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Review

Current advances and research prospects for agricultural and industrial uses of microbial strains available in world collections

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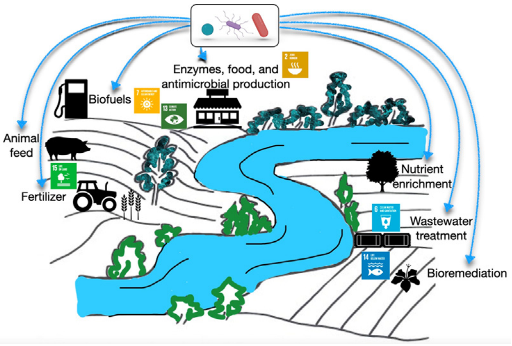
HIGHLIGHTS

- As a source of authenticated biological material, culture collections are crucial in research.
- Collections under WFCC are a bank of around 3.0 million microbes.
- The use of conserved microbes is regulated by biodiversity and biosafety law.
- Preserved microbes are a bioresource for green products and technologies.
- Genetically engineered microorganisms are resources for bioremediation.

GRAPHICAL ABSTRACT



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ABSTRACT

Microorganisms are an important component of the ecosystem and have an enormous impact on human lives. Moreover, microorganisms are considered to have desirable effects on other co-existing species in a variety of habitats, such as agriculture and industries. In this way, they also have enormous environmental applications. Hence, collections of microorganisms with specific traits are a crucial step in developing new technologies to harness the microbial potential. Microbial culture collections (MCCs) are a repository for the preservation of a large variety of microbial species distributed throughout the world. In this context, culture collections (CCs) and microbial biological resource centres (mBRCs) are vital for the safeguarding and circulation of biological resources, as well as for the progress of the life sciences. Ex situ

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conservation of microorganisms tagged with specific traits in the collections is the crucial step in developing new technologies to harness their potential. Type strains are mainly used in taxonomic study, whereas reference strains are used for agricultural, biotechnological, pharmaceutical research and commercial work. Despite the tremendous potential in microbiological research, little effort has been made in the true sense to harness the potential of conserved microorganisms. This review highlights (1) the importance of available global microbial collections for man and (2) the use of these resources in different research and applications in agriculture, biotechnology, and industry. In addition, an extensive literature survey was carried out on preserved microorganisms from different collection centres using the Web of Science (WoS) and SCOPUS. This review also emphasizes knowledge gaps and future perspectives. Finally, this study provides a critical analysis of the current and future roles of microorganisms available in culture collections for different sustainable agricultural and industrial applications. This work highlights target-specific potential microbial strains that have multiple important metabolic and genetic traits for future research and use.

Contents

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1. Introduction

Microbial culture collections (MCC), also known as Biological Resource Centres (BRC), are major suppliers of cultured microorganisms and their replicable parts such as DNA, genomes and plasmids and viable but not yet culturable microorganisms in biological or environmental matrices (Smith et al., 2014; Díaz et al., 2021). Smith et al. (2014) reported a concept that MCC or BRC generally includes "the provision of services and repositories of living cells, genomes of organisms, and information relating to heredity and functions of biological systems. The value of MCC is well documented by the Organization for Economic Cooperation and Development (OECD), which encourages and improves economic well-being and social welfare at an international level (Smith et al., 2014). MCC works mainly for two purposes, first, it plays a vital role in the conservation of agroecosystems through the isolation and preservation of microbial diversity, and second, it makes it easier for the study and preserved microorganisms to the public to generate biotechnological strategies (Díaz et al., 2021).

The first culture collection was established by Prof. Frantisek Král in 1890 at the German University of Prague. Later, several other culture collection centres were established like the Mycothèque de l'Université catholique de Louvain (MUCL) in 1894 in Belgium, the other Collection created in Holland named the Centraalbureau voor Schimmelcultures (CBS) in 1906. These two collections were specialized for fungi. Later, the American Type Culture Collection (ATCC) was established in the United States in the year 1925, which preserves different types of microorganisms (Sharma et al., 2017a,b; Díaz et al., 2021). Currently, the World Federation for Culture Collections (WFCC) is the main organization that synchronizes the activities of MCC globally (Sharma et al., 2017a,b). The WFCC generally aims to promote and support the establishment and monitoring of MCC by providing a platform and sharing information between affiliated culture collections and users (Díaz et al., 2021). It supports the World Data Centre for Microorganisms (WDCM) to compile the data of culture collection, its management, services and promotes the most recent research with an online international database (Sharma et al., 2017a,b). Currently, the WDCM lists 820 collections around the world, of which 303 are located in the Asia region, 259 in Europe, 208 in America, 42 in Oceania, and 19 in Africa (http://ccinfo.wdcm.org/statistics on 12 June 2022). In this way, it is worth mentioning that culture collections globally play a fundamental role in the preservation of microbial diversity, and the accessibility of axenic and stable, promising strains for a variety of applications in agriculture, environment, industrial and medical microbiology, etc. Recently, it was reported that currently a total of 3,348,121 microorganisms have been registered in the WDCM, of which 1,476, 133 are bacteria, 887,812 are fungi, 39,207 are viruses, and 37,923 are cell lines (http://ccinfo.wdcm.org on 12 June 2022).

Rapid exploitation of natural resources and environmental disturbances due to global climate change, soil degradation, and environmental pollution causes problems in the sustainable production of agricultural products and human health. In this context, microorganisms could be the main resources that must be utilized to solve the major challenges of the present day. Over the past 50 years, microorganisms have been exploited to solve essential challenges related to health, agriculture, food processing, and waste management (Thallinger et al., 2013; Singh et al., 2016; De Giani et al., 2021; Fu et al., 2021; Gilmour et al., 2021; Iyer et al., 2021; Kaur et al., 2021; Soh et al., 2021; Liu et al., 2022; Montaño López et al., 2022). In the last decade, the application of microorganisms in different sectors has progressed considerably due to the advancement of modern tools and techniques for the isolation, screening and detection in environmental components such as air, soil, and water. Currently, it has been proven that people rely on microbial-derived products, such as vinegar, proteins, yogurt, types of cheese, wine, bread, pickle, sauces and fermented ethnic foods (Matassa et al., 2016; Singh et al., 2017a,b,c; Rau and Zeidan, 2018; Pham et al., 2019; Choi et al., 2022). Microorganisms are also used to generate attenuated vaccines, antigens, or as such their products to cure several human diseases, including smallpox, polio, diabetes, among others (Jozala et al., 2016; Sanchez-Garcia et al., 2016; Berg et al., 2017; Selas Castiñeiras et al., 2018; Sarsaiya et al., 2019; Maske et al., 2021; Yang et al., 2021a,b). Regarding human health, today, a plethora of available antibiotics is derived from microbial metabolites. Most antibiotics are derived from Actinomycetes, a soil bacterial group (Genilloud, 2017). They are also used to produce industrial enzymes involved in improving detergent quality, cleaning toxic waste, in the processing of paper and pulp, and in the fashion industry (Zumsteg et al., 2017; De Menezes et al., 2021; Intasian et al., 2021; Mazotto et al., 2021). Furthermore, microorganisms and their enzymes/metabolites are also exploited globally for remediation of several xenobiotic compounds and emerging pollutants under different environmental conditions, being used in wastewater treatment to decompose organic matter in sewage as to well as to generate biofuels such as biogas or bioethanol and for oil extraction (Singh et al., 2016; Amadu et al., 2020; Amin et al., 2020; Arias et al., 2021; Zhang et al., 2021; Ahmad et al., 2022). They are used to promote sustainable development goals (SDGs) of the United Nations, including new energy sources, environmental protection, waste management, sustainable agriculture and environmental monitoring (Narancic and O'Connor, 2017; O'Toole and Paoli, 2017; Timmis et al., 2017; Khan Mirzaei and Deng, 2021).

The soil is a habitat for various microflora, which plays a role in various ecological processes and climate regulation and is also necessary to maintain soil functions and health (Jacoby et al., 2017; Abinandan et al., 2019; Sofo et al., 2020; Bertola et al., 2021). However, the composition and diversity of soil microbial communities and their biological functions are negatively affected by climate change as well as by various human activities, such as excessive use of agrochemicals, intensive agricultural practices, discharge of industrial wastes, antibiotics, among others (Zhang et al., 2016; Margesin et al., 2017; Ibekwe et al., 2018; Ji et al., 2018; Díaz Rodríguez et al., 2019; Ou et al., 2019; Zhen et al., 2019; Wang et al., 2020; Wang et al., 2020a; Anand et al., 2021; Khare et al., 2021; Xu et al., 2021; Yang et al., 2021a,b; Feng et al., 2022; Wu et al., 2022). Subsequently, the reduction in the diversity and quality of microbial communities in the soil is directly related to loss of natural resources and the disturbance of the ecosystem (Cavicchioli et al., 2019). It plays a vital role in the hindering of sustainable development in agriculture, industries, food, and health. It is estimated that the benefits of microorganisms are many billions of dollars annually – at a global level – because they cater to the need of society by providing ecosystem services such as (i) social and ecological sustainability, (ii) adaptation and mitigation of climate change, (iii) biotechnological resources for humanity, (iv) biogeochemical cycles, and (v) increase in agricultural production (Rousk and Bengtson, 2014; Zhu et al., 2017; Martínez-Espinosa, 2020; Bakker and Berendsen, 2022). Considerable progress in microbiology brought the need to establish the microbial culture collections to study and preserve the microbial biodiversity in ecosystems and their distribution of promising microbial strains for the improvement of goods and services. Thus, microbial culture collections are the best way to ex situ preserve and catalog the diversity of promising microorganisms (Smith et al., 2014; Sharma et al., 2017a,b; Becker et al., 2019; Reimer et al., 2019; Paton et al., 2020; Smith et al., 2020; Díaz et al., 2021). The microbial culture collections are repositories that preserve microbial strains and provide quality cultures and genetic materials to the stakeholders required for various purposes like research, industrial, or product development, and other uses (Wu et al., 2013; Sharma and Shouche, 2014; Wu et al., 2017). The revival of long lost homoacetogenic bacterium *Clostridium aceticum* is a notable example of a very old stock culture (34 years) that was still available. This strain is now becoming a valuable model for research studies (Braun et al., 1981; Overmann, 2015; Mayer et al., 2018; Atasoy and Cetecioglu, 2021). This review highlights (1) the importance of available global microbial collections for man and (2) the use of these resources in different research and applications in agriculture, biotechnology and industry.

2. Functions of microbial culture collections

The microbial culture collections were started more than 100 years back and many microbes of economic importance had been conserved in many forms but preferred forms are lyophilized form (Freeze-dried) and liquid nitrogen (Frozen form) (Sharma et al., 2017a,b; Singh et al., 2017a,b,c). Besides, all these were also being used today in the study of several areas such as (1) biodiversity (2) discovery of new biomolecules and (3) ecosystem functioning and restoration, (4) biosensor development (5) oil pool recovery (6) crop and soil health promoters (7) human health and (8) in several other areas. The goal of the Biological Resource Centre's (Microbial Culture Collections) is the collection, preservation and distribution of microbial strains, together with the supply and exchange of relevant information. The goals can be achieved by directing resources towards fundamental services and expertise related to (i) specific conservation and quality assurance (ii) identification, authentication and taxonomic classification (iii) data management and sharing. Most of the collections are providing identity and accession numbers to microbes but only some microbial culture collections are providing information on traits of microorganisms in public. Molecular tools and techniques such as next-generation sequencing (NGS) technology, RNA seq, and transcriptomic and metagenomic approaches, have exponentially increased the detection of both culturable and non-culturable microbial biodiversity. It is noteworthy that, with the progressive cost reduction of NGS, it is expected that the identification of novel species will be based on their entire genome in future. In addition, genome sequences of correctly described species can be used as a reliable reference to infer taxonomic lineages of so-far-uncultured microbial species in natural populations. The functionally well-equipped culture collections after receiving cultures are verifying the cultures by characterization for their taxonomic identification but most of the collections are accepting cultures which are well characterized with proof for assigning accession numbers. These collections again re-verifying the identity of culture with facilities available to them and assign accession numbers and preserve them under mid-and long-term storage. Currently, culture collections have adopted new biomolecular techniques to characterize and add value to the services they offer. In addition, with the advancement of biochemical and physiological studies, the conservation of microorganisms has improved a lot. The adoption of standard formats for delivering information and the implementation of state-of-the-art programming interfaces would allow true and effective interoperability of collection information systems with the bioinformatics environment of databases and software (De Vero et al., 2019). In a true sense, in the most cases, attributes of microbes have not been organised and hence, there is a need to develop that microbes should also be assigned attributes apart from identity and accession number. Globally, the functionally well-equipped culture collections are generally having enough staff and funds to run collections over time but some collections do not have enough staff and funds to run smoothly. Running collections are more of service than research type; however, big collections are also conducting research and characterizing microbes for commercial purposes. Generally, freeze-drying is the preferred method for transporting and storing microbial cultures because it offers many advantages over other preservation techniques, including the total sealing of the specimen and protection from infection and avoiding contamination.

3. Regulations associated with microbial culture collections

Most of the microbial culture collections across the globe preserve microorganisms mainly to supply cultures for research purposes in the academic and research institutions but today commercial use of such microbes is exploited at the industry level as well (Díaz et al., 2021). World Federation for Culture Collections (WFCC) is recognising all collections but some of them are defunct due to various reasons and some of them are fully in the functional state working on both research and commercial purposes. There are guidelines developed by WFCC (http://www.cabri.org/guidelines/micro-organisms/M100Ap1.html) and OECD (https://www.oecd.org/science/emerging-tech/23547773.pdf) to establish microbial culture collection worldwide. Besides the guidelines of WFCC and OECD, today every country has its own guidelines for biodiversity management and sharing of bioresources is regulated by its country of origin in the line of Nagoya Protocol (Sharma et al., 2019). Similarly, India has also developed its own guidelines under the umbrella of the Convention of Biological Diversity (CBD) through National Biodiversity Authority (NBA), Govt. of India, Chennai, India, (Govt. of India) which is a nodal body for bioresource/biodiversity regulation along with access and benefit-sharing of biological resources (http://nbaindia.org/uploaded/pdf/Guidelines_for_Designated_Repositories.pdf). Further, India is sharing our microbial resources, especially bacterial type culture with other collections of the world with some restrictions. However, it is falsely propagated by other countries that Indian culture collections are not sharing microbial resources with other repositories but are distributing cultures under the ambit of Biological Diversity (BD) Act 2003 of India regulation through the National Biodiversity Authority (Rahi, 2021). For example, some of our important collections namely MTCC, Chandigarh; NMRC (MCC), Pune; NAIMCC, Mau; ITCC, New Delhi and other designated repositories are sharing the type culture for taxonomic study and other reference strains following extant guidelines of India to other countries. So far in India, culture collections namely MTCC, NMRC (MCC) and NAIMCC have been recognized by International Depository Authority (IDA) for deposition for new taxa (type culture) and patent deposit under Budapest Treaty, 1980. Most of the IDA recognized culture collections, deposit microbes in the category of (1) General deposit (open deposit) for use by any researcher for research work, (2) Safe deposit for commercial purposes and (3) Safe deposit for patent purposes. All general culture collections deposit microbes under general deposit and assign accession numbers.

There are no global criteria existing for grading collections. However, in India, National Biodiversity Authority (NBA) has categorized the "*National Depository*" as all those collections that have all infrastructures to operate a collection and all referral strains are being deposited in these collections for future reference. At the global level, collections are also classified based on biosafety level (BSL) for example Biosafety Level 1 (BSL 1), Biosafety Level 2 (BSL 2), Biosafety Level 3 (BSL 3), and Biosafety Level 4 (BSL 4). Every culture collection has its own policy as per the regulations of the country of origin and the supply of cultures regulated under the ambit of such policy. However, most of the culture collections supply cultures with a nominal fee in case culture is deposited under the "'*General or Open*' category but do not supply cultures which are under the '*Safe deposit or Patent' deposit* category. Most of the cultures under the category of restrictions either have commercial value or are under different BSL 3 and 4 which are hazardous to human beings, animals and the environment. For example, Limburger is called "*smelly cheese*" because of its strong aroma, mainly originating from the rind, rather than the cheese itself. The bacteria involved in "*smelly cheese*" are *Streptococcus thermophilus* and *Lactobacillus delbrueckii* subsp. *lactis* and *Clostridium licheniforme* (*Bacillus licheniformis*) and *Paraplectrum foetidum* are two other bacteria that have been studied and found on the surface of the smear-ripened Limburger cheese (Zheng et al., 2021). All these bacteria are usually belonging to BSL 1. Even if some collections keep some such bacteria in BSL 2 because of their mild pathogenic nature and presence of pathogenic genes that are not much hazardous to humans and the environment but may become hazardous upon overexposure to such bacteria.

4. Study design

In this review, a preliminary scientometric analysis was performed to collect information from Web of Science (WoS) data on preserved microorganisms and highlight their potential applications, which are the worthiest of future exploration. As the literature and citations of preserved microorganisms are growing exponentially on public domains such as Web of Science (WoS), Scopus, and PubMed, the scientific community is interested enough to explore them further. However, this research is not easy because, like several other complex data, the citation data are much more complicated, arbitrary, and multidimensional. Handling these data requires a lot of care and is almost manual browsing. In this context, machine learning tools and data analytics tools such as R have been accelerating the bibliometric process, which has been shown to be the best way to evaluate research productivity systematically (Qu et al., 2019; Lai et al., 2019; Dill-McFarland et al., 2021; Goodswen et al., 2021).

In this study, a total of seven microbial culture collections were selected. Three of these are internationally recognized, namely, American Type Culture Collection (ATCC), China Center for Type Culture Collection (CCTCC), and Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), and 4 Indian microbial culture collections including Microbial Type Culture Collection and Gene Bank (MTCC), National Agriculturally Important Microbial Culture Collection (NAIMCC), The Indian Type Culture Collection (ITCC) and National Collection of Industrial Microorganisms (NCIM). Then, text mining was done to retrieve the keywords from the data of each culture collection. The frequency of the keywords was also calculated and passed through an R script to create a word cloud. The high frequency of keywords has been represented by a larger font size.

Cluster bibliography analysis has been applied to select the most suitable papers and arguments to carry out the work. The Scopus database (https://www.scopus.com/) was consulted on January 10, 2022, to retrieve articles related to potential biotechnological microbial repositories for agricultural and industrial applications.

The following keywords were selected in the combined fields of title, abstract, and keywords: ((microorganism) OR (microbial)) AND (biotechnology) AND ((preservation) OR (conservation)). The resulting papers were 819. Before 2001, only a few papers on the selected arguments were published (less than 10 per year). From 2015 to 2021, a mean value of 50 papers was published each year, in the restricted search area.

Some keywords were found to be of considerably higher frequency. The keywords "ANTIMICROBIAL ACTIVITY" and "FERMENTATION" were the most frequently used words in the literature (Fig. 1). The topic-wise classification was performed according to the WoS mentioned data fields. It is evident that the categories "LIFE SCIENCE & BIOMEDICINE" and "BIOTECHNOLOGY & APPLIED MICROBIOLOGY" contain the highest reports (Fig. 2). Out of the data retrieved from WoS, some studies from international culture collections are compiled in Table 1, with their conserved microorganisms and accession number.

The bibliometric analysis of the obtained results was realised by using VOSviewer software (https://www.vosviewer.com/), with the aim of graphically showing a map able to display the text cooccurrence network. The map highlights the most frequently used bibliographic terms to understand the most active research fields that are grouped in 4 clusters.

Cluster 1 (represented with red bubbles, in Fig. 3) contains general terms correlated with microbial biotechnologies (such as sequence, biochemistry, biological potential, culture collection, genome, genetic engineering, etc.). In addition, it contains also specific worlds connected with the application of microorganisms in agriculture (like climate change, agriculture, ecosystem, and the Earth).

Cluster 4 (represented with yellow bubbles) is mainly addressing pollutants bioremediation. In particular, the main terms highlighted are bioremediation, biodegradation, soil remediation, contaminant, hydrocarbon, and pesticide.

Cluster 2 (represented with green bubbles) is made up of terms related to industrial applications, such as fermentation, temperature, concentration, food, food preservation, food industry, bioactive compounds, enzyme activity, and stability. In particular, cluster 3 (represented with blue bubbles) is mainly addressed to biofuel production (the main terms are biomass, conversion, biodiesel, biofuel, bioethanol, bioreactor, efficiency, energy, feedstock, metabolic engineering, and productivity).

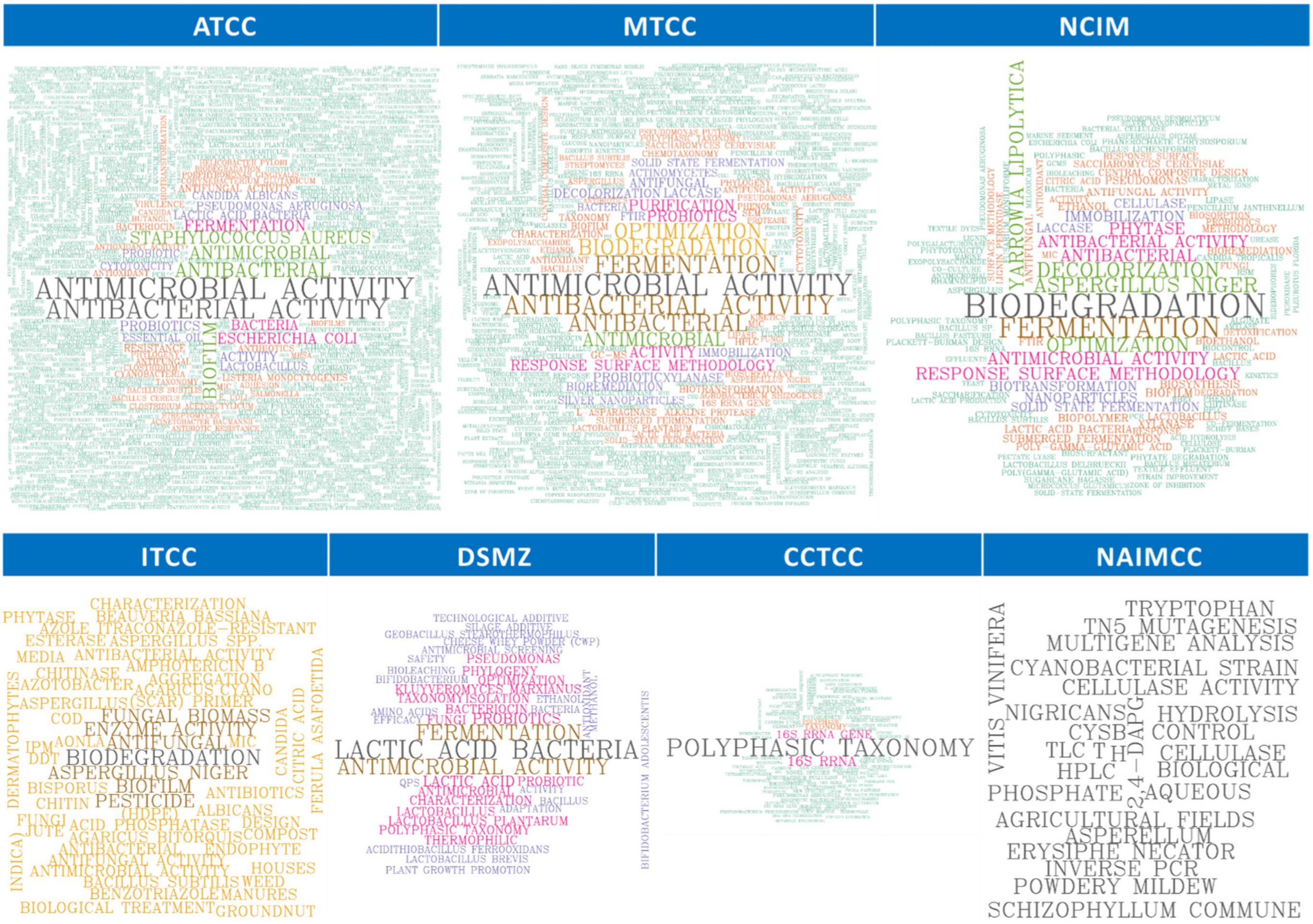
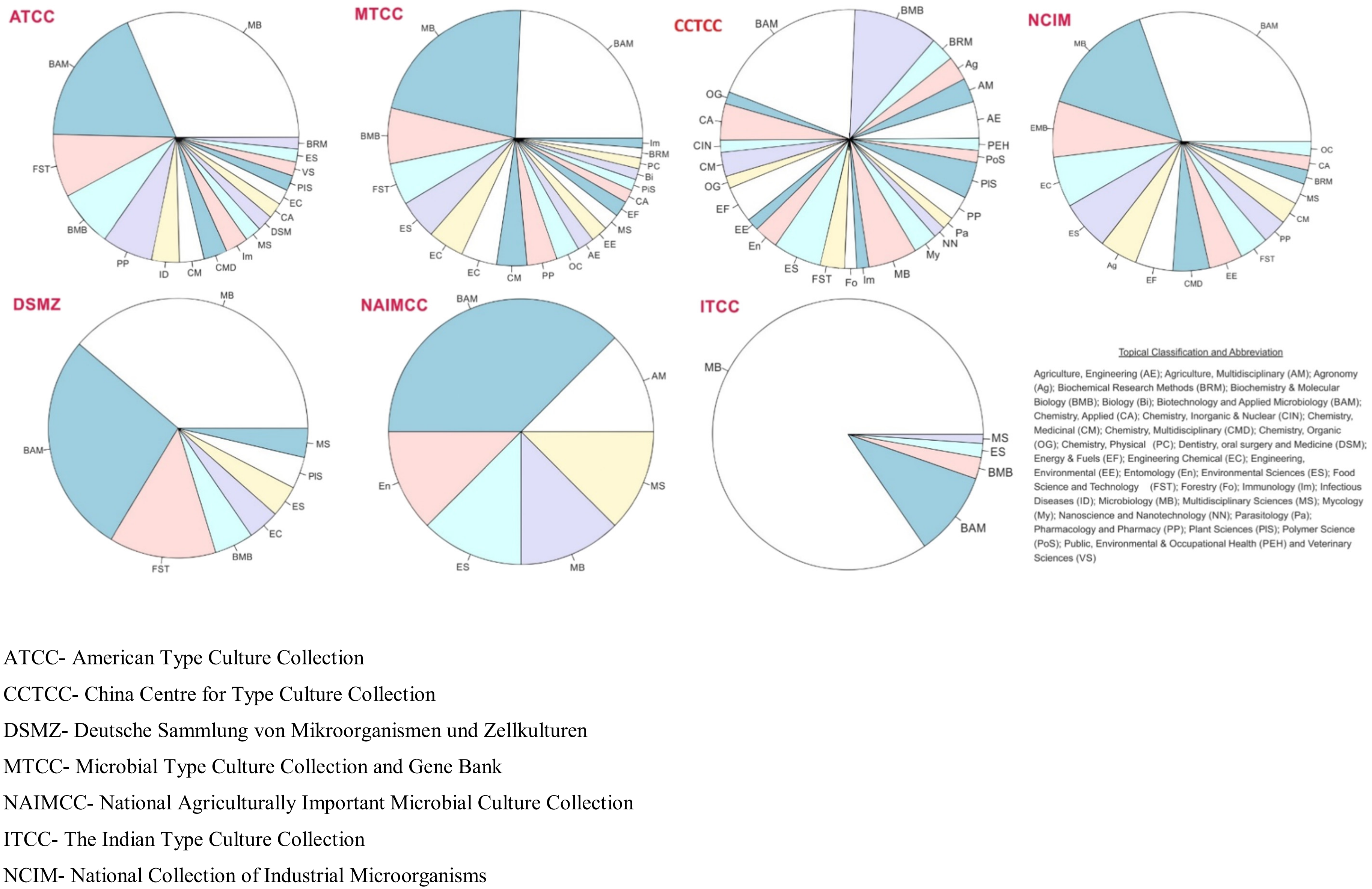


Fig. 1. World cloud after retrieving keywords from the available literature on conserved microbial strains at different culture collections. The sizes of words represent their frequency in the literature.

Data retrieved from scientometric analysis (see Figs. 1 and 2 and Table 1) suggested that the initial interest in microorganisms was centered on antimicrobials. Cluster analysis highlights that the current situation has changed researchers to look for other beneficial properties that can be further classified into three broad groups based on their wide applications, that is, agriculture, bioremediation, and industries. Therefore, Section 3 of the paper is devoted to the application of microorganisms in agriculture, Section 4 is dedicated to microorganisms for bioremediation of pollutants, Section 5 is devoted to the application of microorganisms for different industrial purposes, and Section 6 to future perspectives.

5. Application of microorganisms in agriculture

The growth of microorganisms in the soil is beneficial for plant growth, health, and the environment. This uniqueness of microorganisms with indigenous potentials has made them most appropriate alternative to agrochemicals. Microorganisms are beneficial when provided with the optimal conditions in the environment in order to grow and show their beneficial effects on plants (Iriti et al., 2019; Valenzuela-Aragon et al., 2019; Ney et al., 2020; Ahmad et al., 2020; Szymanek et al., 2020). In agroecosystems, effective microorganisms can be termed agriculturally important microorganisms (AIMs) which are involved in nitrogen fixation, the transformation of organic matter, nutrient cycling, formation and aeration of soil aggregates, carbon sequestration, xenobiotic bioremediation, and plant growth regulation. These AIM-improved processes show that plant potential tolerance to abiotic stress is responsible for carrying out 80 to 90 % of biological processes in the soil (Robles Montoya et al., 2020a,b; Rojas-Padilla et al., 2020). Recently, it was reported that the Culture Collection of Native Soil and Endophytic Microorganisms (COLMENA), Mexico 24 % of 1464 microorganisms are preserved to date characterized using 16 S rRNA for bacteria and 5.8 S rRNA genes for fungi (De los Santos-Villalobos et al., 2021); these values are important, but still not sufficient for the proper preservation of important soil microorganisms. These authors also discussed the activity of various preserved microorganisms such as *Bacillus* sp., *Pseudomonas* sp., *Stenotrophomonas* sp., *Aspergillus* sp., etc. in biocontrol, bioremediation, soil fertility and production of antibiotics in the agroecosystem. Since long, agricultural biotechnologists have thoroughly investigated plant growth-promoting rhizobacteria (PGPR), and arbuscular mycorrhizal fungi (AMF) and the information related to agricultural traits have been stored in databases of the Center for Agriculture and Bioscience International (CABI), UK, Korean Agricultural Culture Collection (KACC), South Korea and Agricultural Culture Collection of China (ACCC). CABI holds a collection of more than 30,000 microbial strains from 142 countries, of which 90 % are unique to CABI. It is one of the world's largest Genetic Resource collections and holds the UK's National Collection of Fungus Cultures (https://www.cabi.org/products-and-services/bioscience-services/). KACC maintains more than 20,900 microorganism cultures, which are available to the public through its website (http://genebank.rda.go.kr) and distributes more than 2000 cultures annually to microbial researchers. Since its establishment, ACCC has collected and preserved more than 20,000 agricultural microbial strains with approximately 250,000 backups. The strains belong to 497 genera and 1774 species and represent one-third of the total agricultural microbial resources in China. Among them, 18,041 strains in the fields of microbial fertilizer, microbial feed, microbial pesticide, microbial food, microbial remediation, and mushroom cultivation are available



Topical Classification and Abbreviation

Agriculture, Engineering (AE); Agriculture, Multidisciplinary (AM); Agronomy (Ag); Biochemical Research Methods (BRM); Biochemistry & Molecular Biology (BMB); Biology (Bi); Biotechnology and Applied Microbiology (BAM); Chemistry, Applied (CA); Chemistry, Inorganic & Nuclear (CIN); Chemistry, Medicinal (CM); Chemistry, Multidisciplinary (CMD); Chemistry, Organic (OG); Chemistry, Physical (PC); Dentistry, oral surgery and Medicine (DSM); Energy & Fuels (EF); Engineering Chemical (EC); Engineering, Environmental (EE); Entomology (En); Environmental Sciences (ES); Food Science and Technology (FST); Forestry (Fo); Immunology (Im); Infectious Diseases (ID); Microbiology (MB); Multidisciplinary Sciences (MS); Mycology (My); Nanoscience and Nanotechnology (NN); Parasitology (Pa); Pharmacology and Pharmacy (PP); Plant Sciences (PIS); Polymer Science (PoS); Public, Environmental & Occupational Health (PEH) and Veterinary Sciences (VS)

ATCC- American Type Culture Collection

CCTCC- China Centre for Type Culture Collection

DSMZ- Deutsche Sammlung von Mikroorganismen und Zellkulturen

MTCC- Microbial Type Culture Collection and Gene Bank

NAIMCC- National Agriculturally Important Microbial Culture Collection

ITCC- The Indian Type Culture Collection

NCIM- National Collection of Industrial Microorganisms

Fig. 2. Topical classification of available literature on conserved microbial strains at different culture collections according to the WoS-mentioned data fields.

Table 1
A list of some studies on conserved microorganisms from three culture collections around the world.

Microorganisms	Culture collection accession number	Application	Reference
American Type Culture Collection (ATCC), USA			
Staphylococcus aureus	ATCC 25923	Imidazolium antiseptics	Hodyna et al., 2018
Halorubrum lacusprofundi	ATCC 49239	Transcriptomic analysis for cold adaptation	Das Sarma et al., 2017
Acanthamoeba castellanii	ATCC 30010	Anti-amoeba activity by disinfecting contact lens	Tanaka et al., 2017
Streptomyces Tacrolimicus	ATCC 55098	Production of tacrolimus	Singh et al., 2017a, 2017b,c
Trametes versicolor	ATCC 200801	Laccase production	Birhanli and Yeşilada, 2017
Corynebacterium glutamicum	ATCC 21799	Production of L-Lysine for making enriched bran	Junior et al., 2016
Bacillus subtilis	ATCC 11774	Chitinase production	Saber et al., 2015
Clostridium acetobutylicum and *Enterobacter cloacae*	ATCC 824 ATCC 13047	Biohydrogen production from industrial wastes	Chen et al., 2015
Lactobacillus rhamnosus GG	ATCC 53103	Used in influenza vaccination	Solano-Aguilar et al., 2015
Bacillus subtilis	ATCC 6633	Biosurfactant production	Sousa et al., 2014
Acidithiobacillus ferrooxidans strains	ATCC 23270 and ATCC 53993	Biomining and bioremediation	Navarro et al., 2013
Trametes trogii (Berk.) and *Trametes versicolor (L.)*	ATCC 200800 and ATCC 200801	Laccase production from lignocellulosic wastes	Birhanli and Yeşilada, 2013
China Centre for Type Culture Collection (CCTCC), China			
Candida utilis	CCTCC M 209298	Biosynthesis of antioxidants	Wang et al., 2012a,b
Aureobasidium pullulans	CCTCC M 2012259	Improves pullulan production	Wang et al., 2018
Bacillus sp. dsh19-1	CCTCC AB 2015426	Production of cold-active alpha-amylase	Dou et al., 2018
Trichoderma harzianum	CCTCC-SBW0162	Triggering the biocontrol of *Botrytis cinerea*	Saravanakumar et al., 2017
Phellinus noxius HN-1	CCTCC M 2016242	Biocontrol activity against cyanobacteria *Microcystis aeruginosa*	Jin et al., 2017
Methylobacillus sp.	CCTCC M2016079	Production of pyrroloquinoline	Si et al., 2017
Geomyces sp.	CCTCC M 2014676	Production of vincamine, a monoterpenoid indole alkaloid	Na et al., 2016
Burkholderia gladioli	CCTCC M 2012379	Biosynthesis of ethyl (*R*)-4-chloro3-hydroxybutyrate	Chen et al., 2016a,b
Actinobacillus succinogenes	CCTCC M2012036	Succinic acid production from sugarcane bagasse	Chen et al., 2016a,b
Pseudomonas plecoglossicida NyZ12	CCTCC AB 2015057	Have the property of cyclohexylamine degradation and studied for complete genome sequence	Li et al., 2015
Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), Germany			
Phanerochaete chrysosporium	DSMZ 6909	Decolorization of synthetic dyes	Hanapi et al., 2018
Azospirillum brasilense	DSMZ 1690	Promotion of plant growth under saline stress	Kadmiri et al., 2018
Clostridium acetobutylicum	DSMZ 79	Production of bio-butanol from waste lettuce leaves	Procentese et al., 2017
Thermotoga neapolitana	DSMZ 4359(T)	Hydrogen and lactic acid production	Pradhan et al., 2017
Bifidobacterium lactis and *Lactobacillus rhamnosus*	DSMZ 32269, and DSMZ 21690	Probiotic capsule against nonalcoholic fatty liver disease	Famouri et al., 2017
Pseudomonas sp.	DSMZ 13134	Plant growth promotion effect on maize	Mosimann et al., 2017
Sphingomonas azotifigens	DSMZ 18530T	Improve the growth of ryegrass due to nitrogen-fixing ability	Castanheira et al., 2017
Trichoderma reesei	DSMZ 970	Production of cellulose from potato peel residues	Taher et al., 2017
Bacillus amyloliquefaciens strain *fiply 3A*	DSMZ 22646	Broad-spectrum antifungal activity	Hajare et al., 2016
Lactobacillus plantarum	DSMZ 12028	Study on probiotics and evaluate innate immunity response	Cammarota et al., 2009
Pseudomonas sp.	DSMZ 13134	Used for rhizospheric engineering	Buddrus-Schiemann et al., 2010

for online sharing (http://www.accc.org.cn/). Out of the data retrieved from WoS, some preserved microbial strains on the application of sustainable agricultural practices are summarized in Table 2.

5.1. Microorganisms for the management of nutrients in soil and plants

Nutrient deficiency in agricultural soils has a significant impact on plant growth and development; subsequently, it disrupts the entire food chain influencing the human diet. Nutrients containing nitrogen (N), phosphorus (P) and potassium (K) are the building blocks of macronutrients such as proteins, lipids, and carbohydrates involved in plant development and improve the nutritional value of agricultural crops (Yin et al., 2018; Ye et al., 2019; Menegatti et al., 2021; Ye et al., 2022). The enrichment of N, P, and K nutrients with an assemblage of microorganisms directly or indirectly helps the productivity of crop plants, as well as the restoration of soil health (Miao et al., 2010; Bledsoe et al., 2020; Du et al., 2021; Baldwin-Kordick et al., 2022; Yang et al., 2022). For example, biofortification is the most promising technique for improving the bioavailability of micronutrients for agricultural crops (Yadav et al., 2022). The use of plant growth-promoting rhizobacteria (PGPR) has been reported to be a suitable alternative to improve crop nutrition (Santoyo et al., 2019a,b; Rojas-Padilla et al., 2020; dos Santos and Olivares, 2021). The reported genera of PGPRs are *Bacillus*, *Bradyrhizobium*, *Azotobacter, Azospirillum, Paenibacillus*, *Pseudomonas*, *Rhizobium*, which help in plant growth promotion and yield (Miao et al., 2010; Compant et al., 2019; Fan and Smith, 2021). The experiments were carried out to improve the uptake of nutrients by inoculated plants under field conditions and to retain the microbial diversity in the soil (Wachira et al., 2014). Symbiotic nitrogen fixation by beneficial bacterial strains such as *Rhizobium* promoted plant growth due to nitrogen acquisition and decreased dependency on nitrogen-based chemical fertilizers (Bhattacharjee et al., 2008; Jesus et al., 2018). Some microbes possess the potential to establish associations with a higher plant and eventually support supplementing crucial nutrients, by solubilizing organic and inorganic nutrient compounds present in the soil, such as phosphate, zinc, potassium, and sulfur (Vaishnav et al., 2015). For example, AMFs play an important role in this category, forming symbiotic associations with host plants and helping to access minerals and water (Shridhar, 2012; Lehmann and Rillig, 2015). Additionally, algal genera, such as *Anabaena*, *Oscillatoria*, and *Phormidium*, are also known to form symbiotic associations with plants and other microbes, contributing to the management of nutrients in plants (Choudhary et al., 2016; Múnera-Porras et al., 2020; Lee and Ryu, 2021).

5.2. Microorganisms for biotic stress management in plants

Microbial mediated resistance in plants is well known to overcome the harmful effect of different biotic factors (Enebe and Babalola, 2019; Nwokolo et al., 2021; Oukala et al., 2021; Pretorius et al., 2021). There are two types of microbial-induced resistance, namely, systemic acquired resistance (SAR) and induced systemic resistance (ISR). In both conditions, plant defenses are stimulated through pre-inoculation with beneficial microbes that result in resistance in plants upon pathogen challenge (Gao et al., 2015; Berendsen et al., 2018; Klessig et al., 2018; Shine et al., 2019;

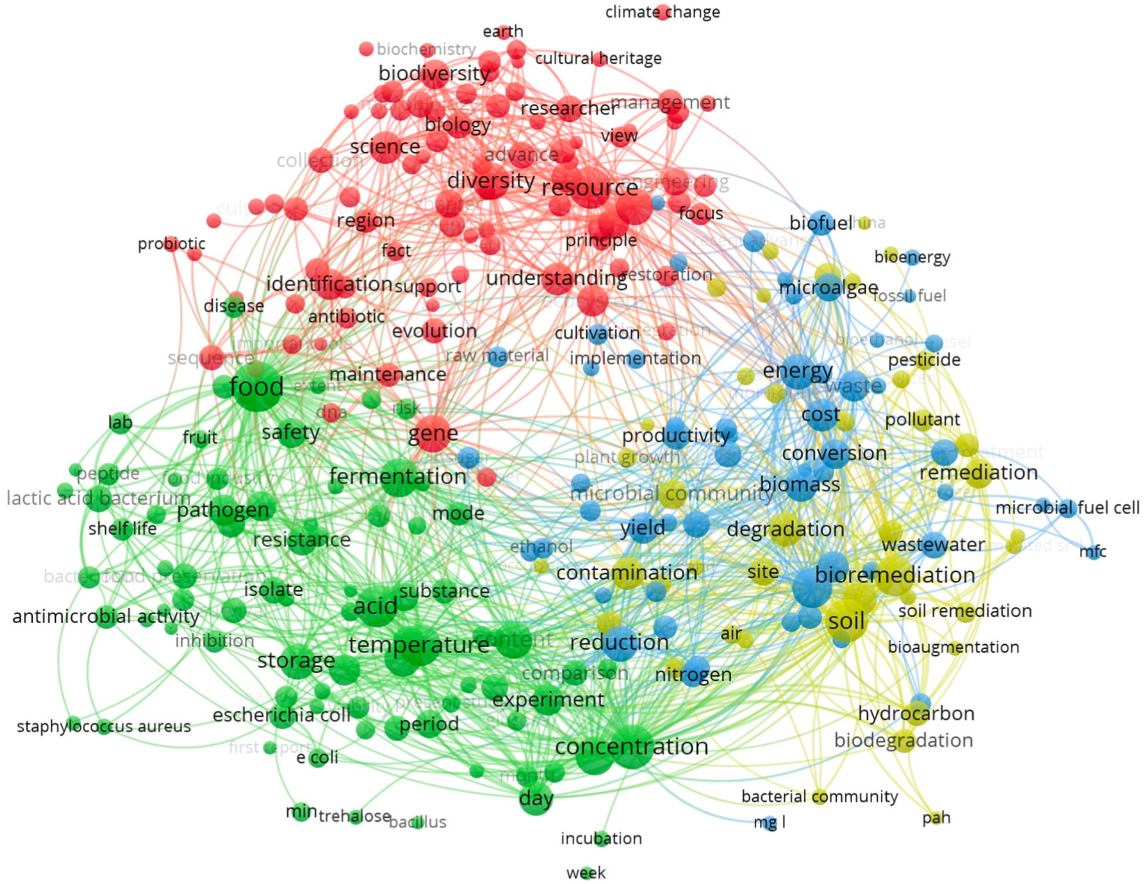


Fig. 3. Bibliographic analysis map of VOSviewer obtained by using the Scopus database. The data was updated on January 10, 2022.

Park and Ryu, 2021; Tzipilevich et al., 2021; Wen et al., 2021). In SAR, pathogenesis-related proteins (PR) and salicylic acid (SA) are induced to control pathogen infection, while ISR promoted jasmonates and ethylene. Other defense-responsive activities are also induced in plants during beneficial microbe interaction. These activities are reprogramming of the antioxidative machinery, the production of phenolic compounds, and the deposition of lignin in the cell wall (Rajput et al., 2019; Nephali et al., 2020).

There are several other modes used by beneficial microbes as mechanisms against plant pathogens, especially allelopathy, niche competition, and antibiosis (Beneduzi et al., 2012; Shahrtash and Brown, 2021). In allelopathy, microbes produced a subset of metabolites including antibiotics, volatiles, enzymes, and others during host interactions (Valenzuela-Ruiz et al., 2019; Valenzuela Ruiz et al., 2020). The action mode of these allelochemicals is very similar to antibiotics and lytic enzymes that inhibit bacterial growth and colonization by rupturing their cell wall (Villa-Rodriguez et al., 2019; Hickman et al., 2021; Ladhari et al., 2022). A volatile compound, hydrogen cyanide (HCN), is produced from various bacterial genera, including *Rhizobium*, *Alcaligenes*, *Bacillus*, *Aeromonas*, *Pseudomonas* and others, which can inhibit microbial growth and suppress several fungal diseases such as root-knot and black rot (Beneduzi et al., 2012; Egamberdieva et al., 2022; Essalimi et al., 2022). In niche competition, beneficial microbes compete with soil pathogens for the acquisition of essential nutrients and better colonization. For example, exopolysaccharides produced by PGPR have better colonization efficiency compared to other microbes, and the mats around the root surface formed by exopolysaccharide (EPS) restrict the growth of plant pathogen (Jain et al., 2018). Siderophore-producing bacteria inhibit the growth of pathogenic fungi by sequestering iron (de los Santos-Villalobos et al., 2012; De Los Santos-Villalobos et al., 2018).

Antibiosis is a self-protective mechanism of microbes against pathogens present in soil. Bacterial genera such as *Pseudomonas* and *Bacillus,* and fungal genera such as *Trichoderma*, *Gliocladium*, *Ampelomyces*, and *Chaetomium* have been widely reported to produce antibiotics to suppress various soil-borne pathogens (Jain et al., 2018). For example, *Bacillus* sp. SJ5 (MCC 2607) produces different volatile antifungal compounds that inhibit the growth of fungal pathogens and the induced defense mechanism in soybean plants (Jain et al., 2016). Sowmya et al. (2012) have reported *Pseudomonas putida* (NAIMCC-B-01212) as a biological control agent for application in soil infested with the nematode *Meloidogyne incognita*. In addition, *Trichoderma asperellum* BHU P-1 and *Ochrobactrum* sp. BHU PB-1 showed biocontrol activity against pure culture of *Fusarium oxysporum* f. sp. *lycopersici* and protected the tomato plant against fusarium wilt (Singh et al., 2019; Vaishnav et al., 2019).

5.3. Microorganisms for the management of abiotic stress in plants

Some plants adapt themselves to adverse environments through habitat-adapted symbiosis, in which the plant improves its ability to maintain through symbiotic associations with microbes (Vaishnav et al., 2014; Harman and Uphoff, 2019; Pankievicz et al., 2019; Hou et al., 2021). Microorganisms have diverse molecular adaptation mechanisms that make them tolerant of a particular extreme event. These stress-tolerant microbes are used as bioinoculants in plants for stress alleviation and tolerance. The concept of microbial-elicited induced systemic tolerance (IST) to abiotic stresses has been reviewed by Vaishnav et al. (2019). Plant growth-promoting rhizobacteria including *Bacillus*, *Pseudomonas*, *Burkholderia*, *Enterobacter*, *Azospirillum*, *Rhizobium*, and *Serratia* have been reported as bioinoculants to induce systemic tolerance (IST) in plants (Glick, 2014; Lau et al., 2020; Saad et al., 2020; Orozco-Mosqueda et al., 2021; Petersen et al., 2021). Indeed, some microbes have the potential to tolerate the stresses, and then promoting plant growth and development. The mechanism of PGPR-mediated IST is the production of ACC-deaminase, volatiles,

Table 2
A list of some microorganisms conserved in Indian culture collections and studied for agricultural purposes such as nutrient management, plant growth promotion, plant protection, etc.

Microorganisms	Culture collection accession number	Application	Reference
Pseudomonas putida	NAIMCC - B-01212	Reduced the growth of *Meloidogyne incognita* and *Erwinia carotovora* and enhanced yield of carrot	Singh et al., 2019
Pseudomonas simiae AU	MTCC 12057	Produce VOCs for improved salt tolerance in soybean	Vaishnav et al., 2015, 2016
Rosealteles terrae	MTCC 9755	Increased N, P, K contents in sugarcane	Muthukumarasamy et al., 2017
Bacillus aryabhattai MDSR14;	NAIMCC-B-01442	Zinc-solubilizing bacteria improve zinc biofortification in soybean and wheat	Ramesh et al., 2014;
B. cereus KMR-5	NAIMCC-B-01509		Khande et al., 2017
Trichoderma afroharzianum	NAIMCC-F-01938	Bio-control against powdery mildew disease	Sawant et al., 2017
T. asperelloides	NAIMCC-F-01965		
Trichoderma. viride	NAIMCC-F-02976	Biocontrol against tomato wilt pathogen, *Fusarium oxysporum*, and chilli damping-off pathogen, *Pythium aphanidermatum*	Singh et al., 2014
Trichoderma koningii	MTCC796	Biocontrol against *S. rolfsii* (causing stem rot on groundnut)	Parmar et al., 2015
Verticillium sp.	MTCC3692	Entomopathogenic	Singh and Prakash, 2015
Metarhizium anisopliae	MTCC892	Larvicidal effects of the entomopathogenic fungus	Vyas et al., 2015
Beauveria bassiana	MTCC2028	Biocontrol agent (entomopathogenic) against the main economic crop pest *Pieris brassicae* L.	Dhawan and Joshi, 2017
Metarhizium anisopliae	MTCC4034	Biological control agent against tea termite *Microtermes obesi* Holmgren	Singh et al., 2011
Metarhizium anisopliae	MTCC4645		
Beauveria bassiana	MTCC4795		
Beauveria bassiana	MTCC4514		
Candida tropicalis	NCIM 3321	Bacterial-derived phytase has plant growth promotion ability	Puppala et al., 2018
Pseudomonas fragi CS11RH1	MTCC 8984	Phosphate solubilization and growth promotion	Selvakumar et al., 2009
Sinorhizobium meliloti	MTCC100	Produced intra- and extra cellular polymers	Devi et al., 2012
Bacillus pumilus	MTCC1640	Biocontrol of *Fusarium* wilt	Akhtar et al., 2010
Pseudomonas alcaligenes	MTCC493		
Pseudomonas putida	MTCC3604	Nodulation in chickpea	Akhtar and Siddiqui, 2009
Pseudomonas alcaligenes	MTCC493		
Paenibacillus polymyxa	MTCC122		
Bradyrhizobium liaoningensis	MTCC10753	Nodulation in soybean	Sharma et al., 2012
Pseudomonas putida	MTCC5279	*P. putida* promotes the growth in *A. thaliana* under salinity, P starved, and P starved-salinity stressed conditions	Srivastava and Srivastava, 2020
Ochrobactrum intermedium BB12	NAIMCC-B-02114	Promotes alleviation of Cd stress in Spinach plant (*Spinacia oleracea* L.)	Renu et al., 2022

MTCC- Microbial Type Culture Collection and Gene Bank.
NCIM- National Collection of Industrial Microorganisms.
NAIMCC- National Agriculturally Important Microbial Culture Collection.

phytohormones, exopolysaccharides and organic acids, which have been used by plants to tolerate environmental stress (Forni et al., 2017; Santoyo et al., 2019a,b; Carlson et al., 2020). Under tolerance to drought and salt, PGPR confers tolerance by regulating the levels of proteins, polysaccharides, and important phytohormones like ACC-deaminase. ACC-deaminase-producing bacteria around the root surface or in the root have the potential to reduce the high level of ACC, and subsequently reduce ethylene production in response to stress conditions (Kumari et al., 2016a). Kumari et al. (2016b) reported that inoculation of wild-type and mutant *Pseudomonas simiae* strains producing ACC deaminase in soybean plants induced longer roots and helped to increase the relative water content of deep soil, under conditions of drought and salt stress (Sandhya et al., 2019; Kumari et al., 2016b). In addition, microbial secreted EPS supports plants in both drought and salt stress conditions through various mechanisms (Ashraf et al., 2004; Coleman-Derr and Tringe, 2014; Getahun et al., 2020; Ma et al., 2020; Morcillo and Manzanera, 2021). EPS can form micro/macroaggregates of soil, increasing moisture retention capacity and cation exchange property content under saline conditions (Gupta et al., 2016; Ayangbenro and Babalola, 2020). They are also of paramount importance in mature biofilm formation and functional nodules in legume–rhizobia symbiosis (Stoodley et al., 2002; Skorupska et al., 2006; Balsanelli et al., 2014; Janczarek et al., 2015).

PGPR are also involved in altering hormonal signaling in plants during stress conditions by producing indole-3-acetic acid, abscisic acid, cytokinin and gibberellic acid hormones that directly affect plant growth (Chen et al., 2007; Porcel et al., 2014; Tsukanova et al., 2017; Kudoyarova et al., 2019). However, there is still a lack of comprehensive analysis of the roles of plant hormones in the interaction of the host plant with the PGPR. Inoculation of PGPR under stress conditions induced osmolytes and antioxidant activities in the plants resulted in the alleviation of the level of reactive oxygen species (ROS) that could damage lipids, nucleic acids and proteins of the plant cellular system (Halo et al., 2015). The bacterial proline synthesis gene proBA was transferred to plants via genetic engineering that increases the free proline content resulting in induced systemic tolerance in transgenic plants. In a recent study, it was reported that *Pseudomonas simiae* AU alleviates drought stress in soybean plants by regulating the expression of osmolyte genes and modulation of phytohormone signaling (Vaishnav and Choudhary, 2018). On the other hand, volatile organic compounds (VOCs) are also microbial mechanisms involved in IST signaling in plants. These VOCs are airborne signals produced below ground but interact with both rhizospheric and phyllospheric parts of plants (Cho et al., 2008; Audrain et al., 2015; Delory et al., 2016; Ninkovic et al., 2016; Schulz-Bohm et al., 2017; Fincheira and Quiroz, 2018; Bouwmeester et al., 2019; Ninkovic et al., 2019; Kong et al., 2021; Raza et al., 2021; Sharifi et al., 2022). The VOCs emitted by PGPR negatively regulate Na^+ levels by regulating HKT1 and Na^+/H transporters in plants under salt stress. Some VOCs, *2R*, *3R*-butanediol, and acetoin, have been reported to regulate the signaling of phytohormones to induce tolerance to drought in plants (Vaishnav et al., 2016). Similarly, Smith and Read (2008) demonstrated that *P. simiae* (MTCC-12057) produces some VOCs, namely, nitroguaiacol, quinoline, and benzothiazole, which participated in IST mechanism and plant growth promotion of soybean under salt stress.

A large group of plant species, including crops, are associated with AMF for nutritional benefits and stress tolerance (Balliu et al., 2015; Thirkell et al., 2017; Diagne et al., 2020). AMF produces structures similar to arbuscules during association, which increases surface absorbing capacity in roots by exposing a large volume of soil and providing macronutrients (N, P, K) and micronutrients (Ca, Zn, S) (Begum et al., 2019). The extra radical hyphae of AMF increase the water uptake ability of roots under water-limiting conditions. Furthermore, AMF symbiosis also regulates phytohormone signaling, antioxidant compounds, and osmolyte contents in plants under drought and salinity stress conditions (Barea et al., 2002;

Egamberdieva and Lugtenberg, 2014; Hashem et al., 2018; Bahadur et al., 2019; Al-Arjani et al., 2020; Pons et al., 2020). AMF can also improve soil characteristics under normal or stressed environmental conditions. AMFs can act as natural growth regulators for the soil microflora. The influence zone of mycorrhizae is known as the mycorrhizosphere, in which AMF also forms a symbiotic association with other microorganisms inside the soil. The functioning of AMF is mediated by the mycorrhizosphere microbiota. The AMF associated with PGPR in the mycorrhizosphere increases the uptake of nutrients by plants under stress conditions (Wu et al., 2014; Diagne et al., 2020). A recent report witnessed that the application of AMF and P-solubilizing *Pseudomonas fluorescens* (ATCC-17400) significantly enhances morphological traits and nutrient content (calcium, potassium, magnesium, phosphorus, iron, and zinc) resulting in high sesame production (Yadav et al., 2021). Additionally, the glomalin content in the soil is believed to maintain the water content under extreme environmental conditions, regulating the homeostasis of water in plants during stress conditions (Taffner et al., 2018).

Archaea (thermophiles, psychrophiles, and halophiles) are present in extreme habitat conditions. Archaea have been reported to colonize the plant environment and improve habitat-imposed stress tolerance in plants by encouraging IAA hormone, nitrogen fixation, siderophore production and nutrient supply under abiotic stress conditions (Grover et al., 2016; Odelade and Babalola, 2019; Alori et al., 2020). Similarly, actinomycetes can also survive under stress conditions, such as extreme temperature, wide pH range, and salinity. Actinomycetes genera such as *Streptomyces, Actinoplanes* and *Micromonospora* have been reported to produce several PGP activities including IAA production, Pi-solubilization, ACC-deaminase production, siderophore production, and biocontrol activity against phytopathogens (Anwar et al., 2016). Several reports are available on the potential role of actinomycetes in alleviating environmental stresses in crop plants (Davis et al., 2003; Smith-Moore and Grunden, 2018; Djebaili et al., 2021).

6. Microorganisms for bioremediation of pollutants

Bioremediation is a promising technology for the absorption or adsorption of xenobiotic compounds, explosives, and several other humans and environmental hazardous compounds through plants or microorganisms (algae, fungi, bacteria, and actinomycetes) or their enzymes by altering them into nontoxic elements and consequently forming innocuous end products (Shukla et al., 2009, 2010; Gkorezis et al., 2016; Ojuederie and Babalola, 2017; Rylott and Bruce, 2019; Cowan et al., 2022; Hui et al., 2022). The possibility to apply a particular bioremediation technology must be evaluated by considering several parameters, such as site conditions, pH, microbial population, nutrients availability, oxygen, temperature, water, and the typology, amount, and toxicity of pollutants (Fig. 4).

To improve the bioremediation process, various approaches have been employed depending on the type of contaminated environment. Among them, biostimulation involves the enrichment of nutrients at polluted sites that support the growth of native microflora for the degradation of pollutants (Shukla et al., 2014; Siles and Margesin, 2018; Ijoma et al., 2019). Biostimulation can be performed by the addition of various forms of rate-limiting nutrients and electron acceptors such as phosphorus, nitrogen, oxygen, or carbon. For example, to biostimulate *Kocuria rosea* MTCC 1532, sucrose and urea were added in the liquid semisynthetic medium (Parshetti et al., 2006). However, in bioaugmentation, the application of wild or genetically modified microorganisms is added to polluted sites, where native microflora fail to degrade contaminants (Perpetuo et al., 2011; Myazin et al., 2021). Furthermore, microbes can adsorb, absorb, precipitate, and transform toxic heavy metals in the plant rhizosphere (Rhodes, 2003). The general mechanisms of microbial-mediated bioremediation are presented in Fig. 5. Some of the studies on microorganisms (procured from culture collections) reported in the bioremediation process are listed in Table 3.

Mycoremediation is an on-site eco-friendly remediation strategy used to remove the hazardous pollutants from a particular contaminated area using fungi (Rhodes, 2013; Shukla et al., 2019). Fungal mycelium is capable of degrading the content of lignin and cellulose by secreting extracellular enzymes and acids. Interestingly, fungal mycotoxins are also a potential candidate to break down aromatic and chlorinated compounds (Chanda et al., 2016). The genus *Penicillium* produces mycotoxins such as citrinin and patulin. Their roles in the biosorption of heavy metals and the metal ions and the biodegradation of hydrocarbons, such as phenol, halogenated compounds, and PAH have been reviewed (Leitão, 2009). In addition, few species of mycotoxin producing *Fusarium* such as *F. graminearum* has also been described for biodegrading carbofuran pesticide (Salama, 1998; Murphy et al., 1996). However, a targeted strategy is required to determine the correct microbial species to target a specific contaminant to strengthen the concept of bioremediation. Recently, use of PGPR in bioremediation of toxic pollutants has been emphasised (Vaishnav et al., 2022), which suggest the exploration of such rhizobacteria that possess both PGP and toxic degradation activities. The biotechnological potential of extremophiles for bioremediation of xenobiotics is reviewed by Shukla and Singh (2020). They concluded that extremophiles could an important group of microbes that play a very crucial role in bioremediation for maintaining environmental sustainability.

7. Application of microorganisms in industry

7.1. Enzyme production

Microorganisms are considered to be the most significant and convenient sources of industrial enzymes. They have the potential to generate large amounts of various industrially relevant enzymes under optimal growth conditions (Gurung et al., 2013; Atalah et al., 2019; Yu et al., 2019; Intasian et al., 2021). The researchers have used a variety of culture media for the cultivation and production of the enzymes in the minimum time possible. Furthermore, it is easy to genetically manipulate microorganisms to enhance the production of desired enzymes and natural plant products at a certain level (Ng et al., 2017; Cubas-Cano et al., 2018; Cravens et al., 2019; McCarty and Ledesma-Amaro, 2019). Thus, the isolation, recovery, and purification processes are naturally easier with microbial enzymes compared to enzyme recovery from animals or plants (Wang et al., 2012a,b). Microbial enzymes have the potential to perform well under a wide range of physicochemical conditions. In this context, microbial enzymes are classified as acidophilic, alkalophilic, and thermophilic (in nature). Microorganisms possess systems to produce thermostable enzymes, which are functionally active at higher temperatures in large-scale industrial reactions and minimize contamination. Thermostable enzymes enhance the mass transfer and reduction substrate viscosity during their activity (Kumar and Takagi, 1999). For example, thermostable xylanase is the best choice in the brewing industries for the mashing process. Additionally, thermostable laccase, derived from plants, is used in textile industries for dyeing, pulping, and bioremediation processes (Karigar and Rao, 2011). Different types of microbial enzymes are applicable for multiple industrial purposes. Acid/neutral proteinase, glucose oxidase, amylase, and xylanase are used in the food industries. Protease, laccase, endoglycosidase, and lipase are used in pharmaceutical industries. Lipase, amylase, alkaline/neutral protease, and xylanase are used in the paper and leather industries. Amylase, pectate lyase, cellulase, laccase, ligninase, protease, collagenase, and cutinase are used in textile industries (Singh et al., 2016). Glycosyltransferase, acyltransferase, glucose isomerase, laccase nitrile hydratase are used in organic acid production (Riffaldi et al., 2006). Manganese peroxidase, tyrosinase, and lignin peroxidase are used for the removal of chlorinated and phenolic compounds from waste effluents. The microbial enzymes have also been utilized to recycle waste materials to recover oil from oilseeds, convert starch to sugar, and convert whey to other useful products (Le Roes-Hill and Prins, 2016).

In addition, microbial enzymes are used for the treatment of human diseases or disorders (Vellard, 2003; Anbu et al., 2017). For example, a congenital deficiency of sucrase-isomaltase is cured by an oral dosage of fucosidase enzyme for the digestion of sucrose (Treem et al., 1999). Similarly, heparinase isolated from *Streptomyces variabilis*

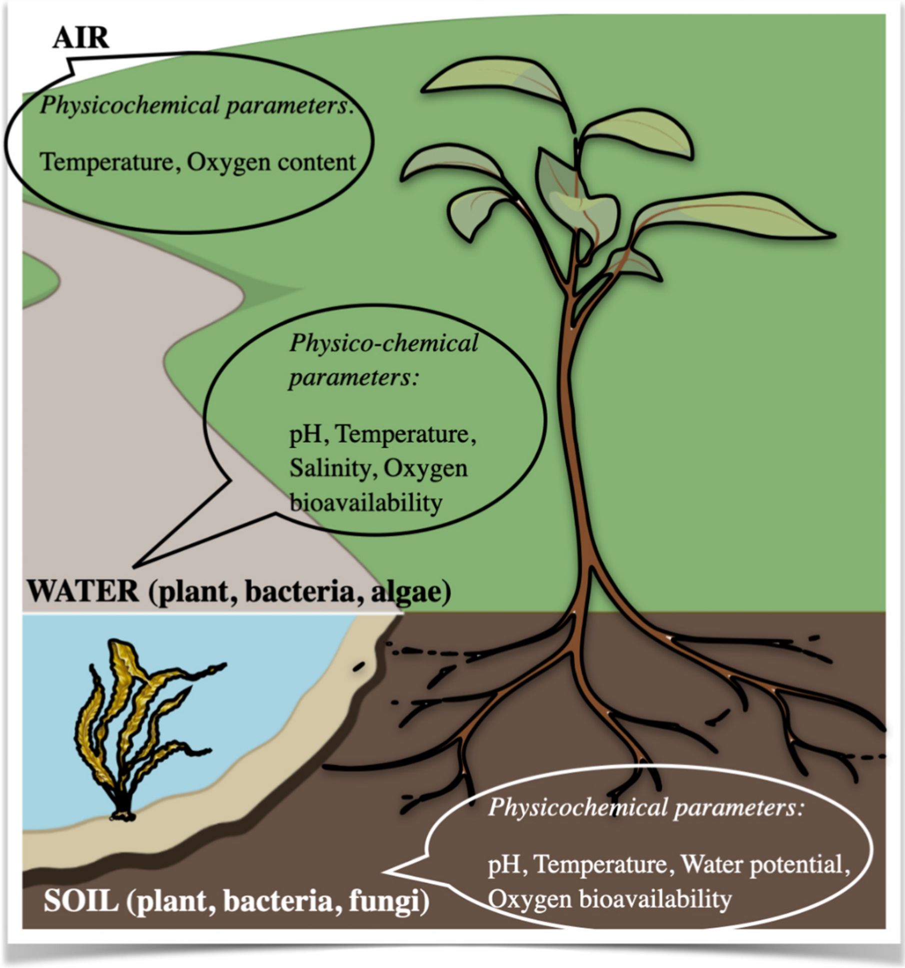


Fig. 4. Factors that affect bioremediation and biodegradation in water, air and soil.

MTCC 12266 can be used for the treatment of cardiovascular disorders such as arterial/venous thrombosis (Singh et al., 2019). Furthermore, phenylalanine ammonia-lyase is used to degrade phenylalanine in genetic phenylketonuria disorder (Sarkissian et al., 1999). Several conserved microbes such as *Trichoderma harzianum* MTCC-4358, *Trichoderma viride* ITCC-1433, *Bacillus* sp. MCC 2727, and *Fusarium*

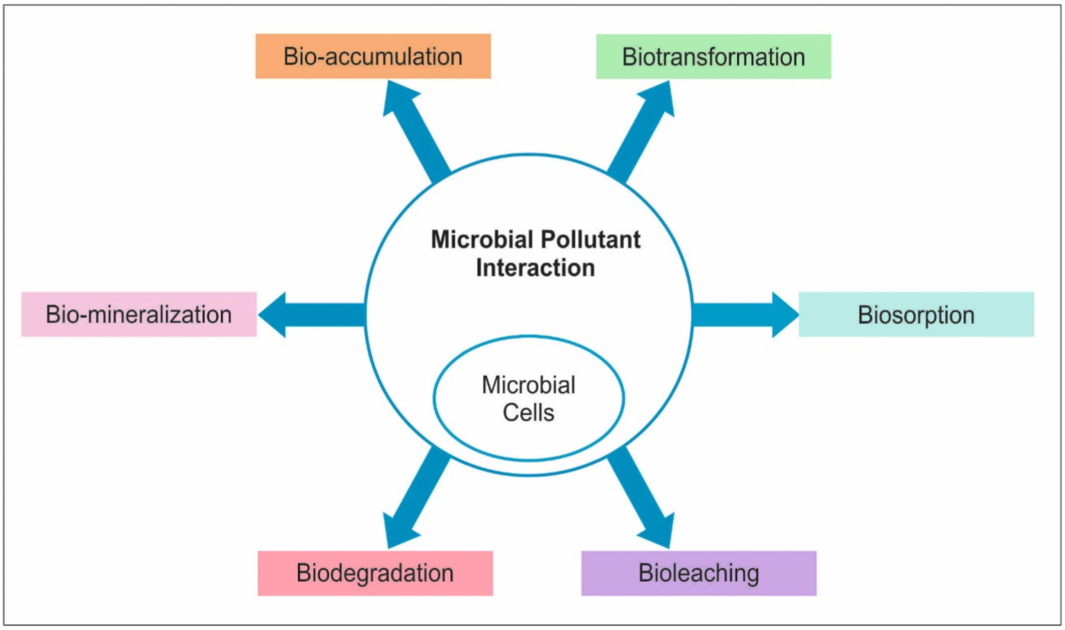


Fig. 5. A diagrammatic representation of different methods for interactions between microbes and pollutants in the bioremediation process.

Table 3

A list of some microorganisms conserved in Indian culture collections studied for the bioremediation of different types of pollutants.

Micrmisms	Culture collection accession number	Application	Reference
Candida tropicalis	NCIM 3556	Phenol degradation	Varma and Gaikwad, 2009
Clostridium sporogenes	NCIM 2337	Produce different solvent using paper mill sludge	Gogoi et al., 2018
Pseudomonas aeruginosa	NCIM 5514	Degradation of petroleum hydrocarbons	Varjani and Upasani, 2016
Pseudomonas aeruginosa	NCIM 5514	Crude oil degradation	Varjani and Upasani, 2017
Bacillus subtilis BMT4	MTCC 9447	Treated automobile contamination in soil	Lily et al., 2009
Kocuria rosea	MTCC 1532	Malachite green degradation	Parshetti et al., 2006
Bacillus cereus	NAIMCC-B-01818	Polythene degradation	Sellamuthu et al., 2018
Pseudomonas putida	MTCC 10510	Decolorization of textile dyes effluent	Garg et al., 2012
Trametes hirsuta	MTCC 136	Degradation of natural organic pollutant	Jeenathunisa et al., 2019
Ochrobactrum intermedium BB12	NAIMCC-B-02114	Promotes alleviation of Cd stress in Spinach plant (*Spinacia oleracea* L.)	Renu et al., 2022

MTCC- Microbial Type Culture Collection and Gene Bank.
NCIM- National Collection of Industrial Microorganisms.
NAIMCC- National Agriculturally Important Microbial Culture Collection.

Table 4

A list of some microorganisms conserved in Indian culture collection studied for industrial purposes like enzyme production, biofuels, antimicrobial compounds, etc.

Microorganisms	Culture collection accession number	Application	Reference
Enzymes production			
Trichoderma reesei	MTCC164	Cellulase	Chandra et al., 2009
Trichoderma citrinoviride	MTCC2418		
Trichoderma koningii	MTCC796		
Trichoderma fasciculatum	MTCC2771		
Trichoderma virens	MTCC794		
Trichoderma harzianum	MTCC 4358	Xylanase	Sakthiselvan et al., 2012
Trichoderma harzianum	MTCC10841	Tannase	Iqbal and Kapoor, 2012
Fomes durissimus	MTCC1173	Mn peroxidase	Singh et al., 2011
Pseudomonas aeruginosa BUP2	MTCC5924	Production of lipase that inhibits rumen of Malabari goat	Unni et al., 2016
Aspergillus niger	MTCC 1323	Production of protease, amylase, and pectinase and their application in biofilm degradation	Singh et al., 2015
Aspergillus foetidus	MTCC6322	Production of alpha-galactosidase and its application in soymilk hydrolysis	Boopathy et al., 2016
Bacillus pumilus	NAIMCC-B-01415	Cellulase enzyme	Padaria et al., 2014
Saccharomyces cerevisiae and *Scheffersomyces stipitis*	MTCC 174 and NCIM- 3497 respectively	Ethanol production	Singh et al., 2014
Bacillus sphaericus	MTCC7542	Polygalacturonase	Jayani et al., 2010
Bacillus licheniformis	MTCC 2617	Production of alpha-amylase	Divakaran et al., 2011
Biofuels			
Pichia stipitis and *Pachysolen tannophilus*	NCIM3498 and MTCC 1077	Ethanol production from peels of *Ananas cosmosus* (L.) Merr.	Bhatia and Johri, 2015
Yarrowia lipolytica	NCIM 3589	Biodiesel production from waste cooking oil by a mutant strain	Katre et al., 2017
Chlorella pyrenoidosa	NCIM 2738	Mitigate the pollution load in dairy wastewater and also produce biofuel	Kothari et al., 2012
Antimicrobial compounds			
Aspergillus giganteus	MTCC 8408	Biosynthesis of low molecular weight antifungal proteins	Dutta and Debnath, 2018
Lactobacillus acidophilus	NCIM 2903	Synthesis of a biosurfactant that inhibits biofilm	Satpute et al., 2018
Others			
Lactobacillus plantarum	MTCC9510	Antitumor activity of bacterial derived polysaccharides	Ismail and Nampoothiri, 2013
Pseudomonas sp.	NCIM 5235	Caffeine-degrading bacteria	Retnadhas and Gummadi, 2018
Hapalosiphon intricatus	NAIMCC-C-00121,	Production of polyphenols and flavonoids under salt stress	Singh et al., 2014
Bacillus circulans	MTCC 8573	L-asparaginase production	Hymavathi et al., 2009
Bacillus subtilis	MTCC 121	Produce extracellular polysaccharide (EPS) like cellulose	Vijayabaskar et al., 2011
Bacillus subtilis	MTCC441	Silver nanoparticles for antimicrobial activity	Venkatesan et al., 2013
Bacillus sphaericus	NCIM5149	Produce polyhydroxybutyrate (PHB) using agro-industrial residues	Ramadas et al., 2009
Oscillatoria acuta	NAIMCC-C-17	Produce antioxidant and polyphenols	Singh et al., 2017a,b,c
Stenotrophomonas sp.	MTCC5978	Microbial silver nanoparticles inhibited the growth of chickpea collar rot pathogen *S. rolfsii*	Mishra et al., 2017
Bacillus brevis	NCIM 2533	Microbial silver nanoparticles have antibacterial activity against pathogenic bacteria	Saravanan et al., 2018
Phanerochaete chrysosporium	MTCC 787	Microbial silver nanoparticles have antibacterial activity against pathogenic bacteria	Saravanan et al., 2018
Bacillus sphaericus	MTCC5100	Monitoring lead in milk	Verma et al., 2011
Flavobacterium indicum	MTCC6936	Cyanide detection using immobilized enzyme	Kumar et al., 2018
Pseudomonas alcaligenes	MTCC5264	To check the caffeine degrading capacity	Babu et al., 2007
Stenotrophomonas sp. *BHU-S7*	MTCC5978	Management of pathogens	Mishra et al., 2017
Streptomyces variabilis	MTCC2266	Heparinase production	Singh et al., 2019

MTCC- Microbial Type Culture Collection and Gene Bank.
NCIM- National Collection of Industrial Microorganisms.
NAIMCC- National Agriculturally Important Microbial Culture Collection.

solani NAIMCC-F-02956, are actively being used to produce various enzymes for industrial applications (Table 4).

7.2. Biofuel production

Recently, the crisis of fuel and increased energy demands have been proposed to be fulfilled by microorganisms such as cyanobacteria, yeasts, and microalgae that are being potentially recognized for the inherent production of bioethanol and biodiesel (Osman et al., 2021). Fermentation is the most important alternative for the production of bioethanol by the conversion of saccharides into alcohol or acid products through the process of anaerobic respiration. Anaerobic microbes have been well proven to convert biomass into energy forms in a process that generates carbon dioxide and methane, and consequently the production of 'biogas' can be used as fuel for the generation of electricity (Harasimowicz et al., 2007). Workers have put forth great interest to increase ethanol fuel production by starch fermentation using different substrates such as molasses, starch-based substrate, sweet sorghum cane extract, lignocellulose, and other waste. *Saccharomyces cerevisiae* (yeast) perform the catalytic digestion of starch-based substrates such as husk (Singh et al., 2014) sugar beet pulp, waste from cassava starch production, etc. leading to the production of ethanol and carbon dioxide as a product (Akaracharanya et al., 2011). On the other hand, researchers are proposing different studies to exploit the potential of photosynthetic bacteria to produce bioethanol. Photosynthetic prokaryotes such as cyanobacteria are studied on a large scale to enhance favorable genetic traits. Genetic manipulations of cyanobacteria have been performed for carbon utilization and resulted in the direct generation of bioethanol through the metabolic pathway (Deng and Coleman, 1999). In addition, the gene coding for ethanol synthesis was isolated from the bacterium *Zymomonas mobilis* and cloned into a suitable vector and then transformed into the *Synechococcus* cyanobacterium (Deng and Coleman, 1999). The recombinant cyanobacteria *Synechococcus* synthesize ethanol directly, which diffuses from cells into the culture medium.

Among these biofuels, biodiesel production gains much impetus and attention due to its high accumulation of lipids (20–75 %), which could be a potential alternative fuel for diesel engines. Microalgae are considered to be as the main contributors to the production of biodiesel worldwide. These algae possess the inherent potential to utilize CO_2 and fix more than 40 % global carbon fixation (Parker et al., 2008). It is reported that most algae can produce energy-rich oils, and various algal species have been found to accumulate high levels of oil in biomass. Microalgae (*Anabaena cylindrica*, *Aphanizomenon flos-aquae, Chlorella pyrenoidosa*, *Dunaliella salina*, and *Arthrospira maxima*) have advantages over terrestrial plants. Algal species, such as *Botryococcus* sp., have the potential to accumulate long-chain hydrocarbons up to 50 % of their total dry biomass (Harun et al., 2010). Although some specific microbes such as *Yarrowia lipolytica* NCIM 3589 and *Chlorella pyrenoidosa* NCIM 2738 are used as a source of biodiesel and bioethanol, none of them were ideal because the large production of biodiesel requires a lot of tools, equipment, energy, water, and nutrients for each step separately (Kothari et al., 2012; Katre et al., 2017).

7.3. Biosensor

A biosensor is a device that is potentially used to associate biomolecules along with transducer molecules to produce a signal that depends on the concentration of analyte (Park et al., 2013; Anand et al., 2022a). Signal generation is due to the result of a change in protons concentration, and further, there may be release or uptake of gases that are transported due to the metabolism of the target compound by the biological recognition element (Lei et al., 2006). The transducer adapts the biological signal to a current or potential. Two main mechanisms by which microbial biosensors can promote a specific reaction during the biosensing process are recognized: a) alteration of cell metabolism in the presence of the detected analyte and b) inhibition of cellular respiration. The change in gene expression of the sensing element induced by the specific analyte can be detected and/or quantified (see Fig. 6).

Various substances such as antibodies, enzymes, receptors, microbes, animals, and plant cells have been used as sensing elements. It was shown that microorganisms offer various advantages over others because they have the potential to sniff a wide range of chemical substances and ease for genetic manipulation, which makes them ideal for biological sensing materials. To date, various microorganisms such as *Pseudomonas putida*, *Bacillus subtilis*, and *P. fluorescens* have been exploited as microbial biosensors (Dai and Choi, 2013). Zhao et al. (2009) isolated a *Methylobacterium organophilium* ME25 (EU567066) which is methanol utilizing strain and prepared a methanol-based sensor using this strain.

Because a microbial biosensor is based on the close association of microbes and transducers, its assembly needs immobilization on a transducer in juxtaposition (Park et al., 2013). In the last decade, a wide development has been made in a variety of biosensors for the detection of different compounds such as ethanol, total sugars, sucrose, *p*-nitrophenol, cyanide, organophosphate, heavy metals such as chromium, penicillin, and trichloroethylene from different environments (Dai and Choi, 2013). It could be due to their low operating cost, longer shelf life, and potential to respond in the full range of optimum pH and temperature (Dai and Choi, 2013). However, some specific areas are of utmost importance to develop microbial biosensors for their application in crop improvement, bioremediation, and the quality of food products. Since microbes residing under moderate temperatures cannot withstand harsh conditions, there is an urgent need to use extremophilic microbes to design biosensors. High-throughput technology in microbial genomics has allowed the use of microbial biosensors for various habitats that are still unexplored and their specific applications in the future (Park et al., 2013; Yeom et al., 2018).

7.4. Probiotic and prebiotic for humans

The intestinal tract is commonly inhabited by various microorganisms after the birth of an individual and in due course of their life circumstances, such as the consumption of antibiotics leads to a reduction in microorganism count in the gut (Francino, 2016; Langdon et al., 2016; Neuman et al., 2018; Konstantinidis et al., 2020; Ramirez et al., 2020; Xu et al., 2020). Bacteria from the gastrointestinal tract and some species of *Clostridium* are harmful to human health. The gut biota is known to maintain interrelations between bacteria and host tissues (Zheng et al., 2020). Probiotics increase the number of microorganisms in the host and induce anti-inflammatory activities (Plaza-Diaz et al., 2019; Cristofori et al., 2021; Raheem et al., 2021). Lactic acid bacteria are considered significant probiotic microorganisms, which are Gram-positive and microaerophilic in nature. Probiotics are generally added to the food material and enhance its nutritional and therapeutic value. Probiotics are embodied by cultures of live microorganisms (beneficial bacteria and some yeasts), which contribute to improving the quality of the end product and are used as antimicrobial medicine (Santos et al., 2009). Prebiotics are mostly used as food ingredients that are used as growth substrates for intestinal microorganisms.

Recent studies suggested that rice bran and its oil have prebiotic potential that could aid in the growth of essential microorganisms in the intestine, such as *Lactobacillus*, which is highly effective in controlling intestinal infections by pathogenic microbes such as *Salmonella* (Kumar et al., 2012; Tamura et al., 2012). Although probiotic research has been on the front line for decades, information on the interaction of complex systems is still modest. Therefore, it is urgent to introduce multiple omics platforms. This will allow the exploration of the microbiome with novel characterization using metagenomics and metatranscriptomics. Integration of these meta-*omics* will provide the datasets to understand the hidden mechanism of the role of probiotics in the immunization host system.

7.5. Nanotechnology

In the current scenario, nanomaterials are at the leading edge of the rapidly developing field of nanotechnology. The use of microbes for the biosynthesis of nanoparticles is a challenging area of bionanotechnology. There is a promising approach and interest in synthesizing nanomaterials

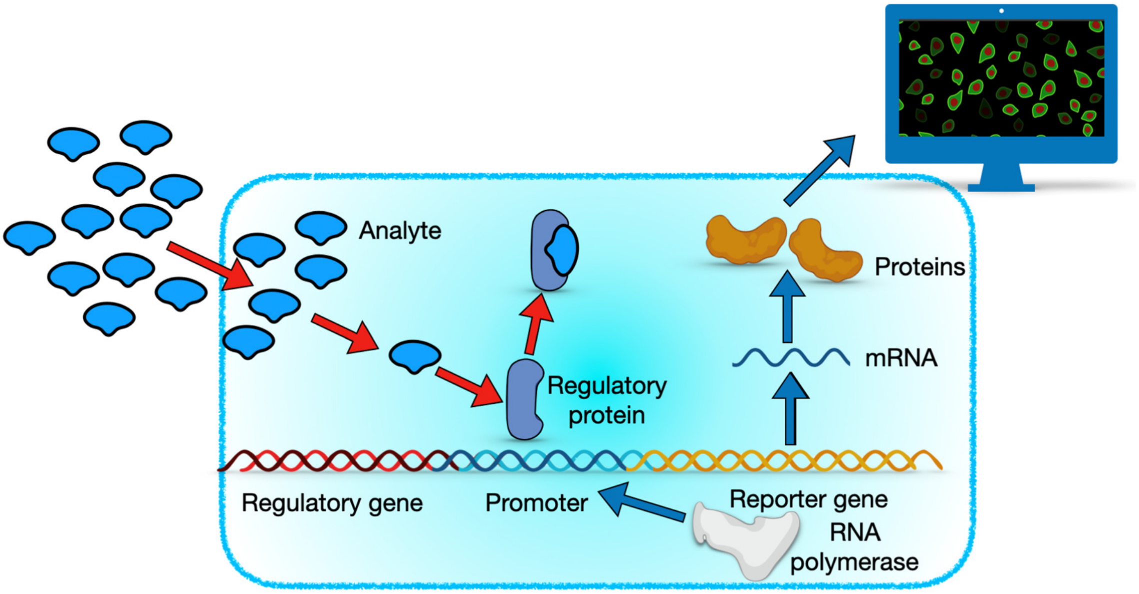


Fig. 6. Schema of a typical microbial biosensor mechanism. The regulatory mechanism is represented: the binding of the analyte to the regulatory protein allows the promoter region of RNA polymerase to express the reporter gene. Then, the expressed reporter protein is detected by a transducer.

due to their unique optical, chemical, and electronic properties (Mandal et al., 2006). The development of nanoscale structures in nanomaterials ensures their significant role in multiple areas for societal benefits. Microorganisms can produce nanosized entities with relevant applications (Kaur et al., 2021; Anand et al., 2022a,b). Different genera such as *Brevibacterium*, *Rhodococcus*, *Rhodobacter*, *Bacillus*, *Pseudomonas*, and other prokaryotes have been used to synthesize different nanoparticles (Ovais et al., 2018). Nanotechnology plays a vital role in agricultural production through the improvement of nutrients, and it can also contribute to the monitoring of water quality and pesticides for sustainable agriculture development (Prasad et al., 2014).

In the agriculture and food industry areas, the pertinent applications of various technologies such as nanotubes, fullerenes, biosensors, controlled delivery systems, and nanofiltration have been observed (Sabir et al., 2014). It is reported that nanotechnology is successfully applied for resource management of the agricultural field as a nanobiofertilizer, drug delivery mechanism in plants and to maintain the fertility of the soil. Nanofertilizers are suggested to be the best alternative to improve soil fertility in soils deficient in nutrients for sustainable agriculture (Elemike et al., 2019). In a study, silver nanoparticles were synthesized from *Stenotrophomonas* sp. MTCC-5978, which inhibited the growth of *Sclerotium rolfsii* sclerotia and chickpea collar rot caused by *S. rolfsii* (Mishra et al., 2017). In the case of bioremediation, microbial-mediated biosynthesis of nanomaterials is a promising biotechnological-based nanomanufacturing process that becomes a ‘green’ alternative approach to physically and chemically synthesized nanoparticles (Grasso et al., 2020). The microbial-mediated biosynthesis of metallic (also as alloys), nonmetallic, or metal oxide nanoparticles has been reported from several microbial strains of bacteria, yeast, molds, and microalgae. Nanoparticles from microbes can be synthesized by the use of extracellular or intracellular materials. After the desired material was recovered from microbes, the whole extract was mixed with metallic salt solution and the synthesis of nanoparticles was monitored by color changes in the solution. Recently, several studies have discussed the importance of microbe-based nanoparticle synthesis in fertilizer and pesticide aspects. Nanoparticle biosynthesis has been performed with bacteria (*Bacillus, Lactobacillus*, *Acinetobacter, Ochrobactrum, Stenotrophomonas* and *Pseudomonas*), fungi (*Trichothecium, Rhizopus, Fusarium, Trichoderma, Aspergillus* and *Penicillium*), yeast (*Saccharomyces, Schizosaccharomyces, Candida*, *Yarrowia, Rhodotorula, Cryptococcus* and *Pichia*), actinomycetes (*Streptomyces*) and algae (*Chlorella, Spirulina, Lyngbya, Oscillatoria willei, Chaetoceros, Isochrysis* and *Tetraselmis*) (Ali et al., 2020; Bahrulolum et al., 2021). Biosynthesis of metal nanoparticles through probiotic bacteria (*Lactobacillus* and *Bifidobacterium*) is most popular for agricultural purposes. Probiotics can directly affect living cells or indirectly regulate diverse metabolites. Probiotics have the potential to attract cations and initiate the nanoparticle biosynthesis process (Bahrulolum et al., 2021). In a recent study, a nanophos was prepared by combining nanophosphorus and phosphate solubilizing bacteria. The application of nanophos to maize plants increased plant growth and biomass and enhanced soil health in terms of the bacterial community and soil enzymatic activities (Chaudhary et al., 2021). However, there is an urgent need to understand the deeper knowledge of the molecular biology and genetic aspects behind microbial nanobiosynthetic pathways.

7.6. Role of microbes in food and antimicrobial products

Most of the foods and their products are undergoing processing before the reach the consumers. In these processes, microorganisms play an important role in the transformation of food into the desired end-product, such as the fermentation of rice, bread, and alcoholic beverages such as beer and wine, as well as various fermented dairy products such as cheese and yogurt. Various dairy foods, such as curd, yogurt, cheese, and kefir, are produced by bacteria. These bacteria include species of *Lactobacillus*, *Lactococcus*, *Streptococcus*, *Bifidobacteria*, *Leuconostoc*, and some yeasts including *Candida lambica*, *Kluyveromyces marxianus*, *Saccharomyces exiguous* and *Torula kefir* are useful to realize various food products for human beings (Alkema et al., 2016). The fermentation process also influences the texture and flavor properties of the food product. These characteristics are produced by specific microbes, flavors are added by adjunct strain in the fermented products (Whetstine et al., 2006; Deetae et al., 2007). Currently, food losses are a prime concern at the global level, especially with an ever-growing world population, and it is reported that approximately one-third of all food produced is either wasted or lost (Gustavsson et al., 2011). Therefore, it is warranted by workers to control measures for the preservation of food commodities using an antimicrobial agent for a longer shelf-life. Lactic acid bacteria comprise a large heterogeneous group of low GC Gram-positive bacteria and have the potential to tolerate acid and also the ability to produce lactic acid as the major metabolic end-product during carbohydrate fermentation. They are found in a variety of habitats such as natural environments, plants, humans, and the animal microbiota. They are commonly used for the manufacturing of various fermented foods and provide shelf-life and nutritional value. Most of the lactic acid bacteria present in fermented foods belong to *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Enterococcus*, *Pediococcus* and *Streptococcus* (Leroy and De Vuyst, 2004). It is reported that species of *Lactobacillus*, *Pediococcus,* and *Leuconostoc* have shown the antifungal activity (Crowley et al., 2013). *Lactobacillus plantarum* is the most studied species and has been tested as an antifungal agent against various fungal species such as *Aspergillus*, *Penicillium*, and *Rhizopus* (Dalié et al., 2010). *Leuconostoc* has also been shown to act as antifungal agents and has been used as a starter in some fermented dairy products. Furthermore, *Pediococcus pentosaceus* has been tested against *Aspergillus flavus* and *Aspergillus niger* species (Scholz and Kilian, 2016).

Bacteria are well known for their ability to produce a large diversity of antimicrobial compounds (Anand et al., 2020). Bacteriocins are extracellular antimicrobial peptides that are generally used in the food industry as preservatives (Subramanian and Smith, 2015). It was reported that phytopathogenic strain *Erwinia carotovora* NA4, isolated from diseased fruits and vegetables, produces the bacteriocin erwiniocin NA4 and *Agrobacterium radiobacter* NA5 produces agrocin NA5 (Jabeen et al., 2004). Another bacteriocin, thuricin 17, is a single small peptide produced by *Bacillus thuringiensis* NEB17, isolated from soybean nodules (Nazari and Smith, 2020). However, recent research has made significant progress in the investigation of the role of yeasts as an antimicrobial property against plant pathogens (Ferraz et al., 2019). Yeasts are ubiquitous in the environment and are used to grow in diverse habitats, such as cereals, vegetables, fruits, meat, and milk, among others. *Meyerozyma guilliermondii* yeasts, *Candida fructus*, and *Candida quercitrusa* are frequently found to be associated with fruits or plant surfaces and showed antagonistic activities against fungal pathogens (Chanchaichaovivat et al., 2008).

8. Future prospective

Reference microbial strains related to ecological, medical, or industrial importance should be explored in detail to confirm and highlight their significance to man. Capacity development to deposit many strains in the next decades is required. Currently, the facilities for deposition and access to biological materials and information are fragmented and there are significant gaps in the materials and support provided. Specific strategies and efficient mechanisms are necessary to help users in order to access the products and services from the Biological Resource Centre (BRC) that are warranted. In this context, Sharma et al. (2017b) documented a list of globally known microbial culture collection and Indian culture collection centres and reported preservation techniques for different microbial genera (Sharma et al., 2017a,b). This type of article is useful for researchers and other users to become aware of such services and understand how to get access. Some of the missing components and constraints are (1) lack of trained taxonomists globally, (2) lack of proper infrastructures and funds in most of the culture collections and (3) no or less recognition of staff engaged in the services of biodiversity conservation, especially microbes. One such strategy is listing authentic microbes with unique traits and technologies developed from such microbes on the website of microbial culture collections may attract the government to recognize the value of these culture collections. Future research and extension would go a long way to the applications of microbes for improving agricultural productivity, the environment, and human health, as well as global climate change, nanomaterials, biosensors, biofuels, and probiotics. Future efforts should be directed towards the investigation of various unexplored habitats of microbial resources and their exploitation for plant health and bioremediation research. The advancement in metagenomics and functional genomics led to exploring the microbial potential in different areas of environmental sustainability such as global climate change, soil fertility, crop production, new drugs and transgenic development.

Furthermore, it is well understood that most collection centres have concentrated on holdings of purified microbial isolates. However, the studies on the consortium and co-cultures approaches are needed to be highlighted in agriculture industrial and biotechnological applications. The practices of preservation of such consortia or whole microbiome have not yet been fully standardized but they are mostly preserved in liquid nitrogen or lyophilized form (Rothrock Jr et al., 2011; Tatangelo et al., 2014; Weißbecker et al., 2017). For example (1) disease suppressive soil is being preserved in liquid nitrogen and (2) starter cultures used in dairy and food industries are being preserved in lyophilized form. The increasing demand for microorganisms in industry and agriculture shows the necessity of preserving a vast diversity of microorganisms in collection centres. Therefore, culture collections are important to man, as they represent a valuable resource of biological and genetic materials to meet the requirements of present, past and future research, biodiversity conservation, and biotechnological applications (Giudice and Rizzo, 2020).

9. Conclusion

The present review documents collective information on microorganisms that are preserved in microbial culture collection centres and highlights their potential application in different sectors. The available information on the WoS database suggests that microbial repositories are a repertoire of hidden sustainable sources in the form of microorganisms for bioactive products with medicinal value, biofertilizers and biopesticides for plant growth promotion and disease suppression, waste management, food technology, nanomaterials for modern technology and enzyme industries. This article will contribute awareness among scientists, researchers, and industrialists and will motivate them to use conserved microorganisms for target-specific research. Moreover, reference strains are important in testing studies of various fields such as clinical diagnosis, food, water, and soil testing. This article also sheds light on the conservation of microbial resources for sustainable living in the future. There is an increasing demand for extremophiles in the agriculture, food, medicine, and other enzyme industries. Extensive research is warranted towards the exploration of extremophiles, their genes, and metabolic pathways to harness their potential for industrial processes. The biotechnological potential of extremophiles in agriculture has become more relevant in recent years for the development of new microbial inoculants. Hence, manipulation of extremophilic genes/enzymes through genetic engineering could generate probable transgenics having superior phenotypes for various biotechnological applications in the foreseeable future.

CRediT authorship contribution statement

All authors of this manuscript have substantially contributed to the concept, literature mining, writing, and methodology of the review, provided critical feedback, and critically revised the manuscript. All authors contributed to the writing or revision of the final manuscript. **Uttpal Anand:** Participated in conceptualization/conceived the study idea, planned and designed the review structure, wrote the first draft of the manuscript, figure preparation, arranged references, revision, addressed reviewer comments, and final draft. **Anukool Vaishnav:** Writing—original draft preparation, prepared the tables and figures, revised the manuscript. **Sushil K. Sharma:** Study idea, writing-review & editing, addressed reviewers comments with inclusion of input in the text and critical suggestions. **Jagajjit Sahu:** Writing-review & editing, performed scientometric and cluster analysis of the literature. **Sarfaraz Ahmad, Kumari Sunita, S. Suresh,** and **Abhijit Dey:** Writing-review & editing, suggestions, response, responded to referee comments. **Elza Bontempi:** Writing-review & editing, investigation, study design, methodology, software, formal analysis, prepared figures, validation, response, suggestions. **Amit Kishore Singh:** Writing—original draft preparation, prepared figures and tables, revision, suggestions, response. **Jarosław Proćków:** Writing-review & editing, response, visualization, attempt reviewers and editor comments, resources, supervision, funding acquisition. **Awadhesh Kumar Shukla:** Conceptualization, planned and designed the review structure, wrote the first draft of the manuscript, figures and tables preparation, arranged references, revision, supervision, addressed reviewer comments, and final draft. All authors have read and approved the final version of the manuscript for submission to this journal.

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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