Review Article

Molecular Characterization of Beneficial Soil Microorganisms: A Strategy for Enhancing CropProductivity

Abstract

The increase in global demand for food necessitates with increasing population has led to relay upon sustainable approaches to enhance crop productivity while maintaining environmental health. Beneficial soil microorganisms, such as *Rhizobacteria*, *Mycorrhizal* fungi, and *Actinomycetes*, play a pivotal role in improving soil fertility, promoting plant growth, and enhancing crop resilience to a biotic and biotic stressors. This review highlights various molecular strategies used for the characterization of these microorganisms, focusing on advanced techniques such as DNA based molecular identification, stable isotopes, arrays,integrated omics, etc. Additionally, it emphasizes the mechanisms by which beneficial microbes enhance crop productivity, including nitrogen fixation, phosphate solubilization, production of phytohormones, and the suppression of pathogens through biocontrol. The integration of beneficial soil microorganisms with precision agriculture and biofertilizer development is explored as a sustainable strategy to reduce chemical input and mitigate environmental challenges. This article provides a comprehensive understanding of molecular characterization techniques and their application in harnessing soil microbial diversity for enhancing crop yield, paving the way for sustainable agricultural practices.

Introduction

The rapid growth of the global population has led to a sharp increase in the demand for food production, posing a significant challenge to modern agriculture**(Petrillo et al., 2021)**. Conventional agricultural practices, heavily reliant on chemical fertilizers and pesticides, have proven effective for short-term productivity but have also contributed to soil degradation, environmental pollution, and loss of biodiversity **(Kour et al., 2020)**. These unsustainable practices threaten long-term food security, necessitating the adoption of eco-friendly and sustainable approaches to enhance crop productivity while preserving soil and environmental health **(Timofeeva et al. 2023)**."Soil is a region on the earth crust where geology and biology unite." Three interrelated factors i.e., physical fertility, chemical fertility and biological fertility compose soil fertility. Physical fertility refers to the physical properties of the soil i.e., structure, texture, porosity, and root fusion. Chemical fertility comprises nutrient status, pH, EC, base saturation of soil which is a decisive factor for a soil to be normal or problematic (acidity, alkalinity and salinity). Biological fertility includes the organisms that live and interact with the other components present in soil**(De Souza et al., 2019)**. The soil organisms are highly dynamic and vary greatly in number but is least explored fertility factor**(Bolton, 1993)**. Beneficial soil microorganisms, including rhizobacteria, mycorrhizal fungi, actinomycetes, archea, algae, insects, annelids, protozoa and other invertebrates have emerged as key players in sustainable agriculture**(Glick, 2010)**.Among them microbial entities are very unique as microbial communities play very important role in plants' functions by influencing their physiology and development via directlyfacilitating plant growth through various

mechanisms, such as nitrogen fixation, phosphate solubilization, production of phytohormones, and suppression of plant pathogens.By improving soil fertility and enhancing crop resilience to abiotic and biotic stresses, beneficial microorganisms not only boost agricultural productivity but also reduce the dependence on chemical inputs **(Zhang et al., 2021)**.In 1904, L. Hiltner for the first time coined the term 'rhizosphere' to describe the highly dynamic region of soil in the proximity of plant roots in which microbiological activity is maximum**(Hiltner, 1904)**. The roots secrete various organic and inorganic compounds such as referred as root exudates **(Table 1)** which help in colonization and survival of various microorganisms that in return encourage the plant growth known as plant growth promoting microorganisms (PGPM) **(Nihorimbre*et al*. 2011)**.In- turn Plants secret out their photosynthetically fixed carbon into direct surroundings, i.e., spermosphere, phyllosphere, rhizosphere, and mycorrhizosphere, thereby nourishing the microbial community and contolling theiractivities **(Nelson, 2004; Frey-Klett *et al*., 2007; Raaijmakers *et al*., 2009; Beredsen*et al*., 2012; Vorholt, 2012)**.In many regions, the healthy microbe population is still being threatened, and not at all promoted by agricultural practices**(Agaras et al., 2015)**.The quantitative measurement of the increased microbial community as well as their activity is measured by the plating technique expressed as a 'rhizosphere effect' or Rhizosphere**(Sukumaran *et al*., 2015)**. Recent advancements in molecular biology have provided powerful tools for characterizing and understanding the diversity, functionality, and mechanisms of beneficial soil microorganisms**(Uzah et al., 2023)**. Techniques such as DNA based molecular identification, stable isotopes, arrays,integrated omics, etc. allow researchers to explore the vast microbial communities present in the soil**(Franco-Duarte et al., 2019; Dabban et al., 2024; Streletskii et al., 2024)**. This review provides a comprehensive overview of the molecular characterization techniques and strategies employed to harness soil microbial diversity. It further explores their mechanisms in promoting crop productivity and discusses innovative approaches for optimizing their application in agricultural systems. By highlighting the role of beneficial microorganisms in enhancing crop yields, this review aims to provide a foundation for future research and practical implementation in sustainable agriculture.

Table 1Microbially secreted compounds found in root exudates (Streletskii et al., 2024)

Sugars	Glucose, fructose, sucrose, xylose, maltose, rhamnose, arabinose, raffinose
Organic acids	Tartaric acid, oxalicacid, malic acid, acetic acid, citric acid, fumaric acid
Amino acids	Leucine, valine, glutamine, asparagines, serine, glycine, glutamic acid, phenylalanine, threonine, tyrosine, lysine, proline, tryptophan
Vitamins	Biotin, thiamine, pentothenate, niacin, choline, inositol, p-amino bezoic acid, pyridoxine, m-methyl nicotinic acid, 'M-factor'
Nucleotide	Adenine, guanine, uridine, cytidine
Flavanones	3,4-deoxy flavanones
Enzymes	Invertase, amylase, protease, polygalacturonase, etc

1. Mechanisms of Soil Microorganisms in Enhancing Crop Productivity

Plant growth promoting microorganisms can affect plant growth by different direct and indirect mechanisms **(Glick, 1995)(Fig 1).**

1.1 Direct mechanisms

1.1.1Phytohormones production: The production of phyto-hormones is considered as one of the major mechanisms for the exclusive promotion of plant growth **(Spaepen*et al*., 2007)**. Phytohormones are the signaling molecules acting as chemical messengers that in extremely low concentrations coordinate cellular activities of plants. The concentration of Auxin (Indole acetic acid) **(Spaepen*et al* 2008)**, gibberellins **(Bottini *et al*., 2004)**, cytokinins**(timmusk*et al*., 1999)**, jasmonic acid and brassinosteroids modulate plant growth and the response to stress**(Masondo et al., 2024; Ali et al., 2024)**.

1.1.2 Indole acetic acid: Many important plants microbial interaction center on the formation of auxins (indole acetic acid as main plant auxins)**(Arora et al., 2024)**. The IAA is responsible for the expansion, division and differentiation of plant cells, promotion of root and shoot elongation, apical dominance, etc**(Fan et al., 2024)**.Generally, IAA released by rhizobacteria intervenes with various plant developmental processes because the endogenous reservoir of plant IAA may be altered by the acquisition of IAA that has been secreted by soil microbiota. IAA are produced by various rhizobacteria, e.g. *Azospirillum, Agrobacterium, Bacillus, Paenibacillus, Pseudomonas* and *Erwinia* **(Costacurta and Vanderleyden, 1995; Glick, 2012)**.

1.1.3Gibberellin: Among all phytohormones, gibberellin producers are still not well understood (Pii*et al*., 2015). Gibberellins (GAs) are a group of phytohormones associated with alterations in plant morphology, mainly in stem and root tissuesstem elongation, dormancy, flowering, germination and fruit ripening **(Spence and Bais, 2015)**. *Acinetobacter calcoaceticus*, *Bacillus pumilus*, *Bacillus licheniformis*and *Promicromonospora*sp. are examples of bacteria that produce gibberellins and result in positive feedback in the endogenous GA of plants **(Richardson *et al*. 2009; Figueiredo *et al*. 2010; Vacheron *et al*. 2013)**. *Bacillus siamensis* is able to produce GA and increases the growth of banana plants **(Ambawade and Pathade 2015; Ahemad and Kibret, 2014)**. In *Azospirillum*, GA3 is the major GA type identified and appears to be involved in promoting plant growth **(Cassan*et al*. 2009)**.

1.1.4 Cytokinins: The role of cytokinin is to promote cell growth and differentiation in plants**(Zhao et al., 2024)**. They help the plant by the inhibition of aging of tissues and thus influence the leaf growth.The apical dominance induced by auxins is down-regulated by cytokinin's**(Sipes and Einset, 1983)**. Cytokinins can be produced in soil by PGPR is an emerging alternative to enhance plant growth to improve yield and quality of crops**(Mughal et al., 2024)**.

1.1.5 Ethylene and Abscisic acid: 1-aminocyclopropane-1-carboxylate (ACC) is a direct ethylene precursor exuded by roots. ACC is converted into α-ketobutyrate and ammonium by the enzyme ACC deaminase produced by PGPR**(Hayat *et al.* 2010; Glick 2014)**. At low concentrations, ethylene mitigates detrimental effects of biotic and abiotic stresses **(Glick 2014)**. Like ethylene, abscisic acid (ABA) also modulates plant development under stressful conditions **(Glick 2015; Spence and Bais 2015)**. *Achromobacterxylosoxidans*, *Bacillus licheniformis*and *Pseudomonas putida* are ABA producing bacteria that favourably influence plant homeostasis **(Sgroy*et al.* 2009; Glick 2014)**.

1.1.6 Phosphate solubilization: Next to nitrogen, phosphorus is the second most important macro-nutrient required by the plants**(Sen et al., 2024; Saber *et al.*, 2005)**. The P content in average soil is about 0.05% (w/w) but because of its fixation and inadequate solubility in soil only 0.1% of the total P is available**(Ducousso-Détrez et al., 2024)**. A diverse group of bacteria (*Pseudomonads* and *Bacillus*), fungal strains (*Aspergilli*, *Penicillium and Rhizoctonia solani*) yeasts (*Yarrowialipolytica*and *Pichiafermentans*), actinomycetes (*Actinomyces* and *Streptomyces*), cyanobacteria (*Anabeana*sp, *Calothrix brauniii*and *Scytonema* sp.) and arbuscular mycorrhizal fungi (*Glomus fasciculatum*) is recognized to be involved in microbial phosphate solubilization**(Saha et al., 2024; Bai et al., 2024; Sharma *et al,* 2013)**.

1.1.7 Siderophore production: The production of **siderophores** is an alternative phenomenon of rhizobacteria**(Bisht et al., 2018)**. These molecules have the efficiency to sequester Fe^{3+} ions, which are considered to play important role in metabolism and cell growth**(Ramos Cabrera et al., 2024)**. In this way, the microbe that inhabit the plant roots compete for available iron present in the soil and may inhibit the proliferation of other pathogenic microorganisms in the rhizosphere **(Kumar *et al.* 2015)**.

1.1.8 Biological nitrogen fixation: Nitrogen is required in the highest amount, and its availability is a major limitation factor for plant growth **(Courty*et al.* 2015; Bhattacharjee *et al.* 2008; Figueiredo *et al.*, 2013)**. In a waterlogged rice field, the combination of *Anabaena* sp., a free-living diazotrophic nitrogen fixer bacterium, and *Azolla* compensate the shortage of nitrogen, hence, *Anabaena* may be referred to as a "biofertilizer" **(Bhuvaneshwari and Kumar 2013; Fosu-Mensah *et al.* 2015)**. In this

way, *Anabaena* contributes high nitrogen amounts (up to 50 kg ha^{-1}), reduces nitrogen loss via ammonia volatilization, and promotes plant growth **(Bhuvaneshwari and Kumar, 2013)**.

1.2. Indirect mechanisms

1.2.1Biocontrols: PGPR can produce a wide variety of antimicrobial compounds for defense such as broad-spectrum antibiotics, lactic acid produced by *Lactobacillus lactis*, hydrolytic enzymes like lysozymes, chitinase, proteases, lipases and β,1-3, glucanases that lyse the pathogenic microbes and numerous types of exotoxins and bacteriocins, which also have bactericidal activity **(Riley and Wetrz, 2002)**.

1.2.2 Antimicrobial compounds: Antibiotics are heterogeneous group of organic, low molecular weight compounds that exert destructive effect on the growth or metabolic activities of other organisms. **(Duffy, 2003; Sharma et al., 2024; Kwon and Kim 2014)**. On the other hand, bacteriocins differ from the traditional antibiotics in relatively narrow bactericidal spectrum i.e. toxic for only closely related to theproducing strains **(Riley and Wetrz,2002)**.Strains of *Leuconostocmesenteroides* subsp. *dextranicum* produce bacteriocins, but the compounds involved have not been completely purified and characterized yet **(Angelini, 2024; Chen et al., 2024)**.

1.2.3 Stress tolerance: Within the major metabolic pathways studied and those involving the participation of rhizobacteria, stands out the metabolism involved in the production of phytohormones in the rhizosphere environment **(Araujo *et al*. 2005)**, and the induction of resistance to biotic and abiotic stresses **(Kang *et al.* 2010)** has been reported. The accumulation of proline in plants acts as an osmoprotectant, maintaining the water potential under deficit conditions and facilitating water uptake from the soil **(Hanson *et al*. 1979)**.

1.2.4 Antioxidant enzymes

Plants produce a range of antioxidant enzymes such as catalases, peroxidases, and superoxide dismutases involved in scavenging free radicals **(Simova-Stoilova*et al*., 2008)**. The introduction of growth-promoting bacteria to the rhizosphere can greatly contribute to the production of antioxidant enzymes in plants**(Araujo and Menezes, 2009; Kumar *et al*. 2009)**. Antioxidants can act directly in neutralizing the action of free radicals or can indirectly participate in enzymatic systems involved in this function **(Moraes and Colla, 2006)**. The main antioxidant compounds with nutraceutical characteristics in plants are flavonoids, which act as potent antioxidants and metal chelators**(Tapas *et al*., 2008)**.

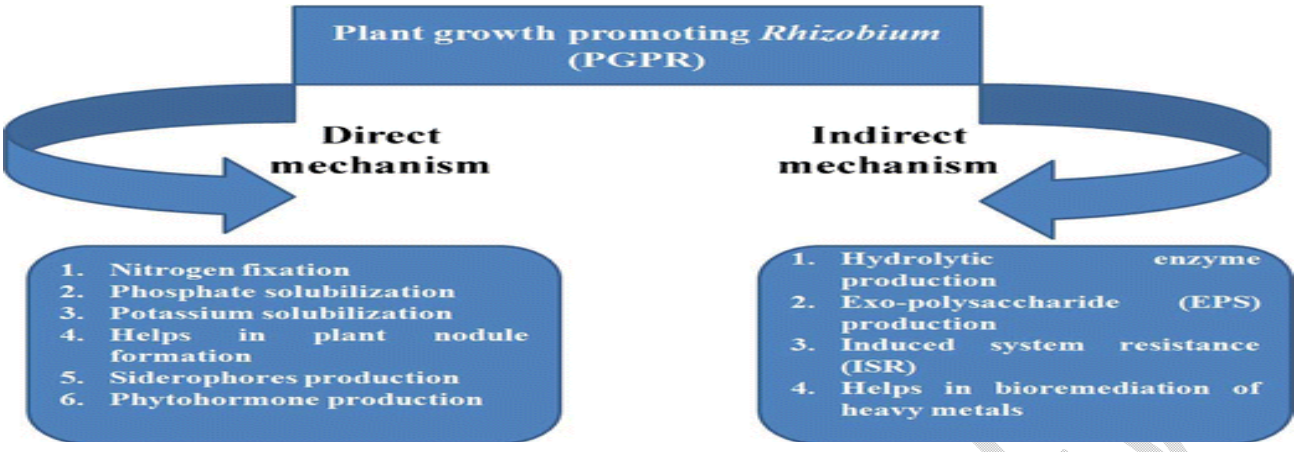

Fig:1 Mechanisms of plant growth promotion by PGPR(Du, et al., 2020).

2. Identification and characterization of beneficial soil microbiota

The term "polyphasic taxonomy" was introduced by Colwell (1970) to refer to phenotypic, biochemical and molecular detection approaches. The first step towards identification of unknown microbe is to understand their phenotypic characters which include morphological characters, cultural characters and biochemical characters of microorganisms**(Bisht et al., 2019)**.

2.1. Phenotypic characterization

The size, shape and arrangement of cells of microorganisms vary with species to which they belong**(Compant et al., 2024)**. The size of some microbes is given in **Table 2**. Bacteria have three basic shapes or morphological type. Coccus, bacillusand spiral **(Fig 2)(Shreshtha et al., 2024)**. Some multicellular microorganisms form the thin-walled, profusely branched filaments called hyphae**(Arellano-Wattenbarger et al., 2024;Banik et al., 2024; Fonseca-García et al., 2024)**.Microorganisms are also recognized on the basis of their cultural characteristics which can provide clues to identify unknown microbes such as shape (circular, filamentous, rhizoid), size (small, medium, large), color, margin(entire, irregular, undulate, lobate), texture(soft, hard, mucoid), optical characters (transparent, opaque,), elevation (flat, convex, raised) and surface (smooth, rough, shiny)**(Sangeetha &Thangadurai, 2013; Woźniaket al., 2019)**

Table 2 Phenotypic and physiological features of some common bacteria(Woźniak, et al., 2019)

Organisms	Significance	Size (µm)	Morphology

Achromatiumoxaliferum	Sulfur chemolithotroph	35 x 95	Cocci
Beggiatoa species	Sulfur chemolithotroph	50 x 160	Filaments
Clostridium botulinum	Food poisoning	3-8	Rods
C. tetani	Tetanus	4-8 X 0.5	Rods
Corynebacterium diphtheriae	Diphtheria	3-6 x 0.6-0.8	Palisade
Escherichia coli	Prokaryotic model organism and indicator of fecal contamination	1x2	Rods
Epulopsciumfishelsoni	Most enignamotic group of gigantobacteria. 16s rRNA subunit is related to *Clostridium*	80 x 600	Rods with tapered end

Lyngbya majuscule	Produce altillatoxin and kaklitoxin, causal organism of seaweed dermatitis	8 x 80	Filaments
Magnetobacteriumbavaricum	Magnetotactic bacterium	2 x 10	Rods
Mycobacterium tuberculosis	Tuberculosis	0.5-4	Rods
Mycoplasma pneumonia	Pneumonia	0.2	Pleomorphic
Neisseria meningitides	Meningitis	1	Cocci
Pasturella pestis	Plague	1- 2	Coccobacilli
Salmonella typhi	Typhoid	1-3 x 0.5-0.6	Rods
Staphylococcus sp	Boils	0.8	Cocci in clusters

Treponema pallidum	Syphilis	6-14	Spiral
Thiomargaritanamibiensis	Largest bacteria ever discovered	750	Cocci in chains
Thiovulum majus	Sulfur oxidizing, fastest swimming bacteria with the speed of 615 µm/sec	18	Cocci

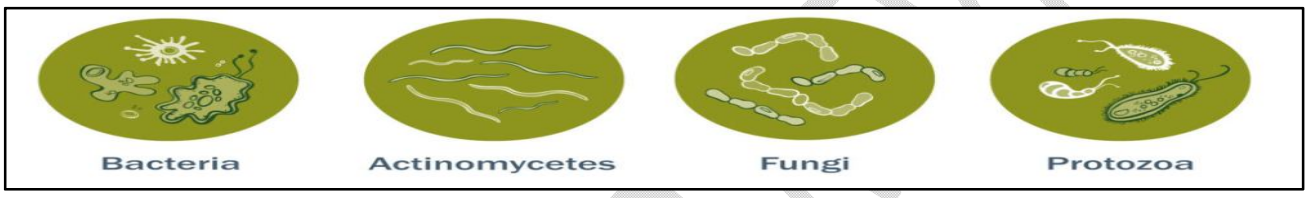

Figure 2 Morphological features of different microorganisms (AgSolutions; Australia; https://agsolutions.com.au/soil-microbes-sustainability/)

2.2Biochemical and physiological characterization

Biochemical characterization of microbes is based on the various enzymes or metabolic products produced by them such as carbon utilization test, citrate utilization test, Voges Proskauer test **(Vedi and Pandey, 2024; Saeed et al., 2024)**. In Fatty acid methyl ester (FAME) analysis, fatty acids are extracted from the membranes of microorganisms, chemically altered to form volatile methyl esters, and analyzed by gas chromatography (GC)**(Zhao et al., 2024)**. The resulting GC chromatogram is compared with reference chromatograms in a database containing data for thousands of bacterial isolates to identify the unknown microorganism **(Fernandes, 2006; Zaratti et al., 2024; Bisht et al., 2019)**.

2.3. Molecular Characterization

2.3 DNA-Based techniques

The techniques include Restriction Fragment Length Polymorphism (RFLP), Amplified Ribosomal DNA Restriction Analysis (ARDRA) and Pulse Field Gel Electrophoresis (PFGE) (**Fusco et al., 2023; William *et al.*, 1990)**.RFLP is preliminary genetic analysis that allows individual to be identified on the basis of their unique pattern of restriction enzyme cutting in specific regions of DNA**(Dabban et al.,**

2024). AFLP uses specific adaptors are ligated to enzyme restricted DNA which is subsequently amplified using primers from the adaptor and restriction site-specific sequences**(Monteiro et al., 2024)**.ARDRA employs digestion of amplified ribosomal DNA with different restriction enzymes and a profile is obtained using the combination of these patterns**(Kalia and Parshad, 2013; Maslow, 1993)**.PFGE uses in situ lysis of bacterial whole-cells in agarose plugs to release DNA which protect the chromosomal DNA from mechanical damages**(Bashbosh et al., 2024; Dubey et al., 2024; Qurbani et al., 2024)**.16S rRNA gene sequence is thus used for inferring the phylogenetic relationship among bacteria based on its universal distribution and highly conserved nature, **(Hammoudeh et al., 2024; Botan et al., 2024)**. Thereafter, sequence comparing software packages such as BLAST and CLUSTAL X are used for alignment of 16S rRNA gene sequence. **(Bisht et al., 2022; Li et al., 2024)**.Characterization of newly isolated strains by different molecular methods is summarized in **Fig. 3.**DNA-DNA hybridization is based on a comparison between whole genome of two bacterial species**(Ansari et al., 2024; Pasquer et al., 2010)**.

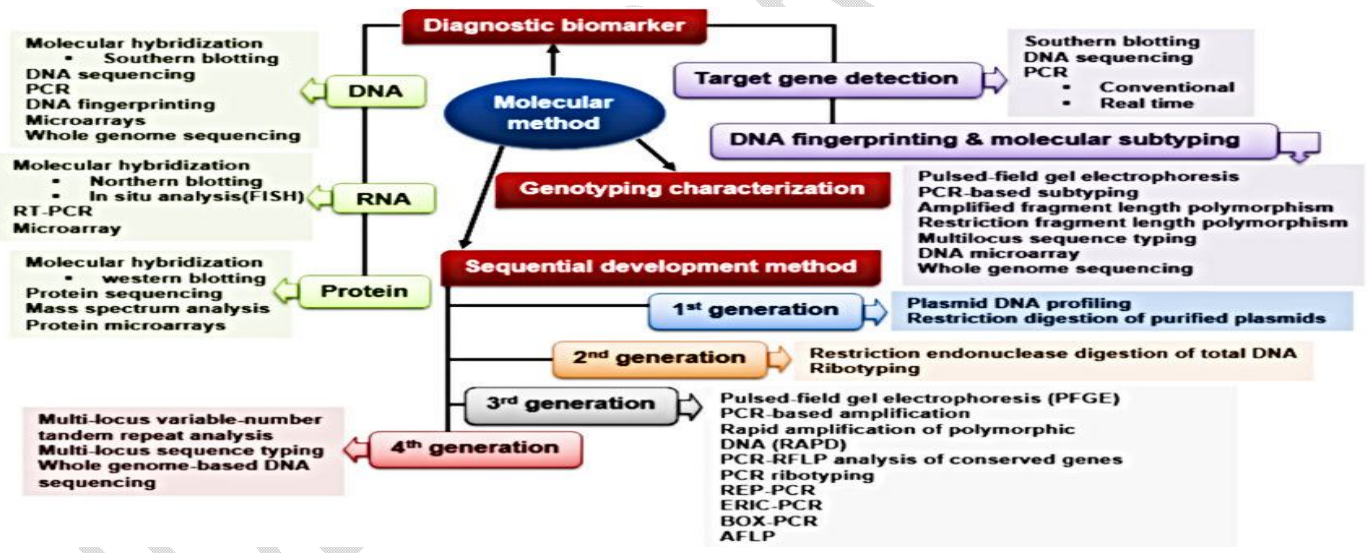

Fig. 3 Characterization of newly isolated strains by different molecular methods(Haque et al., 2021)

2.3.2Other advanced molecular techniques

a. FISH (Fluorescence In Situ Hybridization)

To visualizeRNA and DNA targets, *in situ*—fluorescence (FISH) and chromogenic (CISH) detectionmethods are used (**Román-Lladó et al., 2024)**.With the development of fluorescent labels radioactive labels were replaced by non-isotopic dyes**(Landegent*et al.*, 1984; Pinkel *et al.*, 1986; Pinkel *et al.*, 1988)**. In 1989, DeLong first used fluorescently labeled oligonucleotides for the detection of single microbial cells**(Aggarwal et al., 2024; Kliot and Ghanim, 2016; Luongo et al., 2024; Tseng**

et al., 2024). Oligonucleotides were labeled with horseradish peroxidase (HRP) that used fluorescein–tyramide as a substrate**(Herr et al., 2015; Ye et al., 2014; Yan et al., 2022)**. The sensitivity of FISH in natural samples was significantly increased using polyribonucleotide probes labeled with several fluorochrome molecules **(DeLong *et al*., 1999;Vági, et al., 2014; Zimmer and Wähnert, 1986).**

b. Microautoradiography

A radiotracer is used for incubation of sample to label microbial cell using radioisotopic compounds like soft beta emitters (^{3}H, ^{14}C, ^{33}P) or strong beta emitter like ^{32}P**(Rogers *et al*, 2007)**. After incubation the samples are fixed in paraformaldehyde or ethanol and washed to remove surplus radiotracer**(Song, et al., 2024; Wasmund et al., 2024; Gougoulias et al., 2014;Carman, 2018)**. Silver grain clumps, so developed, can be easily seen clearly using transmission light microscopy/ bright-field microscopy/ phase contrast microscopy/ LSM (Laser Scanning Microscopy)**(Ginige et al., 2005; Ouverney and Fuhrman, 1999).Fig. 4**shows stepwise procedure for microautoradiography**(Nielsen and Nielsen, 2005)**.

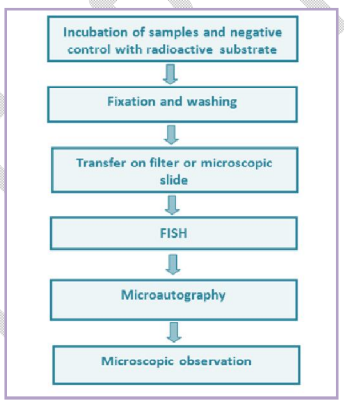

Figure 4: Step wise procedure of microautoradiography

c. Sequencing technology

Due to size limit of Sanger sequencing (i.e., 100 to 1000 base pairs), longer sequences are subdivided into smaller fragments that can be sequenced separately**(Muñoz-Ramírez et al., 2024; Siew et al., 2024; Li et al., 2024)**.Sanger sequencing is still used for sequencing, because of its low rate of error, long read length (> 700 bp) and larger insert sizes (i.e. > 30 Kb)**(Chen *et al*, 2014; Sanger *et al*., 1977; Sood*et al*., 2008; Zaytsevetal., 2024)**.Among the NGS technologies, the 454/Roche and the Illumina/Solexa systems can be applied to metagenomic samples**(Satam et al., 2023; Sharma et al., 2024)**. The pyrosequencing method includes the sequential addition of all four deoxynucleoside triphosphates, which, if complementary to the template strand, are added by a DNA polymerase**(Nafea**

et al., 2024; Mandlik et al., 2024).Illumina/Solexa technologyimmobilizes random DNA fragments on a surface and then performs solid surface PCR amplification, resulting in clusters of identical DNA fragments**(Chettri, et al., 2024; Minoche*et al.*, 2011; Meera Krishna et al., 2019; Raffan and Semple, 2011; Takeda et al., 2019; Bowman et al, 2015; Davis et al., 2013)**. The Applied Biosystems SOLiD sequencer has been extensively used, for example, in genome resequencing. This technology was developed by Life Technology in 2006**(Chettri et al., 2024; Remesh et al., 2024; Ho *et al*., 2011; Mandlik et al., 2024; Chettri et al., 2024)**. This procedure include—hybridization of primer, selective ligation of the probes, four-color imaging, and cleavage of probe—is repeated again and again, the number of cycles detect the eventual read length **(Metzker, 2009)**.

d.Omics techniques:

Omics include an increasingly broad range of fields, which ranges from genomics (the quantitative study of protein coding genes, regulatory elements and noncoding sequences), transcriptomics (RNA and gene expression), proteomics (focusing on protein abundance), and metabolomics (metabolites and metabolic networks)**(Botta et al., 2024; Yow et al., 2022)(Fig. 5)**.

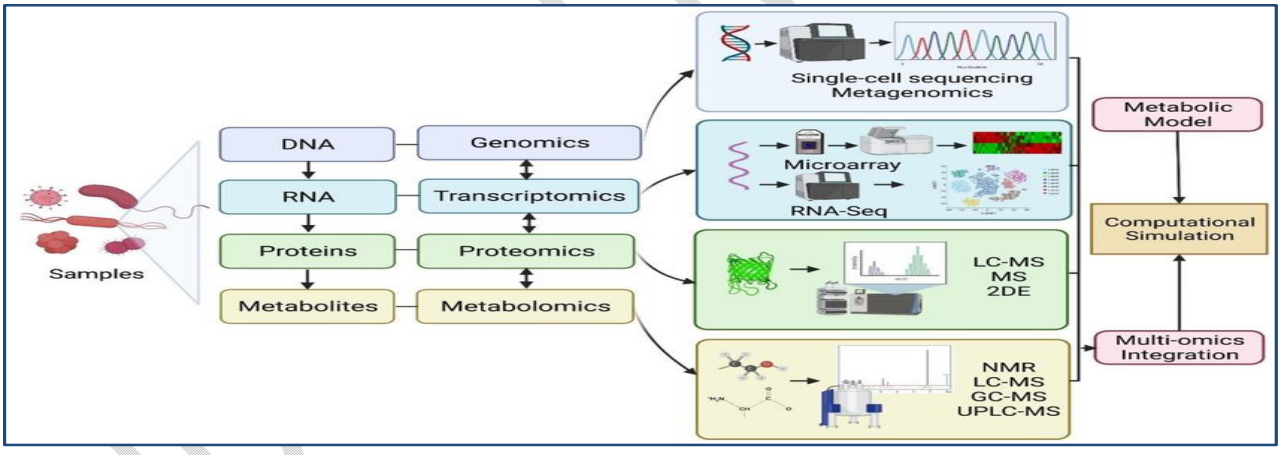

Figure 5:Schematics representation of omics dogma describing the network the processing of DNA, RNA, proteins and metabolites and method used(Yow et al., 2022).

1. Genomics

Genomics is the study of an organism's genome, or genetic material. Genomics is an emerging area of molecular biology where novel techniques were employed in order to get an insight of the complex, biological function of the genome.

1.1 Metagenomics

Metagenomics is the culture-independent technique to analyze complete genome of microbial communities present in a particular environment sample**(Ejaz et al., 2024; Yu et al, 2024).**Phenolics and humic acid interfere with the downstreaming applications such as polymerase chain reaction (PCR) amplification and cloning of genes (metagenomic library construction)**(Debnath *et al* 2010; Devi et al., 2024)**.The idea of cloningDNA directly from environmental samples was first proposedby Pace (**Pace *et al*., 1985; Schmidt *et al*., 1991; Healy *et al*., 1995)**. DeLong's group reported libraries constructedfrom prokaryotes from seawater **(Stein *et al*., 1996; Suwannaphan et al., 2024).**

1.2 Transcriptomics:

Transcriptomics is the overall scanning of the approx. 50,000 known genes that are transcribed into mRNA from the three-billion-letter human genome**(Aslam et al., 2024)**. The advantage of this new technique is that instead of examining one gene at a time, it analyses the complete transcriptome in one single go, which is the full set of all mRNA molecules present at a particular time in a defined cell population**(John Martin et al., 2024; Vohra et al., 2024)**. All genes and most proteins can be considered as instruments to make the biochemical composition and there by the physiological identity of an organism**(Raza et al., 2024)**.

1.3 Proteomics

Proteins are the most important components of major biochemical and signaling pathways, studies at protein levels are crucial to provide insight on molecular mechanisms underlying growth, development, and their interactions with the environment**(Pan et al., 2024; Macaulay *et al.,* 2005)**. The genome contains all of an organism's genes, having the codes for the proteins require for the function. Proteomics is the comprehensive investigation of proteins and their biological functions and processes**(Kaya, 2024; Siddiqui and Saeed, 2024)**.Once the sequence of an organism's genome is obtained, it can be compared to that of other organisms to find genes that are similar to those already known**(Cataldo et al., 2024; Shiaw-Lin *et al.*, 2005; Tasleem et al., 2024)**.

1.4 Metabolomics(metabonomics)

It is the integrated study of the metabolome, the entire set of small metabolites (e.g. hormones, metabolic intermediates, signalling molecules, and secondary metabolites) of biological sample **(Steuer *et al*, 2003)**. The metabolic state reflects the encoded product of genome which is being modified by environmental factors **(Kaddurah-Daouk, 2006).** NMR and other spectroscopic methods such as MS, GC/MS can be used to generate metabolic profiles**(German *et al.*, 2005; Fiehn, 2002; Kristal, and Shurubor, 2005)**.In MALDI-TOF (matrix assisted laser desorption ionization) version of mass

spectrometry, the sample is ionized and vaporized by a laser**(Chen et al., 2023)**. The time of flight (TOF) for each ion depends on its mass/charge ratio- the smaller this ratio**(Bielen et al., 2024; Dash et al., 2024; Fontana et al., 2012)(Fig 6)**.

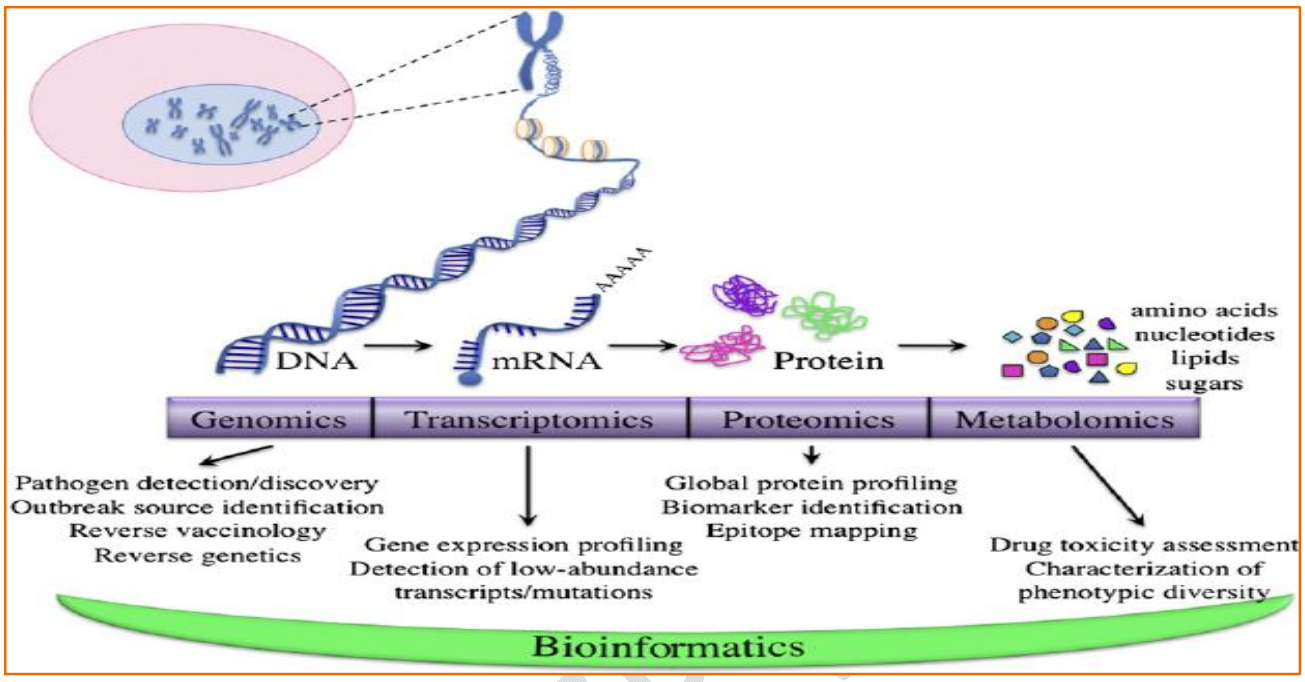

Figure 6:Integrating omics technology:genomics, proteomic, transcriptomic, and metabolomic(Fontana et al., 2012)

e. Arrays

DNA microarrays are a firmly rooted method for determining gene expression levels**(Cummings and Relman, 2000)**.

A. Oligonucleotide Microarrays

Oligonucleotide microarrays have emerged as a preferred platform for genomic analysis beyond simple gene expression profiling**(Chung *et al*., 2009)**. Each chip may contain over 6 million features, each feature comprising millions of copies of a distinct probe sequence **(Gregory *et al*., 2008; Mockler and Ecker, 2005)**. The hybridization events can be detected, owing to the labelling of the bound complementary target, by high resolution scanning or imaging**(Wong and Medrano, 2005)**.

B. cDNA Microarrays

cDNA microarrays are designed by mechanically attaching probes (e.g., amplified PCR products, oligonucleotides, or cloned DNA fragments) onto a solid substrate made up of glass having desired physico-chemical properties (e.g., excellent mechanical stability, durability and chemical resistance) **(Gregory *et al*., 2008; Mockler and Ecker, 2005; Zhou and Thompson, 2002)**.The disadvantages

related with oligonucleotide arrays include the associated costs and low sensitivity due to short sequences used in this technology **(Schulze and Downward, 2001)**.

3. Applications in Agriculture

3.1 Beneficial microbe based biofertilizers

The major limitation of crop yield in developing nations globally, and particularly among resource-poor farmers, is soil infertility**(Vlek and Vielhauer, 1994; Chen, 2006; Garcha and Samredhi, 2024)**.The term biofertilizer (microbial inoculants) can be defined as a preparation having live or latent cells of active microbial strains capable of nitrogen fixing, phosphate solubilizing which can be used for application of seed, soil or composting areas with the objective of increasing the numbers of such microorganisms and accelerate certain microbial process to augment the extent of the availability of nutrients in a form which can assimilated by plant**(NIIR Board, 2004)**.The formulation of inocula, method of application and storage of the product are all critical to the success of a biological product. In general, there are 6 major steps in making biofertilizer**(Bagga et al., 2024)**.First of all, active organisms must be decided**(Santos et al., 2024)**. Then, isolation is made to separate target microbes from their habitation. Usually, organism is isolated from plants root or by luring it using decoy such as putting cool rice underground of bamboo plants**(Fadiji et al., 2024; Kumar et al., 2024)**. At the end, biofertilizer should be tested on large scale to determine the effects and limits at different environment. Usually, biofertilizers are being prepared as carrier-based inoculants comprising active microorganisms**(Schenk et al., 2024; Miranda, et al., 2024) (Fig. 7)**. The properties of a good carrier material for seed inoculation are inexpensive and available in adequate amounts**(Zhao et al., 2024)**.

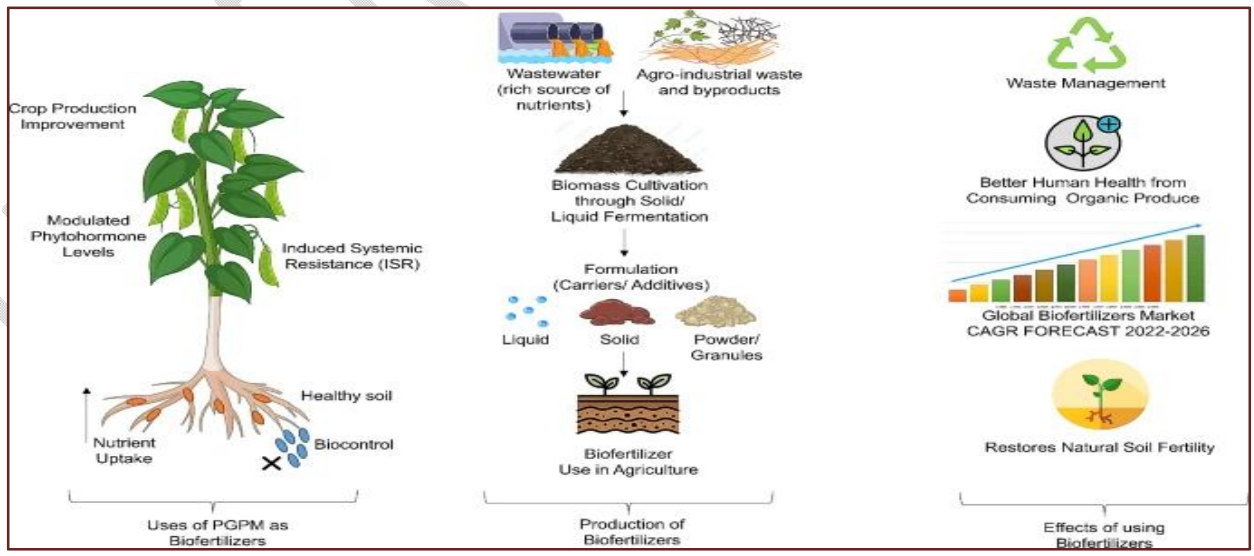

Figure 7:Commercial biofertilizers manufacturing process(Bagga et al., 2024)

3.2Integration with Precision Agriculture

Commonly used microorganisms as biofertilizers are nitrogen fixers, potassium solubilizer and phosphorus solubilizer, or combination of molds or fungi. These bacteria have close relationship with plant roots such as *Rhizobium* has symbiotic association with legume roots, and Rhizobacteria colonize on the surface of root or in rhizosphere soil**(Asad and Ahmed 2024)**. The phospho-microorganism mainly bacteria and fungi make insoluble phosphorus available to the plants**(El-Moustaqim et al., 2024)**. While Rhizobium, Blue Green Algae (BGA) and Azolla are crop specific, bio-inoculants like *Azotobacter*, *Azospirillum*, Phosphorus Solubilizing Bacteria (PSB), and Vesicular Arbuscular Mycorrhiza (VAM) could be regarded as broad spectrum biofertilizers. VAM is fungi that are found associated with majority of agriculture crops and enhanced accumulation of plant nutrients **(Gupta &Samnotra, 2004; Gupta, 2004)**. Examples of free-living nitrogen fixing bacteria are obligate anaerobes (*Clostridium pasteurianum*), obligate aerobes (*Azotobacter*), facultative anaerobes, photosynthetic bacteria (*Rhodobacter*), cyanobacteria and some methanogens**(Rahim, 2002)**.

4.Future Perspectives

There are several views about biofertilizers. It is often perceived to be more expensive than the chemical fertilizers due to the lack of skills and technology to produce biofertilizer products from abundant wastes. Besides, the effect on the crops is slow, compared to chemical fertilizers. Special care such as storage or mixing with powders is also needed to handle microbial inoculum to remain effective for extended use. As biofertilizers contain living microbes, their effectiveness therefore depends on environmental conditions. Hence, outcomes are bound to be inconsistent. Short shelf life, lack of suitable carrier materials, susceptibility to high temperature, problems in transportation and storage are biofertilizer bottlenecks that still need to be solved in order to obtain effective inoculation.

Conclusion

Beneficial soil microorganisms are essential components of sustainable agriculture, offering eco-friendly solutions to enhance crop productivity while minimizing environmental impacts. By improving soil fertility, promoting plant growth, and providing resilience against various stresses, these microorganisms serve as natural allies in addressing the challenges of modern agriculture. The molecular characterization of soil microbial communities using advanced techniques such as DNA based molecular identification, stable isotopes, arrays,integrated omics, etc. has significantly expanded our understanding of their diversity and functional roles. Integrating these microorganisms into agricultural practices through biofertilizers, biostimulants, and precision farming not only reduces dependence on chemical inputs but

also contributes to long-term soil health and environmental sustainability. Despite the advancements, challenges such as scalability, strain-specific adaptability, and knowledge gaps in complex microbial interactions remain. Future research should focus on overcoming these challenges, fostering innovations in microbial engineering, and expanding practical applications to ensure global food security. By harnessing the potential of beneficial soil microorganisms through molecular and biotechnological approaches, we can pave the way for a more sustainable, productive, and environmentally conscious agricultural system. This review underscores the critical role of these microorganisms in shaping the future of agriculture and highlights the need for continuous research to unlock their full potential.

Reference

Adamiak, J., Otlewska, A., Tafer, H., Lopandic, K., Gutarowska, B., Sterflinger, K., &Piñar, G. (2018). First evaluation of the microbiome of built cultural heritage by using the Ion Torrent next generation sequencing platform. *International Biodeterioration & Biodegradation*, *131*, 11-18.

Aebersold, R. & Mann, M., (2003). Mass spectrometry-based proteomics. *Nature*, 422(6928), 198.

Agaras, B.C.; Scandiani, M.; Luque, A.; Fernández, L.; Farina, F.; Carmona, M.; Gally, M.; Romero, A.; Wall, L.; Valverde, C. Quantification of the Potential Biocontrol and Direct Plant Growth Promotion Abilities Based on Multiple Biological Traits Distinguish Different Groups of *Pseudomonas* Spp. Isolates. *Biol. Control* **2015**, *90*, 173–186.

Aggarwal, M., Simadibrata, D. M., Kipp, B. R., Prokop, L. J., Barr Fritcher, E. G., Schneider, A., ... & Chandrasekhara, V. (2024). Diagnostic Accuracy Performance of Fluorescence In Situ Hybridization (FISH) for Biliary Strictures: A Systematic Review and Meta-Analysis. *Journal of Clinical Medicine*, *13*(21), 6457.

Ali, J., Mukarram, M., Ojo, J., Dawam, N., Riyazuddin, R., Ghramh, H. A., ... & Bayram, A. (2024). Harnessing phytohormones: Advancing plant growth and defence strategies for sustainable agriculture. *Physiologia Plantarum*, *176*(3), e14307.

Angelini, P. (2024). Plant-Derived Antimicrobials and Their Crucial Role in Combating Antimicrobial Resistance. *Antibiotics*, *13*(8), 746.

Ansari, F. A., Ahmad, I., & Khan, A. S. (2024). Recent Molecular Tools for Analyzing Microbial Diversity in Rhizosphere Ecosystem. In *Microbial Diversity in the Genomic Era* (pp. 233-246). Academic Press.approach. *International Journal of Biological Macromolecules*, *257*, 128563.

Arellano-Wattenbarger, G. L., Montiel, S., Aguirre-Von-Wobeser, E., de la Torre, M., & Rocha, J. (2024). Contribution of seed-endophytic bacteria to drought tolerance in early developmental stages of native maize landraces from arid milpas. *Plant and Soil*, *500*(1), 213-232.

Arora, P., Tabssum, R., Gupta, A. P., Kumar, S., & Gupta, S. (2024). Optimization of indole acetic acid produced by plant growth promoting fungus, aided by response surface methodology. *Heliyon*, *10*(14).

Asad, M., & Ahmed, S. Y. (2024). Utilizing Biofertilizer for Achieving Sustainable Agriculture and Rural Development Strategy towards Vision 2040, Oman. *Sustainability*, *16*(10), 4015.

Aslam, N., Li, Q., Bashir, S., Yuan, L., Qiao, L., & Li, W. (2024). Integrated Review of Transcriptomic and Proteomic Studies to Understand Molecular Mechanisms of Rice's Response to Environmental Stresses. *Biology*, *13*(9), 659.

Bagga, D., Chauhan, S., Bhavanam, A., GN, N., Meena, S. S., & Mohanty, A. (2024). Recent Advancements in Fermentation Strategies for Mass Production and Formulation of Biofertilizers: Towards Waste Valorization. *Journal of Soil Science and Plant Nutrition*, *24*(3), 5868-5897.

Bai, K., Wang, W., Zhang, J., Yao, P., Cai, C., Xie, Z., ... & Wang, Z. (2024). Effects of phosphorus-solubilizing bacteria and biochar application on phosphorus availability and tomato growth under phosphorus stress. *BMC biology*, *22*(1), 211.

Bajaj, T., Bhattacharya, S., & Gupta, J. (2024). MICROBIAL GENOMICS-the Changing Technological Landscape of Microbiology via NGS. In *Microbiology-2.0 Update for a Sustainable Future* (pp. 307-330). Singapore: Springer Nature Singapore.

Banik, A., Pandya, P., Patel, B., Rathod, C., & Dangar, M. (2018). Characterization of halotolerant, pigmented, plant growth promoting bacteria of groundnut rhizosphere and its in-vitro evaluation of plant-microbe protocooperation to withstand salinity and metal stress. *Science of the Total Environment*, *630*, 231-242.

Bashbosh, A., Ibrahim, S., AL-saadi, H., Ghosh, S., AL-huchaimi, S., & M Fahmy, E. (2024). Study of genetic characterisation of Multidrug-nonsusceptible Escherichia coli from septicaemia: Pulsed-field gel electrophoresis (PFGE) and PCR techniques. *Microbes and Infectious Diseases*, *5*(4), 1413-1424.

Beja, O., Aravind, L., Koonin, E. V., Suzuki, M. T., Hadd, A., Nguyen, L. P., Jovanovich, S. B., Gates,
Bielen, A., Babić, I., Vuk Surjan, M., Kazazić, S., Šimatović, A., Lajtner, J., ... &Hudina, S. (2024). Comparison of MALDI-TOF mass spectrometry and 16S rDNA sequencing for identification of environmental bacteria: a case study of cave mussel-associated culturable microorganisms. *Environmental science and pollution research*, *31*(14), 21752-21764.

Bisht, N., & Tewari, L. (2019). Identification and Characterization of High Efficacy Thermotolerant Yeast for Bioethanol Production from Fruit Waste. *Biotech Today: An International Journal of Biological Sciences*, *9*(1), 81-86.

Bisht, N., Dalal, V., & Tewari, L. (2022). Molecular modeling and dynamics simulation of alcohol dehydrogenase enzyme from high efficacy cellulosic ethanol-producing yeast mutant strain Pichia kudriavzevii BGY1-γm. *Journal of Biomolecular Structure and Dynamics*, *40*(22), 12022-12036.
Bisht, N., Sharma, B., Joshi, N., & Tewari, L. (2018). Role of microbial siderophore in Iron acquisition and amelioration of plant stress in saline soil. *Biotech Today: An International Journal of Biological Sciences*, *8*(2), 7-15.

Board, N. I. I. R. (2004). The complete technology book on bio-fertilizer and organic farming. *National*
Bolton Jr, H. (1993). Microbial ecology of the rhizosphere. *Soil microbial ecology*, 27-63.

Botan, A., Campisciano, G., Zerbato, V., Di Bella, S., Simonetti, O., Busetti, M., ... & Comar, M. (2024). Performance of 16S rRNA Gene Next-Generation Sequencing and the Culture Method in the Detection of Bacteria in Clinical Specimens. *Diagnostics*, *14*(13), 1318.

Botta, C., Tsoureki, D., Gautam, A., Patz, S., Pissaridi, K., Ferrocino, I., ... &Rantsiou, K. (2024). How can DNA-based omics effectively improve microbiological quality control? An explorative study applied to infant food production. In *Food Micro 2024: Scientific Program* (pp. 1-82).

Bowman, B., Kim, M., Cho, Y. J., &Korlach, J. (2015). Long-read, single molecule, real-time (SMRT) DNA sequencing for metagenomic applications. In *Metagenomics for Microbiology* (pp. 25-38). Academic Press.

C. M., Feldman, R. A., Spudich, J. L., Spudich, E. N. & DeLong, E. F. (2000). Bacterial rhodopsin: evidence for a new type of phototrophy in the sea. *Science*. 289(5486), 1902-1906.

Carman, K. R. (2018). Microautoradiographic detection of microbial activity. In *Handbook of methods in aquatic microbial ecology* (pp. 397-404). CRC Press.

Cataldo, P. G., Saavedra, L., & Hebert, E. M. (2024). Proteomic signature in lactic acid bacteria and related microorganisms. In *Proteomics Applied to Foods* (pp. 195-208). New York, NY: Springer US.

Chen, L., Cai, Y., Zhou, G., Shi, X., Su, J., Chen, G., & Lin, K. (2014). Rapid Sanger sequencing of the
Chen, L., Gao, W., Tan, X., Han, Y., Jiao, F., Feng, B., ... & Wang, L. (2023). MALDI-TOF MS is an effective technique to classify specific microbiota. *Microbiology Spectrum*, *11*(3), e00307-23.

Chen, X., Lan, W., & Xie, J. (2024). Natural phenolic compounds: Antimicrobial properties, antimicrobial mechanisms, and potential utilization in the preservation of aquatic products. *Food Chemistry*, *440*, 138198.

Chettri, D., Chirania, M., Boro, D., Saha, M., & Verma, A. K. (2024). Molecular Approaches to Microbial Identification of Industrially Significant Strains. In *Industrial Microbiology and Biotechnology: An Insight into Current Trends* (pp. 129-152). Singapore: Springer Nature Singapore.

Chettri, D., Chirania, M., Boro, D., Saha, M., & Verma, A. K. (2024). Molecular Approaches to Microbial Identification of Industrially Significant Strains. In *Industrial Microbiology and Biotechnology: An Insight into Current Trends* (pp. 129-152). Singapore: Springer Nature Singapore.

Chettri, D., Chirania, M., Boro, D., Saha, M., & Verma, A. K. (2024). Molecular Approaches to Microbial Identification of Industrially Significant Strains. In *Industrial Microbiology and Biotechnology: An Insight into Current Trends* (pp. 129-152). Singapore: Springer Nature Singapore.

Chung, S., Leung, A., Han, B. S., Chang, M. Y., Moon, J. I., Kim, C. H., Hong, S., Pruszak, J., Isacson,
Compant, S., Cassan, F., Kostić, T., Johnson, L., Brader, G., Trognitz, F., &Sessitsch, A. (2024). Harnessing the plant microbiome for sustainable crop production. *Nature Reviews Microbiology*, 1-15.

Costacurta, A. &Vanderleyden, J. (1995). Synthesis of phytohormones by plant-associated bacteria.
Critical Reviews in Microbiology, 21, 1-18.
Cummings, C. A., &Relman, D. A. (2000). Using DNA microarrays to study host-microbe interactions. *Emerging infectious diseases*, *6*(5), 513.

Dabban, I. A., Ahmad, M., Enejiyon, S. O., Hauwau, A. N., Gani, M., Oyewole, O. A., &Adetunji, C. O. (2024). Isolation Techniques Used for Molecular Characterization of Beneficial Microorganisms: Cultural, Biochemical and Molecular Characterization. *Handbook of Agricultural Biotechnology*, 491-545.

Dash, J., Naykodi, A., Mohakud, N. K., & Deb, S. (2024). MALDI TOF-MS for microbial identification and diagnosis. In *Evolving Landscape of Molecular Diagnostics* (pp. 43-57). Elsevier.

Davis, B. M., Chao, M. C., &Waldor, M. K. (2013). Entering the era of bacterial epigenomics with single molecule real time DNA sequencing. *Current opinion in microbiology*, *16*(2), 192-198.

De Souza, R.S.C.; Armanhi, J.S.L.; Damasceno, N.D.B.; Imperial, J.; Arruda, P. Genome Sequences of a Plant Beneficial Synthetic Bacterial Community Reveal Genetic Features for Successful Plant Colonization. *Front. Microbiol.* **2019**, *10*, 1779

Debnath, M., Prasad, G. B., & Bisen, P. S. (2010). Molecular diagnostics: promises and possibilities. *Springer Science & Business Media*, 11-31.

DeLong, E. F., Taylor, L. T., Marsh, T. L., & Preston, C. M. (1999). Visualization and enumeration of marine planktonic archaea and bacteria by using polyribonucleotide probes and fluorescent *in situ* hybridization. *Applied and Environmental Microbiology*, *65*(12), 5554-5563.

Devi, R., Kaur, T., Negi, R., Sharma, B., Chowdhury, S., Kapoor, M., ... & Yadav, A. N. (2024). Biodiversity, mechanisms, and potential biotechnological applications of minerals solubilizing extremophilic microbes: A. *Journal of Applied Biology & Biotechnology Vol*, *12*(5), 23-40.

Du, J., Xu, S., Zhou, Q., Li, H., Fu, L., Tang, J., ... & Du, X. (2020). A review of microplastics in the aquatic environmental: distribution, transport, ecotoxicology, and toxicological mechanisms. *Environmental Science and Pollution Research*, *27*, 11494-11505.

Dubey, D., Rath, S., Subhadarshini, S. S., Purohit, G. K., Tripathy, D., Panigrahi, R., ... &Singhsamanta, D. (2024). Exploring rapid molecular methods for diagnosing Candida species infecting humans: A narrative review. *Microbes and Infectious Diseases*, *5*(1), 336-346.

Ducousso-Détrez, A., Lahrach, Z., Fontaine, J., Lounès-Hadj Sahraoui, A., & Hijri, M. (2024). Cultural techniques capture diverse phosphate-solubilizing bacteria in rock phosphate-enriched habitats. *Frontiers in Microbiology*, *15*, 1280848.

Ejaz, M. R., Badr, K., Hassan, Z. U., Al-Thani, R., &Jaoua, S. (2024). Metagenomic approaches and opportunities in arid soil research. *Science of The Total Environment*, 176173.

El-Moustaqim, K., Sbai, S. E., El Yousfi, Y., Mabrouki, J., &Hmouni, D. (2024). New strategy for the advancement of modern agriculture through the use of microalgae as biofertilizers. *Euro-Mediterranean Journal for Environmental Integration*, 1-15.

Fadiji, A. E., Xiong, C., Egidi, E., & Singh, B. K. (2024). Formulation challenges associated with microbial biofertilizers in sustainable agriculture and paths forward. *Journal of Sustainable Agriculture and Environment*, *3*(3), e70006.

Fan, Y., Song, Q., Li, S., Tu, J., Yang, F., Zeng, X., ... & Wang, G. (2024). Protective Role of Indole-3-Acetic Acid Against Salmonella Typhimurium: Inflammation Moderation and Intestinal Microbiota Restoration. *Microorganisms*, *12*(11), 2342.

Fernandes, M. F. (2006). Fatty acid profiling of soil microbial communities: a comparison of extraction methods and temporal dynamics in plant residue amended soils. *Oregon state University*, 6-18.

Fiehn, O. (2002). Metabolomics—the link between genotypes and phenotypes. In *Functional genomics*, *Springer*, 155-171.

Figueiredo, M. V. B., Seldin, L., Araujo, F. F. & Mariano, R. L. R. (2010). Plant growth promoting rhizobacteria: fundamentals and applications. In: *Maheshwari DK (ed) Plant growth and health promoting bacteria. Springer*, 21–43.

Fonseca-García, C., Pettinga, D., Wilson, A., Elmore, J. R., McClure, R., Atim, J., ... & Coleman-Derr, D. (2024). Defined synthetic microbial communities colonize and benefit field-grown sorghum. *The ISME Journal*, *18*(1), wrae126.

Franco-Duarte , R. , Černáková , L. , Kadam , S., S. Kaushik , K. , Salehi , B. , Bevilacqua , A. , Corbo , M.R. , Antolak , H. , Dybka-Stępień , K. , Leszczewicz , M. , Tintino , S.R. , Alexandrino de Souza , V.C. , Sharifi-Rad , J. , Coutinho , H.D.M. , Martins , S. , Rodrigues , C.F. , Advances in chemical and biological methods to identify microorganisms—from past to present . *Microorganism* , **7** , 5 , 130 , 2019 .

Fukushima, A., Kusano, M., Redestig, H., Arita, M., & Saito, K. (2009). Integrated omics approaches in plant systems biology. *Current opinion in chemical biology*, *13*(5-6), 532-538.

Fusco, V., Fanelli, F., &Chieffi, D. (2023). Recent and advanced DNA-based technologies for the authentication of probiotic, protected designation of origin (PDO) and protected geographical indication (PGI) fermented foods and beverages. *Foods*, *12*(20), 3782.

Garcha, S., &Samredhi. (2024). Biofertilizers: An Imminent Approach for Sustainable Agriculture. In *Metabolomics, Proteomics and Gene Editing Approaches in Biofertilizer Industry: Volume II* (pp. 1-14). Singapore: Springer Nature Singapore.

Garrity, G. M. (2012). Bergey's manual of systematic bacteriology: Volume one: the Archaea and the deeply branching and phototrophic bacteria. *Springer*. 1-119.

German, J. B., Hammock, B. D., & Watkins, S. M. (2005). Metabolomics: building on a century of biochemistry to guide human health. *Metabolomics*, *1*(1), 3-9.

Ginige, M. P., Keller, J., & Blackall, L. L. (2005). Investigation of an acetate-fed denitrifying microbial community by stable isotope probing, full-cycle rRNA analysis, and fluorescent in situ hybridization-microautoradiography. *Applied and environmental microbiology*, *71*(12), 8683-8691.

Glick, B. R. (2012). Plant growth-promoting bacteria: mechanisms and applications. *Scientifica*, 55-70.

Glick, B. R. (2014). Bacteria with ACC deaminase can promote plant growth and help to feed the world. *Microbiological Research*, *169*(1), 30–39.

Glick, B. R. (2015). Beneficial plant-bacterial interactions. *Springer*, 1-221.
Gougoulias, C., Clark, J. M., & Shaw, L. J. (2014). The role of soil microbes in the global carbon cycle: tracking the below□ground microbial processing of plant□derived carbon for manipulating carbon dynamics in agricultural systems. *Journal of the Science of Food and Agriculture*, *94*(12), 2362-2371.

Gregory, N. G. (2008). Animal welfare at markets and during transport and slaughter. *Meat science*, *80*(1), 2-11.

Gupta, A. K. (2004). The complete technology book on biofertilizers and organic farming. *National Institute of Industrial Research Press. India*. 495-549.

Gupta, A. K., &Samnotra, R. K. (2004). Effect of biofertilizers and nitrogen on growth, quality and yield of cabbage (*Brassica oleracea* var *capitata* L.) cv Golden Acre. *Environment and Ecology*, *22*(3), 551-553.

Hammoudeh, Y., Suresh, L., Ong, Z. Z., Lister, M. M., Mohammed, I., Thomas, D. J. I., ... & Ting, D. S. J. (2024). Microbiological culture versus 16S/18S rRNA gene PCR-sanger sequencing for infectious keratitis: a three-arm, diagnostic cross-sectional study. *Frontiers in Medicine*, *11*, 1393832.

Hanson, J., Gordon, M., Peterson, N., Lepak, R., Goldsworthy, C., Brady, V., ... & Hoffman, J. (2024). Stable isotope analysis of western Lake Superior predatory fishes, part one: Trophic niche overlap. *Journal of Great Lakes Research*, 102441.

Haque, M. A., Khan, A., & He, C. (2021). Feed-borne Bacillus cereus: An emerging threat to food chain related hazard, safety and pathogenic potentiality. *Veterinary Pathobiology and Public Health*, *1*, 251-269.

Hayat, R., Ali, S., Amara, U., Khalid, R. & Ahmed, I. (2010). Soil beneficial bacteria and their role in plant growth promotion: a review. *Annals of Microbiology, 60*(4):579–598

Healy, J. M., Schaefer, K., &Haszprunar, G. (1995). Spermatozoa and spermatogenesis in a monoplacophoranmollusc, *Laevipilina antarctica*: ultrastructure and comparison with other Mollusca. *Marine Biology*, *122*(1), 53-65.

Herr, J. R., Öpik, M., & Hibbett, D. S. (2015). Towards the unification of sequence-based classification and sequence-based identification of host-associated microorganisms. *New Phytologist*, *205*(1), 27-31.

Hiltner, L. (1904). Over recent experiences and problems in the field of soil bacteriology and special those into account the Grundungung and fallow. *Arb Deutsche Agricultural Enges*, 98, 59-78.

Ho, P. L., Lo, W. U., Yeung, M. K., Lin, C. H., Chow, K. H., Ang, I., & Lo, J. Y. C. (2011). Complete sequencing of pNDM-HK encoding NDM-1 carbapenemase from a multidrug-resistant Escherichia coli strain isolated in Hong Kong. *PloS one*, *6*(3), e17989.

Huang, R., Xu, C., Grießinger, J., Feng, X., Zhu, H., &Bräuning, A. (2024). Rising utilization of stable isotopes in tree rings for climate change and forest ecology. *Journal of Forestry Research*, *35*(1).

Janovský, M. P., Ferenczi, L., Trubač, J., &Klír, T. (2024). Stable isotope analysis in soil prospection reveals the type of historic land-use under contemporary temperate forests in Europe. *Scientific Reports*, *14*(1), 14746.

John Martin, J. J., Song, Y., Hou, M., Zhou, L., Liu, X., Li, X., ... & Li, R. (2024). Multi-Omics Approaches in Oil Palm Research: A Comprehensive Review of Metabolomics, Proteomics, and Transcriptomics Based on Low-Temperature Stress. *International Journal of Molecular Sciences*, *25*(14), 7695.

Kalia, A., & Parshad, V. R. (2013). Advanced Molecular and Microspectroscopy Toolbox for Deciphering Soil Diazotroph Diversity. In *Geomicrobiology and Biogeochemistry* (pp. 37-60). Berlin, Heidelberg: Springer Berlin Heidelberg.

Kaminek, M., Motyka, V. &Vankova, R. (1997). Regulation of cytokinin content in plant cells. *Physiologia Plantarum*, 101, 689-700.

Kaya, C. (2024). Microbial modulation of hormone signaling, proteomic dynamics, and metabolomics in plant drought adaptation. *Food and Energy Security*, *13*(1), e513.

Kliot, A., & Ghanim, M. (2016). Fluorescent in situ hybridization for the localization of viruses, bacteria and other microorganisms in insect and plant tissues. *Methods*, *98*, 74-81.

Kour, D.; Rana, K.L.; Yadav, A.N.; Sheikh, I.; Kumar, V.; Dhaliwal, H.S.; Saxena, A.K. Amelioration of Drought Stress in Foxtail Millet (*Setaria italica* L.) by P-Solubilizing Drought-Tolerant Microbes with Multifarious Plant Growth Promoting Attributes. *Environ. Sustain.* **2020**, *3*, 23–34.

Kristal, B. S., &Shurubor, Y. I. (2005). Metabolomics: opening another window into aging. *Science of aging knowledge environment*, *2005*(26), 19.

Kumar, A., & Yadav, A. (2024). Next Generation Sequencing in Metagenomics and Metatranscriptomics. In *Multi-Omics Analysis of the Human Microbiome: From Technology to Clinical Applications* (pp. 49-75). Singapore: Springer Nature Singapore.

Kumar, D., Kumar, R., Sakshi, Deepshikha, & Kumar, A. (2024). Commercialization and Market Perspectives of Biofertilizers Through Advanced Approaches. In *Metabolomics, Proteomics and Gene Editing Approaches in Biofertilizer Industry: Volume II* (pp. 339-357). Singapore: Springer Nature Singapore.

Landegent, J. E., De Wal, N. J. I., Baan, R. A., Hoeijmakers, J. H. J., & Van der Ploeg, M. (1984). 2-Acetylaminofluorene-modified probes for the indirect hybridocytochemical detection of specific nucleic acid sequences. *Experimental cell research*, *153*(1), 61-72.

Lathe, R. (1985). Synthetic oligonucleotide probes deduced from amino acid sequence data: theoretical and practical considerations. *Journal of molecular biology*, *183*(1), 1-12.

Li, C., Song, J., Chen, Q., Ge, D., Li, Q., & Yang, Y. (2024). Whole-genome shotgun sequencing unravels the influence of environmental microbial co-infections on the treatment efficacy for severe pediatric infectious diseases. *Frontiers in Microbiology*, *15*, 1308871.

Li, M. N., Wang, T., Wang, N., Han, Q., You, X. M., Zhang, S., ... & Zhang, G. F. (2024). A detailed analysis of 16S rRNA gene sequencing and conventional PCR-based testing for the diagnosis of bacterial pathogens and discovery of novel bacteria. *Antonie van Leeuwenhoek*, *117*(1), 102.

Lin, S. Y., Rai, R., Li, K., Xu, Z. X., & Elledge, S. J. (2005). BRIT1/MCPH1 is a DNA damage responsive protein that regulates the Brca1–Chk1 pathway, implicating checkpoint dysfunction in microcephaly. *Proceedings of the National Academy of Sciences*, *102*(42), 15105-15109.

Lu, X., Bai, J., Ye, F., & Wei, G. (2024). Progress and Prospect of Rare Earth Elements Stable Isotope Analysis Techniques. *Journal of Earth Science*, *35*(6), 2129-2132.

Luongo, F. P., Annunzi, E., Girolamo, F., Belmonte, G., Ponchia, R., Piomboni, P., &Luddi, A. (2024). Assessment of sperm chromosomal abnormalities using fluorescence in situ hybridization (FISH): implications for reproductive potential. *Journal of Assisted Reproduction and Genetics*, *41*(10), 2787-2793.

Macaulay, I. C., Philippa, C., Arief, G., Willem, H. O., Des, F., & Nicholas, A. W. (2005). Platelet genomics and proteomics in human health and disease. *The Journal of clinical investigation*, *115*(12), 3370-3377.

Mandlik, J. S., Patil, A. S., & Singh, S. (2024). Next-Generation Sequencing (NGS): Platforms and Applications. *Journal of Pharmacy and Bioallied Sciences*, *16*(Suppl 1), S41-S45.

Manefield, M., Whiteley, A. S., Griffiths, R. I. & Bailey, M. J. (2002). RNA stable isotope probing, a novel means of linking microbial community function to phylogeny. *Applied and Environmental Microbiology*, 68, 5367-5373.

Manefield, M., Whiteley, A. S., Ostle, N., Ineson, P. & Bailey, M. J. (2002). Technical considerations for RNA-based stable isotope probing: an approach to associating microbial diversity with microbial community function. *Rapid Communications in Mass Spectrometry*, 16, 2179-2183.

Maslow, J. N., Mulligan, M. E. & Arbeit, R. D. (1993). Molecular epidemiology: application of contemporary techniques to the typing of microorganism. *Clinical Infectious Disease*, 17, 153–164.

Masondo, N. A., Gupta, S., Moyo, M., &Aremu, A. O. (2024). The application of phytohormones in plant biotechnology for sustainable agriculture. *Frontiers in Plant Science*, *15*, 1382055.

Meera Krishna, B., Khan, M. A., & Khan, S. T. (2019). Next-generation sequencing (NGS) platforms: an exciting era of genome sequence analysis. *Microbial Genomics in Sustainable Agroecosystems: Volume 2*, 89-109.

Metzker, M. L. (2009). Sequencing in real time. *Nature biotechnology*, *27*(2), 150.
Minoche, A. E., Dohm, J. C., &Himmelbauer, H. (2011). Evaluation of genomic high-throughput sequencing data generated on Illumina HiSeq and genome analyzer systems. *Genome biology*, *12*(11), R112.

Miranda, A. M., Hernandez-Tenorio, F., Villalta, F., Vargas, G. J., & Sáez, A. A. (2024). Advances in the Development of Biofertilizers and Biostimulants from Microalgae. *Biology*, *13*(3), 199.

Mockler, T. C., & Ecker, J. R. (2005). Applications of DNA tiling arrays for whole-genome analysis. *Genomics*, *85*(1), 1-15.

Monteiro, R. C., Yu, C. Z., Dolatabadi, S., Hagen, F., Sandoval-Denis, M., Crous, P. W., ... & Rodrigues, A. M. (2024). Novel amplified fragment length polymorphism (AFLP) markers for typing medically relevant Fusarium and allied fusarioid genera. *Fungal Systematics and Evolution*.

Morris, S. A., Radajewski, S., Willison, T. W. & Murrell, J. C. (2002). Identification of the functionally active methanotroph population in a peat soil microcosm by stable-isotope probing. Applied and Environmental Microbiology, 68, 1446-1453.

Mughal, N., Shoaib, N., Chen, J., He, Y., Fu, M., Li, X., ... & Liu, J. (2024). Adaptive roles of cytokinins in enhancing plant resilience and yield against environmental stressors. *Chemosphere*, 143189.

Muñoz-Ramírez, Z. Y., González-Escobedo, R., Avila-Quezada, G. D., Ramírez-Sánchez, O., Higareda-Alvear, V. M., Zapata-Chávez, E., ... & Muñoz-Castellanos, L. N. (2024). Exploring microbial rhizosphere communities in asymptomatic and symptomatic apple trees using amplicon sequencing and shotgun metagenomics. *Agronomy*, *14*(2), 357.

Murrell, J. C. &Radajewski, S. (2000). Cultivation-independent techniques for studying methanotroph ecology. *Research in Microbiology*, 151, 807-814.

Nafea, A. M., Wang, Y., Wang, D., Salama, A. M., Aziz, M. A., Xu, S., & Tong, Y. (2024). Application of next-generation sequencing to identify different pathogens. *Frontiers in Microbiology*, *14*, 1329330.

Neha Bisht, N. B., Heena Parveen, H. P., & Lakshmi Tewari, L. T. (2019). Batch fermentation of underutilized pear fruits using newly isolated stress tolerant ethanogenic yeast Pichia kudriavezeii BGY1.

Nguyen, T. Q., Dao, T. K., Nguyen, H. D., Phung, T. B. T., Pham, T. T. N., Nguyen, T. V. H., ... & Do, T. H. (2024). Application of PCR-based techniques for the identification of genetic fingerprint diversity of dominant bacteria in fecal samples of children with diarrhea in Vietnam. *Infectious Disease Reports*, *16*(5), 932-951.

Nielsen, J. L., & Nielsen, P. H. (2005). Advances in microscopy: microautoradiography of single cells. *Methods in enzymology*, *397*, 237-256.

Ouverney, C. C., & Fuhrman, J. A. (1999). Combined microautoradiography–16S rRNA probe technique for determination of radioisotope uptake by specific microbial cell types in situ. *Applied and Environmental Microbiology.*, *65*(4), 1746-1752.

Pace, N. R., Stahl, D. A., Lane, D. J., & Olsen, G. J. (1986). The analysis of natural microbial populations by ribosomal RNA sequences. *Springer*,1-55.

Pan, H., Wattiez, R., & Gillan, D. (2024). Soil Metaproteomics for Microbial Community Profiling: Methodologies and Challenges. *Current Microbiology*, *81*(8), 257.

Pasquer, F., Pelludat, C., Duffy, B., & Frey, J. E. (2010). Broad spectrum microarray for fingerprint-based bacterial species identification. *BMC biotechnology*, *10*, 1-9.

Petrillo, C.; Castaldi, S.; Lanzilli, M.; Selci, M.; Cordone, A.; Giovannelli, D.; Isticato, R. Genomic and Physiological Characterization of Bacilli Isolated From Salt-Pans with Plant Growth Promoting Features. *Front. Microbiol.* **2021**, *12*, 715678

Pii, Y., Mimmo, T., Tomasi, N., Terzano, R., Cesco, S. &Crecchio, C. (2015). Microbial interactions in the rhizosphere: beneficial influences of plant growth-promoting rhizobacteria on nutrient acquisition process: a review. *Biology and Fertility of Soils*, *51*(4), 403–415.

Pinkel, D., Gray, J., Trask, B., Van den Engh, G., Fuscoe, J., & Van Dekken, H. (1986). Cytogenetic analysis by in situ hybridization with fluorescently labeled nucleic acid probes. *Cold Spring Harbor Laboratory Press*, 51, 151-157.

Pinkel, D., Landegent, J., Collins, C., Fuscoe, J., Segraves, R., Lucas, J., & Gray, J. (1988). Fluorescence in situ hybridization with human chromosome-specific libraries: detection of trisomy 21 and translocations of chromosome 4. *Proceedings of the National Academy of Sciences*, *85*(23), 9138-9142.

Qurbani, K., Hussein, S., & Ahmed, S. K. (2024). Molecular Biotechniques for the Isolation and Identification of Microorganisms.

Radajewski, S. & Murrell, J. C. (2002). Stable isotope probing for detection of methanotrophs after enrichment with $^{13}CH_4$. *Methods in Molecular Biology*, 179, 149-157.

Radajewski, S., Ineson, P., Parekh, N. R. & Murrell, J. C. (2000). Stable-isotope probing as a tool in microbial ecology. *Nature*, 403, 646-649.

Radajewski, S., Webster, G., Reay, D. S., Morris, S. A., Ineson, P., Nedwell, D. B., Prosser, J. I. & Murrell, J. C. (2002). Identification of active methylotroph populations in an acidic forest soil by stable-isotope probing. *Microbiology*, 148, 2331-2342.

Raffan, E., & Semple, R. K. (2011). Next generation sequencing- implications for clinical practice. *British medical bulletin*, *99*(1), 53-71.

Rahim, K. A. (2002). Biofertilizers in Malaysian agriculture: perception, demand and promotion. In *2002 FNCA Joint Workshop on Mutation and Biofertilizer*, 2023.

Ramos Cabrera, E. V., Delgado Espinosa, Z. Y., & Solis Pino, A. F. (2024). Use of phosphorus-solubilizing microorganisms as a biotechnological alternative: a review. *Microorganisms*, *12*(8), 1591.

Raza, A., Salehi, H., Bashir, S., Tabassum, J., Jamla, M., Charagh, S., ... & Varshney, R. K. (2024). Transcriptomics, proteomics, and metabolomics interventions prompt crop improvement against metal (loid) toxicity. *Plant cell reports*, *43*(3), 80.

Rees, G. (2015). *Verifying the declared origin of timber using stable isotope ratio and multi-element analyses* (Doctoral dissertation, University of York).

Remesh, R. K., &Priyadarsini, G. (2024). Chapter-7 SOLiD Sequencing: A Comprehensive Overview. *ISBN: Book DOI: Price:839/-*, *79*, 115.

Ricciardi, M., Pironti, C., Comite, V., Bergomi, A., Fermo, P., Bontempo, L., ... & Motta, O. (2024). A multi-analytical approach for the identification of pollutant sources on black crust samples: Stable isotope ratio of carbon, sulphur, and oxygen. *Science of The Total Environment*, *951*, 175557.

Richardson, A. E., Barea, J. M., McNeill, A. M. &Prigent- Combaret, C. (2009) Acquisition of phosphorus and nitrogen in the rhizosphere and plant growth promotion by microorganisms. *Plant Soil*, 321,305–339.

Rogers, S. W., Moorman, T. B., & Ong, S. K. (2007). Fluorescent in situ hybridization and micro-autoradiography applied to ecophysiology in soil. *Soil Science Society of America Journal*, *71*(2), 620-631.

Román-Lladó, R., Aguado, C., Jordana-Ariza, N., Roca-Arias, J., Rodríguez, S., Aldeguer, E.& Molina-Vila, M. A. (2023). Fluorescence In Situ Hybridization (FISH) for the Characterization and Monitoring of Primary Cultures from Human Tumors. *Journal of Molecular Pathology*, *4*(1), 57-68.

Saeed, M., Naeem, M., Javed, A., Perveen, S., Sajjad, I., Yousaf, M. Z., ... & Song, X. (2024). Characterization of water-deficit tolerance in Upland cotton (Gossypium hirsutum L.) assessing morphological, biochemical, molecular and yield attributes. *Acta Physiologiae Plantarum*, *46*(1), 13.

Saha, K. K., Mandal, S., Barman, A., Mondal, S., Chatterjee, S., & Mandal, N. C. (2024). Genomic insight of phosphate solubilization and plant growth promotion of two taxonomically distinct winter crops by Enterobacter sp. DRP3. *Journal of Applied Microbiology*, *135*(6), lxae146.

Sangeetha, J., &Thangadurai, D. (2013). Staining techniques and biochemical methods for the identification of fungi. In *Laboratory Protocols in Fungal Biology*, *Springer*, 237-257.

Sanger, F., Nicklen, S., & Coulson, A. R. (1977). DNA sequencing with chain-terminating inhibitors. *Proceedings of the national academy of sciences*, *74*(12), 5463-5467.

Santos, F., Melkani, S., Oliveira-Paiva, C., Bini, D., Pavuluri, K., Gatiboni, L., ... &Bhadha, J. H. (2024). Biofertilizer use in the United States: definition, regulation, and prospects. *Applied Microbiology and Biotechnology*, *108*(1), 1-16.

Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., ... &Malonia, S. K. (2023). Next-generation sequencing technology: current trends and advancements. *Biology*, *12*(7), 997.

Scandellari, F., Attou, T., Barbeta, A., Bernhard, F., D'Amato, C., Dimitrova-Petrova, K., & Sprenger, M. (2024). Using stable isotopes to inform water resource management in forested and agricultural ecosystems. *Journal of environmental management*, *365*, 121381.

Schenk, P., Batool, M., Mirzaee, H., & Abbott, A. (2024). Customized plant growth promotion with soil-and cultivar-compatible microbial biofertilizers. *Agronomy*, *14*(9), 1-16.

Schmidt, T., Jung, C., &Metzlaff, M. (1991). Distribution and evolution of two satellite DNAs in the genus Beta. *Theoretical and Applied Genetics*, *82*(6), 793-799.

Schulze, A., & Downward, J. (2001). Navigating gene expression using microarrays—a technology review. *Nature cell biology*, *3*(8), E190.

Sen, A., Saha, N., Sarkar, A., Poddar, R., Pramanik, K., & Samanta, A. (2024). Assessing the effectiveness of indigenous phosphate-solubilizing bacteria in mitigating phosphorus fixation in acid soils. *3 Biotech*, *14*(9), 197.

Sharma, A., Anurag, Kaur, J., Kesharwani, A., & Parihar, V. K. (2024). Antimicrobial potential of polyphenols: An update on alternative for combating antimicrobial resistance. *Medicinal Chemistry*, *20*(6), 576-596.

Sharma, B., Mishra, A., Sahni, P. K., & Sharma, U. (2024). Next-generation sequencing: role in microbial biofilm study. In *Microbial Biofilms* (pp. 237-247). Academic Press.

Sharma, S. B., Sayyed, R. Z., Trivedi, M. H., & Gobi, T. A. (2013). Phosphate solubilizing microbes: sustainable approach for managing phosphorus deficiency in agricultural soils. *Springer Plus*, *2*(1), 587.

Shreshtha, K., Raj, S., Pal, A. K., Tripathi, P., Choudhary, K. K., Mitra, D., ... & Tripathi, V. (2024). Isolation and identification of Rhizospheric and Endophytic Bacteria from Cucumber plants irrigated with wastewater: Exploring their roles in plant growth promotion and disease suppression. *Current Research in Microbial Sciences*, *7*, 100256.

Siddiqui, S., & Saeed, M. (2024). Proteomics as a Tool for Studying. *Microbial Toxins in Food Systems: Causes, Mechanisms, Complications, and Metabolism*, 127.

Siew, S. W., Khairi, M. H. F., Hamid, N. A., Asras, M. F. F., & Ahmad, H. F. (2024). Shallow Shotgun Sequencing of Healthcare Waste Reveals Plastic-Eating Bacteria with Broad-Spectrum Antibiotic Resistance Genes. *Environmental Pollution*, 125330.

Simpson, A., Wood-Charlson, E. M., Smith, M., Koch, B. J., Beilsmith, K., Kimbrel, J. A., & Wilhelm, R. C. (2024). MISIP: a data standard for the reuse and reproducibility of any stable isotope probing-derived nucleic acid sequence and experiment. *GigaScience*, *13*, giae071.

Sipes, D. L. &Einset, J. W. (1983). Cytokinin stimulation of abscission in lemon pistil explants. *Journal of Plant Growth and Regulation*, 2, 73-80.

Song, Y., Zheng, D., Fan, S., Li, S., Zhang, L., Wang, H., & Li, D. (2024). Simultaneous nitrification/denitrification in a single-chamber stainless steel bioelectrochemical reactor. *Journal of Power Sources*, *591*, 233810.

Spaepen, S., Dobbelaere, S., Croonenborghs, A., &Vanderleyden, J. (2008). Effects of Azospirillumbrasilense indole-3-acetic acid production on inoculated wheat plants. *Plant and Soil*, *312*(1-2), 15-23.

Spence, C. & Bais, H. (2015). Role of plant growth regulators as chemical signals in plant-microbe interactions: a double edged sword. *Current Opinion in Plant Biology*, 27, 52–58.

Steuer, R., Kurths, J., Fiehn, O., &Weckwerth, W. (2003). Observing and interpreting correlations in metabolomic networks. *Bioinformatics*, *19*(8), 1019-1026.

Streletskii, R. A., Astaykina, A. A., Belov, A. A., Cheptsov, V. S., &Vetrova, A. A. (2024). Beneficial soil microorganisms and their role in sustainable agriculture. In *Sustainable Agricultural Practices* (pp. 293-333). Academic Press.

Suwannaphan, S., Suksaard, P., Lueangjaroenkit, P., Aroonluk, S., &Thongrak, P. (2024). Isolation and screening of potential lignocellulolytic microbes from Phra Nakhon Si Ayutthaya Province.

Takeda, H., Yamashita, T., Ueda, Y., &Sekine, A. (2019). Exploring the hepatitis C virus genome using single molecule real-time sequencing. *World Journal of Gastroenterology*, *25*(32), 4661.

Tasleem, M., AL-Shammary, A. A., Shoaib, A., Siddiqui, S., & Saeed, M. (2024). Proteomics as a Tool for Studying of Microbial Toxins. In *Microbial Toxins in Food Systems: Causes, Mechanisms, Complications, and Metabolism* (pp. 127-136). Cham: Springer Nature Switzerland.

Timmusk, S., Nicander, B., Granhall, U., &Tillberg, E. (1999). Cytokinin production by *Paenibacilluspolymyxa*. *Soil Biology and Biochemistry*, *31*(13), 1847-1852.

Tseng, Y. F., Li, Y. C., Lee, Y. H., Hu, H. W., Zhang, M. S., Hung, T. C., & Lien, H. C. (2024). Correlation of In Situ HER2 RNA Expression With HER2 Immunohistochemistry and Fluorescence In Situ Hybridization Categories in Breast Cancer. *Archives of pathology & laboratory medicine*, *148*(3), e48-e56.

Uzah, G. A., Ire, F. S., &Ogugbue, C. J. (2023). Isolation and molecular characterization of microorganisms with biofertilizer potential. *Scientia Africana*, *23*(1), 173-188.

Vacheron, J., Desbrosses, G., Bouffaud, M. L., Touraine, B., Moënne-Loccoz, Y., Muller, D., Legendre, L., Wisniewski-Dyé, F. &Prigent-Combaret, C. (2013). Plant growth-promoting rhizobacteria and root system functioning. *Frontier in Plant Science*, 4, 356.

Vági, P., Knapp, D. G., Kósa, A., Seress, D., Horváth, Á. N., &Kovács, G. M. (2014). Simultaneous specific in planta visualization of root-colonizing fungi using fluorescence in situ hybridization (FISH). *Mycorrhiza*, *24*, 259-266.
Vedi, A., & Pandey, G. C. (2024). Physio-biochemical and molecular characterization of wheat cultivars (Triticum aestivum L.) under post-anthesis heat stress. *Bulletin of the National Research Centre*, *48*(1), 88.

Vlek, P. L. G. &Vielhauer, K. (1994). Nutrient management strategies in stressed environments. *Oxford and IBH Publishing Co., New Delhi, India*. 203-229.

Vohra, M., Kour, A., Kalia, N. P., Kumar, M., Sharma, S., Jaglan, S., ... & Sharma, S. (2024). A
Wasmund, K., Singleton, C., Dahl Dueholm, M. K., Wagner, M., & Nielsen, P. H. (2024). The predicted secreted proteome of activated sludge microorganisms indicates distinct nutrient niches. *Msystems*, *9*(10), e00301-24.

Williams, J. K. G., Kubelik, A. R., Livak, K. J., Rafalsky, J. A. &Tynger, S. V. (1990). DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Research*, 18, 6531–6535.

Woese, C. R. (1987). Bacterial evolution. *Microbiological reviews*, *51*(2), 221.

Wong, M. L., & Medrano, J. F. (2005). Real-time PCR for mRNA quantitation. *Biotechniques*, *39*(1), 75-85.

Woźniak, M., Gałązka, A., Tyśkiewicz, R., &Jaroszuk-Ściseł, J. (2019). Endophytic bacteria potentially promote plant growth by synthesizing different metabolites and their phenotypic/physiological profiles in the Biolog GEN III MicroPlateTM Test. *International Journal of Molecular Sciences*, *20*(21), 5283.

Xiong, Y., Mueller, R. S., Feng, S., Guo, X., & Pan, C. (2024). Proteomic stable isotope probing with an upgraded Sipros algorithm for improved identification and quantification of isotopically labeled proteins. *Microbiome*, *12*(1), 148.

Yan, Y., Qin, X., Liu, J., Fan, H., Yan, W., Liu, L., ... & An, G. (2022). Clonal phylogeny and evolution of critical cytogenetic aberrations in multiple myeloma at single-cell level by QM-FISH. *Blood Advances*, *6*(2), 441-451.

Ye, P., Shen, L., Jiang, W., Ye, Y., Chen, C. T. A., Wu, X., ... & Wu, B. (2014). Zn-driven discovery of a hydrothermal vent fungal metabolite clavatustide C, and an experimental study of the anti-cancer mechanism of clavatustide B. *Marine Drugs*, *12*(6), 3203-3217.

Yow, H. Y., Govindaraju, K., Lim, A. H., & Abdul Rahim, N. (2022). Optimizing antimicrobial therapy by integrating multi-omics with pharmacokinetic/pharmacodynamic models and precision dosing. *Frontiers in Pharmacology*, *13*, 915355.

Yu, J., Yang, S., Zhang, X., Liu, X., Tang, X., Wang, L., ... & Song, C. (2024). Integrating metagenomics and culturomics to uncover the soil bacterial community in Asparagus cochinchinensis

Zaratti, C., Marinelli, L., Colasanti, I. A., Barbaccia, F. I., Aureli, H., Prestileo, F., ... & Macchia, A. (2024). Evaluation of Fatty Acid Methyl Esters (FAME) as a Green Alternative to Common Solvents in Conservation Treatments. *Applied Sciences*, *14*(5), 1970.

Zaytsev, P. A., Rodin, V. A., Zaytseva, A. A., Zvereva, M. I., &Solovchenko, A. E. (2024). Advances of high-throughput sequencing for unraveling biotechnological potential of microalgal-bacterial communities. *Journal of Applied Phycology*, 1-19.

Zhang, J.; Cook, J.; Nearing, J.T.; Zhang, J.; Raudonis, R.; Glick, B.R.; Langille, M.G.I.; Cheng, Z. Harnessing the Plant Microbiome to Promote the Growth of Agricultural Crops. *Microbiol. Res.* **2021**, *245*, 126690

Zhao, G., Zhu, X., Zheng, G., Meng, G., Dong, Z., Baek, J. H., ... & Jia, B. (2024). Development of biofertilizers for sustainable agriculture over four decades (1980–2022). *Geography and Sustainability*, *5*(1), 19-28.

Zhao, H., Zhang, Z., Lu, K., Ye, Y., & Gao, S. (2024). Effects Analysis of FAME on the Engine Characteristics of Different Polymerized Biofuels in Compression Ignition Engine. *Energies*, *17*(10), 2255.

Zhao, J., Wang, J., Liu, J., Zhang, P., Kudoyarova, G., Liu, C. J., & Zhang, K. (2024). Spatially distributed cytokinins: Metabolism, signaling, and transport. *Plant Communications*.

Zhou, J., & Thompson, D. K. (2002). Challenges in applying microarrays to environmental studies. *Current opinion in Biotechnology*, *13*(3), 204-207.

Zimmer, C., &Wähnert, U. (1986). Nonintercalating DNA-binding ligands: specificity of the interaction and their use as tools in biophysical, biochemical and biological investigations of the genetic material. *Progress in biophysics and molecular biology*, *47*(1), 31-112.