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Role of microbial diversity to influence the growth and environmental remediation capacity of bamboo: A review

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ABSTRACT

Soil microorganisms play crucial role in maintaining the global nutrient cycle. Soil health status and its nutrient pool rely upon soil microbial community structure and function. Majority of microbes are associated symbiotically with diverse plant and animal species to maintain the growth of plants as well as their own. Soil microorganisms are highly responsible to regulate the plant metabolism and signaling by producing various metabolic compounds, which facilitate growth of plant and also provides immunity against plant diseases. Bamboo is a taxonomic group of plants which is widely distributed in many tropical and subtropical regions. The rhizospheric microbial communities of the bamboo play significant role in the immobilization of various soil nutrients and also enhances the phytoremediation and environmental restoration capability of bamboo. In this regard, the present review critically spotted light on the plant microbial interactions with major emphasis on the bamboo plantation. The diversity of bacteria and fungi in bamboo cultivated forest and how bamboo cultivation influences the microbial community's dynamic of the soil are critically discussed in the present review. Furthermore, this review cover-up various advance tools and technologies deployed in characterization of bamboo rhizospheric microbial communities. Finally, this review comprehensively explored the phytoremediation and environmental management aspects of bamboo/bamboo biomass along with prospects for the future research.

1. Introduction

According to plant physiologist, soil is not only serving as an efficient source of nutrients to plants but also complex ecosystem which includes animals, bacteria, fungi and protists (Gothandapani et al., 2017; Müller et al., 2016; Zhao et al., 2016). Generally, three types of mechanisms are demonstrated, which relate, how microbes able to enhance growth of the plants, (i) Manipulation of plants hormonal signaling activity (Verbon and Liberman, 2016); (ii) Preventing the growth of pathogenic microbes (Park et al., 2015) and (iii) Stimulating the availability of soil-nutrients (Wagg et al., 2014). Jacoby et al. (2017) reviewed the mechanism, how soil microbes immobilized the bound forms of nutrients/elements and make it bioavailable to the plants. Microbes play a crucial role in biogeochemical processes of the soil, including decomposition of organic matter, mineralization of nutrients, enhancing soil aggregation, sequestration of heavy metals (HMs), biodegradation of organic contaminants, and suppressing the growth of the plant

pathogens (Sun et al., 2020; Cheng et al., 2016; Pant et al., 2016). There are many nutrients such as sulphur (S), phosphorus (P), nitrogen (N_2) etc. gets bound to organic molecules in natural ecosystem hence, bioavailable in minimum concentration for the plants. For accessing these nutrients, plants are totally depending on the activities of interacting soil microorganisms such as bacteria, fungi, archaea, viruses, protozoa etc. together called soil microbiome (Dubey et al., 2019; Jansson et al., 2019). These microbes possess diverse metabolic machineries to mineralize and immobilize the bounded nutrients (Jacoby et al., 2017).

Soil microbiome is the microbial community with their encoded functions, located in soil environment (Crecchio et al., 2018). Soil microbiome serves as a primary inoculum to the rhizospheric soil. Deployment of valuable microbes improves the quality and health of plant, helping in plant residues recycling with lesser environmental impacts. The genotypic and phenotypic differences in plants are also considered as important factor which support development of the

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microbiome to increase the bioavailability of nutrients and simultaneously prevents entry of the pathogens (Dubey et al., 2019). Soil quality also play important role in suppressing the crop disease, maintaining the health resulting, better growth and productivity of the crops (Gu et al., 2016; Xue et al., 2015). Soil microbiome is also served as an indicator of soil quality as it is highly sensitive towards small environmental changes imposed by an environmental stressor (Sharma et al., 2010). Higher species richness and microbial diversity leads to production of high redundancy at the functional level within the soil microbiome, permit rapid recovery from the stresses (Chaparro et al., 2012). The distributional and functional features of key soil microbial activities may have imperative effects on the aboveground plant's growth e.g., bamboo growth (Zhang et al., 2020a).

Bamboo has high dense foliage and fast-growing nature due to which, it is capable of maintaining the thick layer of litter (Mishra et al., 2014). This layer of litter controls microclimate in the soil moisture which is the most essential feature for restoration of contaminated lands (Singh et al., 2020c). According to Emamverdian et al. (2018a,b) phytoremediation is considered as one of the most novel method for the removal of contaminant, mainly HMs from the environment. There are various mechanisms such as rhizosphere bioremediation, phytostabilization, phytotransformation, phytoextraction and rhizofilteration via plants remediate the contaminated site (Prabha et al., 2021; Kumar et al., 2021b). In rhizosphere phytoremediation, plants stimulate the microbial activities and their enzymes via releasing the root exudates from rhizosphere, which also facilitated the fixation of organic carbon in soil (Prabha et al., 2021). The process of phytostabilization decreases the phytoavailability and mobility of contaminants and prevent its re-entry in the environment. Phytotransformation reduces the toxicity of contaminates by transforming it in to non or less toxic form. The process of contaminant absorption by plant and translocate them to different part is known as phytoextraction whereas, rhizofilteration is the process in which pollutants are filtered out by the plant root system. Bamboo species are usually preferred in phytoremediation as compared to other woody plants because of their high growth rate, better absorbability and facile cultivation (Bian et al., 2017, 2018; Were et al., 2017; Zhong et al., 2018) (Fig. 1) (Table 1).

The rhizosphere of the plants is the main place between the roots of plants and the soils which is colonized by diverse groups of living organisms such as rhizospheric and endophytic microbes which promote the plants growth (Pathan et al., 2020; Singh et al., 2020b) (Fig. 2). Some investigators established, the role of rhizosphere microbiome in the process of phytoremediation (Chaparro et al., 2012; Hou et al., 2019). In addition to this, root-associated microbes can enhance bioavailability of metals, provides tolerance towards metal accumulation, increase plant biomass, and promote photosynthesis (Luo et al., 2019). Although, researches come out recently which discussed the role of microbes in productivity of bamboo and vise-versa (Fig. 3), but still a comprehensive review is needed, which compile the existing knowledge.

Considering the above discussion, the focus of the present review is to provide a framework regarding the soil microbial diversity in bamboo forests and their role. A detailed discussion about the plant microbial interaction, change in microbial diversity in bamboo forest, their various influencing factors, advance characterization tools and technologies. Finally, this review comprehensively explored the phytoremediation and environmental management aspects of bamboo/ bamboo biomass along with prospects for the future research.

2. Functional classification of soil microbes and their role

Soil microbes serves as an essential and integral component of the ecosystem (Crecchio et al., 2018; Gothandapani et al., 2017). The complex interaction is observed between the several constituents of soil ecosystem comprising microbial biomass along with chemical contaminants of soil like radionuclides and HMs. In addition to soil properties, soil type, pH and salinity that considerably effects the soil microbial biomass with their activities and dynamic performance may be administered by the type and level of contaminants such as HMs, organic contaminants etc., (Bach et al., 2010;). However, certain microbes such as bacteria, fungi and protista can reduced the HMs and utilizes the organic fractions for their own metabolic products with the help of specific enzymes. Throughout the process the HMs could be transformed into the non-toxic or less toxic forms. The process of bio-precipitation and bio-sorption leads to reduction of the metal bioavailability and its mobility (Ghosh et al., 2018; Xu et al., 2019). Majority of the microorganism are symbiotically associated with plant and animal species to support the growth and development of the plants as well as their own (Mushtaq et al., 2017).

Based on various functional activities, microorganisms have been categorized in to decomposers, predators, ecosystem engineers, microregulators, litter transformers, and soil born pest (Cárenas et al.,



Fig. 1. Schematic representation of phytoremediation/extraction of heavy metal by bamboo plantation.

Table 1

Application of different bamboo species in phytoremediation of heavy metals.

Bamboo species	Type of experiment	Heavy metals and their respective concentration (mg g^{-1})	Observation	Reference
Indocalamus latifolius	Pot	$\begin{array}{l} Cu = 2000 \\ Pb = 2000 \\ Zn = 2000 \end{array}$	Enhanced lipid synthesis and hampered antioxidant enzyme production.	Emamverdian et al. (2018)
Phyllostachys praecox	Natural condition	Cd = 14.5 Cu = 195 Zn = 2980	Better plant growth, and exhibited typical fully expanded green leaves and shoot.	Bian et al. (2018)
Moso bamboo	Natural condition	$\begin{array}{l} Cd=11\\ Cu=99\\ Zn=3608 \end{array}$	Normal growth without any toxic symptoms.	Bian et al. (2017)
Moso bamboo	Pot	Cd = 120	Moso bamboo exhibited tolerant toward Cd concentration.	Li et al. (2016b)
Pleioblastus kongosanensis, Indocalamus latifolius, Sasa fortunei	Pot	Pb = 3000	Impairment symptoms appeared in <i>I. latifolius</i> after 40 days and in <i>P. kongosanensi</i> and <i>S. fortune</i> after 25 days.	Li and Gao (2016)
Moso bamboo	Both hydroponics and pot	Cu = 600	Non-significant difference appeared in the Moso bamboo leaves.	Chen et al. (2015)
Moso bamboo	Hydroponics	Pb = 400	Ultrastructural investigation exposed some interior cell damage, non- significant Pb toxicity signs appeared, plant disease such as asnecrosis and chlorosis appeared.	Liu et al. (2015)
Moso bamboo	Natural condition	Mn = 406 Cu = 28 Zn = 210 Pb = 286 Cd = 0.5 Cr = 58	Both the rhizosphere soil and plant shoots were polluted with terrifyingly levels of Pb.	Yan et al. (2015)
Moso bamboo	Hydroponics	Zn = 400	No substantial variation in root length, sharp reduction in fibrous roots number.	Liu et al. (2014)
Phyllostachys Auresulcata, Pleioblastus Chino	Hydroponics	Cu = 2000	The concentration of malondialdehyde amplified, while the biosynthesis of chlorophyll and the photosynthesis capacity declined.	Jiang et al. (2013)
Pleioblastus fortunei	Both hydroponics and pot	Pb = 3315	The concentration of mineral elements in <i>P. fortune</i> altered significantly, the variations in Na and K concentration was most noticeable, the leaves becomes yellowish.	Zhang et al. (2011)
Arundinaria fortunei, Sasa auricoma	Pot	Zn = 500 Cu = 400 Cd = 20 Pb = 500	A. fortunei was more tolerant to heavy metals than S. auricoma.	Wang et al. (2010)



Fig. 2. Schematic representation of different types of soil microbes residing in rhizosphere as well as endophytes.



Fig. 3. Numbers of publications (2010-2020) related to microbial diversity of bamboo forest.

2017). Soil microbes are also functionally classified into the major groups of macrofauna, mesofauna and soil microbial biome (combined groups of soil microorganism). Macrofauna are also called soil ecosystem engineers, having important role in transforming the soil properties. Mostly macrofauna serve as soil predators and litter decomposers (Abdu et al., 2017). Mesofauna can ingest organic matter along with other soil microorganisms like bacteria and fungi turns to enhance the soil ecosystem performance by varying the microbial population who mediated organic matter decomposition. Mesofauna facilitate dissemination of microorganisms, fungi, and their spores hence, they are termed as catalysts (Socarrás, 2013).

With reference to the positive effects of soil microbes on ecosystem health and soil characteristics, they have been utilized globally to enhance the growth of plants and their yield. The most favorable activities of these microbes include, production of diverse biological catalysts like enzymes and plant hormones, improvement of soil structure, mineralization of organic content of soil, interaction with others soil microorganisms (Liu et al., 2017b). According to, Marschner et al. (2011), there are various mechanism adopted by these microorganisms to enhance the solubility of soil micronutrients (a) Affecting the metabolism of plants and hence altering the root exudates either by symbiotically or by non-symbiotically (b) Affecting the solubility of soil nutrients and ultimately make it bio-available for the plants (Adesemoye, 2009) (Fig. 4). Various roles of microbes and their potential mechanisms involved in plant growth promotion have been comprehensively discussed in the following section.

3. Role of soil microbes in plant growth promotion

There is multiple evidence that plants have advanced strategies to coordinate with soil microbes for enhancing growth and productivity (Hassani et al., 2018). Microbes can benefit plants in various ways like synthesis and release of enzymes, phytohormones etc., to diminish exogenic and endogenic stresses of plants (Liu et al., 2019). The rhizosphere serves as a hotspot for plant-soil microbe and microbe-microbe interactions. The microbes with their interactions can mostly inhibits pathogen outgrowth and also enhance capacity of plants for disease resistance (Durán et al., 2018). Plant microbiota constitute different types of advantageous, pathogenic and neutral microorganisms. Association of microbial communities with their hosts have been shown to stimulate the growth of plant, uptake of nutrients and resistance towards pathogen (Liu et al., 2021; Trivedi et al., 2016; Backer et al., 2018). Soil disease suppressive property depends on multiple factors such as, abiotic and biotic condition, diversity of plant microbiome, genetic background of host as well as pathogen and population of pathogen (Liu et al., 2019; Nail et al., 2019). Plant microbiome can mobilize the nutrients that are not freely accessible to plants like iron and inorganic phosphate, via different processes i.e. through excretion, mineralization and solubilization (Trivedi et al., 2017, 2020). Under the low concentration of inorganic phosphate, plant depends on cooperation of microbial partners, which include arbuscular mycorrhizal fungi and their endophytes to fulfill the necessities of essential nutrients (Bodenhausen et al., 2019). These bacteria can not only enhance plant growth via the process of N₂-fixation but also induce the plants for the production of



Fig. 4. Role plant growth promoting rhizobacteria (PGPR) in growth and developments of the plant.



Fig. 5. Mechanism of plant growth promotion by microorganisms.

phytoharmones, improve the process of nutrient utilization, compete with pathogenic microbes for space, and nutrition etc., (Liu et al., 2017c). Plant growth promoting microbes (PGPMs) can encourage growth of plant by both direct and indirect mechanisms (Naik et al., 2019) (Fig. 5).

3.1. Direct mechanisms

Direct mechanisms of plant growth promotion are performed by diverse microbial communities such as, *actinomycetes*, bacteria, fungi and yeasts through various mechanisms like phytohormones secretion, N_2 -fixation, secretion of exopolysaccharides, solubilization of potassium and phosphate, production of siderophores and decomposition of organic matter etc. (Sahur et al., 2018; Singh et al., 2016). Generally, plant growth promoting microbes associated with the genera of *Bacillus*, *Clostridium, Penicillium, Pseudomonas, Rhizobium, and Trichoderma* have been reported to improve the productivity of crop by enhancing the vegetative growth, making nutrients availability to plants and photosynthesis (Park et al., 2019; Kotoky et al., 2019; Xu et al., 2019) (Table2).

The auxins are the organic compounds having low molecular weight and consist of an aromatic ring. In the groups of auxin compounds, Indole Acetic Acid (IAA) is applied frequently and play significant role in plant growth promotion (Bashri and Prasad, 2016). The production of auxin depends upon certain factors like type of plant, growth rate and sensitivity towards auxins (George et al., 2008). Gibberellins are the compounds contain a different set of phytoharmones that display a vital role in stimulating the development of plants such as seed germination, elongation of stem and development of leaf. The most common gibberellin phytohormone is gibberellic acid (GA) (Sponsel and Hedden, 2010) which stimulates calcium ions absorption along with other nutrients that might be efficiently reduce the oxidative damage of lipid membrane by controlling antioxidant metabolism (Siddiqui et al., 2008). Cytokinin are also a type of plant hormone responsible for division and differentiation of the plant cells (Gajdošová et al., 2011).

Plant Growth Promoting Rhizobacteria (PGPR) possessed ability to increase the availability of nutrients by fixing their supply for promoting plant growth. Plant utilizes N₂ from soil in the form of ammonia, nitrate which are highly important nutrients for the growth (Kumar, 2016). Some PGPR have an ability to solubilize phosphate resulting in released of numerous phosphate ions in the soil (Paredes and Lebeis, 2016). The

Table 2

Role o	of different	bacteria	and	fungi	in 1	plant	growth	promotion.
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Microorganism	Mode of action	Reference
Pseudomonas fluorescens	P. fluorescens SS101 play a vital role in enhancement of plant growth and	Park et al.
00101	systemic resistance towards the	(2010)
	pathogens.	
Serratia marcescens S2I7	S. marcescens S2I7 exhibited	Kotoky et al.
	resistant to heavy metals, it helps in	(2019)
	promoting the growth of Oryza	
	sativa in the soil contaminated with	
D :11	Cd.	
Bacillus aryabhattai	B. Aryabhattai has capability to get	Ghosh et al.
MCC3374	the process of bioremediation along	(2018)
	with promoting the increased plants	
	growth.	
Raoultella sp. X13	It can immobilize and accumulate	Xu et al.
	Cd ²⁺ , also helps in promoting plant	(2019)
	growth.	
Actinomycetes	Endophytic actinomycetes may	Lacava and de
	increases the growth of plants by	Sousa (2016)
	combination of mechanisms like	
	enzyme and growth hormone	
	production with nutrients	
Asperaillus fumigatus TS1	These isolates promote growth	Bilal et al
and Fusarium	activities consisting phosphate	(2018)
proliferatum BBL1	solubilisation siderophore activity	(2010)
protijoratani Draži	along with gibberline and indole	
	acetic acid production.	
Beauveria bassiana	B. bassiana enhance seed	Tall and
	germination.	Meyling
		(2018)

process of biological N₂-fixation can be carried out by either symbiotic or non-symbiotic interaction between plants and microbes. Major microbes involved in the process of symbiotic N₂-fixation are *Bradyrhizobium* sp., and *Rhizobium* sp., (Souza et al., 2015). *Azospirillum* is known as a free-living N₂-fixer with an ability to enhance the growth and productivity of non-leguminous plants (Lin et al., 2015a, 2015b). Siderophores are small organic molecules that stimulate iron uptake capability of plants in presences of other metals like cadmium (Cd) and nickel (Ni). Exopolysaccharides (EPSs) are biodegradable polymers having diverse sugar moleties (Kumar et al., 2018; Thakur et al., 2018). EPSs are synthesized by variety of algae, bacteria and plants (Sanalibaba and Çakmak, 2016; Kumar et al., 2019) and play significant role in maintaining water potential, provide an obligate contact between rhizobacteria and plant roots, and provide tolerance to cope up with adverse environmental conditions (Kumar et al., 2018; Thakur et al., 2018).

3.2. Indirect mechanism

Indirect mechanism of plant growth promotion involves the process, where PGPR inhibits the toxic effects of phytopathogens hence providing a healthy environment. This process helps to grow the plants under various environmental stress condition. Indirect action includes the production of biocontrol agents that inactivate or kill plant pathogens thereby providing a healthy crop environment (Jha, 2015). PGPR produces hydrogen cyanide (HCN) which may check the growth of plant pathogens and simultaneously regulate bioavailability of phosphate (Rijavec and Lapanje, 2016). Additionally, soil microbes are either interact antagonistically or synergistically based on the soil conditions. Amongst the most beneficial interaction, mycorrhiza fungi and soil bacteria interaction are considered as most advantageous one (Chung and Park, 2014; Li et al., 2020). Activities of microbes inside the soil aggregates can stimulate distribution of oxygen (O₂), generating habitats for anaerobes that catalyzes different processes such as denitrification and production of methane. The functional and taxonomic diversity of soil microorganisms can influence the plant root growth, by modifying the rhizospheric soil chemistry via carbon exudation and nutrient absorption (Aislabie et al., 2013). Thiobacillus sp. decrease the soil pH up to 2 which impede the activity of pH-sensitive microbes. The O₂ generated by algae partner in lichen association avert the anaerobic microorganism from colonizing in plant parts (Naik et al., 2019).

Production of antibiotic by various groups of microorganisms are also considered as indirect mechanisms to prevent the growth of plant pathogens. Bacillus, Pseudomonas and Streptomyces bacterial sp., in soil release antibacterial and antifungal antibiotics that avert the growth of harmful microbes (Naik et al., 2019). Various antibiotics along with their specificity and effects have been widely investigated in depth, and few antibiotic producers as bio controller have been commercialized. But there is a problem with relying lavishly on antibiotic-producer as bio controller that may trigger the development of antibiotic resistance in pathogenic microorganism (Glick, 2012). To avoid this, few investigators have applied biocontrol microbes that produced HCN along with antibiotics. Although, HCN may not have considerable biocontrol potency independently, but it performs synergistically impact with bacterial produced antibiotics (Olanrewaju et al., 2017). Few bacterial stains produced enzymes such as chitinases, cellulases, $\beta\beta$ -1,3 glucanases, proteases, and lipases that effectively acts against the certain groups of pathogenic fungi via their lytic activities (Glick, 2012). PGPB that produced these lytic enzymes have been applied as bio controller against various fungal pathogens such as Botrytis cinerea, Sclerotium rolfsii, Fusarium oxysporum, Phytophthora sp., Rhizoctonia solani, and Pythium ultimum (Glick, 2012).

As discussed above the important of microbes and their role in enhancement of the plant growth and productivities. However, there are certain microbes which adversely affect the growth and productivity of the plants especially pathogenic fungi (Mori et al., 2019). Top ten plant pathogenic fungi include Blumaria graminis, Botrytis cinerea, Colletotrichum sp., Fusarium graminearum, F. oxysporum, Magnaporthe oryzae, Melampsora lini, Mycosphaerella graminicola, and Puccinia sp., Ustilago maydis (Kaur, 2019). Phytopathogenic fungi differentiate into a formation of dome shaped appressorium cell to penetrate their host directly through rupturing the cuticle layer. These fungal species are known to drive the plant nutrients and have an adverse impact on plant growth (Doehlemann et al., 2017). Fungal contamination possibly affects the quality of crops directly as well as indirectly. Direct effect includes damaging the quality of grains might be due to the excessive growth throughout the kernel along with ramification of fungal sp. Indirect

impact is associated with contamination which again leads to reduction in yield (Amza, 2018). There have been several reports, which comprehensively discussed the significant impacts of pathogenic fungi on the bamboo plantation. Blight disease in bamboo sp. was primarily reported in Bangladesh where maximum loss in the bamboo productivity was observed (Rahman, 1978). Later on, Jamaluddin et al. (1992), discussed the percent disease incidence (PDI) and symptomology of blight on B. nutans in shore line of Orissa, India. The existence of this fungal disease has been also identified in Kerala, India (Mohanan, 1994). Bambusabalcooa is vulnerable to blight disease, which is observed as the utmost impactful disease (Gogoi et al., 2013). Death of younger culms of B. tulda was identified in Dimapur district of Nagaland, India due to infection of F. semitectum(Gogoi et al., 2013). The groves of B. balcooa is also affected by blight disease, may be one of the foremost issues in falling the cultivation of bamboo in this region (Gogoi et al., 2015). More recently, Yang et al. (2019) reported first time bamboo blight caused by Arthrinium yunnanum on P. heteroclada in Sichuan, China. The above discussion concludes the direct and indirect beneficial as well as harmful impacts of the soil microbes on the plant growth and productivity.

4. Plant microbiome

The plethora of microbes associated with higher level of microorganisms is called as microbiome (Berg et al., 2016). Plant-microbe association is highly important to improve the physiology of plants and their survival capability (Bilal et al., 2020; Singh et al., 2020a). Nowadays, investigators have paid more attentiveness towards explicating the function and composition of soil and plant microbiomes. However, it is well-known, the plants growth is completely dependent on indigenous microbial diversity. Microorganisms live either endosphere (inside) or episphere (outside) of the plant organs. Majority of the plant associated microbes living in the soil environments belongs to fungi and bacteria (Bilal et al., 2020, 2018; Bulgarelli et al., 2012). Soil microbes are responsible for production of metabolic compounds that control the plant metabolism and signaling. Antibiotic compounds such as polymyxin, penicillin etc. are produced by microbes which enhance the utilization of organic matter (OM), increased leakage, and change the cell permeability (Harmsen and Jager, 1962). Microbial communities, widely associated with taxa known as keystone taxa. Individually or in groups these keystone taxa displayed significant impact on shaping the function and structure of microbiome (Dastogeer et al., 2020). Based on the occurrence of microbes in different parts of the plants, microbiome can classify as rhizosphere microbiome, phyllosphere microbiome, and endosphere microbiome.

4.1. Rhizosphere microbiome

Rhizosphere constitute 1-10 mm of the soil zone proximately adjoining the plant roots through mucilage, accumulation of root oozes, and plant dead cells (Hou et al., 2019). The term rhizosphere is most frequently used to illustrate the diverse root systems and physico-chemical properties of soil. It has been also described that the rhizosphere zone has a crucial importance for the health and development of the plants (Hauchhum and Tripathi, 2017). The rhizosphere microbiome is considered as a hot spot where plant-soil-microbe and microbe-microbe interactions take place (Liu et al., 2021). The plants microbes' interactions principally avert growth of pathogenic microbes and improve the plant disease resistance capacity of plants (Durán et al., 2018). A diverse range of microbes living in rhizosphere include algae, archaea, bacteria, fungi, viruses, protozoa, nematodes and oomycetes. Amongst the prokaryotic microbes, bacterial communities are dominated and mostly belongs to Actinobacteria, Acidobacteria, Bacteroidetes, Firmicutes, Proteobacteria and Planctomycetes (Bonkowski et al., 2009; Bulgarelli et al., 2012; Uroz et al., 2010). There are several investigations, which displayed significant changes in the composition of

Table 3

Role of different microbes with their mode of action on diverse bamboo species.

Bamboo species	Microorganism	Mode of action	Reference
Bambusa nutans, Bambusa arundinacea and Dendrocalamus hamiltonii	Bacteria and Fungi	Microbial carbon, nitrogen, phosphorus and soil organic matter was significantly enhanced <i>Bambusa nutans, Bambusa</i> <i>arundinacea</i> and <i>Dendrocalamus hamiltonii</i> growth. It conforms the restoration of abandoned soil nutrient of ecologically fragile hilly region in India	Arunachalam and Arunachalam (2002)
Dendrocalamus strictus (Roxb.) Nees	Azospirillum brasilense, Bacillus polymixa and Glomusaggregatum.	Different types of soil did not influence the response to the microbial inoculation. Application of fertilizer dramatically altered plant response to microbial inoculation resulting in optimum reaction to growth in all soil forms, in both fertilized and unfertilized environments	Muthukumar and Udaiyan (2006)
Phyllostachys edulis	Proteobacteria, Firmicutes and Bacillus	There will be an abundance of species diversity of cultural microbes in the root zones of moso bamboo plants and there are strong discrepancies between endophytic, rhizoplane and rhizospheric bacterial populations.	Han et al. (2009)
Phyllostachys edulis	Acidobacteria, Crenarchaeota and Actinobacteria	Significant amount of nitrogen supplementation increased Soil microbial biomass carbon and the relative abundances of microbial diversity. Intensive maintenance for more than two decades reduced soil pH, improved mineral resource abundance and aggregation.	Li et al. (2016a)
Phyllostachys edulis	Acidobacteria, Actinobacteria, Bacteroidetes and Proteobacteria	Significant change in composition of the soil bacterial population occurred after 15 years of management. After 15 years of management and lower the functional diversity of soil microbiomes when compared with amino acid and carbohydrate processing over 20 years, diversity indexes decreased.	Chen et al. (2019)
Bambusa balcooa Roxb, Bambusa nutans Wall. ex Munro, Bambusa vulgaris var. vittata, Bambusa vulgaris var. striata and Dendrocalamus asper Backer ex Heyne	Azotobacter species, Rhizobium species and actinomycetes	Supplementation of nitrogen fixing microbes such as Azotobacter species, Rhizobium species, actinomycetes along with farm yard manure and vesicular-arbuscular mycorrhizae significantly enhanced bamboo growth parameters like number leaves, number of culms, internodular distances and biomass production.	Singh et al. (2020)
Moso bamboo (Phyllostachys heterocycla f. pubescens)	Bacteria and Fungi	growth of phytopathogenic bacteria and finitotory effect against the growth of phytopathogenic bacteria and fungi and hence, can be used as a natural pesticide for the protection of plants Super-heated steam extract of bamboo culm (at 210 °C) significantly inhibited the growth of gram-negative bacteria (Pseudomonas syringae pv. actinidiae biovar 3 and Erwinia chrysanthemi) and three species of fungi (Botrytis cinerea, Glomerella cingulata, and Trichoderma harzianum)	Mori et al. (2019)
Leaves of different species of bamboo	Fungi	Bamboo leaf was observed to be a prominent source for managing the infestation caused by <i>Pyricularia grisea</i> mostly in production of rice.	Toan et al. (2018)
Bamboo leaf flavonoid	Fungi	Flavonoid extracted from bamboo leaf enhances the control of <i>Pichia caribbica</i> against the growth of <i>P. expansum</i> and accumulation of patulin in apples	Mahunu et al. (2018)

plants rhizosphere and qualities of soil due to microbial activities (Lundberg et al., 2012; Schlaeppi et al., 2014). Some studies have been established the role of microbiomes in phytoremediation of HMs (Chen et al., 2018; Hou et al., 2019), which displayed the important of microbial communities associated with plant rhizosphere.

4.2. Phyllosphere microbiome

Phyllosphere is considered as the plants aerial surface which includes leaves, stems, and flowers (Liu et al., 2019) and recognized as relatively nutrient poor in comparison to endosphere and rhizosphere. The phyllospheric environment is highly dynamic than the endospheric and the rhizospheric environment. The process of microbial colonization is subjected to seasonal and diurnal variations of moisture, temperature and radiation. Additionally, these environmental factors alter the physiological mechanisms of the plants and influences the microbiome composition. Both wind and rain, also influence the temporal alteration of the phyllosphere microbiome (Dastogeer et al., 2020). In the temperate regions phyllosphere is highly dominated with fungal sp., and shows great variation in microbial communities' structure in comparison to tropical areas (Finkel et al., 2011), probably due to different climatic conditions. Few soil microorganisms may firstly enter through the apoplast in xylem vessels root in endosphere and further move to phyllosphere, whereas few microorganisms can enter directly to the phyllosphere through air, water, and dispersion of the soil (Liu et al., 2019).

4.3. Endosphere microbiome

Some microorganisms like endophytes are responsible for the formation of endospheric microbiome by occupying and penetrating the internal plant tissues. The main colonizer of the endosphere includes arbuscular mycorrhizal and endophytic fungi that can symbiotically associated with various plant species (Li et al., 2020; Chung and Park, 2014). Some endophytic microbial species interacts with their own host and facilitate host plant's growth at certain extent (Dastogeer et al., 2017, 2018). Over-all, diversity of the microbial community outside the plant is higher than the endophytic microbiome among different plants species is also affected by the characteristics of plants roots and shoots tissue (Chung and Park, 2014).

5. Microbial diversity in bamboo forest

Soil microbial communities plays significant role in mobilization and recycling of essential micro/macro nutrient and organic matters, which

facilitate development of forest ecosystem (Table 3). Different environmental factors as well as types of forest can affects soil microbial community structure significantly as discussed previously in this review. Soil microbes can affect the development and composition of plant community (Merilä et al., 2010). Invasion of bamboo generally enhances the bacterial diversity and mineralogical characteristics of the soil. Clonal library and pyrosequencing analysis revealed, the phylum Acidobacteria constitutes half of the bamboo soil microbial diversity (Lin et al., 2014). Some studies, observed a wide distribution of the microbial communities amongst numerous soils like agricultural system, tropical and subtropical forests (Meng et al., 2013). There are several advance tools and technologies applied so far to identified the microbial communities in bamboo rhizosphere (Fig. 6). The sequences related to Pseudomonas sp., were sporadic and displayed less abundance in the soil of bamboo plantation. Proteobacteria were also found to be highly abundant in above mention all three communities of the soil along with others (Janssen, 2006). The most abundant class of Proteobacteria in all three communities was α -Proteobacteria, and most of the sequences related to the order Rhodospirillales and Rhizobiales. They include species associated with the process of N2-fixation, decomposition of organic components and promotion of plant growth (Yarwood et al., 2009). In the β -Proteobacteria, Burkholderia is one of the most common bacterial genera in all three above discussed communities. The genus Burkholderia having ability of N2-fixation, plant growth promotion and also acts as biological regulator. The relative abundance of Bacteriodetes observed in cedar community is greater than the bamboo soils. Bacteriodetes were mostly observed in nutrient-rich atmosphere with the capability to degrade organic contaminants (Lin et al., 2014).

In many tropical and subtropical areas, bamboo agroforestry can maintain food, nutritional security pharmaceutical values, and provide economic development too (Kittur et al., 2016; Sawarkar et al., 2020; Tewari et al., 2015). Plant species such as Bletilla striata, Paris polyphylla and Tetrastigma hemsleyanum are the most prominent medicinal herbs in China having anti-inflammatory and antitumor activities (He et al., 2017; Ru et al., 2018; Tewari et al., 2015). Hence, the mechanism of inter-cropping of the medicinal value plants species under mosos bamboo plantation has been studied previously (Luo, 2016). Wang et al. (2017) observed that inter-cropping of Tetrastigma hemsleyanum along with moso bamboo resulting, enhanced leaf characteristics (length, width) with root biomass. Wu et al. (2017) showed, the utilization of the inorganic fertilizer in Tetrastigma. hemsleyanum implanted under the moso bamboo plantation can efficiently advance the photosynthetic fluorescence's characteristics of Tetrastigma. hemsleyanum. Zhang et al. (2019b) revealed that Proteobacteria was observed to be the most dominant along with Acidobacteria in moso bamboo rhizosphere soils, which facilitate the growth of plants.

Xiao et al. (2018) observed the dominance of Acidobacteria followed by phylum Proteobacteria and Chloroflexi in 10 cm upper soil of bamboo forest. Previously the phylum Acidobacteria have been reported to favor an oligotrophic atmosphere (Fierer et al., 2012). Further, the members of Acidobacteria phylum exhibit very low metabolic rates under the conditions of low nutrient contents. Mostly, the taxa of phylum Actinobacteria included copiotrophs are involved in carbon cycling and organic matter degradation (Liu et al., 2017a, b; Yang et al., 2017). The genera Gemmatimona,s showed higher growth rate in the nutritionally enriched plant's rhizosphere (Yin et al., 2013). Candidatus solibacter displayed cellulose substrate degradation property that might be associated with phytodegradation (Pearce et al., 2012). C. solibacter having gene like carbon monoxide dehydrogenase which metabolize carbon as a mixotroph (King and Weber, 2007). Verrucomicrobia plays significant role in certain biogeochemical cycling process like participating in the process of polysaccharide degradation (Martinez-Garcia et al., 2012) and N₂-fixation (Zhang et al., 2019b; Chen, 2014). In case of fungi members, Basidiomycetes are capable of degrading lignocellulosic organic material more efficiently than other fungal groups (Yelle et al., 2008).

Zhang et al. (2020b) investigated the microbial diversities in Cr

contaminated rhizospheric soil of Phyllostachys praecox (commonly known as Lei bamboo). They studied the effect of Cr implementation in bamboo plantation at five different levels such as, low/control (L), low-moderate (LM), moderate (M), moderate-high (MH) and high (H). The Chao and Shannon indices for bacteria were found to be lower in H treatment i.e. (p < 0.05) compared to L, LM, M, and MH treatments. In fungal microbiome, significant differences were observed in Shannon index and the order of value is $L > LM \approx M > H > MH$. The Shannon indices of bacteria and fungi were negatively related to Cr concentrations. Hong et al. (2015) also showed the negative relationship towards the bacterial and fungal abundance and diversities in HM polluted soils. Liu et al. (2018) described that Shannon index of bacterial community was certainly associated with Hg concentration in paddy fields. Sorokin et al. (2014) have isolated and screened few nitrite oxidizer bacterial strains associated to Chloroflexi phylum. The main groups of bacteria observed using biomarkers in LM, M, MH treatments were Acidobacteria, Chloroflexi, Proteobacteria respectively while, Acidibacter, Acidothermus, Candidatus Koribacter and WPS-2 were most abundantly and observed in H treatment with no observed biomarkers applied in L treatment. In fungal communities, the most abundantly found taxa in L treatment included Candida, Exophiala, Trechispora and Pseudaleuria; LM treatment showed the abundance of Cryptococcus, Harpophora, and Hypocrea; Scutellinia was highly predominant in M treatment; MH treatment showed the presence of Verrucostoma, Hydropus and Ascomycota; Auricularia and Polyschema, were the representative of H treatment. The shifting in microbial communities described that the bacteria residing in rhizospheric soil were highly sensitive toward Cr pollution than fungal strains. Ascomycota had an ability to tolerate maximum stress than the Basidiomycota. Ascomycota along with Basidiomycota have been observed as the most dominating fungal phylum in the rhizospheric soil and accounted approximately 90 % of total fungal abundance relatively (Zhang et al., 2020b). Strategies of microbial communities' adaptation to HM contaminated soil, mainly involve change in abundance, diversity and structure (Ma et al., 2019). Proteobacteria are known as copiotrophs, having an ability to grow rapidly in presence of labile substrates (Li et al., 2014). Some strains of Proteobacteria are the promoter of plant growth which can fix N₂ symbiotically (Hassen et al., 2012). Acidobacteria might be negatively related with HMs concentrations (Cui et al., 2017), while according to Guo et al. (2017) Acidobacteria was related positively with certain HMs such as As, Pb, Zn. Narendrula-Kotha and Nkongolo (2017), revealed that the most abundant phyla in HM contaminated rhizospheric soil were Ascomycota and Basidiomycota. It was observed that, phylum Ascomycota, Basidiomycota and Zygomycota indicated highest tolerance against HMs hence, advantageous to develop healthy soil atmosphere required for plant growth.

In China, *Phyllostachys praecox* is significant bamboo species with great economic value to farmers (Liu et al., 2017b). Intensive management of bamboo forest can gradually stimulate bacterial communities in soil (Jansson and Hofmockel, 2018; Zhai et al., 2017). According to Li et al. (2017) intensively maintained bamboo forests enable to modify the abundance and structure of the indigenous fungal population. Lundberg et al. (2012) reported, imperative role of soil in the distribution of the microbes to the plant's rhizosphere. Members of *Proteobacteria* can stimulate the plant growth through the process of phosphate solubilization and N₂-fixation (Zhang et al., 2019b; Chen, 2014), ultimetly leads to better growth and yield of Lei bamboo.

Zhang et al. (2019b) observed and reported, in Lei bamboo forest, the *Proteobacteria* was the predominant root endophytes. This observation also linked the certain association between the soil microbiome and bamboo root endophytes. Intensive management considerably reduced the abundance of *Proteobacteria* while, increased the abundance of phylum *Actinobactria*, *Bacteroidetes*, and *Fermicutes*. Members of phylum *Firmicutes* are able to produce acetone, butanol, ethanol and lactic acid by utilizing carbon sources. Most of the *Firmicutes* and *Bacteroidetes* involve in nutrients cycle as they shown tremendous denitrification potency. Also, *Actinobacteria* inhibits the growth of the harmful



Fig. 6. Application of advance molecular tool and technologies to identify the microbial communities of bamboo rhizosphere; Denaturing gradient gel electrophoresis (DGGE); Temperature gradient gel electrophoresis ((TGGE); Single-strand conformation polymorphism (SSCP); Length heterogeneity polymerase chain reaction (LH-PCR); Terminal restriction fragment length polymorphism (T-RFLP); Ribosomal intergenic spacer analysis (RISA)).

microbes and produce a biological compound, which either directly or indirectly enhances the plant's growth (Barka et al., 2016). Shift in microbial communities were strictly associated to the alteration in the content of the soil nutrient and pH. Relative richness of the Proteobacteria was certainly associated with the soil alkali-hydrolysable N (AN) and available K (AK) whereas, the Bacteroidetes were certainly related with soil available K (AK), total P (TP) and negatively associated with total N (TN) and soil organic matter (SOM) (Zhao et al., 2014). According to Cui et al. (2019), Firmicutes were positively associated with available P (AP) and negatively with pH in rhizosphere and bulk soil of maize. Zhou (2017) showed the effect of mixed ratio of broad-leaved mixed forests and bamboo on inter-species relationship. The existence of broad-leaved trees can potentially enhance the soil fertility as well as create conducive environment for growth of associated bamboo plants. Lin et al. (2014) observed that invasion of bamboo, mostly enhances the bacterial diversity in the soil. Wang et al. (2009) also found highest soil microbial diversity in moso bamboo forest as compared to broad leaved mixed forest and bamboo.

According to Yang et al. (2018) an enhanced understanding of soil microbiome in bamboo-based agroforestry can help in designing and managing of agroforestry. The process of plant invasion can significantly modify the structure along with function of microbial communities (Stefanowicz et al., 2016). According to Ying et al. (2016), moso bamboo invasion into the subtropical forests has become a very huge problem in some areas in southern China. Previously, managing of only moso bamboo forests for harvesting shoots and wood of bamboo was highly advantageous and profitable (Kittur et al., 2016; Sawarkar et al., 2020). But, due to increase in labour cost and decrease in utilization of bamboo products, most of the moso bamboo forests have been deserted as they are no more beneficial (Tian et al., 2020). But its invasion is still going on to adjacent evergreen forests and progressively replacing the local species (Xu et al., 2020). Some studies shown that invasion of moso bamboo could alter the composition and diversity of local plant species (Bai et al., 2013) also change the composition of C, N, P as well as organic matter in the soil (Fukushima et al., 2015; Wang et al., 2016; Shiau and Chiu, 2017). However, Tian et al. (2020) studied that native bamboo invasion can change the microbial communities in litter and soil of the natural forest. Moso bamboo invasion can increased the microbial diversity in soil and litter whereas, some bacteria and fungi showed diverse response to the process of bamboo invasion. The diversities of bacteria (*Acidisphaera, Burkholderia, Luteibacter*) and fungi (*Amphisphaeriaceae, Capnodales, Dothideomycetes, Hypocrea, Trechispora*) in litter at transition zone (slightly invaded by moso bamboo) increased after the invasion of bamboo. Conversely, invasion of bamboo may lead to decrease in abundance of some bacteria sp., like *Enterobacteriaceae* and *Sphingomonas*, which might be due to release of specific growth inhibitors by moso bamboo root exudated (Zhu et al., 2011).

Zhang et al. (2019a) demonstrated that only P-fertilization can alter the structure of soil bacterial community but generated negligible role in stimulating moso bamboo biomass. The growth of moso bamboo might be enhanced by the increase in soil TN, available P followed by Ascomycota and Proteobacteria. Proteobacteria played significant role in bio-availabilities of iron and sulphur (da Silva Neto et al., 2013). Mori et al. (2016) revealed that, rhizospheric fungi belongs to Ascomycota can promote plant tolerance against extreme environment and increases productivity of plant. Intensive management of subtropical bamboo forest reduces microbial diversity and altered community composition. Most prominent phyla in microbial community were found to be Proteobacteria, Acidobacteria, Actinobacteria and Bacteroidetes with 32.8 %, 14.5 %, 11.8 % and 9.0 % respectively. The relative abundance of Bacteriodetes were higher in 15 and 20 years of intensive management (IM15 and IM20). In addition to this, relative abundance of Actinobacteria was observed to be highest in the intensive management of 25 years (IM25) (Chen et al., 2019).

Lin et al. (2015) collected soil samples along six elevations from moso bamboo plantation from 600 to 1800 m in central Taiwan. Previously it was found that, bamboo plantation at high elevation (1200 and 1400 m) were significantly different from below elevation bamboo plantation i.e. (600, 800 and 1000 m), along with greater concentration of soil C, N, soluble organic N and C (Huang et al., 2014). However, changes in bacterial community with geographical elevation is still unexplored. According to Meng et al. (2013) *Acidobacteria* were found pre abundant group of soil bacteria in agriculture, tropical and subtropical forests. Recently Jin et al. (2020), identified the microbial

diversity of bamboo using high throughput sequencing. This investigation revealed the association between the available nutrient content of bamboo and its influence on gut microbial communities of giant panda. The bacterial diversity of bamboo was positively correlated with gut bacterial diversity of giant panda (p < 0.05). Substantial links of certain microbes (mostly bacteria and fungi) present in bamboo and gut of giant panda (p < 0.05) were revealed. 54 and 36 genera of fungi and bacteria respectively were common between bamboo and the gut of giant panda (Jin et al., 2020). In other study, Zhang et al. (2020a), estimated the diversity of bacterial communities' present in bamboo and broad-leaved forest. They analyzed different communities of soil bacteria, its diversity and composition along a relative gradient of 0-40 % mixed-ratio stand of bamboo and broad-leaved forest plants applying the next generation high throughput sequence of the 16S rRNA gene. The stand represented 10-20 % mixed ratio having more bacterial diversity than 20-30 % stand. Amongst the 20-30 % mixed forest soil samples, Acidobacteria was most copious in comparison to mixed soil samples from others stand. Redundancy study displayed that mixed forest stand assembly, pH, organic carbon, TN, and moisture content all influencing the bacterial diversity. The above studies revealed that how bamboo plantation influence the microbial communities' dynamics and vice-versa. Further research studies should deploy more sophisticated tools and technologies which revealed the rhizospheric microbial communities of the bamboo plantation in more systematic manners.

6. Application of bamboo/bamboo biomass in environmental restoration

Bamboo plantation is considered as one of the potential strategies to restore the contaminated lands and carbon-sequestration, due to its fast growth rate and minimum maintenance requirements (Kumar et al., 2021a; Yuen et al., 2017). It is well recognized that, bamboo possess dense foliage which upholds the copious sheet of leaf litter, and these litter foliage act as source of organic matter (OM) which control the microclimate and moisture content of the soil, which facilitate the process of phytoremediation and restoration of degraded land (Kumar et al., 2021a).

6.1. Phytoremediation

Bamboo plants are mostly consisting of leaves, branches, stems rhizomes, roots and shoots. High concentration of HMs was accumulated in the roots. Liu et al. (2014) revealed that under the stress condition, Zn concentration in the roots of moso bamboo ranges from 2329 to 8942 mg kg $^{-1}$. Additionally, concentration of Pb in moso bamboo reached to the highest levels of 4282. 8, 482.2 and 148.8 mg kg^{-1} in the roots stems and leaves respectively (Liu et al., 2015). Bian et al. (2018) observed that, P. praecox showed healthy and fully matured leaves as well as shoots although the levels of Cd, Cu ad Zn were considerably greater than the toxic levels. Chen et al. (2015) revealed that, vacuoles of moso bamboo play a significant role in tolerance of Cu and hence considered as the primary organ for Cu accumulation. Phyllostachys praecox (Lei bamboo) is broadly cultivated in southern Chinese provinces. This bamboo species is cultivated for higher shoot production along with economic benefits (Zhang et al., 2019a). This particular species of bamboo normally grown on HMs (Zn/Cd) contaminated soil having concentration of Cd > 14.5 mg kg⁻¹ and Zn > 2900 mg kg⁻¹ (Bian et al., 2020). The values of translocation and bio-concentration factor were observed in the range of 0.78–1.09 and 0.64 – 0.82 respectively. Hence, the above observation suggests, the P. praecox is not a hyper-accumulator but still could be utilized in the phytoremediation of HMs.

According to Chen et al. (2016) moso bamboo is one of the most potent species for the process of phytoremediation because of its great endurance to HM-contaminated soil. Bian et al. (2017) studied the ability of moso bamboo to remediate HMs alone or in combination with Sedum plumbizincicola. Moso bamboo monoculture, intercropping of *S. plumbizincicola* with moso bamboo and control were well-established in Cd, Cu and Zn-contaminated soil. As compared to control, available Cd, Cu and Zn contents were 48.4, 65.0 and 28.7 % lower in intercropping of *S. plumbizincicola* x moso bamboo while, 45.5, 52.8 and 24.8 % lower in monoculture of moso bamboo. Hence phytoremediation using moso bamboo in combination with *S. plumbizincicola* is highly efficient strategy for the removal of HMs from HM-contaminated soil. Kumar et al. (2021a) suggested that, some species of bamboo namely *Bambusa balcooa, B. bambos, B.vulgaris* are the great accumulators of certain HMs like Cd, Cu and Pb. The above studies revealed the phytoremediation of HMs contaminated soil by different bamboo species. But research endeavors should further focus on to developed a hyper HMs accumulator bamboo species to improve the phytoremediation efficiency.

6.2. Bamboo biochar

In countries, bamboo is used as food and nutrient supplement as well as pharmaceutical agents, (Kittur et al., 2016; Sawarkar et al., 2020). The bamboo biomass harvested from contaminated sites cannot be uses directly as food resources due to presence of HMs, and organic contaminates in their biomass. Therefore, that bamboo biomass can be applied as timber wood, fiber and in fabrication of fiber-based composites (Muhammad et al., 2019). Apart from the aforementioned applications of bamboo, in a recent trend, it is being used for the production of bamboo biochar. Biochar is a carbonaceous material fabricated by thermo-chemical and mechano-chemical conversion of biomass such as crops/agricultural residues (Kumar et al., 2020c), algal biomass (Nie et al., 2020; Kumar et al., 2020a), waste wate sludge (Kumar et al., 2020b) etc. Recently application of bamboo biochar is gaining attention in remediation of environmental contaminants and in biorefinery of biomass as catalyst/catalyst support (Kumar et al., 2020b).

Dong et al. (2019) applied Fe₃O₄ impregnated biochar for degradation of 4-Nonylphenol in marine sediments. This study achieved the degradation of 4-Nonylphenol up to 85.0 % via advance oxidation process using impregnated bamboo biochar. Similarly, Zhang et al. (2020) applied Ti-Sn-Ce functionalized bamboo biochar for enhanced electrocatalytic treatment of coking wastewater in a three-dimensional electrochemical reaction system. The study achieved the removal rate of chemical oxygen demand (COD) and dissolved organic carbon (DOC) in coking wastewater up to 92.91 % and 74.66 %, respectively. Xia et al. (2016) applied bamboo charcoal in anaerobic digestion of bamboo biomass for production of bio-methane. Results of this study revealed that, the bamboo charcoal amended system was able to remove the COD (94.5 \pm 2.9 %) better than control (89.1 \pm 3.1 %). The supplementation of bamboo charcoal improved the quantity of biomass and increased the overall efficiency of the systems. Microbial communities' analysis of the anaerobic digestion system revealed that, amendment of bamboo charcoal improved the microbial diversity and encouraged the activity of various anaerobic microbes such as Methanosaeta, Methanospirillum, and Methanobacterium, which facilitated bio-methane generation in the system.

Bamboo biochar is also used catalyst and catalyst support in biorefinery of biomass. For instant, a sulfonated bamboo biochar along with solid acid catalyst was applied to transform bamboo hemicelluloses into xylooligosaccharides (XOS) and achieved a yield of 54.7 % XOS after 45 min at $150 \ ^{\circ}$ C (Qi et al., 2014). Kumar et al. (2020b) published a comprehensive review which discussed the application of bamboo biochar in environmental remediation and biorefinery of biomass. Still techno-economical and life cycle assessment should be considered in future research to established the economical and sustainable application of bamboo biochar in biorefinery and environmental restoration.

6.3. Carbon sequestration

In forest, carbon sequestration is generally recognized as a process having great potential of reducing CO₂ concentration in the atmosphere (Xu et al., 2018). Bamboo species have great potential for carbon sequestration along with carbon storage due to rapid growth rate as well as huge production of biomass (Yuen et al., 2017; Kumar et al., 2021a). The potential of biomass growth of bamboo is usually greater than the fast-growing exotic plant species. Its capability of existence for longer period without any significant development in the culm stock makes bamboo most significant and potential species for the process of carbon storage and sequestration (Devi and Singh, 2021). Bamboos are useful in carbon sequestration through all main types of forest-based climate change activities particularly afforestation and re-forestation (Dwivedi et al., 2019). Due to the presence of phytolith-occluded carbon (PhytOC), moso bamboo has an immense potential in carbon-sequestration. The carbon-sequestered by moso bamboo forests could vary with management system. Extensively managed moso bamboo practices can sequester 50 % less carbon than intensively managed practices (Lv et al., 2020). A study by Song et al. (2017) estimates the current rate of carbon-sequestration in terrestrial bamboo biomes which was 0.16 ± 0.9 gigatons (Gt) of CO₂-equivalent per year. Tegler (2017) estimated carbon-sequestration rate of bamboo biomass per hectare per year, which was 2.03 tons that may leads to a total of 8.3-21.3 Gt of CO2 sequestered by 2050. Over all these studies revealed the potential role of bamboo in sequestration of CO₂ and its environmental significance.

7. Conclusion and prospects for future research

Soil microorganisms can considerably contribute in the bioavailability of nutrients for the plant. Through varying biological interactions, microbes are synergistically correlated to the plants and contribute to boost up the defense mechanism directly or indirectly under stress conditions. Plant associated microbiomes are highly beneficial to the host plant as it promotes growth, nutrient uptake and resist the entry of pathogens. Bamboo is considered as imperative forest reserve globally as they serve as an outstanding ancillary for woody products along with offers various products as well. Bamboo species are usually preferred for phytoremediation and environmental restoration due to its considerable absorption abilities, higher HMs removal capacity, higher growth rate, easy cultivation at degraded land and occurrence of diverse rhizospheric microbial communities. Bamboo cultivation in agricultural as well as degraded land is highly influence by the indigenous complex microbial communities and vice-versa. Physiological, molecular and microbial studies will helpful in understanding the mechanism involve in phytoremediation of contaminated sites, HM uptake and its tolerance in bamboo species. There have been several reports which shown the influence of bamboo plantation on the microbial diversity of the soils and its mechanisms, along with application of bamboo species in phytoremediation and environmental restoration but still this research domain is infancy. Based on the above discussion following recommendation are suggested for future research to make this novel domain more fruitful for the environment as well as society.

- The role of rhizospheric microorganisms and their interactive mechanism which influence the growth of bamboo, must be emphasized in future research to develop the understanding about their complex mechanisms.
- How bamboo plantation influences the microbial communities and vice-versa; deployment of advance genetic tools and technologies (metagenomic, genomic, proteomic, metabolomics etc.) are desirable to assess the changes.
- Bamboo can grow on HMs contaminated sites, and accumulate HMs in biomass. These HMs could affect further applications of the bamboo biomass, need to explore in future research.

- Development of hyper HMs accumulator bamboo species and understanding about their mechanism could be a good approach to restore degraded land. These types of studies should be emphasized in future research.
- Moso bamboo is rich in PhytOC and has a great capability in carbonsequestration. Still their quantification and estimation studies are limited, that required extensive investigation in future research to developed a good corelation.
- Techno-economic investigation and life cycle analysis of commercial bamboo cultivation on HMs contaminated sites required further investigations to achieve sustainable environment goal.
- Application of bamboo biochar in environmental management and biorefinery required techno-economical and life cycle assessment which should be considered in future research to make these technologies cost-effective and environmentally sustainable.
- The environmental impacts of bamboo cultivation, occupational health and safety of bamboo cultivator need to be considered in future and prudently assessed.

CRediT authorship contribution statement

Priya Fuke: Conceptualization, Writing - original draft. Mohan Manu T: Writing. Manish Kumar: Writing- review, editing, supervision. Ankush D. Sawarkar: Writing and editing. Ashok Pandey: Revision and writing. Lal Singh: Project administration, supervision, writing- review and editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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