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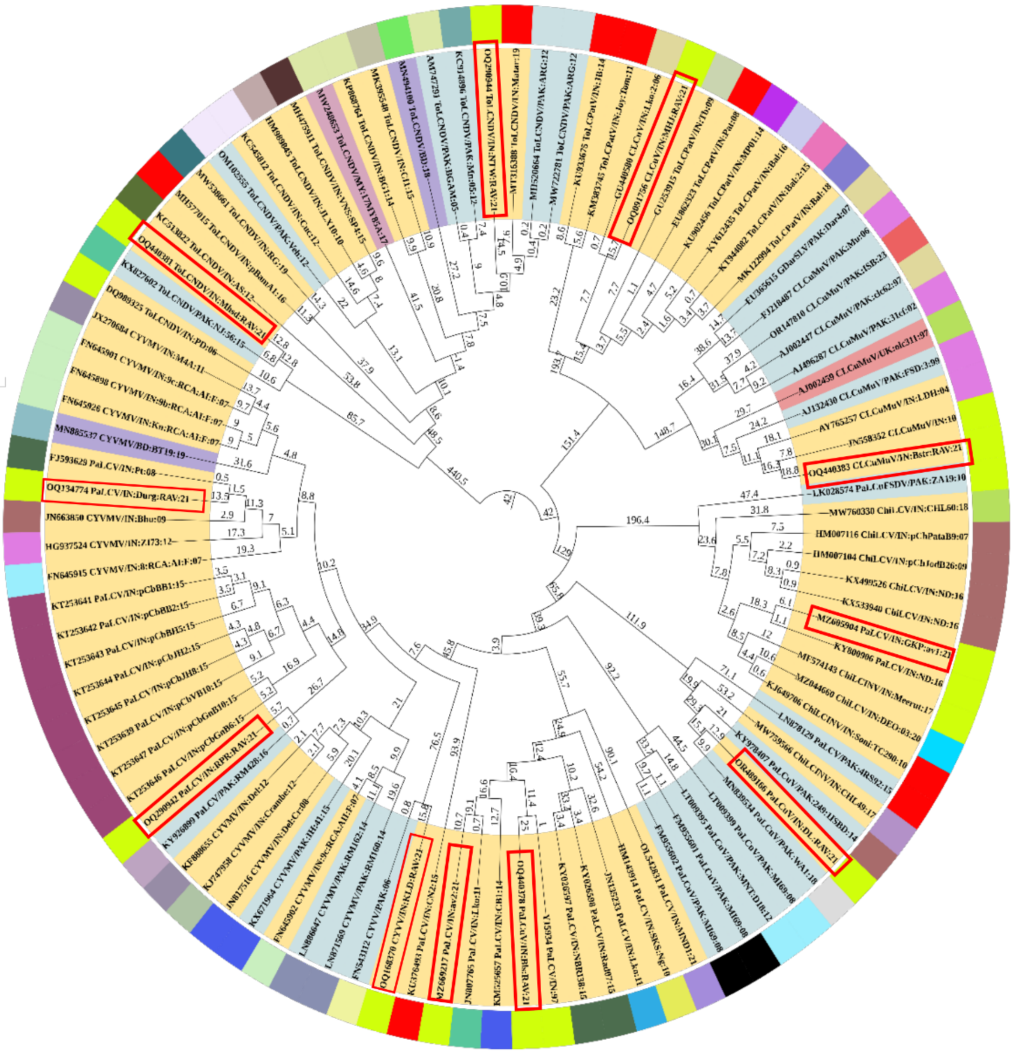
BIOTECH INNOVATORS

Magazine



Phylogenetic analysis of Chilli leaf curl virus

Department of Biotechnology,
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Editorial Committee

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From The Patron Desk

I am happy that the Department of Biotechnology, Deen Dayal Upadhyaya Gorakhpur University is celebrating its 23rd Foundation Day on 31st January 2024. Celebration of Foundation Day reveals the time to remember what has been achieved in the past and acknowledge the faculty members and students who have contributed to the upliftment of the Department. It also provides an opportunity for the faculty members and students to set new goals for the Department. The Department of Biotechnology has immensely contributed in terms of publications, research projects, and administrative responsibilities for the last 23 years. I would like to appreciate the efforts of the faculty members and students to bring a six-monthly magazine "***BIOTECH INNOVATORS***" to encourage students to contribute articles relevant to biotechnology for the welfare of society. In the present time, documentation of the activities is of paramount importance and this magazine will play a significant role in the documentation of the activities and contributions of the faculty members and students regularly.

With best Wishes

Prof. Poonam Tandon
Vice-Chancellor

From The Chief Editor Desk

*It's my pleasure to be part of the new beginning in the year 2024 with an initiative to start a six-monthly magazine named "**BIOTECH INNOVATORS**" reflecting the potential of students of Biotechnology along with the activities and achievements recorded for a period of six months. The first issue of the newsletter is going to be released on 31st Jan 2024, as the day is being celebrated as the foundation day of the Department, marked with the inauguration of the independent building on 31st Jan 2002.*

With more than 23 years of completion of the journey of the Department, it is time to cherish our past achievements and document the upcoming activities of the Department. The Department of Biotechnology was established in the year 2000 and since then 22 batches of M.Sc. Biotechnology students have been awarded degrees. More than 20 students have been awarded Ph.D. in Biotechnology since its inception. We are proud of the achievements of students and faculty members, over the years, to bring the name of the Department to National and International forums.

As Chief-Editor of the newsletter, I would like to acknowledge the sincere support from Prof. Rajarshi K Gaur, Head of the Department along with Prof. Jonnada A.V Prasada Rao, Prof. Sarad Kumar Mishra, Dr. Gaurav Singh and Dr. Pawan Kumar Doharey. I would also like to thank the Ph.D. Scholars namely Kanchan Yadav, Shruti Dwivedi, Varsha Rani, and Vineeta Pandey for contributing articles in the first issue. In the first issue of the magazine, the achievements of the students and faculty members in the last six months (June to Dec. 2023) have been compiled along with the other activities conducted in this duration. I hope the sincere efforts of the students and faculty members to bring the magazine will be highly appreciated and will encourage us to continue for the next issue.

With best Wishes

Prof. Dinesh Yadav

ABOUT THE DEPARTMENT

Biotechnology is amongst the frontiers of science today cutting across various disciplines namely agriculture, medicine, environment, and industry. Realizing the enormous potential of biotechnology several post-graduate programs and research in Biotechnology were initiated at various Institutions/ Universities in the country but the relatively underdeveloped eastern part of Uttar Pradesh encompassing Gorakhpur, Deoria, Basti, Gonda, Beharaich was left out. Keeping in view the importance of Biotechnology, D.D.U Gorakhpur University with funding from the State government and University Grant Commission, New Delhi established the Department of Biotechnology in 2000. It has UGC-sanctioned posts namely Professor (01), Associate Professor (02), and Assistant Professor (04). The department is presently offering M.Sc. and PhD degrees in Biotechnology. The Department has an independent building having seven research laboratories, MSc Laboratories, Classrooms, a Conference Hall, a Seminar Hall and a Departmental Library. The Departmental library has rich collections of over 1100 books related to diverse fields of biotechnology. The present faculty members include Prof. Rajarshi Kumar Gaur as Head, Prof. Jonnada A V Prasada Rao, Prof. Dinesh Yadav, Prof. Sarad Kumar Mishra, Dr. Pawan Kumar Doharey and Dr. Gaurav Singh. In the past, Prof. Anil Kumar Tripathi, Director, Institute of Sciences, BHU, Varanasi, Prof. Dinesh Raj Modi, Head, Department of Biotechnology BBAU Lucknow, Prof. Jagtar Singh, Ex-Coordinator Biotechnology, Punjab University, Chandigarh, Dr. Kirti Srivastava, and Dr. Farrukh Aqil have served the department as faculty members. The major thrust areas of research include Plant Biotechnology, Microbial Technology, Molecular Biology, Bioinformatics, and Enzyme Technology. The Department of Biotechnology has organized several seminars, conferences, and workshops over the years. The research in the Department has gained momentum after procuring basic infrastructural facilities in 2002-03 and to date, several students have been awarded Ph.D. degrees in Biotechnology. Many students have qualified for UGC/CSIR-JRF fellowship, UP-SLET, DRDO, ICMR, and GATE to date. Some students are pursuing their higher education abroad, especially in countries like in USA, Germany, France, and Korea. The research profile of the Department has been strengthened with several project grants received from UGC, DST, UPCAR, UP Govt. The Department has recently received “Centre for Excellence in Genomics and Bioinformatics” from, Higher Education, Govt. of Uttar Pradesh. The research work carried out in the Department has resulted in publications in National and International Journals of repute with high-impact factors. Faculty members have received prestigious fellowships and awards.

EX-FACULTY MEMBERS

Prof. Anil Kumar Tripathi

Prof. Dinesh Raj Modi

Prof. Jagtar Singh

Dr. Kirti Srivastava

Dr. Farrukh Aquil

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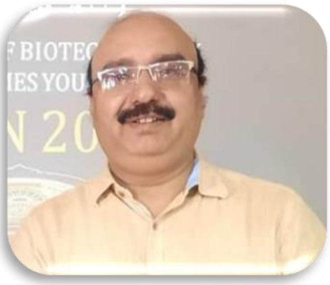
Prof. (Dr.) Rajarshi Kumar Gaur
Head

Prof. (Dr) Dr. Jonnada A.V. Prasada Rao

Prof. (Dr.) Dinesh Yadav



Prof. (Dr.) Sarad Kumar Mishra

Dr. Pawan Kumar Doharey

Dr. Gaurav Singh

ARTICLE-01

FUNGI AS SOURCE OF INDUSTRIALLY IMPORTANT ENZYMES: AN OVERVIEW

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Fungi are lower eukaryotes that are ubiquitous in nature and share diverse morphology. Their macromorphological distinction makes them easy to differentiate and identify revealing their remarkable biochemical diversity (Adedyo et al.,2023). These feed on dead and decaying as absorptive mode of nutrition. The fungal exploitation for baking, and beverage industry drew most of the attention towards these opportunistic hosts (Liu et al.,2017). The wild ability to feed over natural substrates and yield extracellular products makes the enzyme retrieval efficient. Their habitat ranges from pychrophilic artic to Antarctic, covering the tropical fertile lands to extreme thermophilic regions. Biotechnological exploitation of fungal genera *Trichoderma, Aspergillus, Fusarium, Penicillium* and *Rhizomucor* as green agents have expediated the fungal enzymes studies (Nath and Kango 2022). The robust capability to be stable at different range of pH, temperature, pressure and indifferent behavior towards osmolarity induces them as industrial agents. Lower production cost, rapid developments, easy mutations, high catalytic efficacy, low-cost growth media, wide range of substrate affinity even waste, and easy recovery of enzymes makes fungi the dominant ruler of industrial biotechnology (Hasssan et al.,2020). It is projected that the enzyme market would expand at a compound annual growth rate (CAGR) of 7.1% globally between 2020 and 2027, with over 50% of enzymes coming from fungi (Saini et al.,2020). Modern techniques including directed evolution, protein engineering, gene cloning and editing, molecular dynamic simulation, and others are being used to study fungal enzymes in addition to traditional methods. As a result, robust enzymes, intriguing chimeric enzymes, and overexpression systems are being created, and their functional patterns are being discovered (Darwesh et al.,2020).

Despite the advantages and potential of fungal enzymes, out of 100 enzymes sources, only 1% show commercialisation capability. Industries demand enzymes strong to compare chemical methods or equal to them. The choice of isolate governs the kinetic capability of the biocatalyst.

Harnessing indigenous sources and advancing the enzyme production may lead to industry efficient enzymes. The selection of production strategies defines the overall economy of enzyme production and accordingly the source of enzyme production matters a lot. The present article highlights the different sources of fungal enzymes exploited for potential industrial applications Fig. 1.

Sources of fungal enzymes

Endophytic fungal enzymes

Inhibiting plant tissues with infectious quality makes endophytes suitable agents for biocatalysts explorations, Endophytes live inside the plant tissues without causing any sign of infection during all or part of the plant life cycle. They form distinct connections with the plant species, varying from latent pathogens to symbiotic interactions (Bhadra et al.,2022). Many factors, including developmental stage, host genotype, immune system signalling, and environmental conditions, intimately regulate the connection between the plant and the endophyte (Pattanaik et al., 2019). In connection with their host plants, endophytic fungus release proteins thought to support development, nutrition, and defence. In the process these release variety of enzymes that can be harnessed for industrial applications (Mckelvey et a.,2017). The most explored species are of genera; *Acremonium, Microsphaeropsis, Nigrospora, Penicillium, Aspergillus, Fusarium, Thaeendophytic fungi, Cephalosporium,* and *Xylaria.* These fungi are sources of hydrolases, lyases and oxidoreductases mostly contributing to almost all industries (Bhadra et al.,2022).

Rock inhibiting fungi and their enzymatic potential

Their characteristic black microcolonies over rock surfaces are mark of identity (Liu et al.,2022). They are mostly slow growing, produce melanin that imparts the black colour, show meristematic growth and show similarities with yeast. They are typically referring to heterotrophic free-living eukaryotic microorganisms and hence may scarcely be spotted effortlessly, in contrast to lichens, which symbiotically live with photosynthetic microorganisms (Adedyo et al.,2023). In a wide range of extreme environments, including hot tropical deserts, semidry and humid Mediterranean coasts, and McMurdo Antarctic dry valleys with multiple erratic stresses like solar radiation, desiccation and rehydration, and temperature fluctuations, black fungi that live on rocks perform exceptionally well (Hassan et al.,2019). This makes them suitable hosts for enzyme production of incomparable kinetics. Genera of *Dotheideomycetes, Eurotiomycetes Cladosporiales, Capnodiales, Racodiales* and

Arthoniomycetes are common. These fungi are different from other extremophiles as they bear single kind of stress. They contribute in areas of biomedicines and pharmaceutical cosmetic industries (Liu et al.,2022).

Rhizospheric fungi

The soil inhabits association of plant roots and microbial communities. The mycobiota colonizing plant roots hold ecological importance. They maintain the dynamic and functional rhizospheric ecosystem (El-Gendi et al.,2021). The major fungal phyla in the rhizosphere soil of numerous plants include Ascomycota, Zygomycota, Basidiomycota, and Glomeromycota. The majority of land plants have mycorrhizal connections. Plant growth and development, stress tolerance, and phytopathogens are all attributed to the rhizospheric fungi, which also play a critical role in mediating several ecological processes directly or indirectly. In order to maintain a healthy balance for ecosystem function and environmental sustainability, fungi have two roles to play: they promote plant growth and bioremediate harmful heavy metal contamination by increasing metal bioavailability at low levels of contamination and reducing metal bioavailability at high levels of contamination. From food to beverage, animal feed and medicines, these have been the most common commercial sources of enzymes like cellulases, lipases, pectinase, amylases, xylanases and chitinases (Pattanaik et al.,2019).

Marine fungi

Mangrove, sandy, beach, river, and estuarine habitats along coastlines have yielded a remarkable diversity of fungi, indicating that winds and floods are the primary environmental forces that transport terrestrial fungi from land into marine environments (Bonguli and Santos 2015). As a result, fungi that originate in the sea frequently display morphological traits that are comparable to those of their terrestrial relatives. Numerous enzymes have been linked to a variety of actions found in the marine environment, such as antibacterial, antidiabetic, antifungal, anti-inflammatory, antiprotozoal, antituberculosis, antiviral, anticancer, and cytotoxic properties. Indeed, the breakdown of biological stuff is a major activity for them. In this context, lipases, proteases, and a wide variety of hydrolytic and oxidative ligninases are frequently used industrial agents (Dhevagi et al., 2021).

Cold-adaptive fungi

Extremely cold temperatures have the ability to harbour microorganisms that, in reaction to environmental stress, produce rare and unusual enzymes. In industrial biotechnology, these kinds of cold-adapted enzymes prove to be useful instruments. The main reason is that they need less energy to be active than their thermophilic and mesophilic counterparts. The cold-adapted enzymes are highly suited for the waste water treatment, detergent, and baking industries due to their intrinsic qualities, which include high specific activity, low activation energy, and high catalytic activity at low temperatures (Kumar et al., 2021).

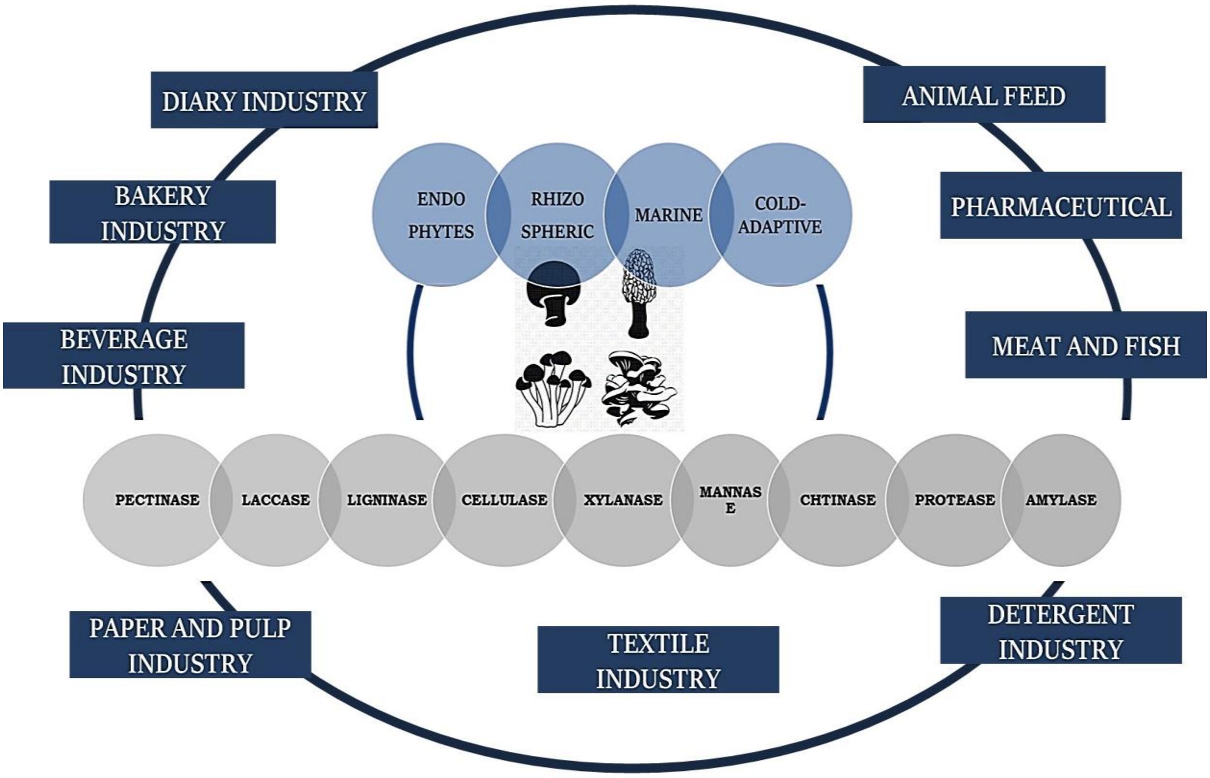

Fig. 1 Fungi and Industrial biotechnology

Fungal enzymes for industrial applications

Limited success has been achieved in the initial attempt to employ enzymes for industrial purposes at the start of the twentieth century. A lack of knowledge about enzyme activity was a major factor (Adedyo et al., 2023). Enzymes and their kinetics have only been characterised and understood since the 1960s (Nath and Kango et al., 2022). Enzymes are now frequently used in many different industrial processes. Addition of proteases and amylases to detergent preparations is the single most important industrial application of enzymes (Dhevagi et al., 2021). The majority of the remaining market is dominated by Carbohydrases, specifically amylases and pectinases. The enzyme glucose isomerase is one of the few non-depolymerases that commands a substantial industrial volume. It is used in the industrial process of producing high-fructose syrup from glucose syrups (Mckelvey et al., 2017).

The food, animal feed, and technical enzymes are the three primary market categories that control the industrial enzyme industry. The majority of sales are made up of technical enzymes including cellulase, amylase, and protease (Liu et al., 2022). The personal care, paper & pulp, textile, leather, detergent, and starch industries all make substantial use of these enzymes. Food enzymes make up the second-largest market sector. Lipase and pectinase are two examples of the enzymes used in the dairy, wine and juice, fats, oils, and baking sectors. The last category is feed enzymes, which includes β-glucanase, xylanase, and phytase (Saini et al., 2020).

One of the most important steps in the commercial manufacture of these fungal enzymes is the fermentation processes, which could be either in the form of solid-state fermentation (SSF) or submerged fermentation (SmF), though SSF is preferred for fungal enzyme production. The superior cultivational benefits, maximum production, quick turnaround, and bioanalyzing capabilities of these fungal enzymes have all been demonstrated. These enzymes can be employed in specific ways in a variety of industrial goods thanks to their hydrolytic characteristics (Hassan et al., 2019).

Due to the lack of need for chemical reagents, the industrial use of fungal enzymes serves as an economical and environmentally friendly substitute. Almost 50% of industrial enzymes are of fungal origin because of these benefits. This chapter emphasised the usefulness of fungi in a wide range of industrial processes, including those in the food, beverage, and wine industries, animal feed manufacturing, paper and pulp industries, textile and laundry sectors (Table 1).

Table 1: The different Genera of fungi exploited for industrial applications

Fungi	Enzymes	Industry	Role in Industrial Processes	Reference
Kluyveromyces sp., Saccharomyces sp., Debaryomyces., Pichia sp., Aspergillus sp., Schizophyllum sp.	Peptidases, Lipases, Proteases	Dairy	Expedite the ripening of cheese, produce acid at a cheap cost using cheese whey as a substrate, remove lactose from milk to create new prebiotics, and practise environmentally friendly clean-in-place.	Knob et al., 2020 Nath and Kango et al., 2022
Rhizomucor sp., Trichoderma sp.,	Amylases Xylanases	Bakery	Reducing pasta's water content,	Ge et al.,2020

Cladosporium sp., Aspergillus sp.	Proteases		strengthening the gluten, increasing dough's volume, texture, and stability, and improving bread's softness, colour, and flavour—all while preventing staling. and improvement of the organoleptic properties of cocoa in cookies & biscuits.	Murthy et al.,2020
Geotrichum sp., Trametes sp., Trichoderma sp., Aspergillus sp.	Pectinases Laccase Cellulose glucoamylase	Beverage	Fruit pectin breaks down to reduce viscosity and clarify juice, starch breaks down for use in industrial processing, and edible vegetable oil's oxidative stability rises.	Ahmed et al. 2020 Guerberoff and Camusso 2019
Pichia sp., Candida sp., Aspergillus sp.,	Proteases Lipases	Meat and Fish	Meat tenderization, fish protein hydrolysates production, skin removal, roe processing, and crosslinking of soy protein.	Sun et al. 2018 Hosseini et al.,2018
Monascus sp., ***Rhizopus sp., Pichia sp., Saccharomycopsis sp., Saccharomyces sp.***	Amylases Glucanases Cellulases, Hemicellulases Xylo pectinases	Beer and Wine	Break down the pectin in brewer's spent grain and improve clarity; speed up the saccharification of sugarcane bagasse and the digestion of grain cell walls; hydrolyse glucans to lower viscosity and improve filterability; and hydrolyse starch in conventional brewing.	Hassan et al. 2020 Liu et al. 2020a Nath and Kango et al., 2022

Trichoderma sp., Aspergillus sp.,	Endoglucanase Xylanase Mannnanase Inulinase Chitosanase	Prebiotic functional food	Concurrent generation of COS and XOS. Corncob xylan hydrolysis produces MOS from guar, konjec, and locust bean gum. Chitosan oligosaccharide degradation	Jana and Kango 2019 Singh et al. 2019 Nath and Kango et al., 2022
Acremonium sp., Chrysoporthe sp.,	Phytase Cellulase Hemicellulases	Animal feed	Using an alkaline environment to break down phytic acid and liberate phosphorous, which is then fed to pigs. Possibility in the saccharification processes of biomass.	Saini et al.,2020 Gonçalves et al.,2020
Rhizomucor sp., Rhizopus sp. Aspergillus sp.,	Amylases Glucoamylase	Starch processing (including food, pharma and ethanol)	High-maltose syrup and better bread quality are produced through starch saccharification. Using cassava bagasse to quickly hydrolyse ethanol	Wang et al.,2020 Escarambonia et al.,2018
Talaromyces sp., Trichoderma sp., Rhizopus sp. Aspergillus sp.,	Cellulases Xylanase Laccases	Pulp and paper	Increasing the pulp bleaching process' effectiveness and releasing decreased sugars and chromophores. Modifying the fibre (making it softer) and de-ink in recycled paper to produce bioethanol.	Saini et al.,2020 Darwesh et al.,2020 Nath and Kango et al., 2022

Phomopsis sp., ***Penicillium sp.,*** ***Aspergillus sp.,*** ***Trichoderma sp.,*** ***Fusarium sp.,***	Cellulases Amylases Pectinases Cold-active Lipases Laccases	Textile	Valuing textile waste Aniline blue's bio scouring, phytopigment processing, bleaching, deinking, and biotransformation	Aggarwal et al.,2019

Conclusion

Fungal enzymes are used in many industrial processes, such as the production of single-cell proteins, lignocellulose saccharification, bioethanol, depolymerization, stain removal, dehairing, bio pulping, bio bleaching, biopolishing, decolorization, biocontrol, organic pollutant remediation, lignin degradation, biosensors, and cancer treatment. These processes offer several advantages over other technologies. High-throughput molecular tools and next-generation proteomics and genomics approaches, including metagenomics, meta proteomics, Meta transcriptomics, and metabarcoding, have revolutionised our understanding of the wide-ranging potential of rhizospheric fungi. Furthermore, these sophisticated instruments offer insights into the composition, structure, and function of rhizospheric fungus, as well as their extensive and unexplored biological activities and latent ecosystem services for the benefit of both the environment and human wellbeing. Target-oriented exploration of the rhizosphere-associated fungal community for the benefit of the human healthcare system, industrial applications, ecosystem functioning, and environmental sustainability is being pursued by the scientific community with great interest in next-generation sequencing methods and chip-based technologies. Despite there has been considerable progress in discovering of new fungal enzymes, there is still a need to implement a new screening program for novel strains in order to optimally maximise the production of enzymes with unique features. As it stands, only 5% of the fungal flora are currently known to exist. A higher-quality yield and an efficient technique with unique features can be supplied by combining the current understanding of molecular biology and biotechnology.

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ARTICLE-02

ELUCIDATING DIVERSE APPLICATIONS OF BIOINFORMATICS IN AGRICULTURE: AN OVERVIEW

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In the era of omics, the bioinformatics is playing a pivotal role for understating different omics especially genomics, proteomics and metabolomics. Bioinformatics is basically a computational intervention which aims for storage, analysis, organization and manipulation of sequences. With the availability of sequence information, researchers in plant biology have been able to determine the genetic architecture of a wide range of plant and microorganism species, including genomes, proteomes, transcriptomes, metabolomes, and even their metabolic pathways (Gomez-Casati et al., 2018). In modern science, sequence analysis is the most fundamental method for obtaining the whole genome sequence of an organism, including DNA, RNA, and proteins. Sequencing entire genomes provides a starting point to understanding the functions of different species and enables the determination of their organization. There are both coding and noncoding regions in a complete sequence data, which can serve as a necessary precursor to any functional gene determining a particular organism's unique characteristics. This sequence includes all regions of the genome, including exons, introns, regulators, and promoters, which results in a large amount of DNA information. Several omics technologies are being developed to examine plants genomes (Gomez-Casati et al., 2018), including next-generation sequencing (NGS), which has expedited the sequencing of several plants genomes.

Bioinformatics databases and tools used by agricultural community

Over the years several innovations in agriculture are being made to achieve the target of attaining global food and nutritional security. Conventional plant breeding, molecular breeding, plant tissue culture, transgenics technology, marker-assisted selection, genomics-assisted breeding, genome editing technologies, next-generation sequencing, omics technologies, and bioinformatics represents the technological advances in agriculture. Due to increasing population, urbanization, industrialization, climate change, and shrinking arable lands, developing crop varieties with higher yields poses a major challenge to agricultural scientists. To feed the growing population on a global scale, technological innovations in agriculture are very important. With the availability of genome sequencing of several crops like *Oryza sativa* (rice), *Triticum aestivum* (wheat), *Sorghum bicolor* (sorghum), *Cajanus cajan* (pigeon pea), *Cicer arietinum* (chickpea), *Solanum lycopersicum L* (tomato), *Eleusine coracana* (Finger millet), etc. intervention of omics technologies comes into the picture. With these technologies, potential agronomic traits can be adequately evaluated by identifying genes/markers/transcription factors. Much effort is being put into genome sequencing, finding novel genes, identifying QTLs, and using marker-aided selection to promote nutritional quality traits in staple crops as a response to abiotic and biotic stresses.

The numerous databases and tools are freely available for agricultural analysis in the field of bioinformatics. Over the year a large number of data has been generated through plant genome sequencing and bioinformatics analysis. These data are submitted to various databases that are publicly accessible. Each database has a specific focus and is unique. For example, MilletDb, is complete multi omics database of six millets consist of information regarding genome, proteome, transcriptome, phenome together with 20 different tools for gene mapping, expression and co expression profiling and GO enrichment analysis (Sun et al., 2023). Having such a database simplifies the research process for those researchers who are working on a variety of millet genomic studies by focusing on using a single database instead of searching through a variety of other databases. In some cases, however, databases are specifically designed and established to cater to all plants, rather than just a particular species or genus, such as the Phytozome database, which has 385 annotated and assembled genomes (http://phytozome-next.jgi.doe.gov/). In contrast, NCBI database as of 2024 contains approximately 2856 plant genomes accessible (https://www.ncbi.nlm.nih.gov/genome/browse#!/eukaryotes/plants). Using such a database is valuable for studies that do not have an exclusive focus on a single species or genus. Consequently, it makes it easier for researchers to access various types of genomic data within one place. In (Table 2), we provide an overview of some of the available plant genome databases that can be accessed by researchers in the agricultural field. There are several other databases like EnsemblPlant available to plant scientists in addition to Milletdb, Phytozome and NCBI databases. EnsemblPlant, a database that provides a comprehensive description of plant species, including their genome sequences, gene models, and functional annotations, together with polymorphic loci, genotypes, population structure, phenotypic characteristics and linkage (Bolser et al., 2016). Additionally, EnsemblPlant provides comparative genomics study for the different plant species of interest, in contrast to NCBI. In this regard, it is clear that this platform offers genome sequence data as well as analytical information about the particular plant species that helps the researcher to conduct their analysis in short time span with less amount of labour. However, the rearchers may need to reassess the data depending on the degree of rigour. In addition to the above-mentioned databases, there are still other plant databases that are useful for retrieving plant genome sequences, such as PlantGDB, and MaizeDIG. In (Table 3), we present a list of tools used in agriculture for genome mining, annotation, function, and structure prediction of candidate gene.

Table 2 Some of the important bioinformatics databases applicable in plant biology research

Function	Server	Details	URL
Genome Database	NCBI	Database for genome, proteome, transcriptome, assembly, bio project and literature	https://www.ncbi.nlm.nih.gov/
	Phytozome	Comparative genomics portal of Plants	https://phytozome-next.jgi.doe.gov/
	MilletDb	multi-omics database to accelerate the research of functional genomics and genetic improvement of millets	http://milletdb.novogene.com/home
	Ensembl Plants	Genomic database (genome sequence, gene models, functional annotation) of more than 33 plant species	https://plants.ensembl.org/index.html
	MaizeGDB	Genetic and genomics database for Maize	https://www.maizegdb.org/
	TAIR	Database of genetic and molecular biology data for *Arabidopsis*	https://www.arabidopsis.org/
	Tomato Functional Genomics Database	Archive of tomato microarray data, metabolite and RNA-seq	https://ted.bti.cornell.edu/
	The Rice Annotation Project Database	Archive of rice genome sequence, structure, and function	https://rice.uga.edu/
	ArrayExpress	Archive for functional genomics data from microarray and sequencing platforms	https://www.ebi.ac.uk/biostudies/arrayexpress
	BarleyGenes	Gene and RNA-seq database for Barley	https://ics.hutton.ac.uk/barleyGenes/
	Expression Atlas EMBL-EBI	Open resource platform for gene and protein expression information	https://www.ebi.ac.uk/gxa/home
	Gene Expression Omnibus	Functional genomics data repository	https://www.ncbi.nlm.nih.gov/geo/
	MaizeDIG	Genotypic-phenotypic database for Maize	https://maizedig.maizegdb.org/

	MaizeMine	Archive to access literature, genomic, interaction and proteomic data for maize	https://maizemine.rnet.missouri.edu/maizemine/begin.do
	PlantProm	Database of plant promoter sequences and experimentally determined transcription start site of various plant species	http://mendel.cs.rhul.ac.uk/ , http://www.softberry.com/
	PlantCARE	Database for promoter sequence analysis and Cis regulatory element identification	https://bioinformatics.psb.ugent.be/webtools/plantcare/html/
	NewPLACE	Database for promoter sequence analysis	https://www.dna.affrc.go.jp/PLACE/?action=newplace
	Rice expression profile Database	Repository of gene expression profiles of rice from microarray analysis	http://expression.ic4r.org/
	PLEXdb	Plant expression database with gene expression profile data sets, structural genomics, and phenotypic	http://www.plexdb.org
	SolGenomics Network	Database and tool of genomics and genetics approach for tomato and some other plant species such as eggplant	https://solgenomics.net/
	PoMaMo	Archive of potato sequences, literature, maps, and tools	https://www.gabipd.org/projects/Pomamo/
	Millet SSR Database	Millets SSR database is an integrated online database for sorghum, foxtail millet, proso millet and pearl millet	http://webtom.cabgrid.res.in/millet_ssr_db/
Transcriptome database	Plant Transcription Factor Database	Database consisting 165 plant species TF	http://planttfdb.gao-lab.org/
	PMDTDb (Pearl Millet Drought Transcriptome Database)	database of drought transcription factors (TFs), gene regulatory network (GRN), SSR and SNP markers of pearl millet	http://webtom.cabgrid.res.in/pmdtdb/
	FmTFDb: a foxtail	for expediting functional genomics in millets	http://59.163.192.91/FmTFDb/index.html

	millet transcription factors database		
Pathway Database	Reactome	Pathway interaction repository	https://reactome.org/
	KEGG	collection of manually drawn pathway maps representing our knowledge of the molecular interaction, reaction and relation networks for metabolism, genetic information pathways, cellular process	https://www.genome.jp/kegg/pathway.html
	PlantCyc	Metabolic pathway reference database from over 350 plant species	https://www.plantcyc.org/
RNA analysis database and tool	Plant rDNA database	providing information on numbers and positions of ribosomal DNA signals and their structures for 2770 plant species	https://www.plantrdnadatabase.com/
	miRBase	the archive for microRNA sequences and annotations	https://mirbase.org/
	psRNATarget	a plant small RNA target analysis server	https://www.zhaolab.org/psRNATarget/
	RNAfold	predict secondary structures of single stranded RNA or DNA sequences	http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi
Chemical Compound Database	ChEBI	Archive of molecular entities that focuses on small chemical compounds	https://www.ebi.ac.uk/chebi/
	PubChem		https://pubchem.ncbi.nlm.nih.gov/
	ChemSpider		http://www.chemspider.com/
	Zinc Database		https://zinc.docking.org/
Metabolomic Database	Metabolights	Consist metabolite structures and their reference spectra as well as their biological roles, locations and concentrations, and experimental data from metabolic experiments	https://www.ebi.ac.uk/metabolights/

Table 3 Some of the important bioinformatics tools and server

S.N	Bioinformatics tools	Link	Application
1.	NCBI	https://www.ncbi.nlm.nih.gov/	Data Mining
2.	UNIPROT	https://www.uniprot.org/	Data Mining
3.	RCSB Protein Data Bank	https://www.rcsb.org/	Protein Data Mining
4.	BLAST	https://blast.ncbi.nlm.nih.gov/Blast.cgi	Homology Search
5.	MEGA	https://www.megasoftware.net/	Multiple Sequence Alignment And Phylogenetic Tree Construction
6.	iTol	https://itol.embl.de/upload.cgi	Phylogenetic Tree Construction
7.	CLC	https://clc-sequence-viewer.software.informer.com/download/	Multiple Sequence Alignment
8.	Expasy Translate tool	https://web.expasy.org/translate/	Protein Sequence Prediction
9.	InterProscan	https://www.ebi.ac.uk/interpro/search/sequence/	Protein Domain Analysis
10	Prosite	https://prosite.expasy.org/	Protein Domain Functional Analysis
11	HMMScan	https://www.ebi.ac.uk/Tools/hmmer/search/hmmscan	Biosequence Analysis Against Collection Of Protein Profile
12	MEME Suite 5.5.2	https://meme-suite.org/meme/tools/meme	Motif Search
13	SWISS-MODEL	https://swissmodel.expasy.org/	Protein Structure Homology Modelling Server
14	PDBSum	http://www.ebi.ac.uk/thornton-srv/databases/pdbsum/	Protein 2D Structure Prediction
15	Primer3	https://primer3.ut.ee/	Primer Designing
16	Ka/Ks calculation tool	http://services.cbu.uib.no/tools/kaks	Gene Duplication Event Prediction
17	Expasy ProtParam server	https://web.expasy.org/protparam/	Physico-Chemical Analysis

18	DeepTMHMM server	https://dtu.biolib.com/DeepTMHMM	Transmembrane Analysis
19	SignalP 5.0	http://www.cbs.dtu.dk/services/SignalP/	Signal Peptide Prediction
20	WOLFPSORT	http://wolfpsort.org/	Subcellular And Nuclear Localization Prediction
21	CB-Dock	https://cao.labshare.cn/cb-dock/	Protein-Ligand docking
22	HADDOCK	https://wenmr.science.uu.nl/haddock2.4/	Protein-Protein Docking

Biotechnology and bioinformatics intervention in plant breeding

Modern agriculture uses transgenic technology to alter or introduce foreign genes into plants or crops for the purpose of making them useful and productive and enhancing their characteristics by using the technology(Jhansi Rani & Usha, 2013). The evolution of various sequencing technologies like NGS and others generates a large number of datasets that requires the use of databases to store the information as previously mentioned. As whole genome sequences are readily available in databases, they can be freely associated with gene sequences, putative functions, or genetic map positions across genomes. By using software to formulate predictive hypotheses, it is possible to incorporate phenotypes desired from complex combinations into plants using genes that score well in breeding and provide higher reliability. A schematic representation of plant breeding using bioinformatics and transgenic techniques is given in Fig. 2. For example for mining of NF-Y genes in finger millet and utilizing these genes for crop improvement program, breeders can choose amalgamation of *In-silco* and wet bench experimentation (Rani et al., 2023). For this agriculture biologist first mined the selected database for putative genes. For example, the MilletDB platform allows searches for NF-Y genes either by using homologous genes or by using keywords. After the putative gene prediction, the gene organization and collinearity analysis can be performed. After that qPCR expression profiling of NF-Y genes can be performed and regulatory network can be constructed. The overall bioinformatics analysis help in prediction of targeted transgene which can be used by breeder in transgenic technique for crop improvement.

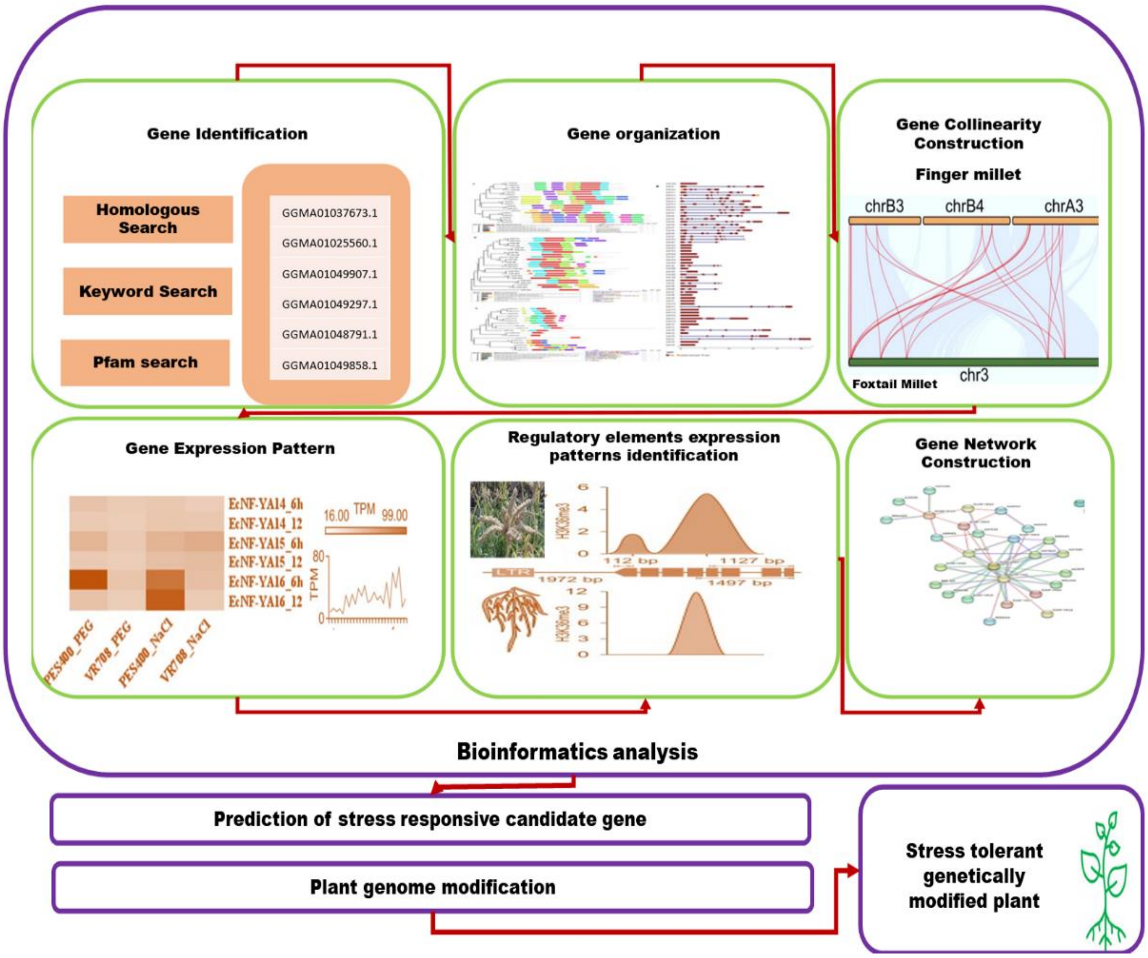

Fig. 2 Schematic representation of application of bioinformatics in plant breeding

Bioinformatics for studying stress resistance in plants

A plant's response to stress environment is crucial for ensuring its growth and development, as well as avoiding the severe crop yield penalties caused by harsh weather conditions (Costa & Farrant, 2019). In order to study and analyze plant transcriptomes in response to biotic and abiotic stress, it is essential to utilize bioinformatic tools. Several stresses in plants are known to induce the expression of numerous transcriptional regulators, which then up-regulate downstream genes involved in self-protection or stress adaptation. The plant transcription factor database (Tian et al., 2020) lists more than 15759 genes encoding 56 families of transcription factors in millets like Jowar, Bajra, Kangni, Kutki, and Chena and overall consisting of transcription factor of 165 plant species. As we all know gene expression begins with the process of transcription, which produces primary RNA transcripts from DNA. Ultimately, this results in the production of a functional protein after translation, which is highly regulated. Hence, transcription factors regulate gene expression and bind to specific DNA sequence known as a promoter, which in turn mediate the important life processes, including cell development, hormonal responses to various biotic and abiotic factors and metabolic pathways. (Gonzalez, 2015). Plants under biotic and abiotic stress responses activate a network of transcriptional factors shown in Fig. 3. It is believed that two groups of genes respond to stress: (1) A set of regulatory genes encodes for receptors, kinases, transcription factors and facilitating the transduction of signaling from stress to downstream genes by altering their expression levels. and (2) groups of genes which encodes for such a kinase which are required for plant recovery during times of stress. Therefore, by using Bioinformatics tools and databases, scientist in the field of agriculture can able to predict stress responsive genes or proteins or transcription factors, which might be playing various role in defence mechanism against stresses like biotic and abiotic.

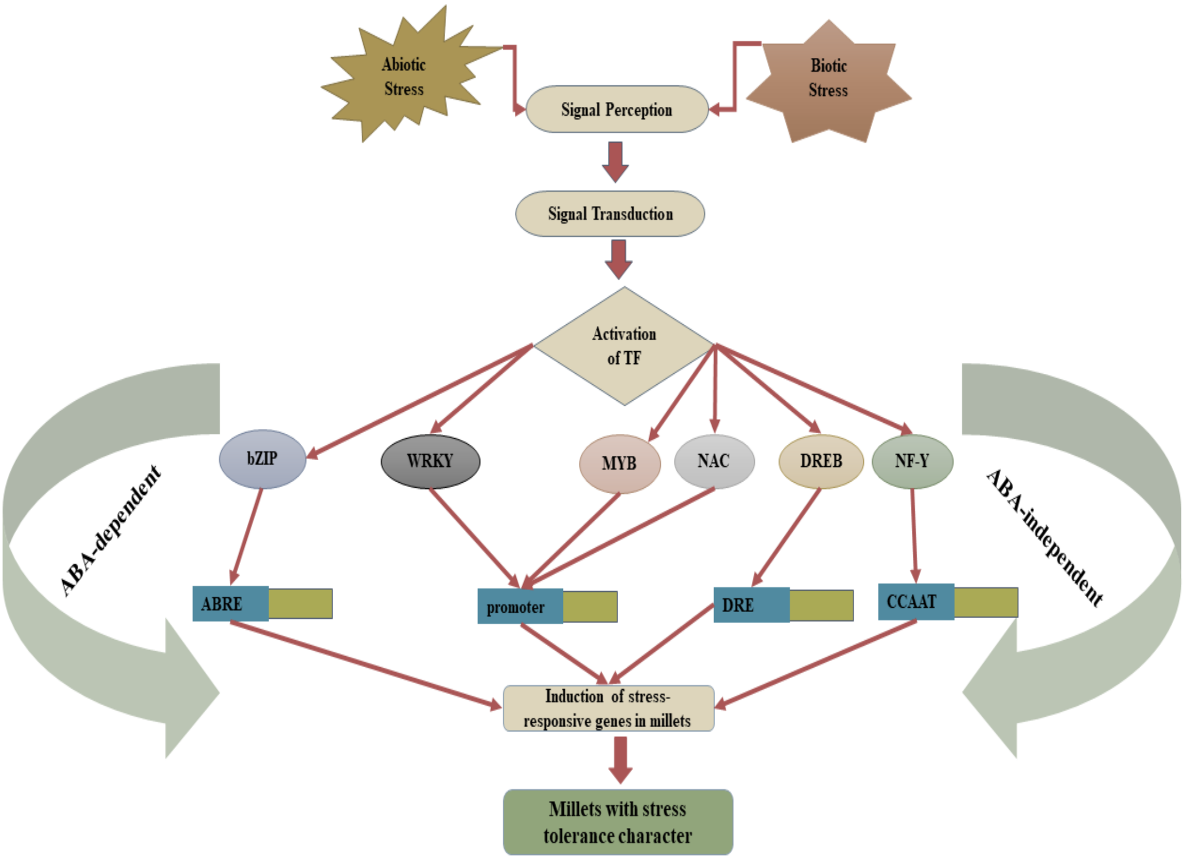

Fig. 3 Activation of various TF in response to several stresses

Bioinformatics in plant- pathogen interaction study

Agriculture crops are susceptible to disease infection caused by fungus effector proteins. The secreted small proteins interact with the host receptor binding partners (effector protein) by penetrating the cells or through the adherence to the apoplastic space (Rozano et al., 2023). It is therefore imperative to understand how effector proteins of fungi interact with host receptor to select (R-gene) plant resistance genes or susceptibility-related genes that may be used by scientist in breeding program to develop new cultivars that are resistant to disease. The P-P interactions between effectors and receptors of plants are characterized using molecular docking simulations. It is anticipated that the computational approaches like molecular docking approach contribute to the sighting of putative interaction partners for effector proteins within plants and support the discovery of effector-aided markers. Thus contributing in the breeding program for development of crops that can be pathogen resistant (Rani et al., 2024).

Conclusion

With the advancement in the sequencing technologies and deciphering of several plant genome sequences, the annotation of these sequences for determining its utility for crop improvements, the role of bioinformatics is of paramount importance. The huge sequence information generated needs to be evaluated for developing strategies for crop improvement either using the modern agricultural tools or the conventional plant breeding approach. Using bioinformatics several genes governing agronomic traits have been deciphered and several markers have been developed. In the field of agriculture, bioinformatics represents a ultimate shift in how researchers examine the living organisms. Understanding complex traits especially stress tolerance has been addressed to some extent by the bioinformatics intervention using whole genome sequences. Recently GWAS has enhanced the modification and improvement of crops by identifying desired QTL and allelic variation associated with particular traits. The application of bioinformatics to plant biotechnology has enabled researchers to gain a systematic and fundamental understanding of economically significant plants. Although bioinformatics has achieved many exciting achievements in agriculture, there is still a long way to go before the whole genome sequencing (WGS) and assembly is annotated and at affordable costs. As a result of the complexity of plant genomes, effective bioinformatic tools are critical to overcoming the challenges associated with providing longer reads with unbiased coverage. This can only be achieved through the development of enhanced algorithms that facilitate mining of data, their analysis and comparison. This entails the importance of researchers in the field of bioinformatics and experts of maths and programming to bring fresh approaches or algorithm to bioinformatics, that not only contribute in the advancement of agriculture sector, but also for humanity's future.

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ARTICLE-03

POTENTIAL OF MICROORGANISMS IN PROMOTING SUSTAINABLE AGRICULTURE: AN OVERVIEW

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The agriculture sector has suffered a significant economic decline over the past few years due to low yield or loss caused by various factors, most prevalently disease and plagues. The plagues are classified into three categories: pathogens, parasites, and predators. They are also referred to as "natural enemies." The procedures and materials employed to resist and safeguard harvests from natural enemies are primarily synthetic and chemical (Bale et al., 2008). Since pesticide and herbicide use negatively influence both the natural environment and consumer well-being, there has been concern in recent years about their application. Even though these seem cheap, eventually, they pollute the environment, harm food, and compromise human health. Thus, synthetic pesticides in agriculture should be reduced or eliminated. Biocontrol agents are a viable option for managing pests in various crops. Biocontrol agents are natural or modified organisms, genes or products that suppress the development of the unwanted organism (pest/pathogen) while enhancing the growth and yield of the desired organism (crops, microorganisms, or insects) (Sandhu et al., 2012). Additionally, Biological Control Agent encourages plant development and prevents plant diseases. They also aid in the uptake of nutrients, acquire disease resistance, and stress management in plants. Biological Control Agent's products can be used as biopesticides, plant strengtheners, and fertilizers according to their actions and outcomes (Cook, 1993). Biological control is the process by which people use non-pathogenic hostile microorganisms to eradicate disease-causing pathogens. Several bacteria, fungi and viruses are utilized to kill pests and weeds and to control diseases. *Agrobacterium radiobacter* strain K 84 was the first bacteria to be identified to exhibit biocontrol activity against crown gall disease in 1979, and *Trichoderma harzianumi* ATCC 20476 was the fungus employed to treat plant diseases (Fravel, 2005). The potential applications of microbes in sustainable agriculture are depicted in Fig. 4.

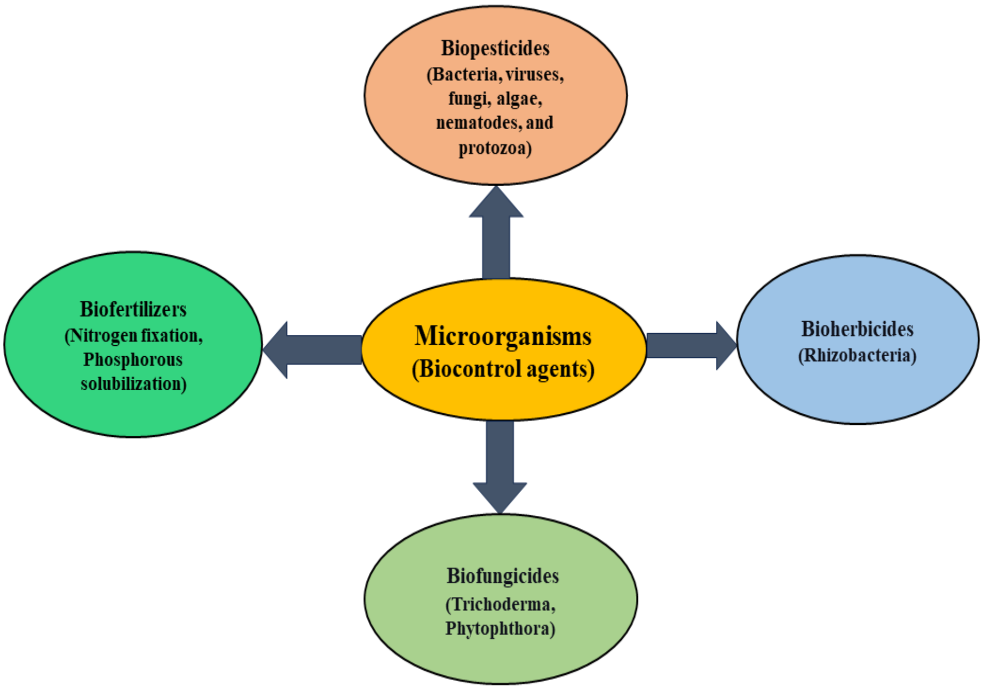

Fig. 4 Applications of microbes in Agriculture

Microorganisms as biofertilizers

Applying chemical fertilizers to supply the growing demand for food and agricultural products has been a major source of environmental contamination. The excessive use of chemical fertilizers is attributed to many difficulties. Therefore, switching to organic farming is essential. The practice of cultivating beneficial plants using biofertilizers that give plants adequate nutrition is known as organic farming. A mixture of live microorganisms known as "biofertilizer" helps increase soil fertility by fixing atmospheric nitrogen, dissolving phosphorus and other nutrients, and stimulating plant development by secreting plant hormones (Barman et al., 2017). Fungi, bacteria, and cyanobacteria are the main providers of organic fertilizers. Several plants, like *Ardisia*, create unique interior holes in their leaves that hold symbiotic nitrogen-fixing bacteria that embrace *Mycobacterium* and *Xanthomonas*, sources of soil fertilizer containing nitrogen (Miller, 1990). Another important class of microorganisms for the environment is called blue-green algae or cyanobacteria. *Trichodesmium*, *Nostoc*, and *Anabaena* are a few cyanobacteria which contribute roughly 36% of the worldwide nitrogen fixation and help enhance the productivity of rice fields so that rice can be grown worldwide (Gallon, 2001; Irisarri et al., 2001; Kundu et al., 1995).

Phosphorus is the second most limiting nutrient for plants after nitrogen, although it accumulates in large concentrations in the soil (Schachtman et al., 1998). However, the majority of it is in an inaccessible form. *Bacillus and Pseudomonas* are examples of phosphorus-solubilizing bacteria that may mobilize phosphorus from states not present in the soil to improve its availability to plants (Richardson, 2001). An active group of microbes, such as *Pseudomonas, Bacillus, Aspergillus, Penicillium, Micrococcus, flavobacterium, Fusarium*, and *Sclerotium*, have been discovered to be efficient in the solubilizing process of phosphorous (Krishnaprabu, 2012). Few reports showed that siderophores and indole compounds produced by *Enterobacter* and *Burkholdenia*, extracted from the rhizosphere of sunflowers, may dissolve phosphate (Ambrosini et al., 2012). It has been discovered that, along with nitrogen-fixing microbes and phosphorus-solubilizing microbes, a few other microbes are also suitable as organic fertilizers, as they produce growth-promoting chemicals that promote plant growth (Bashan, 1998). Reports showed that *Bacillus licheniformis* and Rhizosphere *Bacillus pumilus* produce significant quantities of the plant hormone gibberellin (Gutiérrez-Mañero et al., 2001). Likewise, *Paenibacillus polymyxa* demonstrated numerous beneficial characteristics, such as synthesizing antibiotics and plant hormones, such as cytokinins, phosphorus solubility, nitrogen fixation, and increased soil porosity (Timmusk et al., 1999).

Microorganisms as biopesticides

Biopesticides are live creatures or their byproducts that kill or repel pests or insects. The major microbiological pest control agents are biopesticides derived from bacteria, viruses, fungi, algae, nematodes, and protozoa, along with certain additional chemicals such as metabolites directly generated from these microbes (van Lenteren, 2012). New pest strains resistant to insecticides and synthetic pesticides have emerged due to the abuse of chemical and synthetic pesticides (Nawaz et al., 2016). Therefore, switching to organic farming based on biopesticides is necessary. Over 100 bacteria have been identified as pathogenic insects, and *Bacillus thuringiensis* (Bt) has assumed paramount importance as a microbial agent. Bacillus thuringiensis exhibits insecticidal properties due to its cry protein, which is responsible for the ingestion and death of insects (Khachatourians, 1986). Similar to this, over 1000 viruses have been known from insect species. For example, baculoviruses of the genus Nucleopolyhedrovirus (NPV), which infect insects as well as other arthropods, have been found to have narrow-spectrum insecticidal properties specific to certain species. In fruit trees, Codling moth is managed by *Cydia pomonella* granulovirus, and in potatoes, potato tuber worms are controlled by *Phthorimaea operculella* granulovirus (Arthurs et al., 2008; Lacey et al., 2008). Trichoderma fungi are being developed as biological control agents to combat plant diseases (Vos et al., 2014). Other fungi, mainly *streptomycetes*, also produce toxic chemicals that are effective against insects. Similarly, the actinomycetes *Saccharopolyspora spinosa* generate the active component Spinosyns, a biopesticidal substance sold commercially and effectively against both Diptera and Hymenoptera (Hall et al., 1999).

Microorganisms as bioherbicides: Utilizing microorganisms as bioherbicides has the unique potential to lower the population of invasive weeds through highly focused, self-sufficient impacts, hence aiding in the preservation of the natural environment (Van Driesche et al., 2010). Nematodes, pathogenic and non-pathogenic bacteria, obligate fungal parasites, soilborne fungal pathogens, and non-phytopathogenic fungi are examples of bioherbicidal microbial agents (Kremer, 2005). The Rhizobacteria are a group of microorganisms that are often overlooked as biological control agents for weeds (Schippers et al., 1987). Tropical soda apple (Solanum viarum) and other invasive weeds are being researched as potential herbicides for mechanically transmitted viruses like Tobacco Green Mosaic Virus, which is grown, harvested, and freeze-dried in surrogate host plants (Raghavan, 2001). Since soilborne fungi are applied directly to the soil to kill seedlings shortly after emergence or reduce weed growth by causing seed rot before emergence, they have been regarded as an essential bioherbicide supplement (Jones & Hancock, 1990).

Microorganisms as biofungicides

Natural compounds and microorganisms with the capacity to manage plant diseases are collectively referred to as biofungicides (Abbey et al., 2019). Most of the preparations in this group of substances are regarded as pure due to their source of origin and the low concentration of the active ingredient. Biofungicides are manufactured in many forms, such as tablets, emulsifiers, suspension concentrates, and water-soluble powders (Albert et al., 2020). The method for administering biofungicides involves preparing the planting material, mixing it into the soil, and then misting the developing plant. Few reports showed that Trichoderma pseudokoningii and T. viride suppress Botrytis cinerea in strawberry fruit by the releasing specific secondary metabolites (Tronsmo et al., 1977). The fungus Cercospora rodmanii produces the spores that regulate water hyacinth. Spores of the Phytophthora palmivora fungus control milkweed vines in citrus orchards. Other examples include the biological control capability of Trichoderma harzianum species against Fusarium, Pythium, and Botrytis cinerea, which results in a powdery mildew hyperparasite (Abbey et al., 2019).

Conclusion

Biocontrol agents can replace chemical pesticides. They can be utilized as biofertilizers, biopesticides, and plant development stimulants. The BCA uses different action mechanisms to control plant pathogens. These mechanisms can be direct, including production of lytic enzymes, antibiotics, or hyperparasites, or indirect, which includes nutrient competition, spatial induction, and plant resistance. Biocontrol agents might be developed as part of an integrated pest management (IPM) system to mitigate the adverse effects of chemical fungicides on the environment. Research and development for biocontrol agents require additional funding. It is essential to conduct more research on the dosage, formulation, impact on the activities of Biological Control Agents, and impacts of Biological Control Agents on the native plant microflora under various environmental conditions. To develop more potent antagonists, it is necessary to comprehend the strategy of action of biocontrol drugs completely. The formulation procedures must be enhanced to provide formulations with longer shelf lives. Environmental conditions significantly influence the efficacy of biocontrol agents. Consequently, it is essential to investigate the ecological factors that promote the efficient usage of biocontrol agents. It is also required to find the factors that led to the colonization of the rhizosphere and the impact of Biological Control Agents on the area's indigenous population. Identifying the genes, gene products, and other signalling molecules that cause microbes to act antagonistically is critical. To successfully use gram-negative bacteria, efficient methods for producing Biological Control Agent in large quantities must also be created, technological issues related to this production must be handled, and formulations must be enhanced.

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miRNAS FOR CROP IMPROVEMENT

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The expansion of the human population and global mechanisation are two major factors that contribute to and encourage climate change. Current climate change poses major concerns for agricultural output and creates issues for food security to feed the world's rising population (Molotoks et al., 2021; Farooq et al., 2022; Zandalinas et al., 2021). Plants experience active environmental pressures throughout their lives as a result of climate change. These pressures include both abiotic (drought, salinity, nutrient imbalance, heavy metals, extreme temperatures, anoxia, hypoxia and UV-B radiation) and biotic (virus, insects, bacteria and nematodes and fungus) (Suzuki et al., 2014; Zandalinas et al., 2021; Shahzad et al., 2021; Farooq et al., 2022; Zandalinas and Mittler, 2022). These stresses, alone or in combination, have a major impact on plant growth and output by compromising many physiological, morphological, molecular, and biochemical processes (Suzuki et al., 2014; Zandalinas et al., 2021; Zandalinas and Mittler, 2022). As a result, one of the most difficult challenges for conventional and creative crop improvement is that the development of one appropriate attribute in an emerging crop cultivar is constantly offset by the degradation of one or more valuable attributes (such as yield, growth, or another agronomic attribute). The most secure solution to this quandary is the widespread adoption of regulatory genes, particularly those that provide more effective and accurate regulation in a directed manner. Developments in genomics resources, such as microarrays and next-generation sequencing (NGS), contributed to the finding of many novel protein-coding genes associated with both abiotic and biotic stresses in the previous era (Dhamija and Menon, 2018; Nejat and Mantri, 2018; Varshney et al., 2018, 2020, 2021b). Nonetheless, other unresolved issues remain, such as how these protein-coding genes are controlled. What kinds of gene systems do plants use to respond to diverse stresses? (Zhang, 2015). MicroRNAs (miRNAs), a family of small regulatory RNA molecules identified recently in plant biotechnology, may overcome these challenges (Zhang, 2015; Choudhary et al., 2021). MiRNAs are now recognised as widespread post-transcriptional gene regulatory molecules in plants, actively influencing growth and development by modifying target gene expression (Kar and Raichaudhuri, 2021; Gao et al., 2021b).

MiRNAs appear to influence less than 1% of plant protein-coding genes. Although the number of miRNAs is minimal, most target key transcription factors (TFs), influencing plant growth and development (Gao et al., 2021b; Gangadhar et al., 2021). Plant miRNAs suppress target genes by a variety of methods, including chromatin changes, sequence-specific mRNA cleavage, and translational repression. These short non-coding RNAs operate as post-transcriptional master modulators of gene expression, targeting miRNAs for translation or cleavage inhibition in plants (Gao et al., 2021b; Gangadhar et al., 2021; Kar and Raichaudhuri, 2021). An introduction to miRNA-mediated crop enhancement and sustainable agriculture resulted in various recent achievements in miRNA-mediated crop improvement under abiotic and biotic challenges and several growth-related parameters. Various studies provided an overview of current improvements in sequence technologies for discovering miRNAs linked to agricultural improvement. Various recent studies have discussed the potential of altering miRNA and their target genes as one of the most appealing research avenues for crop development. Existing issues and future directions for genetically modified miRNA targets for building climate-smart crops have also been highlighted.

The a forementioned results demonstrated that miRNA plays an important role in various stress mitigation mechanisms; nevertheless, research is still hesitant to address the molecular mechanism underlying these responses. Maintaining and increasing agricultural productivity becomes critical with the world's population constantly increasing. Abiotic and biotic stressors both have a considerable impact on agricultural production; thus, understanding plant responses to stress and tolerance mechanisms is critical. The isolation and identification of novel stress-responsive, growth-related, and other agronomic trait-associated miRNAs utilising cutting-edge sequencing technologies and computational approaches is a future research direction. Such research can also aid in the discovery of new targets and regulatory pathways governed by miRNAs. Growing scientific data reveals that several stress-associated plant miRNAs and their pivotal role in stress response and tolerance have been identified in models and important field crops over the last few years. Recent improvements in high-throughput sequencing technologies and computational sources, such as in-silico tools and databases, machine learning, and genome-wide documentation of stress-associated miRNAs and their targets, have made genome-wide documentation of stress-associated miRNAs and their targets increasingly practical. Another intriguing area of investigation is the use of miRNAs in agricultural enhancement via genetic engineering.

According to the literature, the data collected regarding stress-responsive and plant development-related miRNAs and their targets could be genetically altered using overexpression or the CRISPR/Cas system to generate stress-smart and superior future cultivars. As a result, the identification of stress-tolerant miRNAs and their roles will aid in the development of commercially important crops that can withstand biotic and abiotic stresses, significantly increasing crop production under various stress situations. The recurrent research on miRNA synthesis and mode of action will provide insights into the regulation of gene expression in plants, with prospective applications in sustainable agriculture and biotechnology to address climate change.

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DEPARTMENT ACHIEVEMENTS

(JUNE-DECEMBER 2023)

RESEARCH PROJECTS SANCTIONED:

S. No.	Title of Project	Principal Investigator/ Co-PI	Funding Agency	Duration	Grant received
1.	Dynamics of photosynthetic apparatus during the pre-zygotic stage of wheat in response to elevated temperature	Dr. Ramwant Gupta and Prof. Dinesh Yadav	UPCAR	3 Yr.	24.86 lac
2.	Improving photosynthetic electron transport and CO2 flow in the leaves of finger millet to enhance yield	Dr. Ramwant Gupta and Prof. Dinesh Yadav	UPCAR	3 Yr.	73.14 lac
3.	Investigations of novel tubulin binding agents with potential anticancer properties using various computational techniques	Prof. Umesh Yadava and Prof. Dinesh Yadav	UPCST	3 Yr.	11.86 lac
4.	To conduct awareness programs related to intellectual property protection	Prof. Dinesh Yadav (Convenor)/ Prof. Umesh Yadava (As Organizing secretary)	UPCST	For one day workshop	80K

PUBLICATIONS:

Editorial Article

- PLC Fonseca, RK Gaur, ERGR Aguiar (2023). Editorial: Using virus specific-signatures during infection to characterize host-pathogen interactions. *Front Genet 14*, 1290714. https://doi.org/10.3389/fpls.2023.1193573

- RK Gaur, Dinesh Yadav and BR Albrectsen. Editorial: Omics driven research for the improvement of industrial crops. Front. *Plant. Sci 14*, 1143571. https://doi.org/10.3389/fpls.2023.1143571

Research Article

- Varsha Rani, Vinay Kumar Singh, D. C. Joshi, Rajesh Singh and Dinesh Yadav (2024). Molecular docking insights into nuclear factor Y (NF-Y) transcription factor and pyrabactin resistance 1 (PYL) receptor proteins reveal abiotic stress regulation in finger millets. *Crop Design* (Elsevier) 100051. https://doi.org/https://doi.org/10.1016/j.cropd.2023.100051

- Ritesh Mishra, Rakesh Kumar Verma, Smriti Mall and R. K. Gaur (2023). Complete genome sequence of eggplant mild leaf mottle virus (EMLMV) infecting eggplant in India. *Indian Phytopathology 76*, 1141–1144. https://doi.org/10.1007/s42360-023-00672-3

- Shruti Dwivedi and Dinesh Yadav (2023). Qualitative and quantitative assessment of metagenomic DNA isolated from diverse soil samples using different protocols. *Ecological Genetics and Genomics (Elsevier) 29,* 10094. https://doi.org/10.1016/j.egg.2023.100194

- R L Maurya, Mukesh Kumar, Ujjwal Sirohi, Priya, Veena Chaudhary, Rakesh Sharma, Dinesh Yadav, and Manoj Kumar Yadav (2023). Effect of silver nitrate and thidiazuron on shoot proliferation, hyperhydricity and assessment of genetic fidelity of microplants in carnation (*Dianthus caryophyllus* L.). *Cytology and Genetics* (Springer) 57, 87-94. https://doi.org/10.3103/S0095452723010061

- Sonali Jaiswal, Anupama Ojha, Sarad Kumar Mishra (2023). Assessment of Plant growth promoting parameters of endophytes isolated from *Calotropis procera* and their performance under irrigated and non-irigated conditions. *Current Microbiology,* Vol: 81 (1), 49**.** 10.1007/s00284-023-03570-z

- Anupama Ojha, Shashank Shekhar, Poonam Gupta, Harikesh Singh, Sonali Jaiswal, Sarad Kumar Mishra, (2023) Study on effect of environmental and occupational pesticide exposure on marker enzymes of malignancies in cancer patience. *International Research Journal of Research in Environmental Science and Toxicology***,** pp 1-5.

Review Article

- Nisha Choudhary, Naveen Dhingra, Amel Gacem, Virendra Kumar Yadav, Rakesh Kumar Verma, Mahima Choudhary, Uma Bhardwaj, Rajendra Singh Chundawat, Mohammed S. Alqahtani, Rajarshi Kumar Gaur, Lienda Bashier Eltayeb, Waleed Al Abdulmonem and Byong-Hun Jeon (2023). Towards further understanding the applications of endophytes: enriched source of bioactive compounds and bio factories for nanoparticles. *Front Plant Sci 14*:1193573. https://doi.org/10.3389/fpls.2023.1193573

- Varsha Rani, D.C. Joshi, Priyanka Joshi, Rajesh Singh and Dinesh Yadav (2023). “Millet Models” for harnessing nuclear factor-Y transcription factors to engineer stress tolerance in plants: current knowledge and emerging paradigms. *Planta*, *258*(2). https://doi.org/10.1007/s00425-023-04186-0

- Aiman Tanveer, Supriya Gupta, Shruti Dwivedi, Kanchan Yadav, Sangeeta Yadav and Dinesh Yadav (2023). Innovations in papermaking using enzymatic intervention: an ecofriendly approach, *Cellulose (Springer) 30*, 7393-7425. https://doi.org/10.1007/s10570-023-05333-2

- Shruti Dwivedi, Kanchan Yadav, Supriya Gupta, Aiman Tanveer, Sangeeta Yadav and Dinesh Yadav (2023) Fungal pectinases: an insight into production, innovations and applications. *World J Microbiol Biotechnol* 39, 305. https://doi.org/10.1007/s11274-023-03741-x

- Kanchan Yadav, Shruti Dwivedi, Supriya Gupta, Aiman Tanveer, Sangeeta Yadav, Pramod K. Yadav, Gautam Anand, Dinesh Yadav (2023). Recent insights into microbial pectin lyases: A review, *Process Biochemistry 134*, 199-217. https://doi.org/10.1016/j.procbio.2023.10.008

- Dinesh Yadav, Shruti Dwivedi, Kanchan Yadav, Supriya Gupta, and Sangeeta Yadav (2023). The diverse industrial applications of microbial pectinases (Feature article), The Microbiologists (*Applied Microbiology International).*

Book Chapter

- Rupali Gupta, Gautam Anand, Satyendra, Pratap Singh, Dinesh Yadav and Rakesh Pandey (2023). Harnessing beneficial rhizospheric microorganisms for biotic stress management in medicinal and aromatic plants (Chapter-11). In Detection, diagnosis and management of soil-borne phytopathogens. Springer nature, Singapore Pte Ltd. ISBN (hardcover: 978-981-19-8306-1), ISBN (eBook):978-981-19-8307-8 (http://doi.org/10.1007/978-981-19-8307-8_11).

- Varsha Rani, Manoj Kumar Yadav, Rajesh Singh and Dinesh Yadav (2023). Genetic diversity assessment in cereal crops. In Sustainable utilization and conservation of plant genetic diversity. Springer nature, Singapore Pte Ltd. ISBN (Hardcover): 978-981-99-5244-1, ISBN (eBook): 978-981-99-5245-8.

- Shruti Dwivedi, Supriya Gupta, Aiman Tanveer, Gautam Anand, Sangeeta Yadav and Dinesh Yadav (2023). Mining of novel microbial enzymes using metagenomics approach for efficient bioremediation: An overview (Chaper-10). In Genomics Approach to Bioremediations: Principle, Tools and Emerging Technologies. Wiley Publisher. ISBN (ebook): 978-1-119-85212-4, ISBN (hardcover):978-1-119-85210-0.

- Chitra Nehra, Dinesh Yadav and R. K. Gaur (2023). Epigenetic response during plant-pathogen interactions: an overview (Chapter-8). In Genomics of plant- Pathogen interactions and the stress response (1st Edition). Francis and Taylor, CRC Press. ISBN (ebook): 9781003153481. https://doi.org/10.1201/9781003153481

- Kanchan Yadav, Sangeeta Yadav, Gautam Anand, Pramod K Yadav and Dinesh Yadav (2023). Hydrolysis of Complex Pectin Structures: Biocatalysis and Bioproducts (Chapter-9). In Polysaccharide Degrading Biocatalysts (1st Edition). Academic Press, Elsevier. ISBN (paperback): 9780323999861, ISBN (eBOOK):9780323983150.

PARTICIPATION OF FACULTY MEMBERS IN CONFERENCES /WORKSHOPS /FACULTY DEVELOPMENT PROGRAMME/ TRAINING PROGRAMME

- Prof. Dinesh Yadav delivered a lecture entitled "*Fungal pectinases: a recent insight into production, innovations and applications'* in National Conference on "Advances and Opportunities in Drug Discovery from Natural Products" jointly organized by Mahayogi Gorakhnath University, Gorakhpur and Translational Biomedical Research Society, Lucknow (15-17th Dec. 2023) on 16th Dec. 2023 **(INVITED LECTURE)**

- Prof. Sarad Kumar Mishra delivered an invited talk on the topic, "Azadirachta indica (Neem): Solution for global health problems" in National Conference on "Advances and Opportunities in Drug Discovery from Natural Products" held at Mahayogi Gorakhnath University, Gorakhpur on (15-17, Dec. 2023) **(INVITED LECTURE)**

- Prof. Dinesh Yadav and Prof. Sarad Kumar Mishra chaired technical sessions in National Conference on "Advances and Opportunities in Drug Discovery from Natural Products" held at Mahayogi Gorakhnath University, Gorakhpur on (15th to 17th, Dec. 2023)

- Prof. Dinesh Yadav delivered a lecture entitled "*Approaches for quality research in NEP 2020: An Overview*" in MMT Training Program- NEP Orientation and Sensitization Program organized by UGC-Malviya Mission Teacher Training Centre, DDU Gorakhpur University, Gorakhpur on 27th Nov. 2023 **(RESOURCE PERSON)**

- Prof. Dinesh Yadav delivered a lecture entitled "*Genomics and Bioinformatics driven research in plant transcription factors and microbial enzymes*" in International Conference on "Recent Trends in Biolgical and Chemical Sciences (ICRTBCS) jointly organized by Institute of Biosciences and Technology, Shri Ramswaroop Memorial University (SRM), Lucknow and Hindu College, University of Delhi (25th Nov. 2023) on 25th Nov. 2023 **(INVITED LECTURE)**

- Dr. Gaurav participated in NEP 2020 Orientation & Sensitization Progamme under Malaviya Mission Teacher Training Programme (MM-TTP) of University Grants Commission (UGC) organized by UGC-Malaviya Mission Teacher Training Centre, D D U Gorakhpur University, Gorakhpur from 22 Nov. to 30 Nov. 2023

- Prof. Dinesh Yadav delivered a lecture entitled "*Elucidating the role of plant transcription factors in millets for global food and nutritional security: An overview*" in National conference on "Current Trends in Biolgical Sciences for Sustainable Agriculture, Environment and Health Under Climate Change" organized by Department of Botany, University of Lucknow (23-25th Nov. 2023) on 24th Nov. 2023 **(INVITED LECTURE)**

- Prof. Sarad Kumar Mishra delivered a special/invited lecture on "*Azadirachta indica* (Neem): A miracle medicinal plant as a source of potential therapeutic compounds for Dengue virus infection" in an International Conference on "Biotech Synergy: Transforming Agriculture, Health and Climate Resilience" held at Invertis University, Bareilly on 03-04, Nov. 2023. **(INVITED LECTURE)**

- Prof. Sarad KumaR Mishra was invited as special guest in the inauguration of an International Conference on "Biotech Synergy: Transforming Agriculture, Health and Climate Resilience" held at Invertis University, Bareilly on 3 to 4th Nov. 2023.

- Prof. Sarad Kumar Mishra delivered talk on "Zero Hunger: A challenge for India" in Faculty Induction Programme (FIP), organized by UGC-Human Resource Development Centre, Pt. Ravi Shankar Shukla University, Raipur on 9th Oct. 2023**(RESOURCE PERSON)**

- Prof. Sarad Kumar Mishra delivered talk on "Recent Developments in Health sector" in Faculty Induction Programme (FIP), organized by UGC-Human Resource Development Centre, Pt. Ravi Shankar Shukla University, Raipur on 9th Oct. 2023 **(RESOURCE PERSON)**

- Prof. Dinesh Yadav delivered a lecture entitled ""*Genomics and Bioinformatics driven research: insights into fungal pectinases & plant transcription factors*" in a webinar on Omics driven research in Biotechnology jointly organized by Department of Biotechnology and IQAC, D.D.U Gorakhpur University on 6th Oct. 2023 **(INVITED LECTURE)**

- Prof. Sarad Kumar Mishra delivered talk on "Recent advances in Biotechnology" in Faculty Induction Programme (FIP), organized by UGC-Human Resource Development Centre and Department of Commerce, D.D.U. Gorakhpur University, Gorakhpur on 18th Sept. 2023. **(RESOURCE PERSON)**

- Prof. Dinesh Yadav delivered a lecture entitled "*Research, Innovations and IPR in NEP 2020: An Update*" in 6th Faculty Induction Programme (FIP) organized by UGC-Human Resource Development Centre and Department of Commerce, D.D.U. Gorakhpur University, Gorakhpur (26th Aug-24th Sept. 2023) on 4th Sept. 2023 **(RESOURCE PERSON)**

- Prof. Sarad Kumar Mishra was **Coordinator**, Faculty Induction Program, UGC-HRDC, DDU Gorakhpur, 25th August - 23rd Sep. 2023.

- Dr. Gaurav Singh delivered a lecture entitled "The Role of Biodiversity Management Committees (BMCs)- Peoples Biodiversity Register (PBR) for conservation of Biodiversity" in One day National Webinar on Biodiversity and its Conservation organized by Govt. P.G. College Amarpatan, Dist.-Satna (M.P.) on 28 Aug. 2023 **(INVITED LECTURE)**

- Dr. Gaurav delivered a lecture entitled "Biodiversity, Conservation of Biodiversity through Biodiversity Management Committees (BMCs) & Peoples Biodiversity Register (PBR)" in One day National Webinar on Biodiversity Conservation: Issues and Challenges on the topic organized by Govt. Science College Pandhurna, Dist.-Chhindwara (M.P.) on 29 Aug. 2023 **(INVITED LECTURE).**

- Dr. Gaurav Singh delivered a lecture entitled "Insights in Biodiversity Management and Conservation in India: Structure and Role of Multi-tier Legal System" in 04 days International Webinar Series on Theme: Biodiversity Conservation and Sustainable Development organized by Govt. M.S. Golwalkar College Rewa, Dist.-Rewa (M.P.) on 26 Aug. 2023 **(INVITED LECTURE)**

- Prof. Sarad Kumar Mishra was **Coordinator**, 5th Refresher Course in Life Science, UGC-HRDC, DDU Gorakhpur university, 23rd July – 05th Aug, 2023.

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PARTICIPATION OF STUDENTS IN CONFERENCES /SEMINARS/ WORKSHOPS / TRAINING PROGRAMME:

- Vineeta Pandey, Ph.D Scholar presented a paper entitled "*In-silico* management approach for ChiLCD: prediction and identification of the chilli protein domain and miRNAs that target the begomovirus” in International conference jointly organized by Ashtha Foundation, Meerut (U.P.) and University of Agriculture Sciences, Raichur, Karnataka, India (18-20th Dec. 2023) on 18th Dec. 2023 **(POSTER PRESENTATION).**

- Priyanka Bharti, Ph.D. Scholar was awarded Young Scientist Award (Second Prize) (Mahant Digvijay Nath Sodh Award). In National conference on “Advances and Opportunities in Drug Discovery from Natural Products”- (BioNatureCon-2023) (15th to 17th December 2023). Organized by Faculty of Allied Health Sciences and Faculty of Pharmaceutical Sciences Mahayogi Gorakhnath University, Gorakhpur in association with Translational Biomedical Research Society, India.

- Sapna Choudhary, Ph.D. Scholar aattended, Two Weeks of Hands-On Training Program entitled “Analytical Techniques: Isolation to Identification” jointly organized by Gujarat Biotechnology Research Centre and Gujarat Technological University, Gujarat. 20thNov to 1st Dec 2023.

- Kanchan Yadav Ph.D. Scholar presented a paper entitled “Potential of fungi in promoting sustainable agriculture and food security: An overview” in National conference jointly organized by Department of Botany, Lucknow University and ISAB, CSUA&T Kanpur (23-25th Nov. 2023) on 24th Nov. 2023 **(POSTER PRESENTATION).**

- Varsha Rani Ph.D. Scholar presented a paper entitled “Bioinformatics intervention in crop improvement: an update” in National conference jointly organized by Department of Botany, Lucknow University and ISAB, CSUA&T Kanpur (23-25th Nov. 2023) on 24th Nov. 2023 **(POSTER PRESENTATION).**

- Supriya Gupta, Ph.D. Scholar presented a paper entitled “Intervention of microbial enzyme in paper industries” in National conference jointly organized by Department of Botany, Lucknow University and ISAB, CSUA&T Kanpur (23-25th Nov. 2023) on 24th Nov. 2023 **(POSTER PRESENTATION).**

- Shruti Dwivedi, Ph.D. Scholar presented a paper entitled “Fungal-pectinase mediated approaches for processing of fruit juices” in National conference jointly organized by Department of Botany, Lucknow University and ISAB, CSUA&T Kanpur (23-25th Nov. 2023) on 24th Nov. 2023 **(POSTER PRESENTATION).**

- Supriya Gupta, Ph.D. Scholar presented a paper entitled “Agricultural waste as a sustainable approach for papermaking” and received First Prize in National Conference on Plant and Microbes; Progress, Potential and Future organized by Department of Botany, D.D.U Gorakhpur University on 30th Sept. 2023 **(ORAL PRESENTATION).**

- Shruti Dwivedi, Ph.D. Scholar presented a paper entitled “Elucidating the role of fungal pectinases for retting of Fibres: an eco-friendly role” in National Conference on Plant and Microbes; Progress, Potential and Future organized by Department of Botany, D.D.U Gorakhpur University on 30th Sept. 2023. **(ORAL PRESENTATION).**

- Supriya Gupta, Ph.D. Scholar attended workshop on “Innovative technologies for wastewater treatment, reuse and resource recovery” organized by Pavitra Ganga Project Partners from IIT Delhi, IHE Delft, IIT Kanpur and VITO. At IIT, Delhi. 27-28 Sept. 2023. And received Second Prize in Technological and management options to complement conventional STP approaches in India **(POSTER PRESENTATION).**

- Varsha Rani Ph.D. Scholar attended “High End Workshop on Advances Techniques in Augmenting Millets for Nutritional Security and Climate Resilient Agriculture” sponsored by Accelerate Vigyan Scheme, SERB (DST), New Delhi organized by Crop Improvement Division ICAR- Vivekanand Parvatiya Krishi Anushandhan Sansthan (VPKAS), Almora, Uttarakhand India (18-28th July, 2023).

- Varsha Rani, Ph.D. Scholar presented a Paper entitled “Bioinformatics intervention revealing structural and functional insight into Nuclear Factor-Y Transcription Factor in Millet” at International Conference on Millets: Breeding, Physiology, Genomics, Biotechnology and Nutraceuticals-2023 (ICM-BPGBN-2023), (5-7th July 2023), Jointly organized by Department of Biosciences & Rajagiri Research & Development Cell (RRDC), Rajagiri College of Social Sciences (Autonomous), Kochi Kerala, India on 6th July **(ORAL PRESENTATION).**

EVENT ORGANIZED IN THE DEPARTMENT

Felicitation of Prof. (Dr.) P.P. Mathur, Hon'ble Vice Chancellor, Birla Global University, Bhubaneshwar

Invited Talk by Prof. (Dr.) Ram Narain , VBS Purvanchal University Jaunpur

Special Lecture by Dr. Alok Tiwari, Synergy Institute & Superspeciality Hospital

Lightning of lamp by Hon'ble Vice Chancellor Prof. Poonam Tandon, DDUGU

Invited Talk by Dr. Hem Chandra Jha, IIT Indore

Invited Talk by Dr. Pragya D. Yadav, NIV Pune

Visit of Schoolchildren G.D Goenka Public School Students

G.D. Goenka Students visits in virology lab of the department

Glimpses of Special Lecture on role of Biotechnology in Cancer Management

Glimpses of Special Lecture on the journey of Indigenous COVID Vaccine in India

Teacher's Day celebration in the Department

Glimpses of Special Lecture on role of Biotechnology in Cancer Management