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Review Article

Biodiversity, Roles, and Potency of Bacteria in Agricultural Land

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Abstract

Biotic and abiotic factors influence biodiversity. Environment and human activities change biodiversity. Human activities to get their food through agricultural activities affect the diversity of bacteria in agricultural lands. Cultivation techniques, plant species, plant growth stadia, and soil influence the diversities of bacteria in agricultural land. The dominant bacteria on agricultural land are from the phyla Proteobacteria, Actinobacteria, Acidobacteria, Bacteroidetes, and Firmicutes. Proteobacteria play a role in the nitrogen, carbon, and sulphur cycles, Actinobacteria in the carbon cycle, and Acidobacteria in the nitrogen cycle. Bacteroidetes work as decomposers of organic matter. Firmicutes are required for biocontrol and plant growth. The high use of pesticides in agricultural land has decreased the diversity of bacteria. Indigenous bacteria that survive in the condition of high pesticide residue contamination have the potential as remediation agents for pesticide residues. Indigenous bacteria can degrade pesticide residues through oxidation-reduction and complexation reactions, thereby reducing the level of pesticide contamination.

Keywords: Biodiversity; bacteria; agricultural land

1. Introduction

Biodiversity is the variation of shape, appearance, number, and properties found in living things (Zid et al., 2018). Biotic and abiotic factors influence diversities. Abiotic factors that influence biodiversity include climate (temperature, rainfall, humidity, wind), edaphic (soil texture, soil structure, soil acidity), and physiography (altitude, distribution pattern). Biotic factors that affect biodiversity are the variations of living things ranging from unicellular to multicellular forms of a community structure. Competition affects community structure (Bayat et al., 2021). Community structures create biodiversity, while genes, species, and ecosystems influence diversity. Marriage or gene mutations change genes, and gene changes lead to species variation. Changes in ecosystems due to natural disasters or human activities, such as deforestation, cause disturbances in the interaction of living things with their environment and ultimately change the structure of biodiversity.

The diversity of microorganisms plays a role in maintaining the balance of the ecosystem as a support system for the biosphere. Microorganisms play an important role in biogeochemical processes such as nitrogen, phosphorus, carbon, sulphur, hydrogen, and oxygen (Fry et al., 2019). Several microbes, such as bacteria, fungi, protozoa, and algae, are beneficial for plants because they promote plant growth and health and increase plant resistance to abiotic stress (Pineda et al., 2013). Because of these roles, a high diversity of microorganisms is a hallmark of healthy soil (Laishram et al., 2012).

The presence of abundant microorganisms in the soil is bacteria, especially in the rhizosphere (Saharan et al., 2011). Closer to the endosphere diversity of bacteria decreases (Edwards et al., 2015). The interaction between plants and bacteria in their rhizosphere areas is mutualistic (Pineda et al., 2013). The rhizosphere is an area around the plant roots with a distance of 1-2 mm from the surface of the plant roots, while the endosphere is the area on the surface of the plant roots to the root tissue. Plants release some of their carbon into the soil used for bacterial growth. Bacteria use the exudate produced by plant roots as an energy source, and plants obtain nutrients from these bacteria (Fernández-baca et al., 2021; Yu et al., 2021).

Many beneficial microbes are found in the roots. Soil with a high diversity of microorganisms is a characteristic of healthy soil. Bioindicators of soil quality are affected by soil and microorganisms in its agroecosystem (Kurniawati et al., 2017). In one gram of soil found, hundreds to thousands of bacterial taxa. Therefore, soil bacteria play an essential role in the world of plants/agriculture. Microorganisms play a role in environmental sustainability. The diversity of bacteria has decreased from the rhizosphere to the endosphere. Rhizobacteria play a direct role in the remediation process through the hormone Indole Acetic Acid, or IAA (Aroua et al., 2019). Rhizobacteria produce the IAA hormone.

Anthropogenic environmental changes cause changes in the diversity of bacteria and their interactions with plants. Anthropogenic such as fertilizers and pesticides. Human activities increase the diversity of soil bacteria but also decrease their diversity. Agricultural land is a suitable habitat for a diversity of microorganisms. However, agricultural land often experiences disturbances caused by the activities of farmers in cultivation processes. Farming activities, such as providing nutrients and organic matter, increase soil bacterial diversity, while harvesting and tillage activities reduce bacterial diversity (Maron et al., 2018). The types of plant cultivation by farmers also affect the diversity of bacteria that grow on agricultural land. A farmer practice that poses a risk to the diversity of microorganisms and soil health, in general, is the use of pesticides. Pesticides are used to protect plants from disease. However, their use is often unmeasured. Thus, they pollute the soil, plants, and surrounding fauna (Iqbal and Bartakke. 2014; Tang et al., 2016).

Changes in nature and human activities affect the diversity of soil microorganisms, including bacteria. Human activities in growing crops cannot be separated from using agrochemical materials, chemical fertilizers and pesticides. Pesticides are favoured by farmers even though they are expensive because of their fast reaction and ease of obtaining them in the market. However, the inappropriate use of pesticides polluted the environment and ultimately contaminated the product. As a result, the diversity of bacteria in agricultural land decrease because not all bacteria survive in these conditions. Thus, this review article aims to determine the diversity of bacteria in agricultural land, the things that affect this diversity, and the role and potential of these bacteria.

2. Methods

This review article was carried out by searching 80 references on the internet using keywords: agricultural bacteria, bacterial diversity, and agricultural management. The selected 51 articles were compiled from Shinta accredited national journals, international journals published by MDPI, PubMed, Sciencedirect, Frontiers, Nature, national proceedings, and international proceedings indexed by Scopus. This review article has been written narratively using 5 accredited national journals, 35 reputable international journals, 4 books, and 7 proceedings from 2011-2022. The obtained results were reviewed and described by the author. This review article described the diversity of bacteria from agricultural land, their role, and their potential as pesticide residue remediation agents. This review article discussed (1) The diversity of bacteria from agricultural land, (2) The effect of cultivation techniques on bacterial diversity, and (3) The potential of bacteria as remediation agents for pesticide residues.

3. Result and Discussion

3.1. Bacterial Diversity from Agricultural Land

The land is an area on the earth's surface characterized by relatively stable soil texture, soil structure, rainfall, and vegetation involved in the biosphere, atmosphere, hydrology, geology, and human activity cycles (Indah et al., 2019). Land used by humans to carry out farming activities is called agricultural land. There are two types of agricultural land: wet and dry. Wet agricultural land is characterized by a place that was quite wet (watery) for a specific time with particular vegetation, such as rice fields, while dry agriculture lands, such as fields, gardens, and fields. Wet agricultural land is used to grow food crops such as rice, corn, cassava, and beans. Dry agricultural land is generally used to cultivate horticulture crops such as vegetables, fruits, ornamental plants, and biopharmaceutical plants.

One of the wet agricultural lands is rice fields. Land conditions affect the diversity of bacteria in the soil (Sengupta et al., 2017) and rice fields. Various kinds of rice fields include irrigated rice fields, rain-fed rice fields, and swamp fields. According to Kurniawati et al. (2017), the highest bacterial diversity is found in rainfed rice fields (37.5%), swamp fields (31.7%), and irrigated rice fields (30.7%). Bacteria in rice fields belong to the Actinomycetes, Bacillus, Chromobacterium, and Pseudomonas fluorescence groups. In addition to land conditions, the fertility of rice fields also affected the abundance of bacteria from the phyla Proteobacteria, Chlorobi, Bacteroidetes, Planctomycetes, and Gematimonadetes (Ma et al., 2021). Cyanobacteria capable of fixing nitrogen are also found in rice fields. During the rice growth stage, *Nostoc punctiforme*, *Nostoc muscorum*, and Anabaena were found (Hendrayanti et al., 2018).

The same varieties of rice planted in different types of soil produce different diversity and abundance of bacteria. Soil affects the abundance of bacteria. Abundant bacteria characterize rice soil with high soil fertility. The most common bacteria found, namely, Nostoc included in Cyanobacteria, which are dominant in paddy fields. Cyanobacteria play a role in fixing nitrogen from the atmosphere.

Dry agricultural land is generally planted with drought-resistant crops, such as corn and sweet potatoes. Walters et al., 2018 state that corn cultivars or varieties affected bacterial diversity. Nitrogen-fixing bacteria, such as Bradyrhizobiaceae, Burkholderia, Rhizobium, Spingomonas, and Oxalobacteraceae, dominated the bacterial diversity in sweet corn (*Zea mays S*) or sweet corn. In comparison, ordinary corn (*Zea mays L*) is dominated by Agrobacterium, Bradyrhizobiaceae, Devosia, Comamonadaceae, Pseudomonas, and Sinobacteraceae (Table 1). Tangapo et al. (2018) reported that rhizobacteria colonies are more commonly found in sweet potato plantations than endophyte bacteria. In the early days of sweet potato plant growth, the bacteria are more diverse and abundant than before the sweet potato harvest.

In addition to food crops, horticultural crops also affect the diversity of bacteria in the soil, such as potatoes, oranges, strawberries, and pineapples. Potatoes and strawberries are widely cultivated on dry upland land. Abundant bacteria found in potato fields included the phyla Proteobacteria, Actinobacteria, Acidobacteria, Planctomycetes, Chloroflexi, Gemmatimonadetes, Firmicutes, and Verrucomicrobia (Gumiere et al., 2019). Proteobacteria from the genus Rhodanobacteria are the most abundant bacteria found in strawberry fields, besides Bacillus from the phylum Firmicutes (Liu et al., 2021).

Oranges (*Citrus sp.*) are widely grown in various countries with different biogeographic conditions. The bacteria in the citrus rhizosphere are closely related to the soil in which they grow. Rhizobacteria from the phylum Proteobacteria such as Pseudomonas, Agrobacterium, Burkholderia, Spingomonas, Devosia, and Rhizobium, are beneficial for plants. Rhizobacteria can potentially increase plant nutrient uptake, hormones, root development, health, and production (Xu et al., 2018).

Pineapple is a plant that grows in semi-arid ecosystems. Semi-arid areas are areas characterized by water scarcity with low rainfall intensity. The stability of plants in this ecosystem is highly dependent on the use of rainwater and the effectiveness of other water resources (Huang et al., 2019). Metagenomic analysis showed that the diversity and abundance of bacteria in pineapple were higher in the rhizosphere than in the endophyte (Putrie et al., 2020). Actinobacteria had the densest colonies, while Proteobacteria from the Gammaproteobacteria and Flavobacteria classes are primarily found in the roots. Acidobacteria and Firmicutes are also abundant in the pineapple root area. Cyanobacteria are found in many host plants. The genus Bacillus was reported as the dominant genus.

Table 1. Diversity of bacteria in various types of crops on agricultural land

Plant Type	Bacteria Group	Source
Paddy (*Oryza sativa*)	Actinobacteria, Firmicutes, Betaproteobacteria, Gammaproteobacteria	Kurniawati et al., 2017
	Acidobacteria, Planctomycetes, Gemmatimonadetes	Edwards et al., 2015
	Cyanobacteria	Hendrayanti et al., 2018
Corn (*Zea mays L*)	Alphaproteobacteria, Betaproteobacteria.	Mendes et al., 2013
	Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria.	Walters et al., 2018
Sweet corn (*Zea mays S*)	Alphaproteobacteria, Betaproteobacteria	Walters et al., 2018
Sweet potato (*Ipomea batatas*)	Alphaproteobacteria, Gammaproteobacteria~~,~~ Bacteroidetes, Firmicutes, Actinobacteria	Tangapo et al., 2018
Potato (*Solanum tuberosum*)	Alphaproteobacteria, (Betaproteobacteria, Delta proteobacteria, Gammaproteobacteria,) Firmicutes, Actinobacteria, Bacteroidetes, Acidobacteria, Gematimonadetes, Verrucomicrobia, Cyanobacteria	Mendes et al., 2013
	Proteobacteria, Actinobacteria, Chloroflexi, Myxococcota	Custer et al., 2021
Orange (*Citrus sp.*)	Proteobacteria, Actinobacteria, Acidobacteria Bacteroidetes.	Xu et al., 2018
Strawberry (*Fragaria* ^{x}*annanasa*)	Proteobacteria, Actinobacteria, Acidobacteria Bacteroidetes.	Wei et al., 2016
	Proteobacteria, Acidobacteria Chloroflexi	Li et al., 2018
Pineapple (*Ananas comosus*)	Proteobacteria: Gammaproteobacteria, Bakteroidetes, Actinobacteria, Acidobacteria, Firmicutes	Putrie et al., 2020

Bacterial abundance from farmland is dominated by Proteobacteria 38%, Actinobacteria 14%, Acidobacteria 12%, Bacteroidetes 10%, Firmicutes 8%, Gematimonadetes 4%, Cyanobacteria 4%, Chloroflexi 4%, Verrucomicrobia 2%, and Planctomycetes 2% (Figure 1). Bacteria abundant in agricultural land were dominated by the phyla Proteobacteria, Actinobacteria, and Bacteroidetes, while Acidobacteria and Firmicutes were less common (Mhete et al., 2020). Figure 2 showed that

Proteobacteria, Bacteroidetes, Actinobacteria, Acidobacteria, Firmicutes, and Chloroflexi dominated the dry land. They were also found in wetlands except for Bacteroidetes and Chloroflexi. Bacteroidetes, Verrucomicrobia, Chloroflexi, and Myxoccota are mostly found in the dry land. Bacterial diversity is related to nutrient cycling, habitat for plant production, and carbon sequestration. So, we have to save microorganisms to save the sustainability of our planet. The life of microorganisms is needed to maintain by reducing the use of chemicals and plastics and not throwing chemicals and plastics into the environment. People do not see the importance of soil microorganisms because they are invisible.

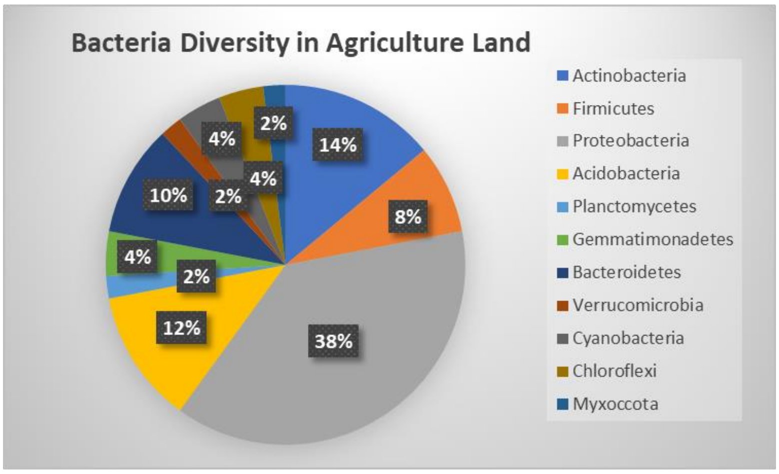

Figure 1. Percentage of bacteria diversity in agricultural land

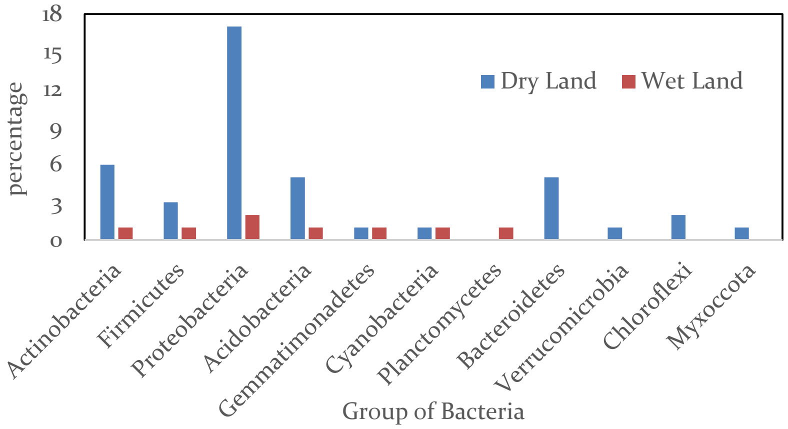

Figure 2. Percentage of bacteria domination in different agroecosystems

Proteobacteria include gram-negative bacteria that play a role in the nitrogen, carbon, and sulphur cycles (Osman et al., 2019). In the carbon cycle, the enzymes work are cellulose enzymes. In the nitrogen cycle, the protease and urease enzymes, while in the sulphur cycle, the arylsulphatase enzymes (Sobucki et al., 2021). Proteobacteria are primarily found in the rhizosphere, saline soils, and semi-arid soils with high availability of soil nutrients. Proteobacteria, including copiotrophs are bacteria that grow fast in an environment rich in nutrients, primarily carbon (Gumiere et al., 2019). Alphaproteobacteria and Betaproteobacteria classes play a role in the degradation of inorganic compounds and nitrogen fixation. In contrast, Deltaproteobacteria play an essential role in the degradation of organic compounds and are involved in the sulphur cycle (Mhete et al., 2020).

Actinobacteria are gram-positive bacteria that play a role in the carbon cycle. Gram-positive bacteria are widely used in bioremediation activities as biocontrol or biological controllers, plant growth promoters, controllers of soil-borne pathogens, and play a role in symbiotic mutualism and commensalism (Ek-Ramos et al., 2019). Actinobacteria are bacteria that survive in extreme environmental conditions such as dry conditions, high temperatures, high salt content, and radiation

(Putrie et al., 2020). Acidobacteria plays a role in the nitrogen cycle and has an excellent ability to change macronutrients, soil acidity, and active transporters of exopolysaccharides. Acidobacteria is oligotrophs, bacteria that grow in low-nutrient environmental conditions (Gumiere et al., 2019). Bacteroidetes function as decomposers of organic matter and live in anaerobic conditions, while Firmicutes are required for biocontrol and plant growth. (Mhete et al., 2020).

So, the global soil bacterial community is dominated by Proteobacteria (Alphaproteobacteria and Betaproteobacteria), Acidobacteria, Actinobacteria, and Planctomycetes (Kanzaki et al., 2021). These bacteria are commonly found in dry land ecosystems (Osman et al., 2019). According to Ma et al. (2021), the bacterial composition is influenced by soil fertility 45.4% and soil parent material(soil type) 23.9% (Table 2). Sandy soil types with low fertility have fewer types of bacteria due to the limited availability of nutrients. Soil acidity also affects the diversity of bacteria in the soil (Osman et al., 2019; Schmidt et al., 2015). Soil type, edaphic conditions, plant phenotype and genotype, and plant growth period affected the interaction between plant roots and soil microbes (Fernández-baca et al., 2021).

Table 2. Soil factors affecting bacterial diversity

	Rich	Poor	Source
Soil fertility	Proteobacteria, Chlorobi, Bacteroidetes, Planctomycetes, Gematimonadetes	Acidobacteria, Actinobacteria, Chloroflexi , Nitrospirae	Ma et al., 2021
	Clay	Sand	
Soil type	Proteobacteria, Chlorobi, Bacteroidetes, Gematimonadetes	Acidobacteria, Chloroflexi	Ma et al., 2021
	Alkali	Acid	
Soil acidity	Actinobacteria, Firmicutes, Bacteroidetes	Proteobacteria , Acidobacteria	Osman et al., 2019

3.2. The Effect of Cultivation Techniques on Bacterial Diversity

There are two types of plant cultivation practices, namely conventional and organic. Conventional farming highly depends on agrochemicals such as inorganic fertilizers and chemical pesticides, while organic farming makes minimal use of agrochemicals. Cultivation practices are human activities to meet their food needs through agricultural activities. This affects the diversity of microorganisms on agricultural land. In these agricultural activities, there are inputs, both organic and inorganic, that are included in the land and outputs transported along with the harvest. The use of agrochemical inputs affects microorganisms up to 50% in crop cultivation practices because non-target organisms are also affected (Wang et al., 2020). Organic farming is more environmentally friendly because it prioritizes using organic materials so that the diversity of bacteria are more abundant (Ares et al., 2021; Peltoniemi et al., 2021).

Agricultural cultivation technology affects the presence and diversity of bacteria in an agricultural ecosystem. According to Aslam et al., 2013 the type of tillage affected the diversity of bacteria in the soil. Microbial diversity in intensive cultivated and uncultivated land is dominated by the same bacterial phylum with different compositions (Figure 3). Soil that did not undergo tillage had more Proteobacteria than the soil that underwent tillage. Proteobacteria are more dominant in the soil that has not undergone processing because it is not disturbed. This was in line with the opinion of Silva et al. (2013) which stated that untreated soil has more bacterial diversity than treated soil except for Firmicutes. Firmicutes have more tolerance than other bacteria phylum for land cultivation.

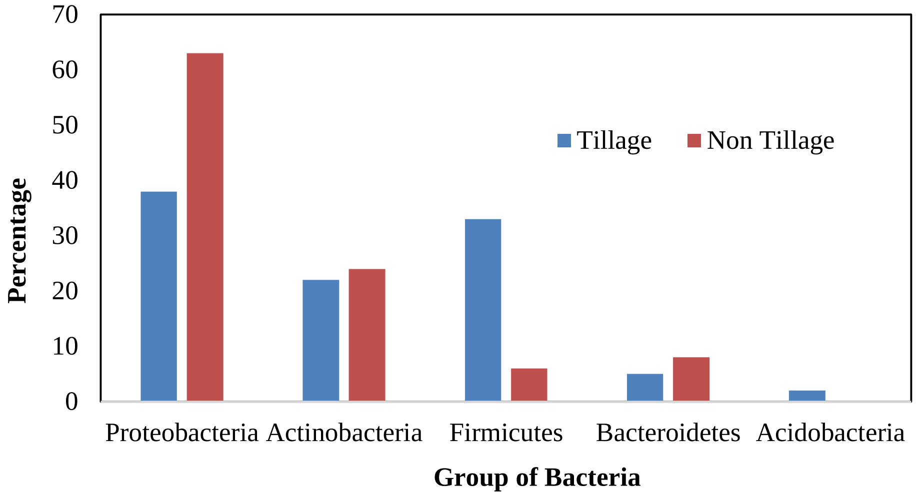

Figure 3. Bacterial composition in different tillage

Month: 1-4 (Rice) 5-8 (Rice) or 5-8 (Palawija) 9-12 (Rice)

(a) **Monoculture cropping pattern**

Chilli and cassava Papaya and eggplant Cauliflower and leek

(b) Intercropping

Figure 4. (a) Monoculture cropping pattern, (b) Intercropping
(Source: Balai Penelitian Lingkungan Pertanian and Personal)

A cropping pattern is a technique of cultivating plants on a plot of land by arranging the order of plant types and layouts at a certain period (Suryanto. 2019). There are several types of cropping patterns in agricultural activities: monoculture cropping patterns such as rice-rice-rice, monoculture by applying crop rotation such as rice-rice-palawija, and intercropping such as chilli-cassava, papaya-eggplant, and so on (Figure 4). Palawija is the second crop that planting after rice, such as corn, nuts, and beans. Corn is included in the group of secondary crops, generally planted in rice fields before the dry season arrives or planted in dry fields. Corn is mainly grown in rice fields for crop rotation. Land undergoing crop rotation produced richer and more diverse microorganisms than land with monoculture systems (Venter et al., 2016).

Cultivating crops on agricultural land is like two sides of a coin. On the one hand, it has a positive impact, namely adequate food availability and improving the economy and human welfare. However, on the other hand, it has negative impacts such as exploitation of the soil due to continuous planting so that soil fertility decreases and excessively used agrochemicals such as fertilizers and pesticides pollute the agricultural environment. These negative impacts affected the diversity of microorganisms, mainly bacteria, in the soil. Bacteria that could survive in unfavourable environmental conditions have the potential to be developed.

3.3. The Potential of Bacteria as Remediation Agents for Pesticide Residues

Pesticides are chemical substances that kill or control pests (Uqab et al., 2016). There are different types of pesticides depending on the target organism. Pesticides with different products have different functions. Chemical pesticides should be used on target, quality, type, time, dose, and way (Moekasan and Prabaningrum. 2011). Improper use of pesticides will cause problems in the future. Because the pesticides applied by farmers are not always on target, about 90% are spread through the soil, water, and air. These pesticides entered surface water, groundwater, sediments, plants, and soil, so they polluted the soil, plants, and even fauna (Iqbal and Bartakke. 2014; Tang et al., 2016). The high use of pesticides on agricultural land cause bacteria to have to adapt to the environment. These indigenous bacteria could be used as remediation agents for pesticide residues.

Another alternative to reduce the use of synthetic pesticides is to use biopesticides. There are 4 types: microbial biopesticides, pheromones, botanical pesticides, and plant protection (Laxmishree and Nandita. 2017). Botanical pesticides are made from certain plant extracts that function as repellants, attractants, antifeedants, and plant growth inhibitors (Ngegba et al., 2022). These plant extracts contained substances that could control insects, worms, fungi, bacteria, and viruses that harm cultivated plants. Botanical pesticides are safe for the environment and health because of their low toxicity. However, farmers do not like it because of its long effectiveness and not always available in the market.

Microorganisms play an essential role in controlling pollutants. Microorganisms work by bioabsorption and bioaccumulation processes in decontaminating pollutants in soil and water (Akinsemolu. 2018). Microorganisms digest these contaminants with certain enzymes so that they become harmless compounds. Indratin et al. (2019) isolated bacteria from three types of agricultural land in the Regencies of Demak, Magelang, and Brebes. The three types of soil were rice fields (Demak Regency), red chili land (Magelang Regency), and dry land shallots (Brebes Regency). The three agricultural lands differed in the intensity of pesticide use, where shallots > red chilies > rice. The isolation results showed 99-100% homology for degraded Pseudomonas alcaligenes, Pseudomonas aeruginosa, and Bacillus amyloliquenfaciens bacteria cypermethrin residues up to 95% at a laboratory scale. Another study was conducted by Wahyuni and Indratin (2015), who isolated soil bacteria from upland vegetable fields in Sukomakmur Village, Kajoran District, Magelang Regency. The study found Azotobacter sp., Sphaerotillus natans, Pseudomonas sp., and phosphate solubilizing bacteria. The consortia bacteria were able to degrade Persistent Organic Pollutants (POPs) pesticide residue compounds by more than 50% after 20 days.

Researchers from Kyrgyzstan successfully isolated the bacteria Pseudomonas fluorescence and Bacillus polymyxa, which reduced aldrin residues on a laboratory scale (Doolotkeldieva et al., 2017). These bacteria came from ex-mining sites that were used as pesticide disposal sites. Researchers from India, Iqbal, and Bartakke (2014) successfully isolated bacteria capable of degrading pesticide residues. The bacteria were Acinetobacter radioresistance, Pseudomonas frederiksbergensis, Bacillus pumilus, Serratia liquefaciens, Serratia marcescens, and Burkholderia gladioli. The bacteria came from local agricultural areas. The pesticide residues that could be degraded include chlorpyrifos, malathion, diazinon, endosulfan, dimethoate, and lindane.

Microbes in a consortium could be used to degrade pesticide residues. Harsanti et al. (2014) conducted ex situ remediation of vegetable land contaminated with organochlorine compounds using sludge enriched with microbial consortia. The microbes used included *Azotobacter chrococcum*, *Bacillus aryabathai*, *Pseudomonas mallei*, and *Trichoderma sp*. The combination reduced heptachlor, dieldrin, endosulfan, Dichloro Diphenyl Trichloroethane (DDT), and Dichloro Diphenyl Dichloro Ethylene (DDE) residues by 47.6; 92; 45.8; 87.6, and 83.1%. Kurnia et al. (2013) conducted an ex-situ study of DDT-contaminated vegetable land from the upstream Citarum watershed using manure and microbial consortia. The results showed that the microbial consortia treatment without manure could degrade DDT up to 100%. The consortium microbes used were *Pseudomonas mallei* and *Trichoderma sp*. These microbes were indigenous microbes from the local land.

Microbes will be more effective in degrading pesticide residues if biostimulants are available. Biostimulants provide the nutrients needed by bacteria. Materials used as biostimulants from agricultural waste include compost, sludge, rice husks, corn cobs, coconut shells, and empty oil palm fruit bunches. Poniman et al. (2017) have carried out in situ bioremediation using coconut shell-activated charcoal urea. Furthermore, corncob-activated charcoal urea was enriched with microbes that reduced endrin residues from the paddy soil by 100%. The microbes used were *Azotobacter sp*., *Azospirillium sp*., *Bacillus sp*., and *Enterobacter cloacae*. Using corncob-activated charcoal urea and urea corncob biochar enriched with microbes reduced residual chlordane in paddy fields by 86.8 and 80.5%, respectively (Poniman et al., 2017).

Indigenous bacteria from land contaminated with pesticide residues can be used as bioremediation agents. Indigenous bacteria will degrade pesticide residues through oxidation-reduction and complexation reactions, thereby reducing pesticide contamination. These consortia bacteria can degrade specific pesticide residues in ex-situ or in-situ. The bacterial consortia will be more effective and last longer if nutrients or biostimulants are available. Agricultural waste can be used as a biostimulant.

4. Conclusions

Agricultural lands are dominated by bacteria from the phyla Proteobacteria, Actinobacteria, Acidobacteria, Bacteroidetes, and Firmicutes. Proteobacteria are involved in the nitrogen, carbon, and sulphur cycle. Actinobacteria are involved in the carbon cycle. Acidobacteria is involved in the nitrogen cycle. Bacteroidetes function as decomposers of organic matter and live in anaerobic conditions, while Firmicutes are required for biocontrol and plant growth. Rhizobacteria predominated on agricultural land. Cultivation techniques, plant varieties, plant growth stages, soil factors, and tillage systems affect the diversity of bacteria in agricultural lands. Organic farming has more diverse bacteria than conventional farming due to the minimal usage of agrochemicals. Bacteria diversity is mostly the same phylum for plant varieties but different in plant growth stages. In the early growth period and before harvesting, bacterial diversity is less than in the active vegetative and generative periods. Low soil fertility, sandy soil, and acid soil have low bacteria diversity than high soil fertility, clay soil, and alkali soil. Non-tillage soil has more abundant bacteria than tillage soil, except for Firmicutes, which are more resistant to tillage. The high use of pesticides in agricultural land affects the diversity of bacteria. Indigenous bacteria that survive in conditions of high pesticide residue contamination have the potential as remediation agents for pesticide residues. Indigenous bacteria can degrade pesticide residues through oxidation-reduction and complexation reactions, thereby reducing pesticide contamination.

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