OFFICE, PRINCIPAL GOVERNMENT TULSI COLLEGE, ANUPPUR
Affiliated to Awadhesh Pratap Singh University Rewa (MP)
Registered Under Section 2 (F) & 12 (B) of UGC Act

E-mail: hegtdcano@mp.gov.in ☎9893076404

Project Report M.Sc 4th Sem Botany

GOVT TULSI COLLEGE ANUPPUR DISTT ANUPPUR (M.P.)

Sub & Department - BOTANY

PROJECT TITLE

Exploitation of Rhizospheric Microbes Including Mycorrhizae

APSU - REWA (M.P.)

Session - June - 2022-23

GUIDDED BY →(Chhaya Shayam)
Prof.Priti Malaiya
Department of Botany

SUBMITED BY
Hushna Bano
M.Sc 4th sem (Botany)
Roll No.- 2013900096
Enroll.No-171021580001

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

OFFICE, PRINCIPAL GOVERNMENT TULSI COLLEGE, ANUPPUR
Affiliated to Awadhesh Pratap Singh University Rewa (MP)
Registered Under Section 2 (F) & 12 (B) of UGC Act

E-mail: hegtdcano@mp.gov.in ☎9893076404

DECLARARION OF THE STUDENT

Name Hushna Bano D/o Mo. Nishar Ansari certify that the project report entitled prepared by me is personal & authentic work under the guidance of Chhaya Shyam.

Date - 08/09/22

Place - Anuppur

Signature of Student

Name - Hushna Bano

Class - M.Sc. IVth Sem.

Roll No. - 2013900096

Enroll No- 171021580001

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

OFFICE, PRINCIPAL GOVERNMENT TULSI COLLEGE, ANUPPUR

Affiliated to Awadhesh Pratap Singh University Rewa (MP)

Registered Under Section 2 (F) & 12 (B) of UGC Act

E-mail: hegtdcano@mp.gov.in ☎9893076404

CERTIFICATE OF THE SURVERED

This is to certify that:- Hushna Bano had visited our office for her project work, her behavior was satisfactory.

Date - 06/09/2022
Place - Anuppur

Signature of Officer
Name ..... R.B. Singh .....
Disigination ..... Sub Divisional Officer Forest Anuppur .....
Office .....

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

OFFICE, PRINCIPAL GOVERNMENT TULSI COLLEGE, ANUPPUR
Affiliated to Awadhesh Pratap Singh University Rewa (MP)
Registered Under Section 2 (F) & 12 (B) of UGC Act

E-mail: hegtdcano@mp.gov.in ☎9893076404

CERTIFICATE OF THE SURVERED

This is to certify that:- Hushna Bano had visited our office for her project work, her behavior was satisfactory.

Date - 06/09/2022
Place - Anuppur

Signature of Officer
Name ..... R.B. Singh .....
Disigination ..... Sub Divisional Officer .....
Forest Anuppur
Office .....

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

E-mail: hegtdcano@mp.gov.in ☎9893076404

ACKNOWLEDGMENT

My self Hushna Bano has done my project work on Chloroquine have completed. My Miss Chhaya Shyam.

I Would like to sincerely thanks from Bottom of my heart for the guidance tendered by.

Without whose valuable help the project would not has been completed. The valuable suggestion received time from her enhanced my under standing at the topic.

HusnaBano

Signature of Student

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

E-mail: hegtdcano@mp.gov.in ☎9893076404

Explotation of Rhizospheric Microbes Including mycorrhizae-

Introduction-

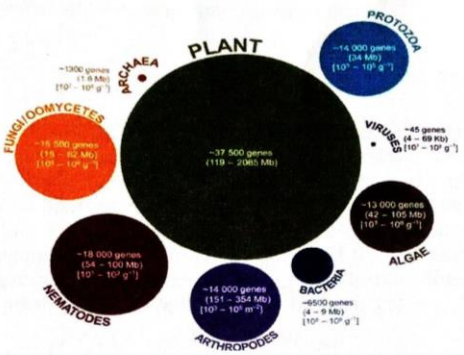
Plants are colonized by an astounding number of (micro)organisms that can reach cell densities much greater than the number of plant cells (Fig. 1). Also, the number of microbial genes in the rhizosphere outnumbers by far the number of plant genes (Fig. 1). An overwhelming number of studies have revealed that many plant-associated microorganisms can have profound effects on seed germination, seedling vigor, plant growth and development, nutrition, diseases, and productivity (Fig. 2). Consistent with the terminology used for microorganisms colonizing the human body (Qin *et al*., 2010; Zhao, 2010; Gevers *et al*., 2012), the collective communities of plant-associated microorganisms are referred to as the plant microbiome or as the plants' other genome. In this context, plants can be viewed as superorganisms that rely in part on their microbiome for specific functions and traits. In return, plants deposit their photosynthetically fixed carbon into their direct surroundings, that is, spermosphere, phyllosphere, rhizosphere, and mycorrhizosphere (Nelson, 2004;Frey-Klett *et al*., 2007;Raaijmakers *et al*., 2009; Berendsen *et al*., 2012; Vorholt, 2012), thereby feeding the microbial community and influencing their composition and activities. To date, the interplay between plants and microorganisms has been studied in depth for various leaf pathogens, symbiotic rhizobia, and mycorrhizal fungi. However, for the vast majority of plant-associated microorganisms, there is limited knowledge of their impact on plant growth, health, and disease. Hence, deciphering the plant microbiome is critical to identify microorganisms that can be exploited for improving plant growth and health.

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

OFFICE, PRINCIPAL GOVERNMENT TULSI COLLEGE, ANUPPUR
Affiliated to Awadhesh Pratap Singh University Rewa (MP)
Registered Under Section 2 (F) & 12 (B) of UGC Act

E-mail: hegtdcano@mp.gov.in ☎9893076404

Figure 1-



Overview of (micro)organisms present in the rhizosphere zoo. The circle's size, except for VIRUSES, is a measure of the average number of genes in the genomes of representative species of each group of organisms; the size (or size range) of their respective genomes is indicated between parentheses. For each of these (micro)organisms, the approximate numbers for their abundance are indicated between square brackets (Alexander, 1977; Brady, 1974; Lynch, 1988; Meeting, 1992; Buée *et al.*, 2009). The endophytic microorganisms, including endosymbionts, are not included. The species selected to illustrate the composition of the rhizosphere microbiome and used to calculate the number of genes and genome sizes are: PLANT: *Glycine max, Populus trichocarpa, Zea mays, Oryza sativa, Arabidopsis thaliana,* and *Vitis vinifera*; PROTOZOA: *Dictyostelium discoideum*; VIRUSES: *Pseudomonas* phage 73, *Fusarium graminearum* dsRNA mycovirus-4, *Agrobacterium* phage 7-7-1, *Rhizoctonia solani* virus 717; ALGAE: *Chlorella variabilis* and *Chlamydomonas reinhardtii*; BACTERIA: *Pseudomonas fluorescens, Bradyrhizobium japonicum, Rhizobium leguminosarum, Bacillus cereus, Bacillus amyloliquefaciens, Burkholderia cenocepacia,* and *Streptomyces filamentosus*; ARTHROPODES: *Metaseiulus occidentalis, Acromyrmex echinatior,* and *Solenopsis invicta*; NEMATODES: *Caenorhabditis elegans* and *Meloidogyne hapla*; FUNGI/OOMYCETES: *Laccaria bicolor, Nectria haematococca, Piriformospora indica, Verticillium dahliae, Metarhizium anisopliae, Fusarium oxysporum, Sporisorium reilianum, Phytophthora sojae, Phytophthora parasitica, Aphanomyces euteiches,*

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

E-mail: hegtdcano@mp.gov.in ☎9893076404

Phytophthora sojae, *Phytophthora parasitica*, *Aphanomyces euteiches*, *Phytophthora cinnamomi*, and *Pythiumultimum*;

ARCHAEA: *Candidatus* Nitrosoarchaeum koreensis.

Figure 2-

Schematic overview of the functions and impact of plant beneficial ('the good'), plant pathogenic ('the bad'), and human pathogenic microorganisms ('the ugly') on the host plant. The terms 'the good', 'the bad', and 'the ugly' are arbitrary as microbial species may be beneficial or deleterious depending on its abundance (Maurhofer *et al.*, 1992). For example, also plant pathogenic and human pathogenic microorganisms may influence several of the functions depicted for the plant beneficial microorganisms. This anthropogenic terminology is merely used to facilitate the description of the complex rhizosphere microbiome environment.

The rhizosphere, that is, the narrow zone surrounding and influenced by plant roots, is a hot spot for numerous organisms and is considered as one of themost

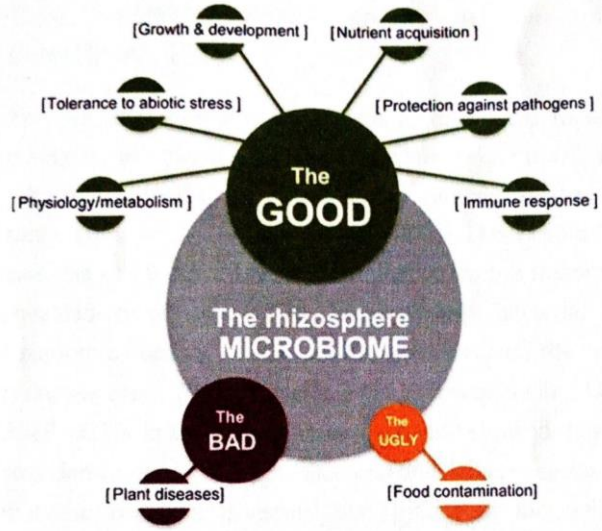
complex ecosystems on Earth (Hinsinger & Marschner, 2006; Pierret *et al.*, 2007; Jones & Hinsinger, 2008; Hinsinger *et al.*, 2009; Raaijmakers *et al.*, 2009). Organisms found in the rhizosphere include bacteria,

fungi, oomycetes, nematodes, protozoa, algae, viruses, archaea, and arthropods (Fig. 1; Lynch, 1990; Meeting, 1992; Bonkowski *et al.*, 2009; Buée *et al.*, 2009; Raaijmakers *et al.*, 2009). Most members of the rhizosphere microbiome are part of a complex food web that utilizes the large amount of nutrients released by the plant. Given that these rhizodeposits (e.g. exudates, border cells, mucilage) are a major driving force in the regulation of microbial diversity and activity on plant roots, Cook *et al.* (1995) postulated that plants may modulate the rhizosphere microbiome to their benefit by selectively stimulating microorganisms with traits that are beneficial to plant growth and health. Others have argued that exudates are passively 'released' as overflow/waste products of the plant (Hartmann *et al.*, 2009; Jones *et al.*, 2009; Dennis *et al.*, 2010). So, whether plants are using exudates to 'cry for help' or are 'just crying' remains to be addressed.

Rhizosphere organisms that have been well studied for their beneficial effects on plant growth and health are the nitrogen-fixing bacteria, mycorrhizal fungi, plant growth-promoting rhizobacteria (PGPR), biocontrol microorganisms,

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

E-mail: hegtdcano@mp.gov.in ☎9893076404



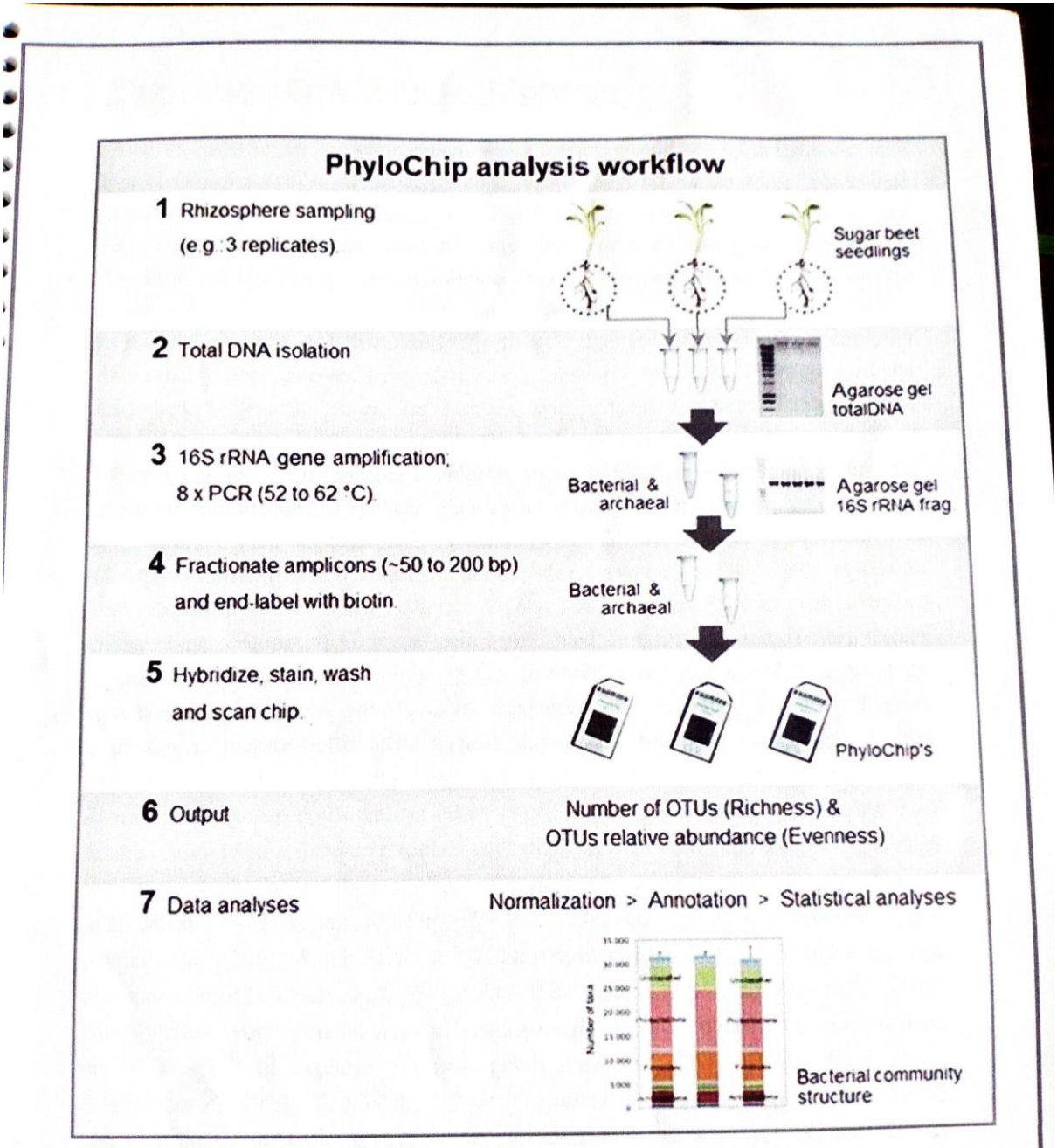
The rhizosphere microbiome –

Culture-independent approaches have shown that microbial diversity of soil and rhizosphere microbiomes is highly underestimated. Next-generation sequencing technologies have demonstrated that only a minority (*c.* up to 5%) of bacteria have been cultured by current methodologies and that a significant proportion of the bacterial phyla detected by these technologies has no cultured representative yet. For example, the rarefaction curve built from 16S rRNA gene sequencing data obtained in a soil metagenome study failed to reach saturation and revealed that, of 150 000 sequencing reads obtained for a soil clone library, < 1% exhibited overlap with the sequencing reads of other independent soil clone libraries (Tringe *et al.*, 2005). In one of the first studies in this research field, Torsvik *et al.* (2002) estimated that the number of bacterial species in a gram of boreal forest soil was *c.* 10 000. Following the same strategy with substantial computational improvements, Gans *et al.* (2005) predicted that 1 g of soil can contain more than 1 million distinct bacterial genomes, exceeding previous estimates by several orders of magnitude. Two years later, Roesch *et al.* (2007) obtained 139 819 bacterial and 9340

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

OFFICE, PRINCIPAL GOVERNMENT TULSI COLLEGE, ANUPPUR
Affiliated to Awadhesh Pratap Singh University Rewa (MP)
Registered Under Section 2 (F) & 12 (B) of UGC Act

E-mail: hegtdcano@mp.gov.in ☎9893076404



PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)

E-mail: hegtdcano@mp.gov.in ☎9893076404

Conclusions and outlook-

Although the importance of the rhizosphere microbiome in the functioning of plant ecosystems has been widely recognized, traditional approaches to unravel these functions are limited in their capacity and for the vast majority of rhizosphere organisms, no knowledge exists. Coupling traditional approaches with advanced next-generation sequencing techniques to assess organismal or community ecology and physiology will bring new insights to understand microbial life in the rhizosphere. Identification of the exudates, signals, and key players in the rhizosphere microbiome will provide chemical and microbial markers to elucidate whether and how plants recruit and stimulate beneficial (micro)organisms. Unraveling the rhizosphere microbiome also holds potential to improve crop protection and to uncover numerous yet unknown soil microorganisms, functions, and genes for diverse applications. Another challenge we face is how to prevent human pathogen proliferation in plant environments to critical doses causing human disease. Therefore, a better understanding of the factors and cues that enable human pathogens to find a suitable niche on plant surfaces is essential to safeguard human health.

To keep plant and human pathogens in check, different and complementary strategies should be developed that redirect the rhizosphere microbiome in favor of microorganisms that prevent pathogens to germinate, grow, attach, and invade the root tissue. One potential approach is to initiate plant breeding programs that are directed toward unraveling the molecular basis of interactions between plant lines and beneficial members of the rhizosphere microbiome. The initial studies by Smith *et al.* (1999) on QTL mapping of tomato lines for traits that support beneficial rhizobacteria provide an excellent framework for this. Combined with in-depth analysis of the rhizosphere microbiomes of wild relatives of economically important food crops, it should be feasible to resolve whether modern plant breeding can select for plant traits that are essential for hosting beneficial microorganisms. This approach of going 'back to the roots' will most likely also lead to the identification of new rhizosphere microorganisms, genes, and traits that can be exploited for other applications. To reduce the impact of plant diseases, we propose to design a 'core microbiome' that is effective against soilborne pathogens in different agro-ecosystems. Analogous to the concept of the core microbiome in human

PRINCIPAL
Govt. Tulsi College Anuppur
Distt. Anuppur (M.P.)