to be a source of many valuable chemicals including ethanol, acetone, enzymes, perfume, antibiotics. In the last few decades, thousands of antibiotics have been discovered. Rhizosphere bacteria from Pseudomonas and Bacillus on leguminous and non leguminous plants have been identified [1], [2], as well as in Hartapel variety potato plants [3]. These findings make it possible to identify isolates or strains of bacteria from the soil for biochemical, physiological, industrial and pharmacological purposes. The number and species of microbes in the soil depend on environmental conditions such as availability of nutrients, soil texture, presence of moisture in the soil and the type of vegetation cover, and other environmental conditions.
Rhizosbacteria are plant root colonizing bacteria that can provide a plant-stimulating effect through hormone production and facilitate the availability of nutrients for plants and can be antagonistic to soil borne pathogenic bacteria and fungi. There are various types of microbes and their activities are related to roots [4]. The narrow zone of soil around the root system is referred to as the rhizosphere, whereas the term "rhizobacteria" is a group of rhizosphere bacteria that have the ability to colonize roots [5], [6]. These organisms can also benefit plants by stimulating growth. PGPR can affect plant growth by different direct and indirect mechanisms [7]. The rhizosphere is the ecological environment of the soil where plant microbial interactions occur through the colonization of microorganisms where associative, symbiotic, naturalistic, or parasitic interactions occur depending on the nutritional status of plants in the soil, the soil environment, and the types of microorganisms that proliferate in the rhosferosphere zone [8]. Soil bacteria that aggressively colonize the root zone and promote plant growth are commonly referred to as Rhizobacteria. In this study it has been found that some bacterial isolates produce important biochemical and physiological factors.

2. Methods

2.1. Sampling and sources of rhizobacteria
Ten grams of soil from the roots of corn plants were taken at three different points in several planting locations on the islands of Ambon and Seram as test samples. Soil samples were put into sterile bags and immediately transferred to the laboratory for isolation.

2.2. Sample preparation and isolation of bacteria
Every 10 g of soil samples from different maize planting sites were mixed with 90 ml of sterile water in 250 ml different beakers and homogenized in a flask for ten minutes using an orbital shaker at 110 rpm. Subsequently, 1 ml of each sample was transferred aseptically into 9 ml of sterile water and thoroughly mixed using a vortex. Homogenate is serially diluted to 10⁻⁵; thereafter, 0.1 ml aliquot of the appropriate dilution is properly spread on a starch petri agar dish. The scattered petri dishes were incubated at 32ºC for 48 hours. Bacterial isolates that showed different colony morphology were taken and purified using nutrient agar media.

2.3. Morphological characters of bacterial isolates
The isolated pure culture was cultured on nutrient broth media. The scattered petri dishes were incubated at 32ºC for 24-48 hours. The colony morphology of the isolates was observed including: shape, margin, elevation and color.

2.4. Biochemical character

2.4.1. Gram reaction test
The gram reaction test uses a 3% KOH solution as much as one drop dripped on the slide. A total of one ose of bacterial isolate is taken which is then transferred onto a slide and mixed or smeared slowly until it forms mucus. A positive test is indicated by no mucus formation and a negative test is indicated by the formation of mucus when mixed with 3% KOH.

2.4.2. Motility test
This test can be used to check the ability of bacteria to migrate away from the inoculation line. To perform this test, the bacterial sample is inoculated into the motility medium using a needle and incubated at 37 ° C for 24 hours and examined for bacterial migration.

2.4.3 Catalase test
This test is carried out to determine the ability of isolated bacteria to degrade hydrogen peroxide by producing enzymes, catalase or peroxidase. A drop of 3% hydrogen peroxide is added to the bacterial colony on a sterile glass slide and mixed well. The production of air bubbles was observed for one minute. The production of air bubbles indicates positive catalase and no bubbles indicates negative catalase.
2.4.4. Oxidase test
The oxidase test is carried out to determine the presence of the oxidase enzyme in bacteria. Oxidase reagents contain reducing agents that change color when oxidized. One loop of bacterial colony was etched on oxidase paper. Observations were made by looking at the reaction caused, if the results of blue streaks on oxidase paper indicate that the tested bacteria have a positive oxidase enzyme and if there is no change in color, it shows a negative oxidase result.

2.4.5. Mac Conkey Agar media Test
This test is to detect gram-negative bacteria. Growing gram-negative bacteria can be distinguished in their ability to ferment lactose. Colonies of bacteria that ferment lactose are brick red. Bacteria that do not ferment lactose are usually pathogenic. This group of bacteria did not show any changes in the media. This means that the colony color is the same as the media color. Colony colors can be seen in a separate colony section. Isolates were grown on Mac Conkey Agar solid media using a scatter plate technique which was incubated at 37°C for 24 hours.

2.5. Ability of phosphate solubility and nitrogen fixation
2.5.1. Phosphate solubitation test
Phosphate dissolution was tested by referring to the Pikovskaya method [9], [10]. The 24-hour-old bacterial isolate suspension was grown on solid Pikovskaya media containing tricalcium phosphate (Ca3PO4) by the spread method. The zone of emergence around the bacterial colony shows dissolving activity. The ability of bacterial isolates to report phosphate dissolving by clear zone, phosphate dissolving efficiency and phosphate dissolution index. Measurement of dissolved phosphate concentration using liquid Pikovskaya media. Thirty ml of culture isolate was cultured in Pikovskaya medium for 7 days and in a shaker. The bacterial suspension was filtered (Whatman No.1) then centrifuged for 15 minutes at 10,000 g. Five 5 ml of supernatant pipette and 0.5 ml of concentrated reagent added (Concentrated reagent: 12 g ammonium molybdate, 0.277 g potassium antimolyltrate). Before measuring the absorbance, the level of phosphate dissolution, the pH of the filtrate solution was measured for the acidity. The absorbance was measured on a 693 nm UV-VIS spectrophotometer. The standard PO4 (titrisol) curve was made from dilution with concentration with the regression equation Y = 0.191 x + 0.048 where R2 = 0.957.

2.5.2. Free nitrogen fixation
The ability of bacterial isolates to fix free nitrogen was tested using free Burk N media [11] and Ashby media [12]. Bacteria that are able to grow on both media are indicated as bacteria capable of fixing nitrogen.

2.6. Production testing of growth enhancing compounds
2.6.1 Screening isolate of producing acc deaminase
Screening of ACC deaminase-producing bacterial isolates was carried out by growing 24-hour culture of rhizoforous bacterial isolates on minimal salt media Dworkin-Foster (DF) [13] enriched with ACC as the only source of nitrogen [7]. Isolates that were able to grow on this medium were indicated as ACC deaminase producing isolates.

2.6.2 Indole Acetic Acid (IAA) production
The production of indole-3-acetic acid (IAA) auxin was tested using by nutrient broth (NB) media and Salkowski's reagent [14]. Bacterial isolates were cultured on NB media supplemented with L-tryptophan (0.1g l-1) at 28 0C. The supernatant was added to 1 ml of Salkowski reagent (12 g l-1 FeCl3 in 429 l-1 ml H2SO4) [7]. The mixture was stored for 24 hours at 28 °C in dark conditions and the absorbance was measured at 535 nm on a UV-VIS spectrophotometer. The change in pink indicates IAA production. Auxin concentrations were measured using the IAA standard curve with the regression equation Y = 0.064 x + 0.09 where R2 = 0.995, made from serial dilutions of IAA stock solutions.
2.6.3 Gibberelic Acid (GA3) production
Gibberelic acid production is based on standard methods [15], which are modified. One ml of bacterial isolate was added to the media and incubated at 37 0C. After incubation the cultures were centrifuged at 8000 g to separate bacterial cells. 15 ml of culture was added to 2 ml of zinc acetate, added to 2 ml of potassium ferrocyanide solution and centrifuged at 8000 g. The supernatant was added to 30 percent hydrochloric acid and incubated at 27 0C for 75 minutes. The absorbance was measured at 254 nm on a UV-VIS spectrophotometer. The concentration of GA3 is measured using the standard GA3 curve with the regression equation Y = 0.888 x + 0.441 where R2 = 0.921, made from serial dilutions of GA3 stock solution.

3. Results and discussion
3.1. Morphological character
Isolation and characterization of bacterial isolates from corn rhizofer obtained as many as 37 bacterial isolates. The morphologically identified isolates showed differences. The bacterial isolates identified colonizing corn roots differed in shape, margin, elevation and color as well as gram reactions. Observation of colony and cell morphology is still needed as an initial stage before further identification such as physiological characterization and DNA identification are carried out. The rhizosphere is the zone between the surface of the roots and soil, and is adjacent to the roots. The bacteria that live in this zone can remain in the soil. Morphologically, the bacterial isolates isolated from the root rhizosphere of maize in various varieties showed diversity in shape, margin, elevation and color. The rhizosbacteria isolates from the rhizosphere of maize were isolated from various varieties, 19 (51.4%) were circular, 16 (43.2%) irregular and 2 (5.4%) filamentous isolates. The results of the observations on the margins and elevation of the rhizosbacteria isolates observed are presented in Table 1. The colony colors observed were dominated by white to dull white. The shape, margins and elevation of observed bacterial isolates refer to Figure 1.

Figure 1. Colony morphology: form: bacteria (a) circular, (b) irregular and (c) filamentous and colony color (d) white, (e) dull white and (f) yellowish white

| No. | Isolate Code | Origin of Rhizosphere | Colony of Morphology |
|-----|--------------|-----------------------|----------------------|
|     |              | Location              | Variety              | Shape       | Margins     | Elevation | Color         |
| 1   | PB01         | Poka                  | Bonansa              | Irregular   | Filiform    | Raised    | White         |
| 2   | PU01         | Poka                  | Uric (asal MTB)      | Irregular   | Undulate    | Raised    | Yellowish white |
| 3   | PU02         | Poka                  | Uric (asal MTB)      | Irregular   | Undulate    | Flat      | White         |
| 4   | PU03         | Poka                  | Uric (asal MTB)      | Circular    | Entire      | Raised    | White         |
| 5   | PU04         | Pока                  | Uric (asal MTB)      | Irregular   | Filiform    | Raised    | White         |
The similarity in shape, margin, elevation and colony color of bacteria does not always show the same gram reaction or similarity in gram reaction does not always show the same morphology of the isolates. Furthermore, it can be assumed that 37 bacterial isolates that have various morphological variations and gram reactions have the potential to also have various different biochemical characters. Table 1 shows that the bacteria colonizing the roots of maize plants varied greatly in terms of morphology, thus indicating the existence of various types of bacteria that cycological plant roots.

3.2. Biochemical character
The gram reaction test and motility test, catalase, oxidase and MacConkey Agar showed differences between isolates. The results of the Gram reaction test using KOH showed that most of the bacteria were Gram positive, reaching 70.3% or as many as 26 isolates. Other test results are presented in Figure 2 and Table 2.

**Table 2. Biochemical character of corn plant rhizosphere bacteria isolates**

| No. | Isolate Code | Gram Reaction Test | Motility Test | Catalase Test | Oxidase Test | Test Mac Conkey Agar Media |
|-----|--------------|-------------------|--------------|--------------|--------------|--------------------------|
| 1   | PB01         | G +ve             | +            | -            | +            | -                        |
| 2   | PU01         | G +ve             | +            | -            | +            | -                        |
| 3   | PU02         | G +ve             | +            | -            | +            | -                        |

The similarity in shape, margin, elevation and colony color of bacteria does not always show the same gram reaction or similarity in gram reaction does not always show the same morphology of the isolates. Furthermore, it can be assumed that 37 bacterial isolates that have various morphological variations and gram reactions have the potential to also have various different biochemical characters. Table 1 shows that the bacteria colonizing the roots of maize plants varied greatly in terms of morphology, thus indicating the existence of various types of bacteria that cycological plant roots.
|   |   |   |   |   |
|---|---|---|---|---|
| 4 | PU03 | G +ve | + | - | + | - |
| 5 | PU04 | G +ve | + | - | + | - |
| 6 | PU05 | G +ve | - | - | + | - |
| 7 | PU06 | G -ve | + | - | + | + |
| 8 | PU07 | G -ve | + | - | + | + |
| 9 | PU08 | G -ve | + | - | + | + |
|10 | PU09 | G -ve | - | - | + | + |
|11 | PU10 | G -ve | + | + | - | - |
|12 | PU11 | G +ve | + | - | + | - |
|13 | PU12 | G +ve | + | - | + | - |
|14 | PU13 | G -ve | + | + | - | - |
|15 | BT01 | G +ve | - | - | + | - |
|16 | BT02 | G +ve | + | + | - | - |
|17 | BT03 | G -ve | - | - | + | + |
|18 | BT04 | G +ve | - | - | + | - |
|19 | BT05 | G +ve | - | - | + | - |
|20 | BT06 | G +ve | - | - | + | - |
|21 | BT07 | G +ve | - | + | - | - |
|22 | BT08 | G +ve | + | + | - | - |
|23 | BT09 | G +ve | - | + | - | - |
|24 | BT10 | G -ve | - | + | - | - |
|25 | BT20 | G -ve | + | - | - | - |
|26 | BT21 | G -ve | + | + | - | - |
|27 | BT31 | G +ve | - | - | + | - |
|28 | BT32 | G +ve | - | - | + | - |
|29 | BW01 | G +ve | - | - | + | - |
|30 | BW02 | G +ve | + | - | + | - |
|31 | BW03 | G +ve | - | - | + | - |
|32 | BW04 | G +ve | + | - | + | - |
|33 | BW06 | G +ve | - | - | + | - |
|34 | BW07 | G +ve | + | + | - | - |
|35 | BW08 | G +ve | + | + | - | - |
|36 | PT01 | G -ve | + | + | - | + |
|37 | PT02 | G +ve | - | + | - | - |

Figure 2. Biochemical character of bacterial isolates (a) gram reaction test, (b) motility test, (c) catalase test and (d) results of Mac Conkey Agar test (formation of mucoid)
3.3. Ability to phosphate solubitation and nitrogen fixation

The ability of phosphate solubitation and producing nitrogen and fixing nitrogen is presented in Table 3.

**Table 3.** The ability of starch degrading bacteria to phosphate solubitation and nitrogen fixation

| No. | Isolate | Ability of Phosphate Solubitation | Nitrogen Fixation |
|-----|---------|-----------------------------------|-------------------|
|     |         | Hallo Zone (mm) | Hallo Zone Diameter (mm) | Index of Phosphate Solubitation | N Burk Test | Ashby Media |
| 1   | PB01    | -             | -                        | -                              | +          | +          |
| 2   | PU01    | 14.5          | 2.2                      | 0.78                           | -          | -          |
| 3   | PU02    | -             | -                        | -                              | -          | -          |
| 4   | PU03    | 14.5          | 1.3                      | 0.41                           | -          | -          |
| 5   | PU04    | -             | -                        | -                              | -          | -          |
| 6   | PU05    | 14.5          | 8.3                      | 0.41                           | -          | -          |
| 7   | PU06    | 12.7          | 8.7                      | 0.31                           | +++        | +          |
| 8   | PU07    | 14.5          | 7.5                      | 0.48                           | +          | +          |
| 9   | PU08    | -             | -                        | -                              | -          | -          |
| 10  | PU09    | -             | -                        | -                              | -          | -          |
| 11  | PU10    | -             | -                        | +++                            | +          | +          |
| 12  | PU11    | 13.5          | 7.3                      | 0.46                           | ++         | +          |
| 13  | PU12    | -             | -                        | -                              | -          | +          |
| 14  | PU13    | -             | -                        | ++                             | +          | +          |
| 15  | BT01    | -             | -                        | ++                             | +          | +          |
| 16  | BT02    | -             | -                        | +                              | -          | -          |
| 17  | BT03    | 15.7          | 7.7                      | 0.51                           | ++         | +          |
| 18  | BT04    | -             | -                        | +                              | -          | +          |
| 19  | BT05    | -             | -                        | -                              | -          | +          |
| 20  | BT06    | -             | -                        | ++                             | +          | +          |
| 21  | BT07    | 14.3          | 8.4                      | 0.43                           | +++        | +          |
| 22  | BT08    | 14.8          | 7.8                      | 0.47                           | +          | +          |
| 23  | BT09    | -             | -                        | -                              | -          | +          |
| 24  | BT10    | -             | -                        | +                              | -          | +          |
| 25  | BT20    | -             | -                        | -                              | -          | -          |
| 26  | BT21    | 12.7          | 3.2                      | 0.74                           | ++         | +          |
| 27  | BT31    | 14.8          | 9.4                      | 0.36                           | -          | -          |
| 28  | BT32    | -             | -                        | -                              | -          | +          |
| 29  | BW01    | -             | -                        | -                              | -          | -          |
| 30  | BW02    | -             | -                        | -                              | -          | -          |
| 31  | BW03    | 12.3          | 5.1                      | 58.5                           | +++        | +          |
| 32  | BW04    | 9.3           | 5.5                      | 0.41                           | +++        | +          |
| 33  | BW06    | -             | -                        | -                              | -          | -          |
| 34  | BW07    | -             | -                        | -                              | +          | +          |
| 35  | BW08    | -             | -                        | -                              | -          | -          |
| 36  | PT01    | 12.6          | 6.2                      | 0.51                           | -          | -          |
| 37  | PT02    | -             | -                        | -                              | -          | -          |

Soil is a habitat for a variety of organisms including micro flora and fauna. Soil microorganisms play a very important role in soil fertility not only because of the ability of microbes to carry out biochemical transformations but also because of their importance as a source and reserve of mineral nutrients. This process occurs in general soils due to the exo enzymes released by microbes in the environment and degrade soil components.

The soil in a growing garden is a rich source of microorganisms. Biologically active enzymes can be extracted from living organisms. The enzymatic activity of bacteria correlates with the physiological function of bacteria in promoting growth through hormone production for the benefit of plant growth. It can also be explained that rhizobacteria isolates that are capable of producing hormones such as IAA and GA have the ability to dissolve phosphate and nitrogen fixation.
The phosphate solubitation ability of the tested isolates refers to the formation of a clear zone around the bacteria on Pikovskaya media containing tricalcium phosphate (Figure 3). The formation of a clear zone is a degradation process of tricalcium phosphate as a form of the ability of bacterial isolates to dissolve phosphate. Of the 37 bacterial isolates that were inoculated into the solid Pikovskaya medium, there were only 13 isolates capable of dissolving phosphate with different abilities seen from the wide diameter of the clear zone formed around the bacterial colony, the dissolution index, and the level of solubilated P concentration.

Figure 3. Bacterial isolates that can degrade phosphate

The qualitative size of the diameter of the clear zone indicates the size of the bacteria's ability to dissolve phosphate. The low concentration of dissolved phosphate is thought to be due to the reuse of dissolved phosphate by culture as a source of nutrition for metabolic activity and a decrease in the number of bacterial cell populations which will affect the activity of bacteria in dissolving phosphate. The results presented in Table 3 show that the phosphate dissolution index varies or there is a difference in the phosphate dissolution index. The greater the phosphate dissolution index is thought to have a tendency for the large dissolved phosphate concentration. This shows that the resulting P dissolution index can determine the ability of bacteria to dissolve phosphate.

The test results showed that from 37 bacterial isolates cultured on Burk N-free medium, 16 isolates were able to grow on the media with different fixation levels, while 20 isolates were able to grow on Ashbi media. Based on several research results, bacteria that are able to grow on Burk N-free media are indicated as bacteria capable of fixing nitrogen [16], [17], [18], [19], [20] and can form pellicles [21], [22], can produce ammonium [23], [24] and have nitrogenase activity [22], [25]. The difference in nitrogenase activity is thought to be due to the influence of the nifH gene system as a control for bacterial nitrogenase activity [26], [27], [28], [29], [30], [31], [32], [33].

3.4. Identification of the ability of enzyme and hormone producing bacteria

Bacteria isolated from the roots of corn plants have the ability to produce ACC-deaminase enzymes and hormones. Details of the ability of these isolates are presented in Table 4. The results of testing the IAA production capability of 34 isolates capable of producing IAA with different abilities after being grown on culture media with the addition of L-tryptophan. This difference in ability indicates a difference in the concentration produced. The ability of bacterial isolates to produce IAA was detected by a change in pink color after the addition of Salkowski's reagent in culture (Figure 4), besides that it can be explained that the difference in IAA concentrations produced by various bacterial isolates tested was due to differences in the ability of bacteria to utilize tryptophan or due to different pathways. IAA biosynthetic mechanism.
The concentration of IAA produced by bacteria depends on the activity and number of cells, the availability of nutrients and the L-trp substrate in the media. In connection with that, it can be explained that there are three pathways for the formation of IAA, namely the IPyA pathway (Indole-3-Pyruvic Acid), the TAM pathway (Tryptamine) and the IAN pathway (Indole-3-Acetonitril). In bacteria there are only two pathways, namely the TAM and IPyA pathways, which are inducible by tryptophan compounds. Tryptophan is the main precursor in the biosynthesis of IAA. IAA production will increase according to the increase in tryptophan concentration from 1-100 μg / ml (Ahmad et al. 2005). Based on the IAA production capability testing method with the addition of L-tryptophan to the culture media as a precursor, it shows the ability of bacterial isolates to produce IAA.

All tested isolates had the ability to produce gibberellic acid (GA3). Gibberellic acid produced by bacterial isolates is presented in Table 4. It is estimated that bacteria can increase GA levels in bacterial isolate cultures due to the production of GAs, deconjugating GAs from root exudates or hydroxylating inactive GA [34].

Table 4. Ability of bacteria to produce ACC-deaminase enzymes and hormones (IAA and GA)

| No | Isolate Code | ACC-deaminase | Capability of Production | IAA Concentration (mg/l) |
|----|--------------|---------------|--------------------------|-------------------------|
|    |              |               | IAA                      |                         |
| 1  | PB01         | +             | +                        | 1.05                    | 6.53                    |
| 2  | PU01         | +             | +                        | 1.15                    | 5.79                    |
| 3  | PU02         | -             | -                        | -                       | 5.25                    |
| 4  | PU03         | +             | ++                       | 2.04                    | 6.89                    |
| 5  | PU04         | +             | ++                       | 2.05                    | 6.14                    |
| 6  | PU05         | +             | +                        | 1.01                    | 5.23                    |
| 7  | PU06         | +             | ++                       | 2.08                    | 5.87                    |
| 8  | PU07         | +             | +++                      | 4.05                    | 5.49                    |
| 9  | PU08         | +             | ++                       | 2.51                    | 4.23                    |
| 10 | PU09         | +             | +                        | 0.16                    | 6.02                    |
| 11 | PU10         | +             | ++                       | 2.02                    | 5.68                    |
| 12 | PU11         | +             | ++                       | 2.62                    | 5.67                    |
| 13 | PU12         | +             | +                        | 0.17                    | 4.85                    |
| 14 | PU13         | +             | ++                       | 2.59                    | 5.53                    |
| 15 | BT01         | +             | +                        | 0.03                    | 4.76                    |
| 16 | BT02         | +             | +++                      | 4.51                    | 6.79                    |
| 17 | BT03         | +             | +                        | 0.19                    | 4.58                    |
| 18 | BT04         | +             | ++                       | 2.53                    | 5.88                    |
| 19 | BT05         | +             | +                        | 0.11                    | 4.21                    |
| 20 | BT06         | +             | +                        | 0.18                    | 4.32                    |
| 21 | BT07         | +             | +++                      | 5.01                    | 6.07                    |
4. Conclusion

Thirty-seven bacterial isolates tested had various morphological characteristics ranging from the shape, elevation and colony color and there were various abilities of biochemical reactions through the gram reaction test, the ability of bacterial migration (motility), degradation of hydrogen peroxide, the production of oxidase enzymes, and the ability to sequester phosphate, nitrogen fixation and producing phytohormones (IAA and GA).

5. References

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