

Review

Application of Synthetic Consortia for Improvement of Soil Fertility, Pollution Remediation, and Agricultural Productivity: A Review

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Abstract: Climate change, inadequate possessions, and land degradation all pose obstacles to modern agriculture. In the current scenario, the agriculture industry is mainly dependent on the use of chemical-based pesticides and fertilizers that impact soil health and crop productivity. Moreover, water scarcity leads farmers in drastically affected regions to use heavy metal-enriched water sources mainly originating from industrial sources for field crops irrigation. Soil pollutants can be carried into the human body via dust and water, creating negative health effects varying from simple symptoms, e.g., nausea and diarrhea and reaching death in critical cases. Thus, to clean soil contaminants, and improve soil fertility and agricultural production, alternatives to chemical fertilizers must be developed. Therefore, using beneficial microbes found in plant-associated soil microorganisms offers an effective strategy to alleviate some of these challenges, improving soil fertility, and crop yield, and protecting plants from stress conditions. Through the use of synergistic interactions, the synthetic consortium strategy seeks to improve the stability of microbial communities. In this review, synthetic consortia and their potential use in agriculture were discussed. Further, engineering new effective synthetic consortia was suggested as an effective approach in the concept of environmental bioremediation of soil pollutants and contaminants.

Keywords: synthetic consortia; soil fertility; pollution remediation; agricultural productivity; heavy metals; pesticides; plants' diseases management

1. Introduction

Purifying toxic-pollutants contaminated soil is an important task. Soil pollutants include chemical and pharmaceutical compounds, pesticides and fertilizers. However, they may not only present short term-impacts on microbial and enzymatic activities but also long term-ones. As a result of increased human awareness, modern agricultural systems to eliminate contaminants were considered to preserve soil, and its microbial populations, along with the maintenance of good agricultural and healthy production [1]. Harmful contaminants can be eliminated from the environment via different methods, e.g., chemical, biological, and phytochemical degradation [2,3]. Centrifugation, coagulation, and phytodegradation are all physical and chemical strategies for eliminating contaminants but these methods, however, are expensive and have a limited impact [4]. On the other hand, the biological breakdown of pollutants is a low-cost and environmentally benign way of purifying contaminated soils. Several degrading enzymes are produced by microbes, which cleave the original bonds of toxic chemicals and mineralize them into inorganic forms. This method transforms dangerous chemicals into less toxic forms using microorganisms [5]. Numerous studies have demonstrated that it is challenging for a single strain to complete the degradation of contaminants. Bacteria with varied elimination capacities are mixed; different strains have diverse metabolic pathways. Therefore, a microbial consortium can combine the benefits of each strain to ensure effective pollutant destruction [6]. The biodegradation of soil contaminants can be greatly accelerated by co-cultivating a microbial consortium, which is more efficient than single bacteria. A pyrene-degrading microbial consortium has been reportedly discovered in Thai mangroves which consists of five microorganisms: *Mycobacterium* spp., *Novosphingobium* sp., *Bacillus* sp., and *Ochrobactrum* sp. The microbial consortium degraded pyrene more quickly than a single bacterium due to synergistic interactions of the consortium [7].

One prevalent environmental issue is the excessive discharge of heavy metals such as manganese and cadmium from various industrial effluent sources into the ground and drinking water [8]. It has been demonstrated that the excessive intake of heavy metals can have neurotoxic consequences on humans [9]. Additionally, remediating soil contaminated with heavy metals is an environmental and economic issue that needs to be resolved as is a global environmental problem [10]. In the biological system, heavy metal bioremediation is crucial and can effectively mitigate the damage caused by organic contaminants. In order to effectively precipitate cadmium (Cd) and cause heavy metals to change from an ionic state to their stable form, researchers have created a stable urease-producing consortium that reduces the mobility and toxicity of hazardous metals [11]. *Bacillus* sp. and *Sphingobacterium* isolated from manganese-contaminated (Mn-contaminated) sediment were combined and grown to produce an Mn-oxidizing bacterial consortium, which used various carbon sources and performed better [9].

Nanotechnology, via nano-farming, has tried to address such environmental issues; however, it failed to fully protect the soil ecosystem from disruption [12], which emphasized the incorporation of synthetic consortia in the synthesis of nanoparticles (NPs) with less environmental threat and higher agricultural effectiveness. Microbial inoculants offer great opportunities for ecological farming approaches to promote crop productivity and plant growth [13,14]. For agricultural sustainability, various bioinoculants with single or multiple microbial strains in a single formulation (consortium) might be used [15–17]. Single-species microbial inoculants frequently fail to colonize plants under field conditions or do not produce the desired results [18]. On the other hand, it is becoming more widely acknowledged that using synthetic microbial communities help to overcome these problems [19]. Different effective microbial strains in a consortium are being used in a

currently growing concept [20–22]. The inoculation of microbial consortia containing *Enterobacter* sp. (nitrogen fixer), *Microbacterium arborescens* (phosphate solubilizer), and *Serratia marcescens* (IAA producer) in wheat cultivation led to significant increases in growth, yield, and nutrient uptake [23]. Ghorchiani et al. [24] investigated the effect of co-inoculating *Pseudomonas fluorescens* (*P. fluorescens*) (phosphorus-solubilizing bacteria) and *Funneliformis mosseae* (*F. mosseae*) (arbuscular mycorrhiza fungi; AMF) in maize cropping. The microbial consortium effectively increased the growth and yield of maize in contrast to the single inoculation and control treatment. Microbes such as *Mesorhizobium* sp., *Pseudomonas*, *Burkholderia* sp., and AMF, when combined, were found to increase chickpea growth and production under rainfed conditions [25]. Tsolakidou et al. [26] reported that a bacterial consortium reduces tomato *Fusarium* wilt symptoms. According to Carrión et al. [27], the combination of *Chitinophaga* and *Flavobacterium* consistently protects sugar beet from *Rhizoctonia solani* (*R. solani*) infection. The synthetic microbial consortium improves crop performance both directly by supplying nutrients and hormones and indirectly by modifying the composition of the microbial population in the rhizosphere [19].

Random microbial species cannot be combined into consortia and lead to a successful bioremediation process, the mitigation of plant yield reduction and viruses/diseases invasion. Therefore, corresponding microbial populations (i.e., bacteria, fungi) should be chosen based on their potential to remove pollutants, increase plant yield and reduce virus toxicity on host plants. This includes long and minute engineering of each microbe, testing in-vitro and on-field applications, then combining two or more engineered microbes in a synthetic consortium to deal with one of the aforementioned aspects.

In this review paper, the role of synthetic consortia in the remediation of contaminated sites, disease suppression, and the improvement of crop productivity and soil fertility was discussed. Numerous review studies have investigated the role of individual bacteria or fungi in the degradation and/or removal of pesticide pollutants. However, the main concern of the current review is to outline the effect of synthetic consortia on bioremediation processes of pesticides and heavy metals, improvement of soil fertility and agricultural productivity through complex metabolisms and modes of action. It also outlines the gap in the literature regarding the engineering of suitable microbial consortia destined for application in agricultural technology via NPs synthesis. Therefore, this review will be a reliable platform on which researchers can rely to engineer suitable microbial consortia for maximized pollutants removal, soil fertility, and plant production.

2. Synthetic Consortium as Bioremediation Agent of Pesticides

The hazardous and extensive use of pesticides was needed to improve crop yields in order to meet the rise in the global population and meet sustainable development (SDG2) goals. The application of pesticides has resulted in extreme pollution as well as human health risks as a result of their bioaccumulation in water, soil, and subsequently cultivated crops (Figure 1). Drastically, soil pollution can directly affect crop growth, productivity as well as the products' composition, and subsequently human health. Several strategies were adopted for the bioremediation of pesticides in soil; among them are classified: bioaugmentation, biostimulation, and phytoremediation. All three methods are cost-effective, eco-friendly, and efficient [28]. The main concern of the current review is bioaugmentation which consists of introducing one or more microorganism(s) for contaminant removal through degradation. A combination of microorganisms from two or more species used for such a purpose is called a synthetic consortium. Chemically, pesticides used for crop protection can be classified as carbamates, organochlorine pesticides, organophosphate pesticides, and synthetic-pyrethroid pesticides [29]. However, they all result in detrimental impacts on soil health and quality, especially in terms of microbiota and subsequent deleterious effects on grown crops and the degree and capability of degradation of each pesticide type.

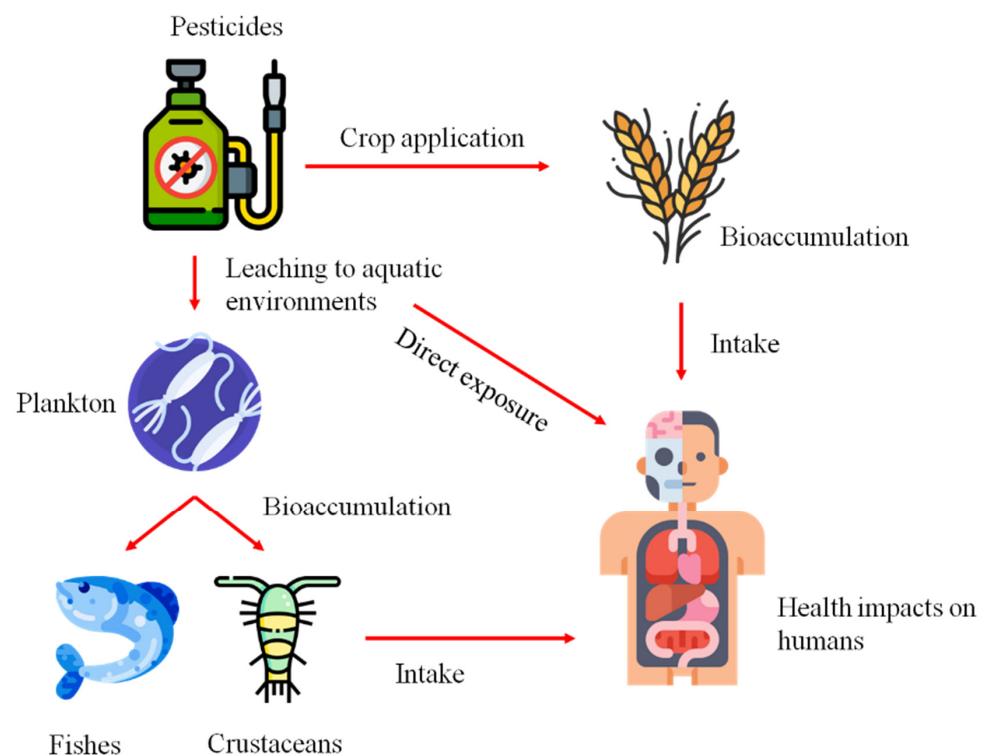


Figure 1. Risks of pesticides applications on water and plant species and human health.

Microbial consortia are reported to have high self-organization enabling them to improve resource interception with higher efficiency in metabolites exchange. Moreover, they have higher adaptability and viability regarding several influencing environmental factors such as pH, temperature, water content, and organic compounds (real representatives of the pollutants). In this context, the first incorporation of microorganisms' consortium in pesticide component removal was reported in the USA. More precisely, a microbial consortium was used successfully to remove coumaphos (an organochlorine compound pesticide) [30]. Organochlorine pesticides, especially coumaphos have a relatively high vapor pressure that makes their volatilization and/or degradation relatively difficult. Such types of pesticide have a long half-life (around 360 days) and can be effectively degraded when alkali-treated, or mineralized and co-metabolized. The combination of Gram-negative bacteria (e.g., *Pseudomonas* and *Bacillus* spp.) is highly efficient for pesticide removal from stagnant water sources such as lakes and ponds. These bacterial strains metabolize pollutants and use them as nitrogen sources for their growth and proliferation. For instance, López et al. [31] studied the removal capacity of a bacterial consortium found in an oligotrophic pesticide-polluted-lake. They found that a consortium composed of *Pseudomonas pseudoalcaligenes* (*P. pseudoalcaligenes*), *Micrococcus luteus* (*M. luteus*), *Bacillus* sp., and *Exiguobacterium aurantiacum* (*E. aurantiacum*) had a considerable removal capacity for pesticides. Bacterial consortia generally act by the hydrolysis of carboxyl ester bonds found in soil and water-accumulated pesticides and the cleavage of diaryl linkage. This explains how a bacterial consortium of *Enterobacter*, *Microbacterium*, *Ochrobactrum*, *Pseudomonas*, *Hyphomicrobiaceae*, and *Achromobacter* was effective in the degradation of β -cyfluthrin in soil and water [32]. Gram-positive bacterial consortia react by ring cleavage against pesticidal contaminants. Such a reaction results in the destabilization of the transition state and thus, the inhibition of any covalent bonding and the formation of an acyclic structure. However, in some cases, separate Gram-positive and Gram-negative consortia face strong polar carbon-oxygen bonding. This makes the mineralization of these pollutants and/or their ring cleavage a difficult task to attain. Therefore, the combined consortia of both Gram-positive and Gram-negative bacteria shall be evaluated for their potential of acting on both verges. In this regard, a two-membered microbial consortium consisting of *No-*

cardioides sp. (a Gram-positive bacterial strain) and a Gram-negative bacterium yielded cyanuric acid which showed a great potential to degrade atrazine (herbicide) [33]. However, synthetic consortia consisting of Gram-negative bacteria can promote catabolic enzymes responsible for pesticide degradation, and the trigger of reactive oxidation and hydroxyl radicals, along with carbon dioxide, water and inorganic ions liberation. This could explain the effectiveness of a microbial consortium consisting of *Alcaligenes xylosoxydans* (*A. xylosoxydans*) subsp. *denitrificans*, *A. xylosoxydans* subsp. *xylosoxydans*, *Pseudomonas putida* (*P. putida*), *Pseudomonas marginalis* (*P. marginalis*), and *Providencia rustigianii* (*P. rustigianii*) in the degradation of two herbicides: atrazine and alachlor with the latter's degradation as the precursor of the former's one [34]. The degradation of atrazine could be also attributed to the big role of *atzB* (microbial gene) [35]. Moreover, synthetic microbial consortia promote several enzymes such as hydrolases, esterases, oxidases, and glutathione-S in two subsequent phases leading to the degradation and removal of pesticides. In this regard, synthetic microbial consortia effectively removed both atrazine and diclofop methyl, which are considered anthropogenic pesticides [36,37].

Microbial consortia outline a synergetic degradation metabolism of pesticides, which reduces the half-time persistence of the latter. On the other hand, diuron, an algicide and herbicide impacted soil microbes inhibiting their growth. Purposely, Villaverde et al. [38] proposed a novel diuron-degrading microbial consortium that succeeded to remove around 98.8% of the available diuron concentrations within a few days. Villaverde et al. [39] tested the effect of five microbial consortia on diuron mineralization; they found various mineralization percentages ranging between 22.9% and 78.6% with a reduction in the half-life from 700 days to 171–546 days. This denotes the synergetic mineralization mechanisms of engineered microbial consortia. Góngora-Echeverría et al. [40] outlined an increase in biobeds' efficiency and remediation potential in agricultural effluents and soils contaminated by pesticides (above 90% removal) besides a decrease in the half-life persistence of carbofuran, diazinon, and glyphosate. Moreover, ametrin (fungicide) degradation was possible with the use of a packed-bed microbial consortium, and metabolite profiles were generated in vitro [41]. Therefore, it shows that the packed-bed system allows for the higher retention of microorganism concentrations found in the microbial consortium and thus higher pesticide degradation capacity.

Obsolete pesticides have a high sensitivity to the degrading ability of microbial consortia owing to their high enzymatic activity. This was approved by Doolotkeldieva et al. [42] who reported the use of a microbial consortium (association of *Micrococcus flavus* (*M. flavus*), *Bacillus polymyxa* (*B. polymyxa*), *P. fluorescens*, and *Flavobacterium* sp.) with successful removal of around 81.5%, 97.9% and 99.9% of β -BHC, 4-heptachlor-epox and dieldrin pesticides, respectively. Khatun et al. [43] elaborated a synthetic bacterial consortium based on two *Escherichia coli* (*E. coli*) strains to detect organophosphorus pesticide degradation efficiency. The consortium succeeded in the hydrolysis of the latter to *p*-nitrophenol, and subsequently to β -galactosidase production for colorimetric detection.

Pesticide accumulation in agricultural wastes showed to be an alarming issue nowadays. However, the incorporation of synthetic microbial consortia played a major role in the biosorption of pesticide pollutants. In this context, several bacterial consortia showed varying pesticide removal efficiencies from *Loofah* sp., corncob depending on the state of the pollutant (immobilized or not): 12.0–95% for carbendazime [44]; 87.0–89.7% for chlorophenols [45] and 55–98% for methyl parathion [46]. The isolation of a *Bacillus* sp. consortium from agricultural fields led to the biodegradation and removal of around 90% atrazine, malathion, and parathion [47,48]. A cow-dung microbial consortium proved potentiality in the bioremediation of several pesticides, i.e., chlorpyrifos, cypermethrin, fenvalerate, and trichlopyr butoxyethyl ester in contaminated surface soils after their mineralization [49]. Moreover, the genus and strain of bacteria and fungi combined in consortia play a big role in the increase or decrease in degradation rates. In other words, the expression of functional genes is a factor determining potential pesticide degradation. The synergetic interaction of five strain-composed microbial consortia (*Variovorax* sp. strain WDL1, *Delftia acidovorans*

(*D. acidovorans*) WDL34, *Pseudomonas* sp. strain WDL5, *Hyphomicrobium sulfonivorans* (*H. sulfonivorans*) WDL6, and *Comamonas testosteroni* (*C. testosterone*) WDL7) showed an improved linuron (herbicide) degradation rate compared to individual degradation rates [50]. The specific strains used showed improved degradation rates. A 50 genera-microbial consortium named ACE-3 degraded around 50 mg/L of acetamiprid in 144 h [51].

Gram-positive bacteria, e.g., *Streptomyces* spp. help in the improvement of lytic enzymes responsible for pesticide degradation. Moreover, the addition of strain activators and/or biosurfactants to synthetic consortia can enhance pesticide removal. For instance, a consortium based on *Streptomyces* spp. showed high removal percentages of chlorpyrifos of around 40.2% (free cells) and 71.0% (immobilized cells) but low removal percentages of pentachlorophenol (5.2% for free cells and 14.7% for immobilized cells) [52]. Noteworthy is the higher removal of pesticides with immobilized cells compared to free ones. Furthermore, a consortium of *Pseudomonas*, *Klebsiella*, *Stenotrophomonas*, *Ochrobactrum*, and *Bacillus* degraded 82% of available chlorpyrifos in a soil-water-based slurry system within 10 days; whereas the addition of a crude rhamnolipid biosurfactant improved this degradation by 30% within only 6 days [53]. Ortiz-Hernández and Sánchez-Salinas [54] outlined the ability of a bacterial consortium—composed of *Stenotrophomonas malthophilia* (*S. malthophilia*), *Proteus vulgaris* (*P. vulgaris*), *Vibrio metschnikovii* (*V. metschnikovii*), *Serratia ficaria* (*S. ficaria*), and *Yersinia enterocolitica* (*Y. enterocolitica*)—to degrade tetrachlorvinphos (an organophosphate insecticide). Several microbial consortia based on three microorganisms (*Brevibacterium frigoritolerans* (*B. frigoritolerans*), *Bacillus aerophilus* (*B. aerophilus*), and *Pseudomonas fulva* (*P. fulva*)) showed high degradation percentages (97.6–98.3%) of phorate (an organophosphorus pesticide) [55].

Phenylurea herbicides are considered dangerous pollutants endangering the water ecosystem. Such types of herbicides cannot be degraded until the mineralization of 3-(4-isopropylphenyl)-1-methylurea and 4-isopropyl-aniline. The degradation of linuron—a phenylurea herbicide using a bacterial consortium based on *Diaphorobacter* sp. strain LR2014-1 and *Achromobacter* sp. strain ANB-1 was shown to be promising due to the synergetic catabolism leading to improved mineralization [56]. Zhang et al. [57] reported an accelerated degradation of dicarbomixide fungicides using a *Providencia stuartii* (*P. stuartii*) JD and *Brevundimonas naejangsanensis* (*B. naejangsanensis*) J3-based consortium with a more efficient removal from soils when these strains are immobilized.

3. Synthetic Consortium as Bioremediation Agent of Heavy Metals

Heavy metals are potentially toxic elements known as high pollutants in soil and subsequently crops by inducing a reduced photosynthesis capacity. These pollutants are generally translocated from soil to fruits and vegetables [58–63]. Several approaches were adopted to reduce heavy metal hazardous disposal in the environment in agricultural practices by using fungal species in growing media [64–69]; other studies focused on the growth of crops with a higher tolerance to heavy metals [70,71]. Although succeeding in reducing these pollutants in soil, these approaches are still built on an experimental scale and not on a large-scale benefiting the whole countries' economy.

Microorganisms including bacteria and fungi require the degradation and consumption of mineralized heavy metals to survive and proliferate. They also show high tolerance and resistance to extremely high pollutant levels. In this context, copper sulfide ores, copper, and arsenic were bio-leached by a five-bacteria-strain consortium composed of *Acidithiobacillus thiooxidans* (*A. thiooxidans*) sp. Licanantay, *Acidiphilium multivorum* (*A. multivorum*) sp. Yenapatur, *Leptospirillum ferriphilum* (*L. ferriphilum*) sp. Pañiwe, *Acidithiobacillus ferrooxidans* (*A. ferrooxidans*) sp. Wenelen and *Sulfobacillus thermosulfidooxidans* (*S. thermosulfidooxidans*) sp. Cutipay [72]. The bioleaching of heavy metals may have occurred via thiosulfate or polysulfide pathways. This consortium showed a high efficiency (owing to a high functional potential) against the high tolerance of copper to microbial degradation and oxidation activity. Copper degradation is considered tough as it requires a very low pH in the polluted environment. This outlines that microbial consortia used for heavy

metals may play a role in the reduction in pH, thus leading to an easier degradation of heavy metals. The balance of iron and sulfur metabolism can be maintained using synthetic microbial consortia [73]. These synthetic consortia can combine both culturable and previously non-culturable microorganisms, thus helping in the explanation of hindered gene functionality besides increasing a consortia's productivity and stability. However, the detailed function mode of microorganisms within these consortia is still scantily investigated. Cultures' consortia have shown a superior metabolism for the biosorption of heavy metals and were considered more appropriate for field applications compared to the individual implication of microorganisms.

Microbial consortia decrease the mobility of heavy metals in soil and water by solubilizing them from a higher oxidation state to lower oxidation one. As a result of partial or complete immobilization, the microbial consortia can degrade the potentially toxic elements and mineralize them for further use as nitrogen sources. For instance, Roane et al. [74] used a consortium of metal-accumulating strains and *Ralstonia eutropha* (*R. eutropha*) JMP134 to enhance Cd-contaminated soil remediation. Dell'Anno et al. [75] studied the potential of a five-bacterial-strain-consortium (*Halomonas* sp. SZN1, *Alcanivorax* sp. SZN2, *Pseudalteromonas* sp. SZN3, *Epibacterium* sp. SZN4, *Virgibacillus* sp. SZN7) on heavy metal reduction in polluted sediments. They noted a decreased mobility of arsenic (As), Cd, and lead (Pb) promoted by their lower fraction bioavailability and higher partitioning. Duarte et al. [76] used a bacterial consortium consisting of *P. putida*, an unidentified *Pseudomonas* sp., *S. malthophilia*, and *Rhodococcus erythropolis* (*R. erythropolis*) for the purpose of bioremediation of sulfurous-oil-containing soils. They outlined a desulfurization capacity of 20–78%. A sulfate-reducing bacterial consortium successfully treated chromium-contaminated (Cr (VI)-contaminated) soils [77]. A four-bacterial-consortium (*Viridibacillus arenosi* (*V. arenosi*) B-21, *Sporosarcina soli* (*S. soli*) B-22, *Enterobacter cloacae* (*E. cloacae*) KJ-46, and *E. cloacae* KJ-47) showed Cd, copper (Cu), and Pb removal percentages of 85.4, 5.6, and 98.3%, respectively, from contaminated soils [78]. However, the aforementioned engineered microbial consortia failed to be specific, especially for heavy metals that show potential resistance to enzymatic activity. This proves again the need to engineer specific microbial consortia for Cd, Cu and Pb removal based on the synergetic effect of potentially robust metabolisms. Lee et al. [79] engineered a microbial consortium based on the biodegradation ability of hydrophobicity and emulsifying activity. This consortium consists of seven microbial strains namely: *Acinetobacter oleivorans* (*A. oleivorans*) DR1, *Corynebacterium* sp. KSS-2, *Micrococcus* sp. KSS-8, *Pseudomonas* sp. AS1, *Pseudomonas* sp. Neph5, *Rhodococcus* sp. KOS-1 and *Yarrowia* sp. KSS-1, it succeeded in the bioremediation of heavily contaminated soil by heavy metals and diesel fuel. A consortium of five actinobacteria (*Streptomyces* spp. A5, A11, M7, and MC1, and *Amycolatopsis tucumanensis* (*A. tucumanensis*) DSM 45259) removed 83.0–100.0% of Cr (VI) from soil [80]. Fungal communities bioaccumulate heavy metals first, then liberate several metabolites such as organic acids and siderophores that precipitate those potentially toxic elements via a biosorption process. Therefore, a combination of fungal and bacterial communities in a synthetic consortium would result in the complete mineralization and biosorption of heavy metals in a polluted environment. For instance, a microbial consortium based on bacteria (*Bacillus* sp., *Streptococci* sp., *Salmonella* sp., *E. coli* sp., *Pseudomonas* sp. and *Micrococcus* sp.), fungi (*Aspergillus* sp., *Mucor* sp., *Penicillium* sp. and *Rhizopus* sp.) and Actinomycetes (*Nocardia* sp., *Micromonospora* sp. and *Rhodococcus* sp.) showed an excellent bioremediation potential of Cd, Cu, and iron (Fe) (98.5, 99.6, and 100.0%, respectively) in soils contaminated by heavy metals [81]. The combination of synthetic consortium (bioremediation) with a phytoremediation process resulted in promising heavy metals removal and reduced accumulation in plant shoots and roots. Dary et al. [82] mentioned the efficient reduction in Cd, Cu, and Pb accumulation in plant roots after inoculation of a consortium of PGPRs (*Bradyrhizobium* sp., *Ochrobactrum cytisi* (*O. cytisi*), and *Pseudomonas* sp.) with *Lupinus luteus* (*L. luteus*) leading to increased biomass. PGPRs release several metal-degrading enzymes, organic acids, and metal chelators that result in a decreased pH, and an environment suitable for heavy metal degradation, especially Cd, Cr,

and Cu. A bacterial consortium based on *Acinetobacter* sp. and *Arthrobacter* sp. reduced Cr contamination by 78.0% [83]. Nwaehiri et al. [84] engineered two bacterial consortia for the bioremediation of soils contaminated by heavy metals. The first consortium was based on *Serratia marcescens* (*S. marcescens*), *Pseudomonas pyogenes* (*P. pyogenes*), *Erwinia amylovora* (*E. amylovora*), and *E. cloacae* while the second one was based on two strains: *Bacillus subtilis* (*B. subtilis*) and *Staphylococcus aureus* (*S. aureus*). Although the second consortium was not much effective, the first one showed a high Cr removal rate. The low effectiveness of a synthetic consortium against heavy metals could be due to antagonistic activities of used microbes and/or high resistance of pollutants in the polluted site. Shen et al. [85] outlined that *Bacillus* sp., *Escherichia* sp., *Micrococcus* sp., and *Staphylococcus* sp. when added in consortium removed around 80% of the total heavy metals. It was recently found that filamentous fungi such as *Aspergillus* spp. have a higher potential to degrade specific heavy metals due to their ability to liberate organic acids that mineralize pollutants. Moreover, these fungal communities combined in a synthetic consortium have a high resistance to extreme heavy metal concentrations. A two-strain fungal consortium based on *Aspergillus flavus* (*A. flavus*) and *A. fumigatus* showed a 70% removal of Cr (VI) [86]. This heavy metal's toxicity was also reduced using a bacterial consortium in an aqueous solution outlining an enzyme-mediated process [87]. A 12-strain bacterial consortium showed resistance to facing heavily chronically polluted soil by heavy metals and diesel oil. It succeeded in the removal of around 75% of the total pollutants [88]. While PGPR are strong metal decomposers, arbuscular mycorrhizal fungi can live in symbiosis with heavy metals reducing their toxicity to plants. Rhizobia can deal directly with heavy metals through chelation, precipitation or transformation into other non-toxic metals. Therefore, a combination of these microorganisms would lead to a strong microbial consortium against pollutants. Lampis et al. [89] mentioned that a consortium of growth-promoting rhizobacteria increased soil arsenic (As) removal from 13% (control) to 35% along with an increase in *Pteris vittata* (*P. vittata*) biomass by around 45%. The consortium association of *P. putida* 710A and *Commamonas aquatica* (*C. aquatica*) 710B reduced Cd accumulation in the soil by 69.4% within one day and by 25.1% and 41.0% in roots and shoots of cultivated mung bean plants, respectively [90]. An improved bioremediation process of soils was recently acknowledged by Belimov et al. [91]. These authors inoculated a consortium of arbuscular mycorrhizal fungus, PGPR, and rhizobia with a pea gene mutant proving an increased tolerance and accumulation of Cd. Wan et al. [9] presented a Mn-oxidizing bacterial consortium that succeeded in the removal of 76.0–98.0% of Mn (II) from polluted sediments when associated with several heavy metals, e.g., Cu (II), Fe (II), Mn (II), Ni (II) and Zn (II). Although very few studies have investigated the effectiveness of *Firmicutes*-based consortia against heavy metals, they showed excellent mineralization of the latter. For instance, the construction of a urease-producing consortium based on three *Firmicutes* genera caused a 92.9% Cd mineralization in soil within only eight hours [11]. Endophytic bacteria play a big role in the production of indoleacetic acid (IAA) and other plant growth promoters. This pushed several researchers to include them in synthetic microbial consortia for heavy metal bioremediation associated or not with a phytoremediation process. For instance, the inoculation of endophytes consortia associated with a phytoremediation process played a crucial role in the removal of Cd and Pb from contaminated soils [92,93]. Moreover, such consortia had a promising bioremediation potential when associated with *Brachiaria mutica* (*B. mutica*); Cd accumulated 44, 55, and 95% more in the latter's leaves, shoots, and roots, respectively [94].

4. Bioengineering of Synthetic Consortia

Non-engineered microbes have generally a low performance and must be chosen minutely based on their chelating, degrader, solubilizer and precipitator potential. Selected microbes are nitrogen fixators, carbon producers, phosphorus solubilizers, and surfactant producers. These properties are essential to managing the potentially toxic elements found in agricultural soil and pesticides found in agro-industrial wastes applied to plants, as well as to promote vegetative development and ensure good pest management. After

microbial selection, genetic optimization is required. This implies the identification of specific interest genes based on modular DNA parts and computational modeling that help in DNA fragments assembling to form suitable genes. The used tools include a Quorum Sensing (QS) system which coordinates between signaling molecules and binds the corresponding receptor to the transcription promoter and a bidirectional communication tool that activates the output within a selected strain. This is followed by an exogenous addition of inducer molecules to expressing genes with each strain of the synthetic consortium under engineering [95]. Finally, gene editing is performed where selected genes were crossed or merged to obtain genetically engineered microbes than can be combined into synthetic microbial consortia with relatively high performance. However, those engineered consortia should be not only tested in in-vitro conditions but also in field conditions before any large-scale application. Figure 2 summarizes the bioengineering steps of a synthetic microbial consortium.

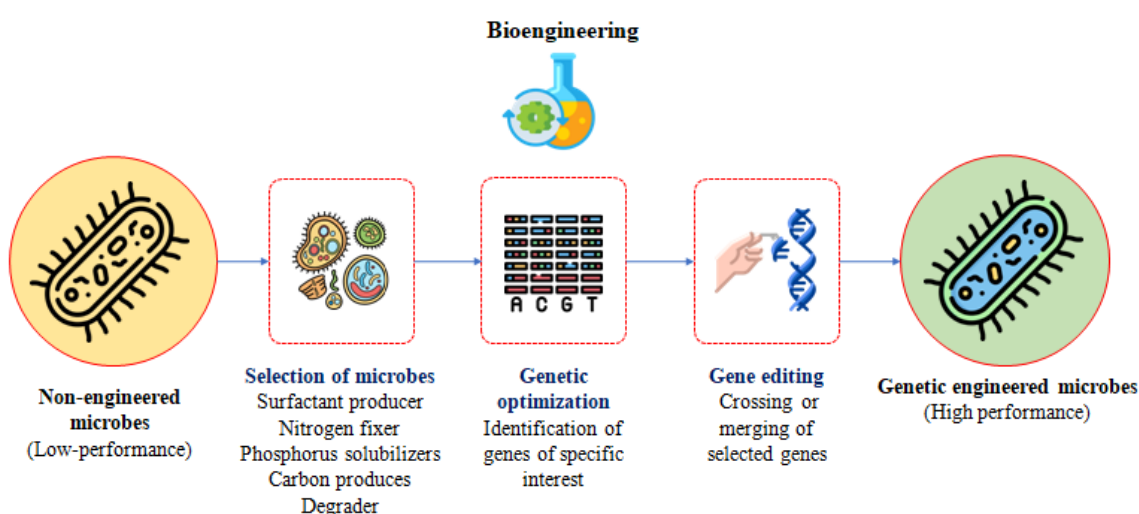


Figure 2. Bioengineering steps of synthetic microbial consortium.

5. Incorporation of Microbial Communities in Agricultural Nanotechnology

Particles with at least one dimension less than 100 nm are known as nanoparticles (NPs), which are thought to be the basis of nanotechnology. Nanotechnology has shown promising potential in promoting sustainability in the agricultural field. It plays a significant role in crop production and protection with a focus on nano-enabled remediation techniques for contaminated soils, nano-enabled fertilizers, nano pesticides and nano biosensors [28]. However, the increased use of NPs in various sectors promoted environmental contamination. Abiotic elements, i.e., water, soil and air that are closely linked to human health, may be affected by NPs released into the environment by industrial or commercial sectors [96]. Some NPs are excessively utilized in consumer items; particularly, silver NPs (Ag NPs) accounted alone for around 20% of NPs utilization, which is roughly three times that of the second most frequently used carbon-based NPs [97]. Due to the use of hazardous chemicals or the production of toxic by-products, NPs synthesis via chemical methods is often not totally safe or environmentally friendly. However, NPs synthesis via green methods is considered both cost-effective and environmentally safe. Green methods play a vital role in the biosynthesis of NPs making them an eco-friendly and sustainable tool [98].

Several bacteria and fungi or the by-products of their metabolism can be used for the biological synthesis of inorganic NPs, which act as stabilizing and reducing materials. Biological synthesis is comparatively sustainable, economical, clean, non-toxic, biocompatible and simple, and offers wide adaptability of NPs [99]. Bacteria were among the first organisms utilized for the synthesis of NPs due to their ease of isolation, quick manipulation, and the existence of built-in mechanisms for metal ion detoxification and extracellular secretion of enzymes. There are different bacterial species that were involved in NPs

synthesis such as *Bacillus megaterium*, *Rhodococcus* and *Bacillus licheniformis*. Additionally, fungi were considered smart agents for the biological synthesis of metallic NPs, due to their easy handling, high tolerance to metals, the efficiency of biomimetic mineralization, high secretion of intracellular or extracellular enzymes and effective reduction and stabilization of NPs [100]. Currently, several fungal species such as *Aspergillus*, *Alternaria*, *Agaricus*, *Acremonium*, *Amylomyces*, *Sclerotium*, *Trichoderma*, and *Verticillium* were successfully exploited for the production of biologically effective metallic NPs [101]. The production of NPs from the dead cell walls of microbial consortia decreases their production costs. In this context, Dameron et al. [102] produced Cd NPs from the cell walls of *Candida glabrata* and *Schizosaccharomyces pombe*. Moreover, gold NPs (Ag NPs) were synthesized using *Candida albicans*, *Candida utilis*, and *Saccharomyces boulardii* [103]. On the other hand, filamentous fungi showed the potential to biosynthesize Au NPs and Cu NPs. This could be due to the role of fungal proteins in the capping of Au NPs and Cu NPs [104]. Furthermore, the secretion of secondary metabolites along with the large surface area make Actinomycetes promising candidates for NPs formulation. For instance, Au NPs were synthesized using a variety of Actinomycetes [105]. Liao et al. [106] moved the soil bioremediation process of heavy metals to a whole new level. They developed a bio-nanocomposite (hybrid iron-, sulfate- and phosphate-based nanocomposite) that succeeded in immobilizing the most deleterious heavy metals, i.e., As, Cd, and Pb in severely contaminated soil by 62.3, 31.3, and 59.9%, respectively. Although they are chemically stable and synthesized by engineered microbial communities, the mechanism of microbial-synthesized NPs is still unclear and not understood in Academia. Therefore, the choice of suitable microbial consortia for large-scale NPs production is still risky and pushes for further and deeper research.

6. Role of Synthetic Consortium in the Improvement of Crop and Soil Properties

The associations of plant growth-promoting bacteria (PGPB) and beneficial fungi with plants played a crucial role in agriculture. It was known that a single application of these microbes could exert beneficial effects on plants. In addition, when these combined microbes were applied, they played additive or synergistic roles in plants [107–109]. This happens because two or more species can perform various tasks in an ecosystem, such as the rhizosphere [110]. The latter is a dynamic zone of biotic and abiotic interactions between plant roots and soil-borne microbes [111]. In addition, the rhizosphere provides a more favorable environment for plant and microbial growth than bulk soil [112].

Microbial consortia consisting of bacteria and fungi have various applications in sustainable agriculture [113]. The synthetic microbial consortia are subjected to development for plant growth and quality in a sustainable manner, which constitutes the soil microbiome of high-quality crops. The formulations of microbial consortia make these microorganisms capable to adapt to the new environment. Nowadays, available bio-formulations consist of single strains; mixed microbial cultures or simultaneous inoculation with other microbes provide a better approach to plant growth and development. So far, several studies have been conducted with microbial consortia in plant growth and productivity. For instance, Maiyappan et al. [114] studied the bio-formulations of a consortium consisting of bacterial genera *Streptomyces* spp., *Bacillus* spp., *Frateria* spp. and *Azotobacter* spp. was made as a wettable powder and found to be beneficial in black gram. The bioformulation consortia of *Burkholderia* sp. and three other growth-promoting bacteria were also used with carrier materials such as sawdust, sugarcane bagasse, rice husk, cocoa peat, charcoal, wheat bran, paneer, and rock phosphate. This study confirmed a growth enhancement in pigeon pea plants [115]. In addition, other practices such as co-inoculation of rhizobia with mycorrhiza showed better results in leguminous plants. Therefore, the dual inoculation of rhizobia and mycorrhiza not only increases the nutritional status of leguminous plants but also improves the stress tolerance in soybean [116], lucerne [117], chickpea [118], pigeon pea [119], and broad bean [120]. Other studies also suggested that the co-application of nodule-forming and phosphate-solubilizing bacteria stimulate legume growth [121]. However, as a consortium, microalgae, cyanobacteria, and *Azotobacter* can be applied as biofertilizers and

bio-stimulators in various crops [122]. In addition, growth-promoting *Bacillus* strains as a consortium of vegetative cells or endospores positively impacted seed germination and promoted oat growth followed by colonization of the root and rhizosphere of plants [123].

Microorganisms present in soil are the active engineers of soil. They make suitable environmental conditions for the growth of plants through the production of necessary growth regulators and nutrient availability. Natural microbial populations also played diverse functional roles in adhering and desorbing inorganic nutrients to physical surfaces and degrading organic residues to make them part of the soil [124,125]. The cumulative role of plants and microbe attributes is essentially the soil fitness for farming and agriculture [126]. Applications of rhizosphere bacteria have also increased soil fertility and encouraged plant growth in a sustainable manner [127]. However, improvement in plant performance is a complex phenomenon that involves interaction with selected microbes or microbial consortiums. Likewise, diverse communities of soil fungi have been detected, which affect soil formation and stabilization at the macro/micro aggregate levels via different mechanisms such as physical, biochemical, and biological processes [128,129]. Soil health is defined by its functionality and ecological equilibrium which relies on various physical properties, i.e., soil moisture, porosity, texture, and chemical factors, i.e., soil nutrients, organic matter, carbon (C), and nitrogen (N), and biological factors, i.e., soil respiration, microbial biomass, and diversity [130]. In recent years, the beneficial role of plant growth-promoting bacterial strains has been explored in plants leading to the commercialization of microbial inoculants [131,132]. In some cases, different strain mixtures of the same species can also be considered consortia and exhibit improved activities. Bacterial consortia have increased beneficial plant traits compared to a single strain because of diverse plant growth promotion and biocontrol mechanisms [133]. A bacterial consortium is a feasible approach for improving the uptake of nutrients in crops [134]. In addition, some bacterial consortia can also take part in nitrogen fixation, the transformation of unavailable nutrients, and the production of plant hormones and chelate iron, which plays a crucial role in maintaining soil quality and health [135].

Microbial communities in the rhizosphere significantly interact with plants for sustainable crop production. These microbial communities function as beneficial aspects of the soil-plant microbiome to create a sustained food source and to maintain soil and plant health [136]. The beneficial rhizosphere organisms, such as mycorrhizal fungi, nitrogen-fixing bacteria, plant growth-promoting rhizobacteria (PGPR), biocontrol organisms, mycoparasite fungi, and protozoa, have been extensively investigated concerning plant health [137]. However, microbial communities connected to the roots and rhizosphere are the main factors influencing a positive impact on the root microbiome. Legumes can be used to enhance the native diazotrophic bacteria, substrates, or non-microbial bio-stimulants in the root microbiome. Alternatively, inoculating microbial strains into an already existing microbial community to change the structure of those communities could also be used to accomplish such objectives [138]. In addition, plants release various molecules from roots into the rhizosphere to support microbial activity or attract soil microbial diversity through root exudation. The root's exudate mostly consists of primary (amino acids, organic acids, and sugars) and secondary metabolites (glucosinolates, terpenes, and flavonoids). They not only serve as a source of energy for microbial growth but also change microbial communities by acting as signaling molecules [139]. The exudations also permit the plant to recruit microbial communities in the rhizosphere. In relation to synthetic microbial consortia (SMC), they could potentially reshape the structure and function of the plant microbiome. The synthetic fungal and bacterial consortia can build novel microbial communities [140–142]. Furthermore, synthetic communities (SynCom) induced the enrichment of bacteria from the phyla Firmicutes, Actinobacteria, and Cyanobacteria in the rhizosphere. The relative abundance of fungi from the phyla Chytridiomycota and Basidiomycota significantly increased in the SynCom treatments through a shift in the fungal communities [17]. Table 1 lists the beneficial effects of microbial players in the rhizosphere such as plant-growth-promoting bacteria (PGPB) and fungi on plant growth, soil fertility, and soil microbiome.

Table 1. Influence of synthetic consortium on crop yield improvement, soil fertility, and soil microbiome.

Synthetic Consortium/ Microorganisms	Test Plant	Impact on Plant Growth/Yield	Effects on Soil Fertility	Soil Microbiological Activity/ Soil Microbiome	Reference
<i>Bacillus licheniformis</i> , <i>B. subtilis</i> , <i>B. polymyxa</i> , <i>B. megaterium</i> , <i>B. macerans</i> , <i>P. putida</i> , <i>P. fluorescens</i> , <i>S. cerevisiae</i> , <i>N. orallina</i> , <i>T. viride</i> with Biosolve (humic acid substance)	Blueberry	It increased the shoot and dry weights of plants	It improved the nitrogen and potassium uptake of plants as well as nitrate content in the soil	It changed the composition of the rhizobacterial community in the soil	[143]
<i>B. thuringiensis</i> -1312 (BT1) <i>B. thuringiensis</i> -1310 (BT2), <i>B. licheniformis</i> (BL) as consortium of vegetative cells and endospores	Oat	It had positive effects on seed germination and enhanced the total dry biomass of plants	-	It colonized plants' rhizosphere without modifying the overall structure of microbial communities	[123]
SynCom candidates, <i>Arthrobacter</i> sp., <i>Enterobacter</i> sp., <i>Brevibacterium</i> sp., <i>Plantibacter</i> sp.	Cotton	It increased the germination, plant height, shoot biomass as well as the number of flowers and yield	It enhanced nitrate content and soil nutrient availability by increasing soil fertility	It triggered the enrichment of bacterial members of the phyla Firmicutes, Actinobacteria, and Cyanobacteria in the rhizosphere. However, a shift in fungal communities was observed with the increase in the relative abundance of Basidiomycota and Chytridiomycota	[17]
<i>Azotobacter</i> , potassium mobilizing bacteria, zinc solubilizing bacteria, phosphorus solubilizing bacteria, inorganic fertilizers	Wheat	It improved plant growth and increased chlorophyll content was noticed in biofertilizer plus RDF treatments. However, the yield was higher in biofertilizer consortia 2 with RDF	Physical and chemical properties were above critical limits	-	[144]
<i>P. fluorescens</i> mvp1-4, <i>P. fluorescens</i> 1m1-96, <i>P. fluorescens</i> Q2-87; <i>P. fluorescens</i> Phl1c2, <i>P. protegens</i> Pf-5, <i>P. protegens</i> CHA0, <i>P. kilonensis</i> F113, <i>P. brassicacearum</i> Q8r1-96	Tomato	It enhanced plant growth	-	It produced changes in the resident community diversity and composition and an increase in the relative abundance of initially rare taxa. However, the beneficial role of microbial consortium can be indirect on diversity and composition.	[145]
<i>S. rhizophila</i> , <i>R. sphaeroides</i> , <i>B. amyloliquefaciens</i>	Oilseed rape	The use of microbes significantly increased the total N content in plants	The application of microbes-maintained soil fertility	It selectively enhanced the growth of <i>Pseudomonadaceae</i> and <i>Flavobacteriaceae</i> as well as the recruitment of diazotrophic rhizobacteria such as members of <i>Cyanobacteria</i> and <i>Actinobacteria</i> in the rhizosphere	[146]
<i>B. amyloliquefaciens</i> , <i>B. pumilus</i> , <i>B. circulans</i>	Golden kiwi	The application of microbes improved kiwifruit growth	The complex bacterial inoculant was able to increase the availability of N, P, and K contents in soil	-	[147]

Table 1. Cont.

Synthetic Consortium/ Microorganisms	Test Plant	Impact on Plant Growth/Yield	Effects on Soil Fertility	Soil Microbiological Activity/ Soil Microbiome	Reference
<i>Enterobacter</i> sp., <i>B. megaterium</i> , <i>B. thuringiensis</i> , <i>Bacillus</i> sp.	French lavender	The combined use with sugar beet residue was the most effective in increasing shoot and root dry biomass	It improved the total N content in the soil	It increased the microbiological and biochemical properties	[148]
<i>Anabaena torulosa</i> used as a matrix for agriculturally useful bacteria (<i>Rhizobium</i> , <i>Azotobacter</i> , <i>Pseudomonas</i> , <i>Serratia</i>)	Wheat	It enhanced plant growth with an increase and the nutrient uptake of wheat	Soil fertility was improved	-	[149]
<i>T. viride</i> – <i>Bradyrhizobium</i> , <i>T. viride</i> – <i>Azotobacter</i> , <i>T. viride</i> – <i>Bradyrhizobium</i> , <i>Anabaena</i> – <i>T. viride</i>	Mungbean and soybean	The treatment enhanced the fresh and dry weights of plants	It exhibited a high dehydrogenase activity in the soil and nitrogen fixation	The use of microbial treatments enhanced microbial activity in the rhizosphere	[150]
<i>B. cereus</i> BT23, <i>Lysobacter capsici</i> ZST1-2, <i>L. antibioticus</i> 13-6	Chinese cabbage	The use of microbes improved plant yield	It decreased soil acidity	The presence of Bacteroidetes and Proteobacteria was relatively more abundant in rhizosphere and Firmicutes as unique phyla	[151]
Microbial consortia product (MCP) (EuroChem Agro GmbH, Mannheim, Germany)	Maize	The plant growth was improved and MCP inoculation stimulated root length development	C, N, and P-turnover in the rhizosphere were slightly affected by MCP inoculation, as deduced from extracellular soil enzymes activities	It increased the abundance of bacteria in the rhizosphere and the auxin production capacity of rhizosphere bacteria	[152]
<i>R. irregularis</i> , <i>P. jessenii</i> , <i>P. synxantha</i>	Wheat	This application improved grain yield in wheat plants	It enhanced the dehydrogenase and alkaline phosphatase activities in the soil	Improvement in the PGPR colonization and soil microbiological properties were noted	[153]

B. subtilis: *Bacillus subtilis*; *B. polymyxa*: *Bacillus polymyxa*; *B. megaterium*: *Bacillus megaterium*; *B. macerans*: *Bacillus macerans*; *P. putida*: *Pseudomonas putida*; *P. fluorescens*: *Pseudomonas fluorescens*; *S. cerevisiae*: *Saccharomyces cerevisiae*; *N. orallina*: *Nocardia orallina*; *T. viride*: *Trichoderma viride*; *B. thuringiensis*: *Bacillus thuringiensis*; *B. licheniformis*: *Bacillus licheniformis*; *P. protegens*: *Pseudomonas protegens*; *P. kilnensis*: *Pseudomonas kilnensis*; *P. brassicacearum*: *Pseudomonas brassicacearum*; *S. rhizophila*: *Stenotrophomonas rhizophila*; *R. sphaeroides*: *Rhodobacter sphaeroides*; *B. amyloliquefaciens*: *Bacillus amyloliquefaciens*; *B. pumilus*: *Bacillus pumilus*; *B. circulans*: *Bacillus circulans*; *B. cereus*: *Bacillus cereus*; *L. antibioticus*: *Lysobacter antibioticus*; *R. irregularis*: *Rhizophagus irregularis*; *P. jessenii*: *Pseudomonas jessenii*; *P. synxantha*: *Pseudomonas synxantha*.

7. Role of Synthetic Consortium/Bio-formulation in Plant Disease Management

The diseases in crop plants caused by the attacks of pathogenic microorganisms (bacteria, fungi, nematodes, oomycetes, and viruses) represent a major constraint for crop production in all agricultural and horticultural systems. They are primarily microscopic organisms and drive their nutrition by growing in or on the host plant. Plant diseases have caused severe economic losses to humans in several ways. The estimated yield losses caused by plant pathogens are up to 16% worldwide [154]. In previous years, disease management relied mainly on the indiscriminate use of chemical-based pesticides including fungicides, bactericides, and insecticides that are toxic to fungal, bacterial pathogens, and insects or insect vectors, respectively [155]. However, the negative impact of these chemical inputs is highly detrimental to the environment, human health, and animals [156]. Therefore, these adverse effects on the agricultural ecosystem may be overcome by developing more promising and sustainable alternatives for plant disease management. In this regard, microbial biocontrol agents or formulations, usually bacteria and fungi, may be used to prevent infections caused by plant pathogens [157].

The application of beneficial microorganisms in agriculture for the biocontrol of plant diseases caused by pests and pathogens has emerged as a potential alternative to chemical-based pesticides [158,159]. In general, microorganisms are commonly used as biocontrol agents for plant protection that rely on the use of individual microorganisms. On the other hand, microbial consortia are commonly referred to as a wide range of beneficial organisms that can act together in a community [160]. The potentiality of microbial consortia is determined by the selection of compatible beneficial microorganisms, which include fungi and bacteria, for the development of stable and versatile biocontrol products aiming for crop protection against a wide range of diseases [161]. The application of consortia is a feasible approach for managing plant pests and pathogenic infections in crops [162]. On the other hand, microbial bio-formulations are defined as any biologically active substances derived from microbial biomass or products consisting of microorganisms and their products. These bio-stimulants could be used as a tool by involving living and non-living products consisting of rhizosphere microbes such as PGPR and beneficial fungi. These bio-formulations could be used against plant pathogens as a suppressive agent in a sustainable manner [163].

The most common microbial species employed in microbial formulations, including genera, belong to bacteria, i.e., *Rhizobium*, *Azotobacter*, *Bacillus*, and *Pseudomonas*, and abundantly used fungal genera such as *Trichoderma* species. However, growth-promoting bacterial and fungal genera can also release metabolites with antibiotic and antifungal activities. The metabolites secreted from bacteria and fungi have been reported to have anti-phytopathogenic activities. Beneficial organisms have also become more popular with biocontrol activity towards soil-borne pathogens in a sustainable way for protecting plants. The significant limiting barriers of biocontrol microbes in disease-suppressive roles are insufficient host colonization and growth inhibition of soil-borne pathogens due to abiotic and biotic factors acting in complex rhizosphere conditions [109,164,165]. The biocontrol consortia with two or more strains (multi-strain biological control agents, MSBCAs) are combined to increase the efficiency and stability of disease suppression in plants [109,164,166,167].

The microbial consortia with multi-strain organisms have been successfully employed to control soil-borne diseases of valuable crops caused by fungi, bacteria, and nematodes. Various microbial combinations of consortia are possible, i.e., fungus to bacterium, fungus to fungus, and bacterium to bacterium to have a bio-control activity. Multi-strain bio-control agents also have the diverse mode of action for disease control, i.e., resource competition and niches [168–170], production of antimicrobials [171,172], induction of systemic resistance [109,173] in comparison with single strain bio-agents.

The microbial consortium consisting of *B. amyloliquefaciens* (ACCC1111060) and *Trichoderma asperellum* (*T. asperellum*) (GDFS1009) was studied on *Botrytis cinerea* (*B. cinerea*) (gray mold disease); it was found to be effective against infection as compared to single strains organisms [174]. Similarly, *Trichoderma virens* (*T. virens*) (GI006) was applied with

Bacillus velezensis (*B. velezensis*) (Bs006), which boosted the efficiency of *Fusarium wilt* in Cape gooseberry [175]. However, *Flavobacterium* sp. 98 and *Chitonophaga* sp. 94 as bacterial consortia have conferred more consistent protection against root-rot infection in sugar beet caused by *R. solani* than members of the individual community [27]. Additionally, a bacterial strain combination of *B. subtilis* S2BC-1 and GIBC-Jamog showed higher antifungal activity against the pathogen that causes vascular wilt, *Fusarium oxysporum* (*F. oxysporum*) *F. sp. lycopersici* in tomato than each strain [176]. Similarly, in vitro testing of *P. fluorescens* T5 against *R. solani* revealed no inhibition. However, it significantly inhibited the growth of *R. solani* when combined with four bacterial strains that were not antagonistic and had been isolated from the *Tamarindus* rhizosphere [177]. *Trichoderma* and *Azotobacter* were described by Woo and Pepe [167] as anchoring microorganisms for developing their respective consortia for enhancing plant health and reducing stress situations.

Bacteria with low abundance also played a crucial role in artificial or synthetic communities, and among them, only some bacterial taxa enriched in diseased roots were associated with disease resistance [178]. A consortium of biocontrol agents (BCAs), *Pseudomonas aeruginosa* (*P. aeruginosa*) DRB1, and *Trichoderma harzianum* (*T. harzianum*) CBF2 were combined to create liquid formulations, talc powder, and pesta granules and alginate beads. These formulations with microbial consortium are a promising way to enhance growth and induce significant biochemical changes in bananas leading to the suppression of Foc-TR4 [179]. Microbial inoculants consisting of *Azospirillum lipoferum* (*A. lipoferum*), *B. megaterium*, *Bacillus sporothermodurans* (*B. sporothermodurans*) as well as biocontrol agents *T. viride* and *P. fluorescens* performed better than individually in terms of plant growth promotion and disease management of ginger [180]. However, adding chitin or its derivatives increased the *B. subtilis* multiplication and its fungicidal activity to control *Fusarium wilt* [181]. Similarly, mixing chitin and dry olive waste with alginate encapsulates *Penicillium janthinellum* (*P. janthinellum*) [182]. This three-component formulation could increase phosphate-solubilizing fungal activity, while the alginate-chitin formulation displays a biocontrol potential in suppressing the soil-borne pathogen, *F. oxysporum*. Table 2 lists synthetic consortia or bio-formulations that act through various mechanisms in managing plant diseases and pathogens.

Table 2. Effects of synthetic consortium/bio-formulations in plant disease management.

Microbial Consortium/Bio-Formulations	Disease	Pathogen	Mode or Mechanism of Action	Reference
<i>Bacillus megaterium</i> -KAU-PSB, <i>B. sporothermodurans</i> -KAU-KSB, <i>A. lipoferum</i> -KAU-AZO and Bioagents <i>T. viride</i> -KAU-TV and <i>P. fluorescens</i> -KAU-PF	Rhizome rot and leaf blight	<i>R. solani</i>	It reduced the rot and blight incidence in ginger	[180]
<i>Enterobacter amnigenus</i> -A167, <i>Serratia plymuthica</i> -A294, <i>S. rubidaea</i> -H440, <i>S. rubidaea</i> -H469, <i>Rahnella aquatilis</i> -H145	Soft rot disease	<i>Dickeya</i> spp. and <i>Pectobacterium</i> spp.	Potato disease suppression occurred by induction of biosurfactants, siderophores, and antibiotic compounds	[183]
<i>T. harzianum</i> -CBF2, <i>P. aeruginosa</i> -DRB1	Wilt disease	<i>F. oxysporum</i> f.sp. <i>cubense</i>	It induced the production of chitinase and 2,4-diacetylphloroglucinol in banana	[184]
<i>T. harzianum</i> -TNHU27, <i>B. subtilis</i> -BHHU100, <i>P. aeruginosa</i> -PJHU15	White rot	<i>Sclerotinia sclerotiorum</i>	It enhanced oxygen species with induction of systemic resistance in disease management of pea	[185]
Formulations of <i>T. harzianum</i> -CBF2 and <i>P. aeruginosa</i> -DRB1	Wilt disease	<i>F. oxysporum</i> F. sp. <i>cubense</i> (Foc-TR4)	Applied formulations increased the defense response in the host through phenolic and proline contents improvements which in turn reduced root damage in banana	[179]
Bacterial community <i>Rhizobium</i> sp., <i>Stenotrophomonas</i> sp., <i>Advenella</i> sp. and <i>Ochrobactrum</i> sp.	Root rot	<i>F. oxysporum</i>	Plants were protected through the synergistic response of highly abundant bacteria with the inhibition of fungal growth. Less abundant bacteria-induced systemic resistance in <i>Astragalus mongholicus</i>	[178]
Mixture of <i>B. cereus</i> , <i>B. firmus</i> , <i>P. aeruginosa</i>	Bacterial leaf blight	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	The mixture showed a good ability to reduce bacterial blight infection in rice	[186]
SynCom1 (<i>P. azotoformans</i> -F30A, <i>T. harzianum</i> -T22, <i>B. amyloliquefaciens</i> -CECT 8238), SynCom2 (<i>P. azotoformans</i> -F30A, <i>B. amyloliquefaciens</i> CECT 8238 and CECT 8237, <i>T. harzianum</i> -22 and ESALQ1306, <i>Pseudomonas chlororaphis</i> -MA 342)	Root and foliar pathogen	<i>F. oxysporum</i> and <i>B. cinerea</i>	Both consortia controlled the pathogens effectively under any of the application schemes through induced systemic resistance and direct antagonism in tomato	[161]
<i>B. firmus</i> -E65 C32b, <i>B. cereus</i> II.14, <i>P. aeruginosa</i> , <i>S. marcescens</i> -E31	Rice blast, sheath, and bacterial leaf blight	<i>Pyricularia oryzae</i> , <i>R. solani</i> , and <i>X. oryzae</i> pv <i>oryzae</i>	Formulations were effective towards leaf and sheath blight while less effect was observed on rice neck blast disease	[187]

Table 2. Cont.

Microbial Consortium/Bio-Formulations	Disease	Pathogen	Mode or Mechanism of Action	Reference
<i>B. subtilis</i> -SM21, <i>B. cereus</i> -AR156, <i>Serratia</i> sp.-XY21	Phytophthora blight	<i>Phytophthora capsici</i>	Alternations were observed in the bacterial community of soil in sweet pepper plants	[188]
<i>B. cereus</i> -MBAA2, <i>B. amyloliquefaciens</i> -MBAA3, <i>P. aeruginosa</i> -MBAA1	Charcoal and stem rot	<i>Macrophomina phaseolina</i> and <i>S. sclerotiorum</i>	It induced the production of siderophore, ammonia and beta-1,3 glucanase, cellulose, and chitinase enzymes in soybean	[171]
<i>B. subtilis</i> -SM21, <i>B. cereus</i> -AR156, <i>Serratia</i> sp.-XY21	Wilt disease	<i>Verticillium dahliae</i>	It induced a systematic resistance and secreted antifungal metabolites in cotton plants	[189]
<i>P. aeruginosa</i> -LV strain compounds from cell-free supernatant of a bacterial culture. The fraction (F4A) consisted of two main compounds (antibiotic and phenazine-PCN)	Stem rot	<i>Pectobacterium carotovorum</i> subsp. <i>Carotovorum</i>	Elicit systemic acquired resistance (SAR) in tomato	[190]
<i>B. velezensis</i> AP136, <i>B. mojavensis</i> AP209, <i>L. macrolides</i> AP282, <i>B. velezensis</i> AP305	Black rot	<i>X. campestris</i> pv. <i>Campestris</i>	PGPR strain mixtures had the potential to elicit induced systemic resistance challenged with black rot pathogen in cabbage plants	[191]
<i>Pseudomonas</i> sp. (PF5, CHA0, Q8R1-96, Q2-87, MVP1-4, 1M1-96, Phl1C227, F113)	Bacterial wilt	<i>Ralstonia solanacearum</i>	It resulted in a competition of resources among bacteria and caused interference with wilt pathogen in tomato	[170]
Bioformulations of <i>P. fluorescens</i> and <i>B. coagulans</i>	Seedling damping-off disease	<i>R. solani</i>	A reduction in sugar beet mortality disease was observed	[192]
<i>B. cereus</i> -BT-23, <i>Lysobacter antibioticus</i> -13-6, <i>L. capsici</i> -ZST1-2	Clubroot disease	<i>Plasmodiophora brassicae</i>	Microbial consortia suppressed the disease incidence by recovering the imbalance in the indigenous microbial community composition	[151]
<i>P. fluorescens</i> Aur6, <i>Chryseobacterium balustinum</i> Aur9	Rice blast	<i>Pyricularia oryzae</i>	The disease incidence was reduced by the induction of systemic resistance in rice	[193]
<i>P. aeruginosa</i> (PHU094), <i>T. harzianum</i> (THU0816), <i>Rhizobium</i> sp. (RL091)	Collar rot	<i>Sclerotium rolfsii</i>	A disease suppression through antioxidant mechanisms was followed by the activation of phenylpropanoid pathway (PPP) and deposition of lignin in chickpea	[194]
Mixture of <i>Azotobacter chroococcum</i> , <i>B. megaterium</i> , <i>P. fluorescens</i> , <i>B. subtilis</i> , <i>T. harzianum</i>	Wilt	<i>Pythium</i> sp. and <i>Fusarium</i> sp.	It showed growth-promoting and disease-suppressing abilities in cabbage	[195]

Table 2. Cont.

Microbial Consortium/Bio-Formulations	Disease	Pathogen	Mode or Mechanism of Action	Reference
<i>Pantoea vagans</i> -C9-1, <i>P. fluorescens</i> -A506	Fire blight	<i>E. amylovora</i>	Compatible strain mixtures had greater biological activity suppressing the blight disease in the pear	[107]
<i>Bacillus</i> sp., <i>B. licheniformis</i> , <i>S. fradiae</i> , <i>P. aeruginosa</i>	Sunflower Necrosis Virus Disease (SNVD)	Sunflower Necrosis Virus (SNV)	The reductions in virus disease symptoms were associated with a concomitant increase in plant growth and ISR enzymes in sunflower	[196]
<i>Pseudomonas</i> community	Bacterial wilt	<i>R. solanacearum</i>	The density of pathogens in the rhizosphere was reduced along with a reduction in the disease incidence because of resource competition and interference with the pathogen in tomato plants	[170]
Neem extracts and chitin with <i>P. fluorescens</i> (Pf1) and <i>B. subtilis</i>	Dieback and fruit rot	<i>Colletotrichum capsica</i>	It reduced the fruit rot incidence by the induction of chitinase, peroxidase (POX), β -1,3 glucanase, phenylalanine ammonia-lyase (PAL), polyphenol oxidase (PPO), and accumulation of phenols in chili pepper	[197]
Isolates of <i>Bacillus</i> spp., <i>Pseudomonas</i> spp., <i>Streptomyces</i> spp., <i>Trichoderma</i> spp.	Wilt disease	<i>F. oxysporum</i> F. sp. <i>cubense</i> (TR4)	Mixtures of antagonists (synthetic microbial community, SynCom) might provide effective biocontrol against fusarium wilt of banana	[198]

B. sporothermodurans: *Bacillus sporothermodurans*; *A. lipoferum*: *Azospirillum lipoferum*; *T. viride*: *Trichoderma viride*; *P. fluorescens*: *Pseudomonas fluorescens*; *S. rubidaea*: *Serratia rubidaea*; *T. harzianum*: *Trichoderma harzianum*; *P. aeruginosa*: *Pseudomonas aeruginosa*; *B. subtilis*: *Bacillus subtilis*; *B. cereus*: *Bacillus cereus*; *B. firmus*: *Bacillus firmus*; *P. azotoformans*: *Pseudomonas azotoformans*; *B. amyloliquefaciens*: *Bacillus amyloliquefaciens*; *S. marcescens*: *Serratia marcescens*; *B. velezensis*: *Bacillus velezensis*; *B. mojavensis*: *Bacillus mojavensis*; *L. macrolides*: *Lysinibacillus macrolides*; *B. coagulans*: *Bacillus coagulans*; *S. fradiae*: *Streptomyces fradiae*; *R. solani*: *Rhizoctonia solani*; *F. oxysporum*: *Fusarium oxysporum*; *B. cinerea*: *Botrytis cinerea*; *X. oryzae*: *Xanthomonas oryzae*; *S. sclerotiorum*: *Sclerotinia sclerotiorum*; *X. campestris*: *Xanthomonas campestris*; *E. amylovora*: *Erwinia amylovora*; *R. solanacearum*: *Ralstonia solanacearum*.

8. Conclusions

The application of bacterial consortia improves microorganisms' ability to breakdown organic and inorganic contaminants. Microbial metabolism reduces the content of soil pollutants thus providing a long-term solution. These consortia have multiple functions such as soil health improvement, disease prevention, and crop productivity improvement. The addition of microbial consortiums to the soil would have a positive impact on environmental sustainability, contributing to an ecologically friendly restoration of contaminated land and opening a new path for sustainable development. However, microbial consortia are rarely used in agricultural commercial processes. Furthermore, the identification of root exudates, signals, and key players in the rhizosphere microbiome will provide chemical and microbial markers to elucidate whether and how plants recruit and stimulate beneficial microorganisms. The hindrance to adopting microbial consortia might be due to insufficient baseline empirical data to model the risks and benefits of sustainable farming across multiple crop systems. Therefore, a better understanding of the molecular and biochemical pathways is needed to effectively benefit from the advantages of soil microbiomes and their host crops in agricultural development.

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