‘Life Under Lens’
The Annual Magazine of Sukshmjeev Society

Vol. 5 | March 2019

MICROCOSMOS

Unveiling the world of Microbiomes

Department of Microbiology
(under the aegis of Star College Scheme, DBT, Govt. of India and IQAC)
Bhaskaracharya College of Applied Sciences
University of Delhi

'MicroCosmos', not a standard dictionary word, was taken up as the title of the 5th issue of 'Life under Lens'. The inspiration for such was based on finding a word that best describes a world of microbes as an independent one. Coincidentally, in 1996, filmmakers Claude Nuridsany and Marie Perennou created a documentary film MicroCosmos. The documentary dramatizes the daily life of Insects living in a French meadow. The documentary has won many accolades for its amazing cinematography. Looking back, at Sukshmjeev Society, we did what we like doing the most: used a higher magnification.

This issue is being brought to you on the occasion of:

A One-day Seminar on 'Advances in Sequencing Technologies: Accelerating progress in Biological Sciences'

and

MicroQuest 2019

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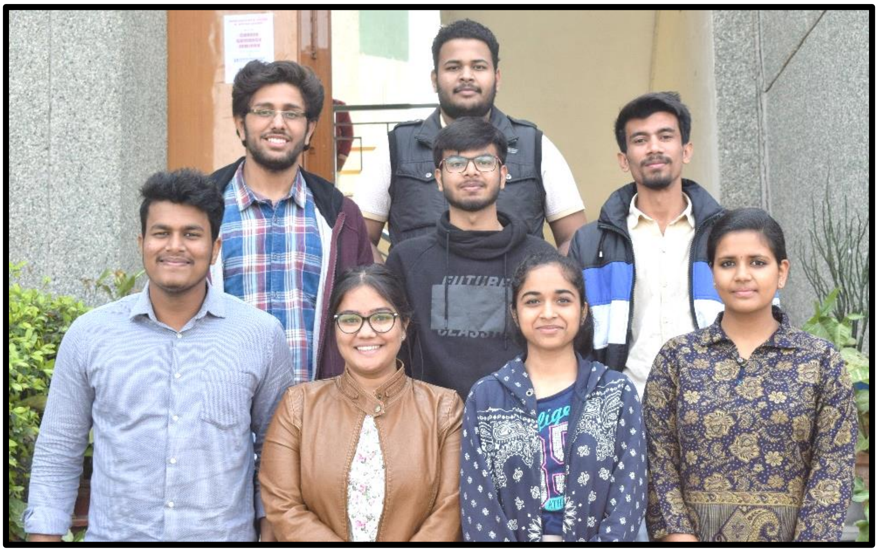
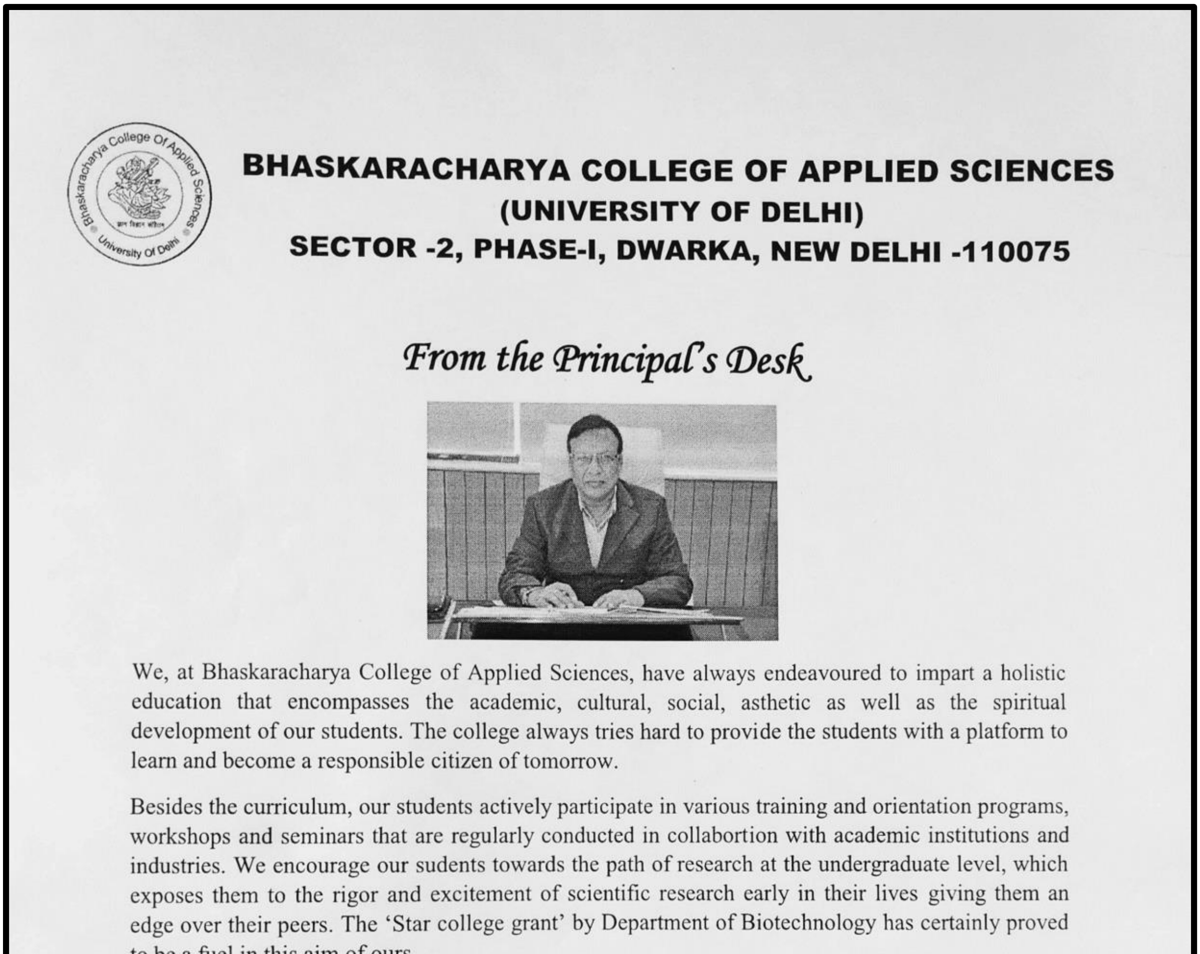
Message from the Editorial Team



This issue has been carefully curated and handcrafted with amalgamation of months of diligent and committed hard work of the Sukshmjeev Society. The tremendous efforts, the wonderful life forms around us and the urge to know more cumulatively has made this magazine a yet another captivating reason to present before you the enthralling entities of the MicroCosmos.
The topic has been chosen keeping in mind that it is virtually impossible to mention every astounding aspect of the world of microbes, as they never fail to prove that they can be beyond the reach of our wildest imaginations. We have tried our best to reach the most extreme adaptations, observe the most important roles they play, to uncover mysteries, study problems they pose and the solutions they offer. While reading the articles, the reader would find that we have tried to paint a picture in an investigator's perspective and have tried to put suggestions forward based on developments from recent research in this field. The articles will take you on a journey of fascination and amazement with topics ranging from battle of the microbes to unique survival strategies to a major apocalyptic threat to an immunity boosting agent that can literally stopper death even the curse of a dead Pharaoh living beyond the sands of time. Your reading will make you appreciate the intricate network and balance of nature. This might seem like a lot to inculcate but the magazine is specially designed to help budding scientific investigators absorb the knowledge, inculcate curiosity and ask new questions about the marvellous creatures surrounding us.

This magazine is an effort to study creations of the most successful 'simulated chain reaction' there ever was and we hope that your reading continues even after you are done with this issue.

We hope you all will enjoy and appreciate the beauty of 'microbial life' as much as we did while putting this together for you. Happy reading!!



BHASKARACHARYA COLLEGE OF APPLIED SCIENCES
(UNIVERSITY OF DELHI)
SECTOR -2, PHASE-I, DWARKA, NEW DELHI -110075

From the Principal's Desk

We, at Bhaskaracharya College of Applied Sciences, have always endeavoured to impart a holistic education that encompasses the academic, cultural, social, asthetic as well as the spiritual development of our students. The college always tries hard to provide the students with a platform to learn and become a responsible citizen of tomorrow.

Besides the curriculum, our students actively participate in various training and orientation programs, workshops and seminars that are regularly conducted in collabortion with academic institutions and industries. We encourage our sudents towards the path of research at the undergraduate level, which exposes them to the rigor and excitement of scientific research early in their lives giving them an edge over their peers. The 'Star college grant' by Department of Biotechnology has certainly proved to be a fuel in this aim of ours.

Our college is also very proud of the dedicated, well qualified, young and enthusiastic faculty as well as the non-teaching staff members who work tirelessly to provide a wholesome learning environment, conducive to the all-round development of our students. The Department of Microbiology has unequivocally acquitted well in this regard. It is one of the youngest Departments of our College but has come up as one of the best.

'Sukshmjeev', the society of the Department of Microbiology, is one of the most active societies in the college that organizes several academic and co-curricular events every year. The society has been also bringing out its annual magazine 'Life under lens' on several pertinent themes on the occasion of Microquest. I wish the department all the very best for the upcoming one-day seminar on 'Advances in Sequencing Technologies: Accelerating Progress in Biological Sciences.' and the annual microbiology festival, Microquest 2019. I eagerly look forward to many more such initiatives.

Dr. Balaram Pani
Principal

Dr. Saurabh Raghuvanshi
Associate Professor
Dept. of Plant Molecular Biology
University of Delhi South Campus
New Delhi-110021

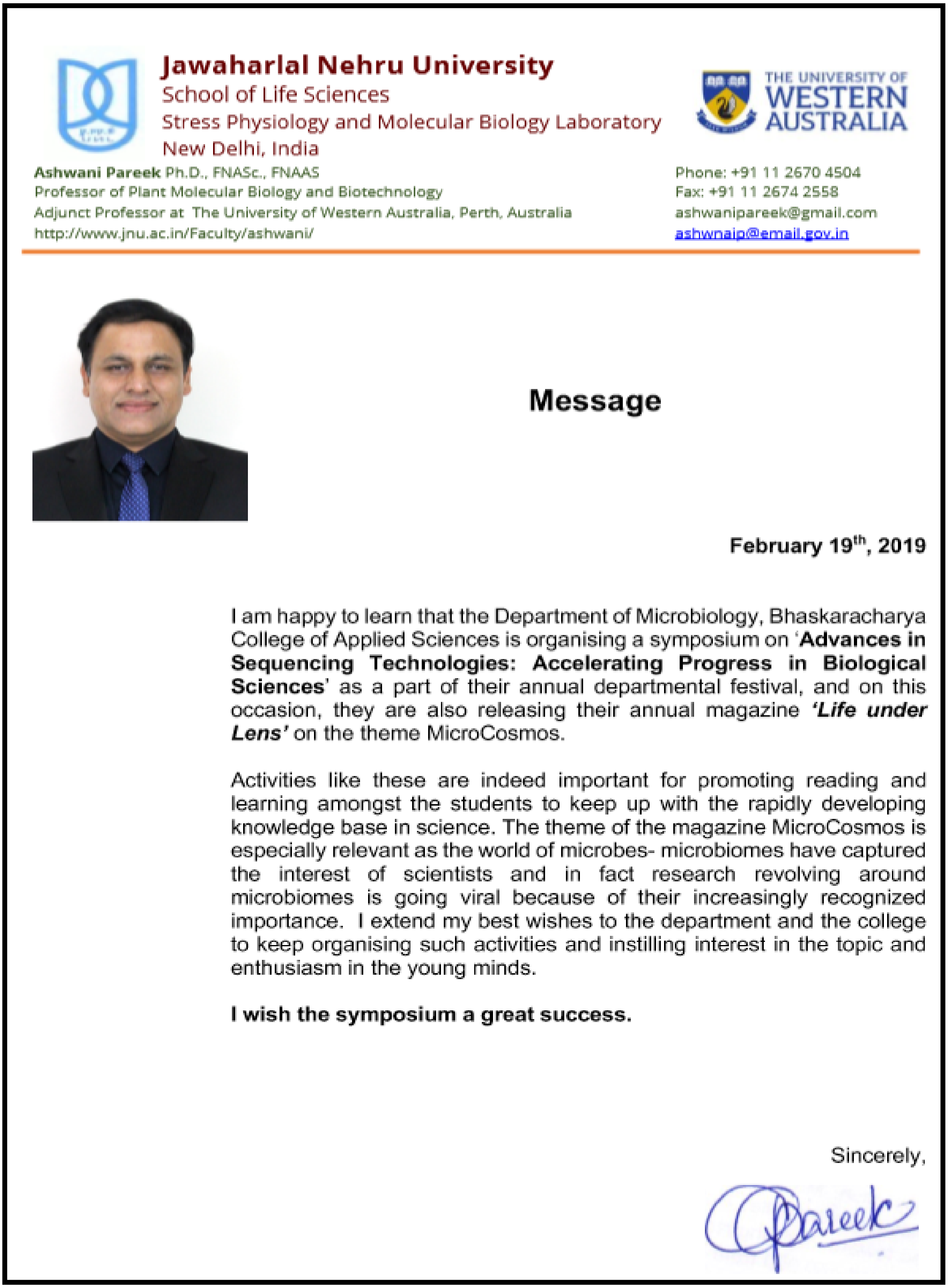
MESSAGE

I am very pleased to know that the Department of Microbiology is organising a seminar on ‘Advances in Sequencing Technologies: Accelerating Progress in Biological Sciences’ and the Annual Microbiology Festival ‘Microquest 2019’on 6 March, 2019. Phenomenal developments in the field has enabled the scientists to embark on efforts that aim to sequence the genome of every organism on our planet (Earth BioGenome Project).

I also congratulate the team for bringing out a magazine entitled ‘MicroCosmos’. Research on Microbiomes is essential to better understand the impact of these microbes on human health as well as stabilizing the ecosystem. Insights into this topic will surely inspire young minds to explore the magnificence of the microbial world.

It is my pleasure to convey my best wishes to all.

Dr. Saurabh Raghuvanshi



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Message

February 19th, 2019

I am happy to learn that the Department of Microbiology, Bhaskaracharya College of Applied Sciences is organising a symposium on '**Advances in Sequencing Technologies: Accelerating Progress in Biological Sciences**' as a part of their annual departmental festival, and on this occasion, they are also releasing their annual magazine ***'Life under Lens'*** on the theme MicroCosmos.

Activities like these are indeed important for promoting reading and learning amongst the students to keep up with the rapidly developing knowledge base in science. The theme of the magazine MicroCosmos is especially relevant as the world of microbes- microbiomes have captured the interest of scientists and in fact research revolving around microbiomes is going viral because of their increasingly recognized importance. I extend my best wishes to the department and the college to keep organising such activities and instilling interest in the topic and enthusiasm in the young minds.

I wish the symposium a great success.

Sincerely,

Pareek

Prof. Swati Saha
Department of Microbiology
University of Delhi South Campus
New Delhi-110021

MESSAGE

I am pleased to learn that the Sukshmjeev Society of the Department of Microbiology, Bhaskaracharya College of Applied Sciences, is organising a seminar on ‘Advances in Sequencing Technologies: Accelerating Progress in Biological Sciences’ as part of their Annual Departmental Festival, also bringing out the 5th volume of their annual magazine ‘Life Under Lens’ entitled ‘MicroCosmos’ on this occasion.

Microbes hold immense potential as resources and as tools for discovery. Some of the most exciting findings in biological sciences have come from simple, yet ingenious experiments carried out using bacteria, viruses and yeasts. With burgeoning research in microbiomes the chosen theme is of immense importance. I laud the efforts of the faculty members and students in putting together a magazine carrying articles written by students - this has given the students an opportunity to explore science beyond text books and gain new insights in various areas of biology, simultaneously igniting their curiosity, and perhaps even unearthing new interests!

It is my absolute pleasure to wish all the faculty members, staff and students of the department the very best as they continue this exhilarating journey in pursuit of knowledge and excellence.

Best Wishes,

Swati Saha

Swati Saha

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ARTICLES

| Human Gut – An Electric Power Plant

Riya Bongirwar (II Year)

The human gut performs many functions like storage, transportation, digestion of food and absorption of nutrients, but can it generate electricity as a miniature electric power plant? Is electricity constantly being produced in our gut? The answer to this question is surprisingly yes!! Researchers in University of California, Berkley have found that many bacteria reside in our gut and form a conspicuous part of gut flora which generate electric current.

Gut bacteria-the workers of electric power plant:

One can imagine these electrogenic gut bacteria as workers of the human gut- electric power plant. A number of electrogenic bacteria that reside in exotic environments like mines, bottoms of lake etc. have been known. Scientists have only recently found microorganisms in human gut to do the same too. Many of these sparking bacteria are natural component of gut flora and other species of bacteria which interact with human gut as either pathogens or probiotics are also electrogenic. For example, a common diarrhoea causing bacteria called *Listeria monocytogenes* has been found by researchers at University of California to produce electricity. The bacteria that cause gangrene (*Clostridium perfringens*) and hospital-acquired infections (*Enterococcus faecalis*), and some disease-causing streptococci also produce electricity. Other electrogenic bacteria, like Lactobacilli, are important in fermenting yogurt, and many are probiotics.

Why and how gut bacteria generate electricity?

Bacteria generate electricity by removing the electrons which are produced due to metabolism in order to produce cellular energy. In animals and plants electrons are generated at the end of electron transport chain and are transferred to oxygen in mitochondria of each cell. They also require an electron acceptor molecule, but since they live in oxygen deprived environment of the human gut, they use electron acceptor molecules other than oxygen. In the case of gut microbes, they live in abundance of one very effective electron acceptor called flavin. This molecule is made up of vitamin B12, which is essential for the function of our cells and so is usually abundant in the body. Hence, these gut bacteria employs a special external electron transport mechanism to transfer the electrons from cytoplasm to extracellular electron acceptor, the flavin molecule to generate electricity. Scientists have used electrodes to estimate the amount of electricity streaming from these electrogenic gut bacteria and were amazed to find that each bacterium can generate approximately 500 milli amperes of current.

Future aspects of electrogenic gut bacteria:

Scientists believe that electrogenesis might be a key to understand the interaction of different bacteria in our digestive system, and to understand if they have a role in gut's influence over our emotions and decision making. Microbiologists believe that colonies of these electrogenic gut bacteria might be used to generate sustainable electricity through microbial fuel cell or bacterial batteries.

| *Fusobacterium nucleatum*: An Opportunist

Tanu Bansal (III Year)

Human beings are the most precocious and supreme creatures on earth. Besides sharing the earth with other organisms, we also share our body with the mighty microorganisms. We have more number of microbial cells living inside our body than our total number of cells. These microorganisms exhibit different characteristics and occupy different habitats in our body. They exhibit either commensalistic or mutualistic relationships with the human host (in some cases, being pathogenic to humans too!). The friendly microorganisms too may become outrageously pathogenic and result in a disease in the host.

The gram negative, anaerobic bacilli *Fusobacterium nucleatum* is a symbiotic bacteria and a part and parcel of human oral, gastrointestinal and placental microbiome. The presence of this bacterium in the microbiome associated with colorectal cancer was the first indication that it may be pathogenic too.

Fusobacterium nucleatum: an opportunistic, symbiotic oncobacterium

***Fusobacterium* in oral cavity**: It has been reported that *F. nucleatum* has evolved itself to live in close association with the tissues of oral cavity and the oral microbiota. With other microbial species such as *Streptococcus spp.*, *Porphyromonas gingivalis*, *Aggregatibacter actinomycetemcomitans*, *Candida albicans* etc. it forms multispecies biofilms which are both beneficial and detrimental. In dental plaque biofilms, it acts as a bridge organism helping in co-aggregation of other microbial species in oral cavity and hence, connects the primary colonizers to secondary colonizers and frame the biofilm. Besides building the dental plaque biofilms, *F. nucleatum* also causes periodontal disease: a situation in which inflammation affects the tissue surrounding the teeth thus leading to swollen or bleeding gums, loosen teeth, bad breath. It has been observed that *F. nucleatum* is a genuine colonizer of placental tissue and is also a part of natural and healthy placental microbiome. At the same time, it has been shown to play an important role in many placental infections too. Thus it can be present in a commensal association but can erode the barriers to cause infections too.

***Fusobacterium* in colorectal cancer:** It has been observed that *F. nucleatum* lives in very close association with the colorectal crypts. The origin of the bacterium being the oral cavity, observations conclude that it can infect many sites in our body leading to devastating diseases. It is mostly found intracellularly in the cancerous cells. In fact, in model organisms, the bacterium influences the formation of pro-inflammatory tumorigenic environment which leads to increase in chances of colorectal cancer. This tumorigenic microenvironment is thought to be achieved by evading anti-cancer immune responses. An interesting study reveals that presence of *F. nucleatum* cells in colorectal cancer tissue promotes resistance to chemotherapy.

Thus *Fusobacterium nucleatum* is an opportunistic bacterium. Though all strains of *F. nucleatum* are not bona-fide pathogens, care must be taken as prevention is better than cure!

| Peizophiles

Nandini Sabharwal (I Year)

Earth's oceans are very similar to those in the extraterrestrial ocean worlds, but the closest analog is found in the deep-sea hydrothermal vents. In there, microbes cycle nutrients and energy across a wide variety of geochemical states and conditions. This type of ecosystem has a specific, common physical parameter, that is, high hydrostatic pressure, piezophily, which is generally found to be the characteristic of life in the deep oceanic spaces. This high-pressure adaptation confers a competitive advantage to piezophiles, allowing them to access additional energy sources and expand habitable niches. Peizophiles (formerly called barophiles) are known to be a part of hadal trenches and oceanic locations deeper than 6000 m, which confers them the distinct abilities for high hydrostatic pressure tolerance. The pressure required for their optimal growth varies from < 10 MPa for piezotolerants to > 50 MPa for hyperpiezophiles.

There are many mechanisms that help in enhancing pressure-resistance of cells i.e., alteration of the membrane lipid composition to increase membrane fluidity, the presence of intracellular stabilizers (salts, sugars) and the presence of an S-layer around the cell membrane. The general pressure tolerance of non-piezophilic prokaryotes can also be enhanced by utilizing various means such as adaptation to environmental stresses like high temperature, high salt concentration or decreased water activity. The majority of the marine piezophilic microorganisms described so far are Gram-negative, facultatively anaerobic bacteria with *Shewanella spp*. as most frequently isolated. As per records, 50 piezophilic and piezotolerant strains of Bacteria and Archaea have been recovered from various sea habitats. *Archaeon pyrococcus*, CH1 was the first hyperthermophilic obligate piezophile isolated from the depth of 4100 m in the mid-Atlantic ridge.

Sampling and cultivation methods of piezophiles

Deep-sea animals, water and sediments are the sources of piezophiles. Piezophiles can be isolated utilizing animal traps and other samplers (multi-bottle water sampler, sterile bag sampler and multicoring sediment sampler). After obtaining samples, these can be maintained and cultivated in pressurized vessels. Various labs have designed specific instruments for isolation and cultivation of piezophilic microbes without performing any decompression. One such equipment is a Deep Bath system which consists of a pressure retaining sampling device, a dilution device, isolation device and cultivation device of maximum 3L capacity. The pressure and temperature of 0.1–65 MPa and 0–150°C, respectively, is maintained in the system. The high pressure vessel is used for cultivation of sample after mixing it with liquid medium. Moderate piezophiles and piezotolerants can be isolated by plating methods from liquid culture. Obligatory piezophiles are isolated at low melting point agar by pressure bag method, whereas dilution-to-extinction method is used for thermophilic piezophiles.

| A Digestive Enhancement

L.S. Pranathi Ganti (II Year)

Rumen is a big pre-gastric anaerobic fermentation chamber in cattle harbouring the complex rumen microorganisms, that catalyses the anaerobic degradation of ingested plant biomass into biological energy. Rumen microbiome is composed of all domains of life, consisting of bacteria (nearly 95%), fungi, archeae, ciliate protozoans and also bacteriophages. Rumen is an ideal microbial habitat because it is favourable for survival and growth of microorganism. Water and saliva provides moist environment for microbial growth. Rumen microbiome is a continuous culture system which operates as biological fermentation unit like a chemostat under well-defined conditions. Ruminal microorganisms have important roles in feed digestion and act synergistically to ferment plant structural and non-structural carbohydrates and proteins. Fermentation products of rumen microbial activity are mainly volatile fatty acids (VFA) which serve as a major source of energy for animals. End products of fermentation are removed by absorption into blood or eructation. Absorption coupled with buffering effect provided by salivary secretion regulate ruminal pH. Ruminal environment is anaerobic containing carbon dioxide (65%), methane (35%) and small amount of other gases. The type of metabolism that occurs in the rumen is fermentation in which terminal electron acceptor is organic or inorganic compound other than oxygen.

The ruminal microorganisms belong to three domains: Eubacteria, Archae and Eukarya. Majority of ruminal bacteria are obligate anaerobes, although facultative anaerobic may also exist. These are predominantly Gram negative bacteria (80-90%). Certain species of ruminal bacteria (*Butyrivibrio fibrisolvens*) have typical Gram positive cell wall but stain Gram negative. Gram positive bacteria population increases in grain fed animals. Most ruminal bacteria are rod shaped, some are spherical and some are also spiral shaped. Some common genera of ruminal bacteria are *Streptococcus*, *Clostridium*, *Treponema*, *Lampropedia*. Lipolytic bacteria found are *Anaerovibrio lipolytica* and *Butyrivibrio fibrisolven*. Celluloses are digested by *Ruminococcus flavefaciens*. Some proteolytic bacteria like *Ruminobacter amylophilus* and *Butyrivibrio fibrisolvens* are also found. Proteins are broken down into polypeptides then into short peptides and finally into amino acids. The methanogens present in the rumen mainly belongs to *Methanobacterium*, *Methanobrevibacter*, *Methanosarcina*, *Methanomicrobium* and *Methanoculleus*. Methanogens usually grow using hydrogen and formate as their energy source and utilise electron derived from hydrogen. They use formate to reduce carbon dioxide to methane. Some species can use methyl groups from methanol, methyl amines or acetate to produce methane. Protozoans were the first rumen microorganisms to be discovered because of their perceptible cell size and activity. Ruminal protozoa actively participate in ruminal digestion and they possess hydrolytic enzymes which are used to ferment the fibrous feed. Some common protozoans are *Isotricha*, *Charonina*, *Metadinium*.

Anaerobic fungi as a member of ruminal microbial population were discovered by Colin Orpin in 1975. These fungi produce hydrolytic enzymes like cellulases, hemicellulases, pectinases, lyases, amylases and proteases required to breakdown major components of plant biomass, the enzymes include. Ruminal fungi carry out mixed acid fermentation. They can metabolise hexoses or pentoses to produce acetate, formate, lactate, carbon dioxide, hydrogen etc.

Bacteriophages have also been found in the rumen microbiota. Polymers are major components of ruminant diets and include carbohydrates, nitrogenous substances, lipids and lignins. Except for lignins, the polymers are hydrolysed to monomers which are then metabolised to various fermentation products chiefly acids and gases. Lignins are polymers of phenolic compounds and are virtually indigestible.

Ruminal microorganisms possess glycosyl hydrolases that breakdown glycosidic bonds to produce oligosaccharides and then disaccharides and monosaccharides. Common examples of carbohydrate fermenting bacteria include *Streptococcus*, *Lactobacillus*, *Bifidobacterium*. Combining multidomain quantitative metatranscriptomics with the gas and VFA profiling, active rumen microbiome was obtained during feed degradation. Holistic assessment of rumen microbiome dynamics using quantitative metatranscriptomics showed multifunctional redundancy during anaerobic feed degradation. Methane emissions and VFA concentration increased drastically sometime after feed intake. The mRNA profiling revealed a dynamic levels of carbohydrate activating enzymes' transcripts, transcripts involved in VFA production and methanogenesis.

Bovine rumen has a complex microbiota which is helpful in cattle's ability to convert indigestible plant mass into energy. The quality and quantity of the microorganisms in the rumen can influence an animal's ability to harvest energy, and indirectly affect mankind as these animals are used as a source of products for human consumption.

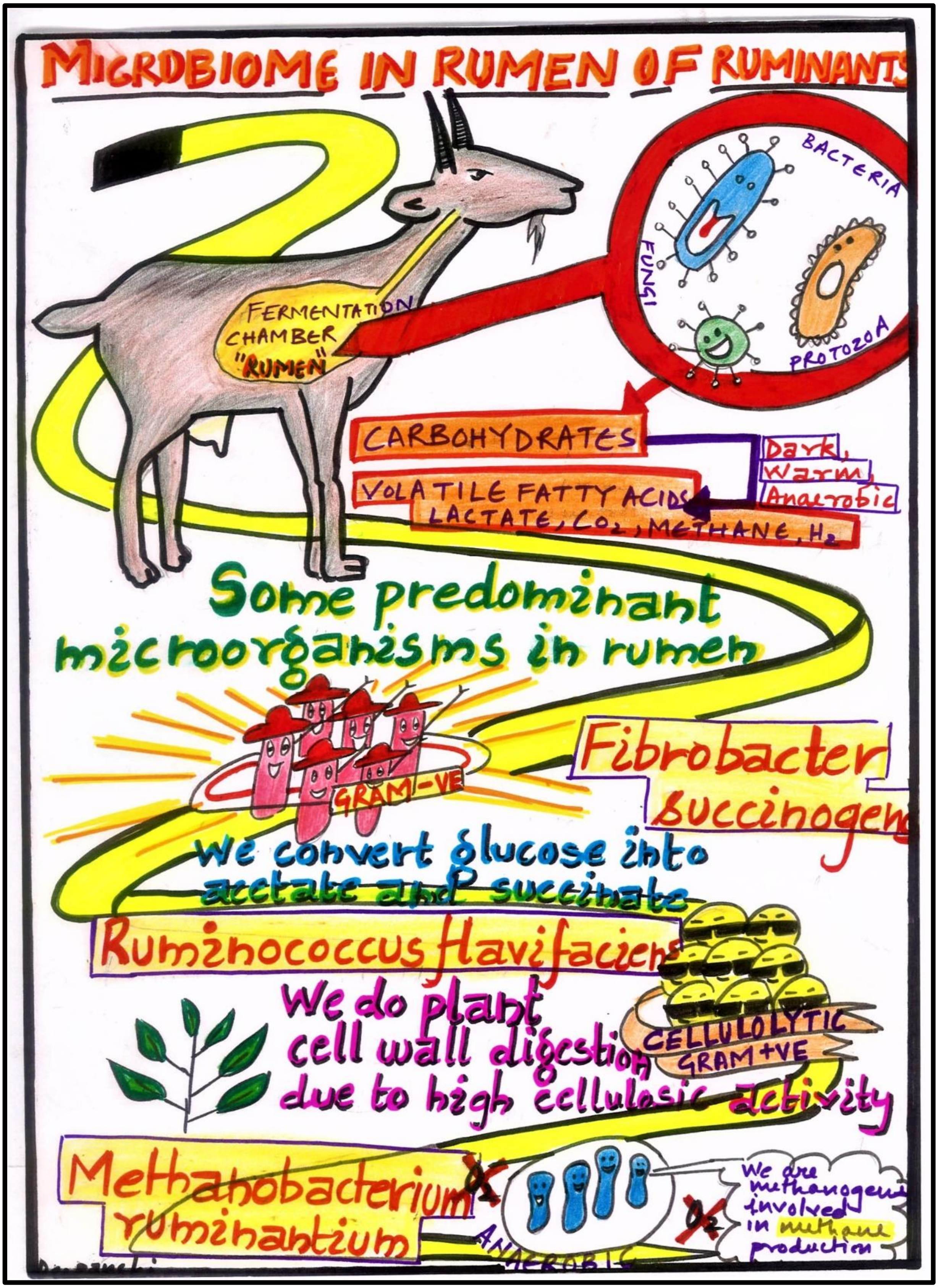
| Community Lifestyle of Microbes

Anirban Adhikary (III Year)

We microbiologists are generous people. We provide rich and abundant nutrient sources and optimum growth conditions while culturing microbes in our labs. Outside our labs, the scenario happens to be very contrasting. Microbes need to constantly battle for survival with both other organisms as well as with the transient conditions of their own habitat. In their quest for survival they deal with scarce nutrient availability, low water availability, toxic environments, invaders, and adverse temperature and pressure conditions. Evolution only allows survival of the fittest. In order to survive and reproduce, they need to find novel strategies to handle variety of challenges. Something that we find so astonishing about these very simple life forms is their remarkable flexibility and ability to regulate their ways of interaction with their immediate surroundings down to the molecular level. One such remarkable example of survival strategy of microorganisms is living together as a community in the form of Biofilms. They are found on almost every non-sterile surface irrespective of environmental parameters. Presence of an aqueous environment enhances biofilm formation. Free-floating mat-like biofilms are found on stagnant water bodies. They can grow in the most extreme of environments ranging from extreme hot temperatures, acidic and alkaline environments to frozen glaciers. Stromatolites, the oldest records for life on earth are actually biofilms of cyanobacteria.

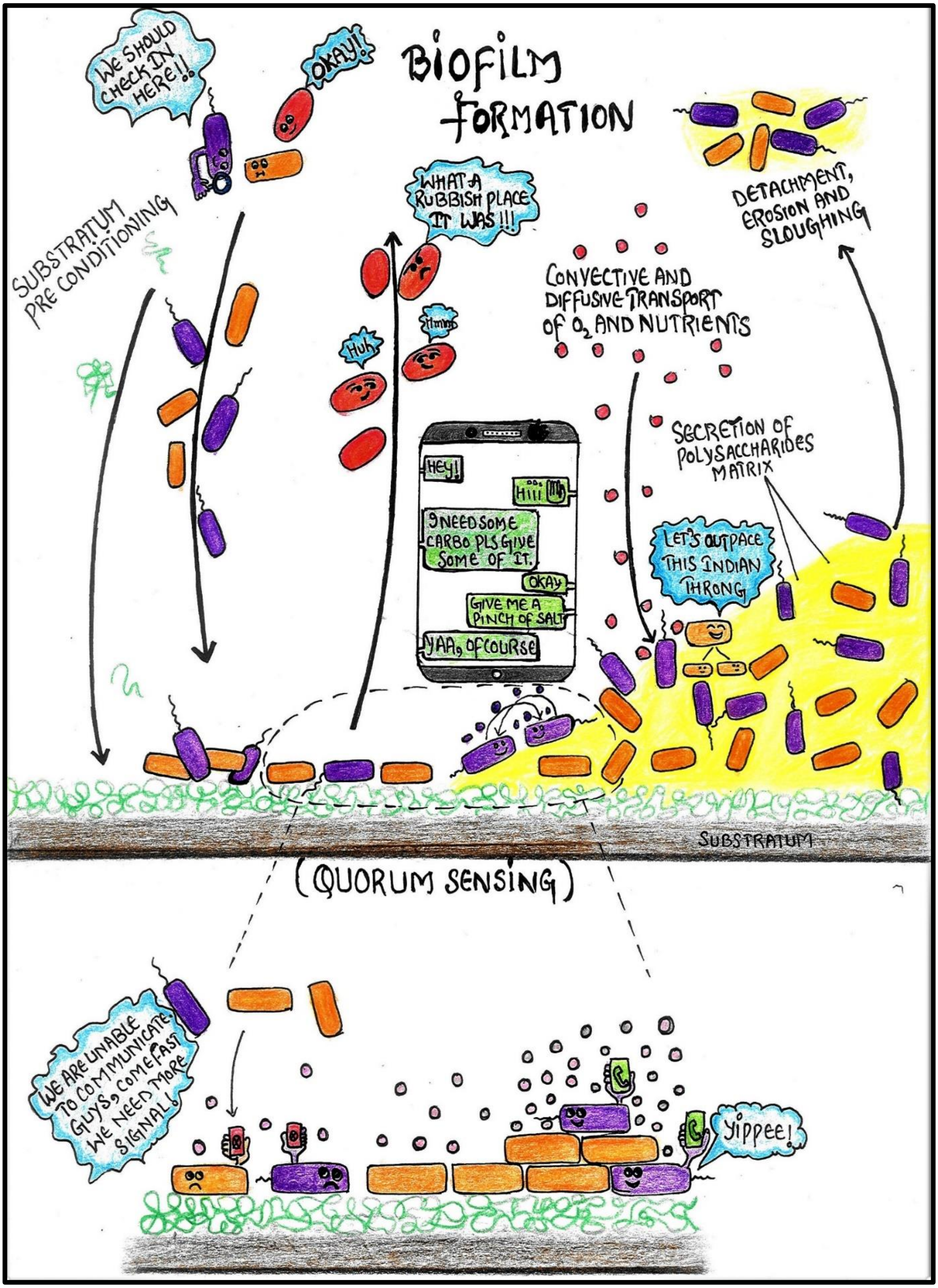
IUPAC defines Biofilms as, "Aggregate of microorganisms in which cells that are frequently embedded within a self-produced matrix of extracellular polymeric substances (EPSs) adhere to each other and/or to a surface". Inhabitants of a biofilm can adjust internally to external environmental conditions. Biofilm formation can be triggered by certain factors like: recognition of a solid adhering surface, presence of nutrition source, detection of sub-inhibitory levels of anti-microbial substances by planktonic or free-floating cells. On detection of any such factor, a cell switches from a planktonic to a biofilm mode of life. This is due to activation and differential regulation of certain group of genes. Cells forming a biofilm show rapid genetically regulated morphogenesis. Microscopic study of a biofilm shows morphologically distinct cells present at different layers of the biofilm. The morphological distinction is actually a result of different degrees of metabolic activity. This makes a biofilm not only a structural organization, but also a functional living entity. Biofilm formation initiates with adherence of a single cell to a solid surface, which then divides rapidly.

"A digestive enhancement"



Doodle by Deepanshi Koul (III Year)

"The Social life"



HEY!

Hiii

I NEED SOME CARBO PLS GIVE SOME OF IT.

OKAY

GIVE ME A PINCH OF SALT

YAA, OF COURSE

Doodle by Ujjwal Sagar and Ankit Saraf (III Year)

There are evidences suggesting that adherence is not a deciding factor for biofilm formation. Certain bacteria can produce biopolymers that help them adhere to each other, thus producing flocculants, which then adhere to form a free floating structures. Motility facilitates biofilm formation as structures such as pili or fimbriae enhance capability of the cells to adhere to a solid surface. Bacterial biofilms are encased in a capsule of EPS. It can be made up of a wide range of components such as polysaccharides, nucleic acids, amyloid fibres, lipids, blood cells etc. During biofilm formation, cells can communicate with each other through quorum sensing. A completely mature biofilm consists of physiologically dormant cells at the center. These cells often contain spores. The peripheral regions are rich in cells that are metabolically more active. They produce certain primary and secondary metabolites that help the community to sustain.

The EPS of a biofilm is known to contain certain extracellular enzymes that help in breaking down of complex substrate, followed by its intake. Biofilms are known to contain networks of water channels which are necessary for cell viability as well as nutrient intake At the end of its life, a biofilm releases the spores into the surrounding environment. The spores germinate on availability of favourable growth conditions.

Biofilm formation provides certain advantages to the microbes. They increase resistance to certain antibiotics. The structure and physical properties of the capsular material of the biofilm does not let the antibiotic seep into their site of action, thus protecting the cells. Higher dose of antibiotics are often required to treat diseases cause by organisms with the capability to form biofilms. This one advantage provided by biofilms is a major problem faced by humans to treat infectious diseases. Biofilms protect the cells from being recognized by immune cells and antibodies, thus they avoid host immune response against them. Modern medical science is looking for substances with potential anti-biofilm activity to treat microbial infections. Bacterial cells in a biofilm tend to gain antibiotic resistance much faster than their planktonic counterparts because of proximity of cells to each other. This is due to lateral gene transfer.

A study in 2003 showed that the human body facilitates biofilm formation by beneficial gut microbiota in the large intestine. The findings were supported by the detection of two molecules abundantly produced by the immune system that support biofilm formation. It is hypothesized that the appendix helps to re-inoculate the gut with useful microorganisms.

Biofilms grow easily in human-made environments that provide moist and warm conditions. They are a major cause of corrosion of sewage pipes. They reduce heat transfer in water heating or cooling systems. Biofilm formation on boats and ships are a major cause of biofouling, which causes major economical damage. Bacterial biofilms are reported to grow on ocean plastic debris.

Biofilms are ubiquitous in nature and they are actually allowing microbes to better adapt in nature. Plant pathogens grow in the form of biofilms on leaf surfaces and also in the interior regions of the plant's body. Symbiotic relationships between plant and micro-organisms are actually mediated by biofilms that are involved in nitrogen-fixation. Biofilms are found extensively in soil. Decomposition of dead and biodegradation is mediated by microbes that grow as biofilms. Extensive formation of biofilm can result in bio-clogging which reduce water seepage into the soil because the pores of soil get clogged by cells EPS material, cell and other by-products.

The properties of biofilms can be utilized to benefit humans. It has been observed that the efficiency of microbial extracellular enzymes is highly enhanced when present within a biofilm.

Bio-leaching utilizes microbial biofilms that can grow on metal ores. The microbes cause degradation of the ores easing extraction. Biofilms that are called flocs are used extensively in sewage treatment. Biofilms can eliminate petroleum oil from contaminated ocean habitats. The oil is degraded by hydrocarbon-degradation of microbial communities. Biofilms are used in Microbial Fuel Cells to generate electricity from complex organic waste material. Biofilm formation is a desirable trait in probiotic bacteria. The colonization of gut by beneficial bacteria prevents colonization by harmful bacteria. It also prolongs the effect of probiotics. To sum up it would be safe to say, if we are talking microbes, we are talking microbial biofilms.

| All about Plastisphere: Existence of Microbial Communities on the Marine Plastic Debris

Tanu Bansal (III Year)

"*Everything is everywhere, but the environment selects*"**- Sir Lourens Baas Becking**

The ecological diversity of earth is so vast that one can find flora and fauna in any part of the world ranging from hotter deserts to saline lakes and snowy mountains. Besides nurturing our planet, we humans have made earth a difficult place to live. From accumulating plastics in water bodies and on the land to deterioration of air and many other natural resources, our activities have depleted our ecological diversity as it has raised a question on its survival in present conditions.

Microorganisms, though being the smallest creature on earth, can survive in varying environment and on different nutritional substrates. The presence of microbes on the plastic marine debris came into picture when some researchers noticed no such significant increase in the plastic accumulation in open ocean even with an increase in the production, use and dispose of plastic into the oceanic bodies. They initially hypothesized photo-degradation and physical shearing as possible mechanisms by which plastic had been degraded, but how could these mechanisms degrade plastic into such finite pieces that it passed through the standard sampling net?

This led scientific community to ponder over the probable mechanism of plastic degradation in nature. Further, with the help of scanning electron microscopy (SEM) and next generation sequencing they found microorganisms embedded in the pits of plastic surfaces which are actually facilitating degradation of plastic. These marine microbial communities were recognized as plastisphere- which refers to the ecosystem evolved to live on man-made plastic rich environment. Further analysis also revealed that microbes actively participate in hydrolysis of the hydrocarbon polymer. These microorganisms were so different from the surrounding environment that scientists called plastic as novel ecological habitat in the ocean itself, comprising hydrocarbon degrading bacteria. Plastic serves as a good source of nutrition for the microorganisms as it has a longer half-life than most of the naturally occurring substrates in the water. Its hydrophobic surface also promotes microbial colonization and biofilm formation. This makes plastic perfect for the microorganisms to attach, grow and act upon.

While combating the problem of gradual increase in the plastic levels on the earth, the use of microorganisms can be one of the mechanism to degrade them and solve many related issues.

|Marine Ecosystem Degradation and Solutions: A Microbial Perspective

Arnab Kakati (I Year)

What really comes in our mind when we think of an ocean? The deep blue colour, tides, fishes and islands and many more. It would be really abstract if we neglect the tiniest members of the blue planet, the microorganisms. Surprisingly, the marine microbiome is considered to account for the largest population of the microorganisms on this planet. The vastness of the oceans and seas helps in the achievement of such huge number of microorganisms. These microorganisms are the true force in maintaining the marine ecological balance. The major question is that why and how are these microorganisms so influential for other aquatic organisms? Are all microorganisms a boon for the aquatic life?

The variety and variability of the microorganisms in marine habitat makes it difficult to study their precise functions and metabolic processes. Hence, metagenomic sequencing is used to study the genetic material of the microorganisms, and find out their potential to produce useful products without having them to culture them. The microorganisms found in the deepest part of the oceans are thought to consume most of the CO_2 found in the atmosphere of the planet and convert them into organic matter. These microbes have been playing a great role in maintaining the ecological balance for a long time.

The marine microorganisms can also be applied to conserve the coral reefs. They make the coral reefs resistant to various diseases and other similar problems arising in ocean. One of the ways to conserve coral reefs by inoculating them with appropriate microbes and then transplanting these healthy corals into affected reefs.

Marine microbes also play a significant role in tackling pollution problems in oceans and seas. Increase in plastic pollution in the oceans has raised serious concerns globally. However, the newly evolved microbes serve as a remarkable solution to this problem. Bacteria that grow and feed on plastics are used extensively in the removal of plastics from seas and oceans on a large scale. For example, *Ideonella sakaiensis* helps in the degradation various plastic bottles which are disposed by humans in aquatic bodies. Research is underway to utilize these microorganisms in production of sustainable bio-plastics.

Apparently, marine microorganisms are of great importance in the field of biotechnology. Such microorganisms have the capability of surviving in various adverse environmental conditions. The biomolecules that allow them to survive under such conditions are important research tools with important potential applications. For example, scientists have isolated a *Pseudomonas sp*. which secrets a natural polymer called polyhydroxyalkanoate used in the production of various biodegradable plastics.

Various human wastes influence the growth of *E. coli* in coastal water and if they are somehow ingested, can cause intestinal problems and other major organ damages. Diseases such as fin rot and fish dropsy are caused by bacterium *Pseudomonas fluorescens*. Some species of bacteria belonging to the genus *Vibrio* are involved in causing vibriosis in salmon and many other fishes. Many fishes are also affected by the *Mycobacterium tuberculosis,* the causative agent of tuberculosis. Furthermore, the viruses causing Hepatitis A, Hepatitis E, polio and protozoans causing giardiasis and cryptosporidiosis are found mostly in costal water and estuaries.

Climate is one of the most influential factors that affect the marine microbiome and all other aquatic life forms supported by the ocean. With an increase in the amount of CO_2 produced due to human activities, the temperature of oceans has become warmer and also led to the rise in its acidic nature. A rise in the temperature of the oceans also causes severe harmful events such as formation of algal blooms leading to depletion of many nutrients and release of toxic substances.

The Pseudo-nitzschia bloom in 2015 had a great impact in the fish industry in US West Coast. It affected many marine organisms as well as the humans who consumed it. Plastic pollution is one of the major problems in present scenario and accumulation of the plastic degrading bacteria in large number has a negative impact on the marine microbiome. Also, the pollutions caused by oil fields and deposition of various sediments from mining activities also have a negative impact on the marine microscopic life. Thus, it is evident that though marine microbes have a significant role in maintaining aquatic life, but due to countless human atrocities, they have been struggling for their own survival. Therefore preserving and maintaining the seas and oceans is very important to solve multiple environmental issues.

| Under the Sea, Across the Sky!

Shreya Sharma (II Year)

Why we humans take so much time to analyze goodness behind everything? We, as a community have to broaden our thinking and visualise the various aspects of nature. The amount of pollution created by us as a whole is causing grave damage to the environment. Due to human activities, the level of green house gases has been increasing, causing the depletion of ozone layer which further posses threat to human health and the ecological balance. Therefore, some new, strong and better inventions and discoveries have to take place for betterment of mankind and environment as well. A discovery was made to reveal the glorious and useful world buried deep inside the sea, capable of bringing about a revolutionary change in the working of industries.

Researchers, from University of Florida, found a bacterium named *Thiomicrospira crunogena* deep inside the ocean, producing carbonic anhydrase, while being able to withstand high temperature (the enzyme which helps to remove carbon dioxide in organisms and is also capable of neutralizing large amount of industrial carbon dioxide in the earth's atmosphere). One of the major greenhouse gases is carbon dioxide which is mostly produced by the combustion of fossil fuel (fuel gas), and its use is raising concerns. This gas can be sequestered by *T. crunogena*. This bacterium is found near hydrothermal vents, so the enzymes that it produces by them is accustomed to high temperature and converts carbon dioxide into harmless compound.

This little creature has evolved to deal with the extreme temperature and pressure, therefore it has well adapted to the conditions prevalent in industrial settings. The enzyme catalyses the chemical reaction of carbon dioxide with water. This interaction of the enzyme with the atmospheric carbon dioxide converts it into bicarbonate, which can be further used in the production of baking soda and chalk. In an industrial setting, the carbonic anhydrase would be immobilized with solvent inside a reactor vessel that serves as a large purification column. Further, when the fuel gas will pass through the solvent it would eventually convert the carbon dioxide into bicarbonate using carbonic anhydrase.

The industrial quantity of carbon dioxide would require a large amount of carbonic anhydrase for neutralisation. Researchers have found out the way to produce this enzyme without having to harvest from the sea beds. They have started producing the enzymes by genetically engineered *E. coli*. The enzyme is not so efficient in converting carbon dioxide to carbonate as compared to the bacteria present in the sea floors.

At last, it is important to design tools that can help us utilize the potential of microorganisms buried deep inside the sea to combat increasing carbon dioxide load in the atmosphere.

| A tete-a-tete between Microbes…

Archana (III Year)

A team of researchers led by the Netherlands Institute of Ecology (NIOO-KNAW) have demonstrated for the first time that two different types of micro-organisms i.e., bacteria and fungi use volatile organic compounds (VOCs) such as terpenes, to hold conversations in-between. "We actually believe that terpenes are the most popular chemical medium on our planet to communicate through," they said. The researchers explained how a soil rhizospheric bacterium *Serratia plymuthica* can smell the volatile terpenes produced by a plant pathogenic fungus *Fusarium culmorum*. It responds by showing motility in the non-motile cells and by producing many volatile compounds of its own.

Researchers working on organic compounds such as terpenes found that they are by no means the only volatile organic compounds which are essential for a good chat. They have also found other volatile compounds, but because of the efficiency and ubiquitous appearance of terpenes, they were chosen as universal communicating molecule between microorganisms. Plants have also been known to communicate via volatile organic compounds. These VOCs are either emitted in the air as volatile compounds or they are secreted in the soil where they solubilize and travel through the pores and air pockets in the soil. Moreover, some studies have also indicated that plants communicate with each other via rhizospheric fungus. The fungus present in the form of network in the soil, carries the molecular messengers between plants.

A study was conducted by observing a range of fragrant or volatile compounds synthesized by the fungus *F. culmorum*. They observed that the bacterium *S. plymuthica* responds to the VOCs by switching the expression of genes. The VOCs affect the bacterial cell motility without disturbing the bacterial cell numbers. With the help of transcriptomic and proteomic data, they successfully identified the proteins with altered gene expression. The proteins such as Flis- a flagellin specific chaperone, Fimbria A and chemotaxis protein IV showed enhanced expression. These proteins were involved in the flagella production, cell adhesion and movement of bacterium towards stimulus for colonization and growth. Besides the expression of motility factors, the bacterium also showed enhanced expression of genes and proteins involved in signal transduction. These proteins were found to regulate motility, cell growth, cell envelope biogenesis, tolerance to multiple drugs and nutrient uptake. Experiments have shown that VOCs considerably enhance the bacterial cell wall permeability. The metabolomics study revealed that VOCs also activate certain gene clusters involved in secondary metabolite production. The volatile terpenes produced by the fungus up-regulates the synthesis of a terpene synthase gene by producing an unusual and unique volatile compound ‘Sodorifen’ by the bacterium. These microorganisms not only exchange the messages with the help of terpenes but also sense the changes in their environment caused by the change in the terpene levels and in return adapt themselves to the change accordingly. Thus, the studies conclude that VOCs which are considered to be the metabolic wastes of microorganisms, are in-fact very crucial for fungi and bacteria to hold long distance communications.

| Microbes: The Kings of Restoration

Saurav Malik (III Year)

Ecological restoration is a globally important and well-financed management intervention to combat biodiversity declines and land degradation. Ecosystem restoration is increasingly relied upon to combat global decline in biodiversity, ecosystem services, and land quality.

The degradation of ecosystems due to human activity has increased in intensity in the last century or so. Ecological restoration is the only solution to this problem; repairing and, indeed, in some places replacing these damaged systems with ones that are healthier and provide more ecosystem-derived goods and services.

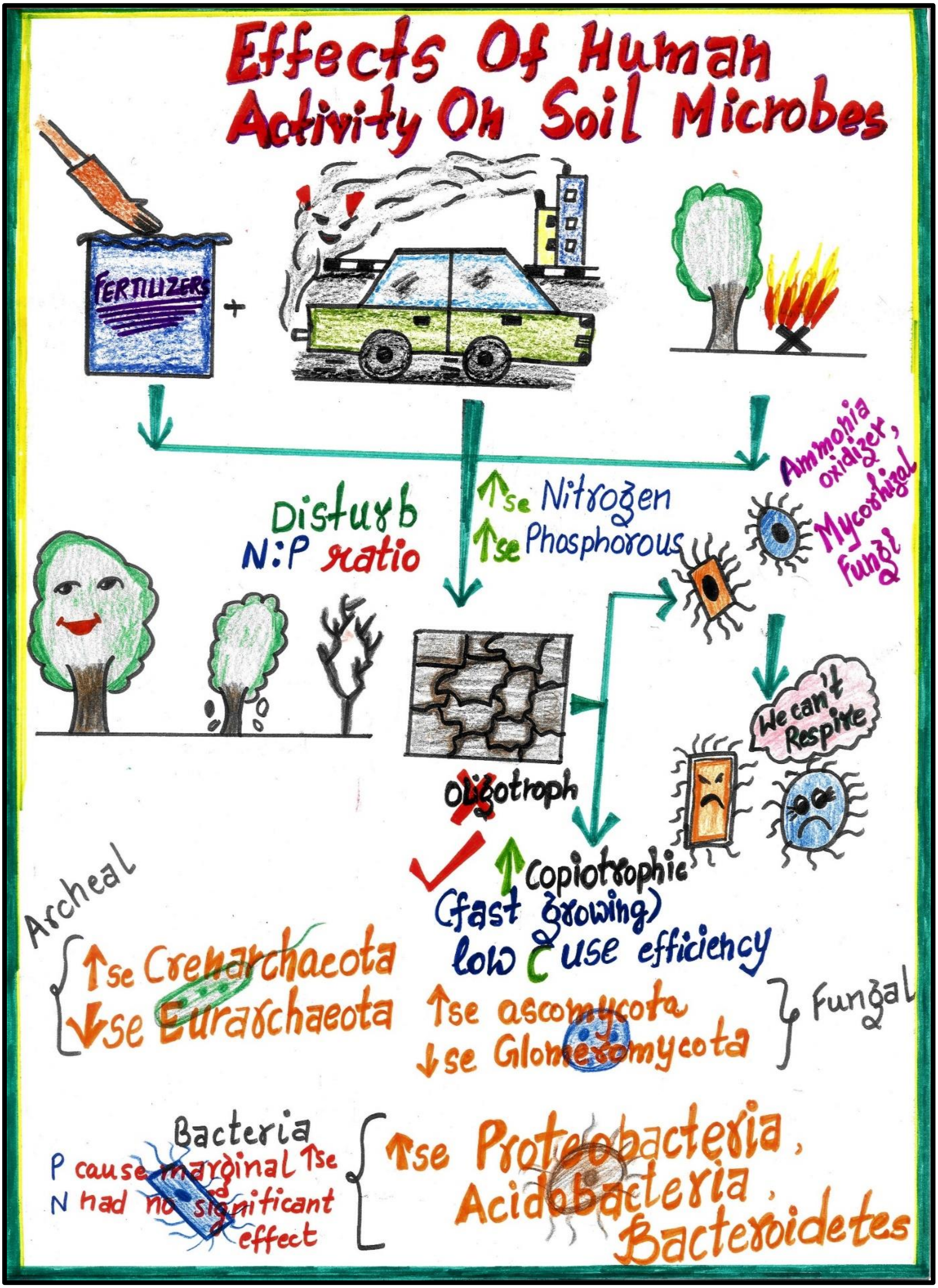
Until now, successful ecological restoration has involved rather crude techniques, such as soil removal, deep ploughing, and both herbicidal and mechanical removal of species. It is well known that microorganisms are essential to the soil structure and soil function, particularly for the degradation of organic matter and nutrient cycling, in regulating plant productivity and community dynamics. Hence, the study of soil microorganisms is an extremely important part of any program aimed at restoration of an ecosystem.

Recently, microbes have been investigated in two ways in relation to restoration. Their relative presence is used to indicate the state of the ecosystem in reference to target sites' conditions, and manipulation of the soil microbiome is also being explored so as to enhance the speed with which the system can be moved along to the desired state (by overcoming biotic barriers, either the absence of desirable components (such as mutualists) or the presence of undesirables (such as invasive plants)).

The use of soil microbial community to indicate the condition of soil-based ecosystems has long been in practice. There is a clear evidence that as intensive use of sites is deliberately decreased to restore a more natural state, the ratio of fungal to bacterial biomass increases, as more-complex organic material enters the soil matrix in these systems and physical disturbances decrease. This ratio of fungal to bacterial biomass increases further with forest development as systems move from early to later successional stages. This suggests that the microbial community is greatly influenced by what is going on above-ground and can be used as an indication of the impact of restoration-management practices.

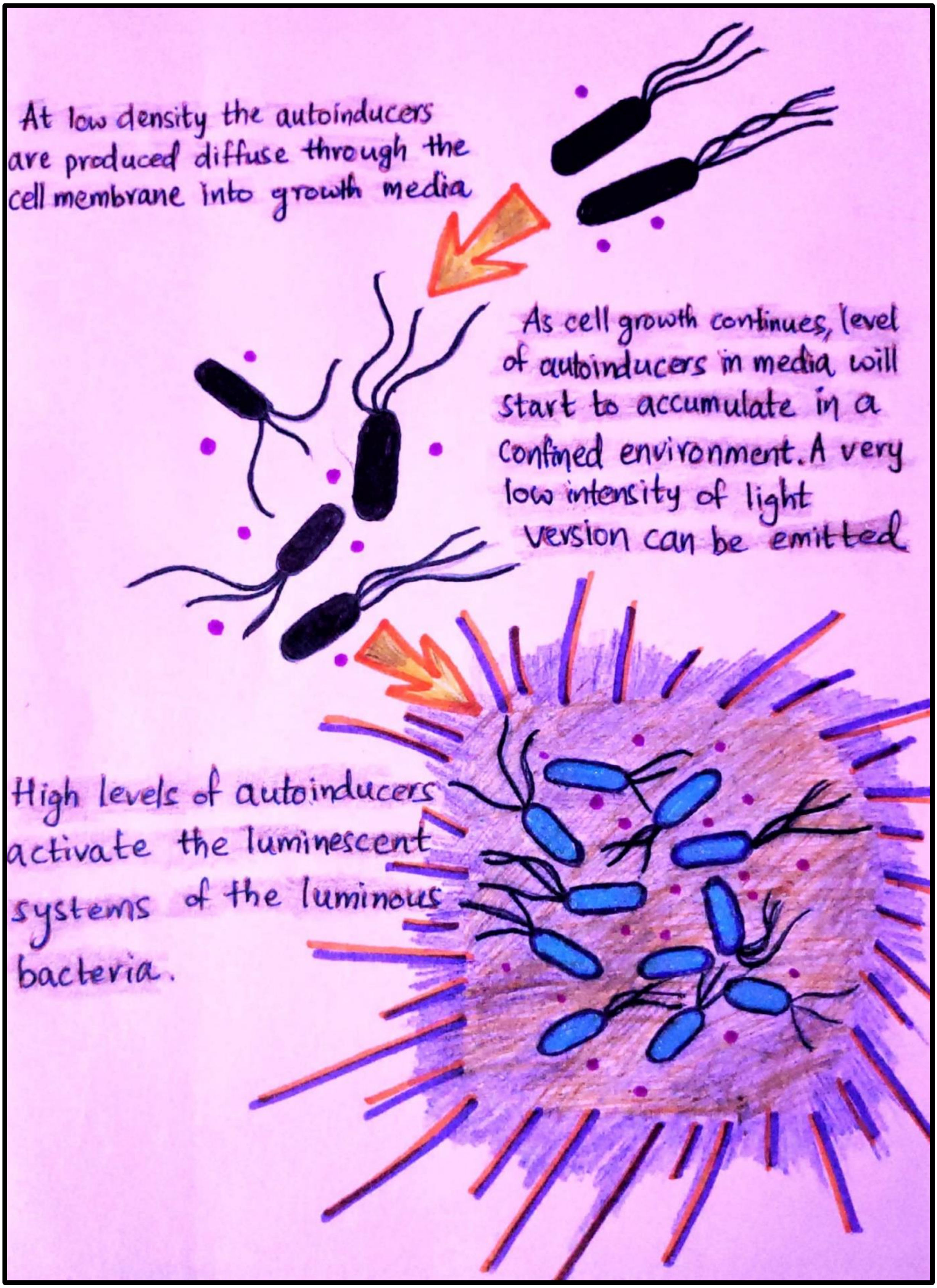
Mycorrhizae, the association of plant roots with fungi, has been known to markedly improve the establishment and the successful existence of the target plant species and have also been linked to plant diversity and productivity. This association is a win situation for the fungus as well as the plant as the fungal partner gains ready access to photosynthates; the plants gain access to mineral nutrients and protection from pathogens and drought. In the restoration of extensively disturbed areas, such as large-scale mining, mycorrhizae offer an economical means of establishing plant communities. The investigation of soil microbial communities in systems undergoing restoration is providing important insights into how pristine ecosystems work. As ecosystems mature, there is an increase in the proportion of fungal biomass in comparison to the bacterial biomass, and around mid succession as the root exudates peak, the total microbial biomass in soil reaches its maximum. With the predominance of fungal biomass in the rhizosphere, there is a decrease in the diffusion of plant exudates. The restoration programs aim to cut short this course by establishing fungal dominance at an early stage. The status of different systems under restoration can be determined by measuring the size, composition and activity of the microbial community of the soil. Given the importance of microorganisms in establishing of a pristine land or restoration of an extensively disturbed land, they are indeed the kings of restoration!

“Observing the change”



Doodle by Trisha Bainiwal (III Year)

“Let there be light”



At low density the autoinducers are produced diffuse through the cell membrane into growth media

As cell growth continues, level of autoinducers in media will start to accumulate in a confined environment. A very low intensity of light version can be emitted

High levels of autoinducers activate the luminescent systems of the luminous bacteria.

Doodle by Areef Kammugari (II Year)

|Interactions between Human Immune System and Microbiota

Lakshay Kumar (I Year)

The general misconception about the microbial world is that the presence of microbial species inside the human body can only be an indication of imminent disease or physiological disorder. Such an idea is actually completely inaccurate and oblivious of the undeniable fact that most of the microbial species found in the human body are indeed beneficial, if not necessary, atleast for orderly metabolism. The microbial species that colonize the human body, mainly the gastrointestinal tract (GIT) and skin, are collectively referred to as the human microbiota. Through the course of evolution, the human microbiota has co-evolved with its host to exhibit symbiosis or commensalism in the human body. Therefore, these microorganisms are fundamental for human health. Any unfavourable stimuli might result in an alteration of the gut microbiota, a process called dysbiosis. Dysbiosis has been correlated with many disorders including Irritable Bowel Syndrome (IBS), Inflammatory Bowel Disease (IBD), obesity, autoimmune disorders and allergies. The significance of gut microbiota is clear considering the widescale consumption of probiotics, or live non-pathogenic microbes with beneficial effects on the host. Prebiotics are non-digestible carbohydrates which act as nutrient sources for probiotic microbes. A combination of probiotics and prebiotics is referred to as synbiotic.

When we talk about human microbiota, we need to consider the potential pathogenicity of these microbial species. In this case, we need to understand that pathogenicity is in fact contextual i.e., the ability and tendency of any microbial species which is part of the human microbiota is dependent on a variety of factors, including state of activation of the host, genetic predisposition of the host, and localisation of that microbial species in the body. However, the presence of such a large amount of microbial species in the human body does pose a considerable threat of pathogenesis. Therefore, a large amount of work done by the immune system is aimed at the regulation of the activities of the microbiota. The host achieves this security via limiting the contact between the microbes and epithelial tissue surfaces, thereby preventing inflammation and microbial translocation. In the gastrointestinal tract, the gut microbiota are contained by the mucosal firewall- a collection of immune cells, epithelial cells, IgA antibodies, antimicrobial peptides and mucus.

Mucus acts as the primary shield between the gut microbiota and the epithelial cell surface. Along with mucus, intestinal epithelial cells also produce antimicrobial peptides, which induce antimicrobial effects in case of failure of containment via enzymatic digestion of the bacterial cell wall or disruption of the inner membrane. E.g. Reg3G or Reg3 gamma creates a physical separation between the microbiota and the host intestine referred to as the 'demilitarized zone', having a direct bactericidal effect on gram-positive bacteria. IgA antibodies are produced when intestinal dendritic cells carrying microbial commensals interact with B cells in the Peyer's patches. These IgA immunoglobulins regulate host commensal interaction by impacting microbial gene expression as well as preventing adhesion of bacteria to the epithelial surface. Most activated and memory T cells reside in regions of the body that are colonized by the microbiota, such as the skin and the GIT. The antigen presenting cells (APCs) of the body have co-evolved with the gut microbiota and hence exhibit the ability to phagocytose antigens while maintaining immune tolerance to the microbial species normally present in the GIT, in spite of being in close proximity to them. The APCs exhibit a unique phenotype called inflammation anergy i.e. the noninflammatory profile of intestinal macrophages even when they encounter microbial stimuli in homeostatic conditions. E.g. Intestinal macrophages do not produce pro-inflammatory cytokines when they encounter microbe-associated molecules such as Toll-like receptor (TLR) ligands.

These microbial species, play a very major role in immune homeostasis. However, due to the complexity of both the microbiota and the immune system, the exact underlying mechanism of their interaction has not been yet elucidated. A lot of these species have a positive effect on the immune system. For example, *Akkermansia muciniphila* has a protective effect against obesity and type 2 diabetes. It also lowers body fat mass, improves glucose homeostasis, decreases adipose tissue inflammation and increases gut integrity. *A. muciniphila* produces a wide range of fermentative products, including short chain fatty acids (SCFAs) through mucin degradation. The major SCFAs produced by intestinal fermentative anaerobic bacteria include acetate (C2), propionate (C3) and butyrate (C4), which are found in different concentrations in different parts of the alimentary canal; specifically, about 13 mM in the ileum, 130 mM in the caecum and 80 mM in the descending colon. They act as substrates for the intestinal cells, providing 5-10% of the human basal energy requirement. These SCFAs provide protection against gut inflammation and regulate leucocytes via stimulation of endogenous free fatty acid receptors (FFAR) like FFAR2 and FFAR3 (thereby stimulating increase in the expression of polypeptide YY or the satiety hormone and increasing gut motility), as well as inhibition of histone deacetylase (HDAC). SCFAs also regulate production of cytokines (TNF-α, IL-2, IL-6, IL-10) and facilitate recruitment of circulating leucocytes to inflammatory sites.

Several studies have shown that a lot of diseases are accompanied by dysbiosis, indicating a correlation between these diseases and the gastrointestinal microbiota. The normal gut contains the phyla Firmicutes, Actinobacteria, Verrucomicrobia, Bacteroidetes and the species *Faecalibacterium prausnitzii*. The gut of a patient suffering from obesity exhibits lower levels of Bacteroidetes, Verrucomicrobia and *Faecalibacterium prausnitzii* and increased levels of Actinobacteria and Firmicutes. GIT in case of autism spectrum disorder shows significantly reduced levels of Bacteroidetes and increase in the bacterial genera *Clostridium*, *Collinsella*, *Corynebacterium*, *Dorea* and *Lactobacillus*, as well as increased proportions of the yeast *Candida spp*. Another example is shown by Crohn's disease (an IBD). Patients suffering from Crohn's disease have shown an increase in *Ruminococcus gnavus*, and decrease in *Faecalibacterium prausnitzii*, *Bifidobacterium adolescentis* and *Dialister invisus*, in the GIT, along with an unknown species of *Clostridium*.

Hence, it is clear that the human microbiota play a significant role in both innate and adaptive immune homeostasis. It is also clear that dysbiosis can severely impair physiological functioning of the body, and lead to various diseases and autoimmune disorders. Therefore, it is necessary to understand and regulate all those human practices that can alter the gut microbiotic composition, such as antibiotic treatments, vaccination, hygiene practices and dietary conditions.

In a study, the gut microbial composition of the faecal matter of European and rural African children was compared. The diet of African children is rich in fiber, starch and plant polysaccharides and low in fat and animal protein, whereas the diet of European children is high in sugar, starch and fat and low in fiber. As compared with the European cohort, the microbiota of the African cohort showed a significant depletion in Firmicutes and an increase in Bacteroidetes. An interesting aspect of this study showed that the bacterial genera *Prevotella* and *Xylanibacter*, which encode genes for metabolizing plant polysaccharides, were present in the African cohort but absent in the European cohort completely. The African cohort also displayed much higher levels of anti-inflammatory molecules like SCFAs proving the hypothesis.

|How do Microorganisms evade host Immune System ?

Saumen Sain (III Year)

Immunity is the ability to resist a particular disease especially through preventing development of a pathogenic microorganism or by counteracting the effects of its products by the action of specific antibodies or sensitized white blood cells. Multicellular organisms possess very sophisticated defense mechanisms that are developed to counter the continuous microbial attack of the environment within the host. However, pathogens have achronic infections. There are numerous virulence strategies used by pathogens to infect humans with few general mechanisms that are being shared among the pathogens in order to exploit the immune system. The ability of pathogen to mount an anti-immune response in infected host organism can ultimately result in acute disease, chronic infection, or pathogen clearance. The ability of a pathogen to evade host immune system is termed as "Anti-Immunity".

An organism fails to establish itself and could not cause any disease if it is easily recognized and destroyed by the host immune system. However, the immune system does not always succeed in its task, as the invading organisms often evolves strategies for evading or suppressing the host's immune response to that organism.

There are different strategies evolved in different organisms against host immunity:

Various strategies directed against adaptive immunity

•**Molecular mimicry:** Microorganisms mimic the chemical or genetic buildup of the host so that they can reside in host cells without being attacked by the host immune system. The bacterium *Bacteroides*, for example, can avoid evoking an immune response in mice. *Mycobacterium paratuberculosis* has been demonstrated to use this strategy in animals.

•**Suppression of immune system:** In this system, the pathogens specifically target those immune cells that react against them. By doing this, the organisms prevent the body from mounting an immune response against them. Two notable bacteria that suppress the body's reaction against them are; *Mycobacterium leprae*, the causative agent of the disease leprosy, and *Mycobacterium tuberculosis*, the causative agent of the disease tuberculosis. In both cases, the Interleukin-2 response to the bacteria is reduced.

Immune suppression is a general mechanism found in many microorganisms. For example, Staphylococci produce toxins like Staphylococcal enterotoxins and toxic shock syndrome toxin-1 (Toxic Shock Syndrome) that act as superantigens. Superantigens are proteins that bind the antigen receptors of very large numbers of T cells, stimulating them to produce cytokines that cause significant suppression of immune responses. Extreme case of immune suppression is Acquired Immune Deficiency l so evolved various mechanisms to overcome innate and adaptive immunity, thereby causing disease or Syndrome which is caused by the infection of a viral pathogen (HIV).

Hiding inside cells: Various bacterial pathogens avoid host immune responses by hiding inside the immune cells. By doing so, they prevent antigen presentation which is responsible for evoking an immune response. These pathogens multiply inside these cells, and then further invade the host body after increasing its number. Microorganisms such as *Brucella sp.*, *Listeria sp.*, *Mycobacterium leprae* and *Mycobacterium tuberculosis* infect macrophages, the phagocytic cells that are normally responsible for destroying invading bacteria. *Mycobacterium leprae* can also invade and inhabit cells that are not a part of the immune system, e.g. skin cells.

•**By altering antigen:** One way in which infectious agents evade immune response is by altering its antigens. This is particularly important for extracellular pathogens, against whose surface antigens antibodies are produced. The methods by which a pathogen alters its antigens include antigenic drift, antigenic shift and programmed rearrangements in the DNA of the pathogen.

Normally, the antigen of an invading organism or a pathogen that is recognized by the host immune system exists on the cell wall or the outer membrane of that organism. Some organisms, however, release these antigens from their cell walls to float freely in the bloodstream, where they will eventually meet their antibody, and will bind to them, thus rendering those antibodies ineffective and useless against the invading organism.

Strategies directed against Phagocytic cells

Phagocytes, i.e. the Macrophages and Neutrophils, are the cells responsible for engulfing and destroying invading pathogens. Many microbial strategies for survival against phagocytes include:

•**Inhibiting Chemotaxis**: Chemotaxis is the chemical phenomenon by which the phagocytes are guided to the site of infection, so that they can begin their task. Some bacteria, such as *Staphylococcus aureus* produce toxins or factors like macrophage migration inhibition factor which inhibit the movement of phagocytes, preventing their accumulation at the site of infection.

•**Inhibiting Phagocytosis:** In order to phagocytose infectious agents, phagocytes must interact, internalize and express them. Some bacteria evade phagocytosis by preventing peptide presentation.

•**Killing the Phagocyte:** Some bacteria are capable of releasing toxins that are lethal to phagocytes. Thus, the invading organisms successfully destroy the phagocytes. E.g. *Mycobacterium tuberculosis*, *Streptococcus pyogenes*, Staphylococci and *Bacillus anthracis* (the bacterium that causes Anthrax).

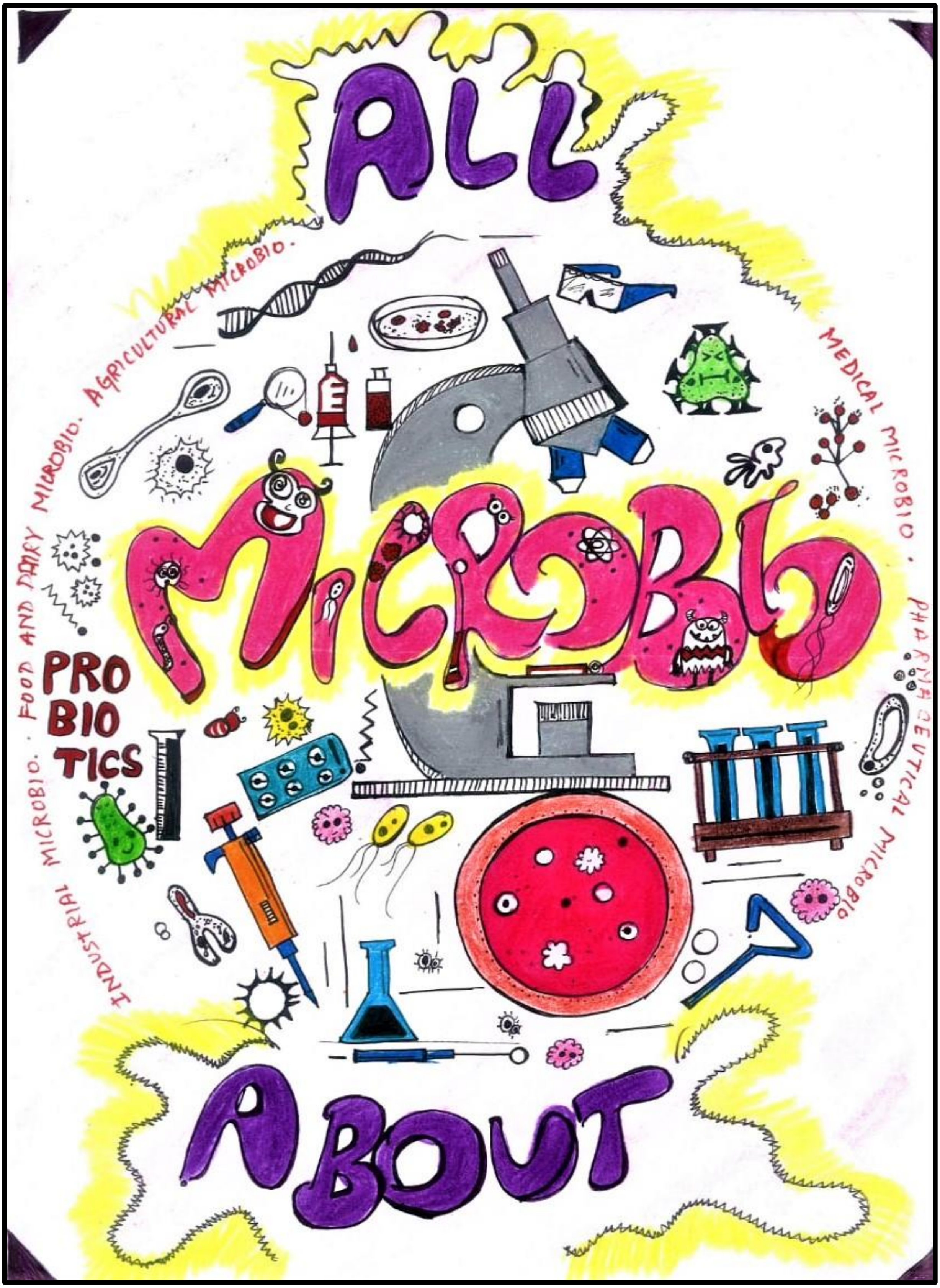
Viruses must replicate and produce viral proteins to cause infection. However, viruses which replicate rapidly can be readily detected by T lymphocytes, which control them in normal cases. Some viruses, however, can enter a state known as latency. In the latent state, the virus does not replicate and thus does not cause any disease and because there are no viral peptides present in the host system to get recognized, the viruses cannot be eliminated. Such latent infections can be reactivated in later part of life and result in recurrent illness. Herpes simplex viruses often enter latency.

Viruses such as Varicella zoster (chickenpox) and Herpes viridae (Herpes simplex viruses, Varicella Zoster virus, Cytomegalovirus etc.) evade the immune system by hiding in neuronal and non-neuronal cells, where they may persist for many years. They emerge as in pathogenic forms when the host resistance is low. This is the case also for bacteria i.e., *Borrelia burgdorferi* and *Burkholderia pseudomallei* (causative agents of Lyme disease and melioidosis, respectively) where reports suggested that symptoms of infection have re-emerged after few months to years (*B. burgdorferi*), and even up to 60 years (*B. pseudomallei*) after the initial infection.

Viral pathogens do need to invade a host cell to complete their replication cycles. One of the most dangerous pathogens to emerge in recent years is the human immunodeficiency virus (HIV) which hijacks the CD4+ T-lymphocytes to degrade the host's ability to counter the infection with a strong cell-mediated immune (CMI) response. The immune evasion methods used by HIV are so far-reaching, that they have obstructed progress towards the advancement of developing an effective vaccine. Firstly, HIV gains access to a naive subject in immune-privileged sites, such as the vagina or rectum, these areas are not well supplied by the lymphatic tissues; subsequently the virus utilizes co-receptors (CCR5/CXCr4) to gain access to CD4+ host cells. The outcome is a gradual loss of CD4+ T lymphocytes with gradual reduction of CMI function in the host and an increased susceptibility of the host to other infections (bacterial pneumonia) or to tumors (e.g. Kaposi's sarcoma). The host is also susceptible to the opportunistic pathogen infection. HIV cases are controlled by anti-retroviral drugs, while successful vaccines are still being identified and evaluated.

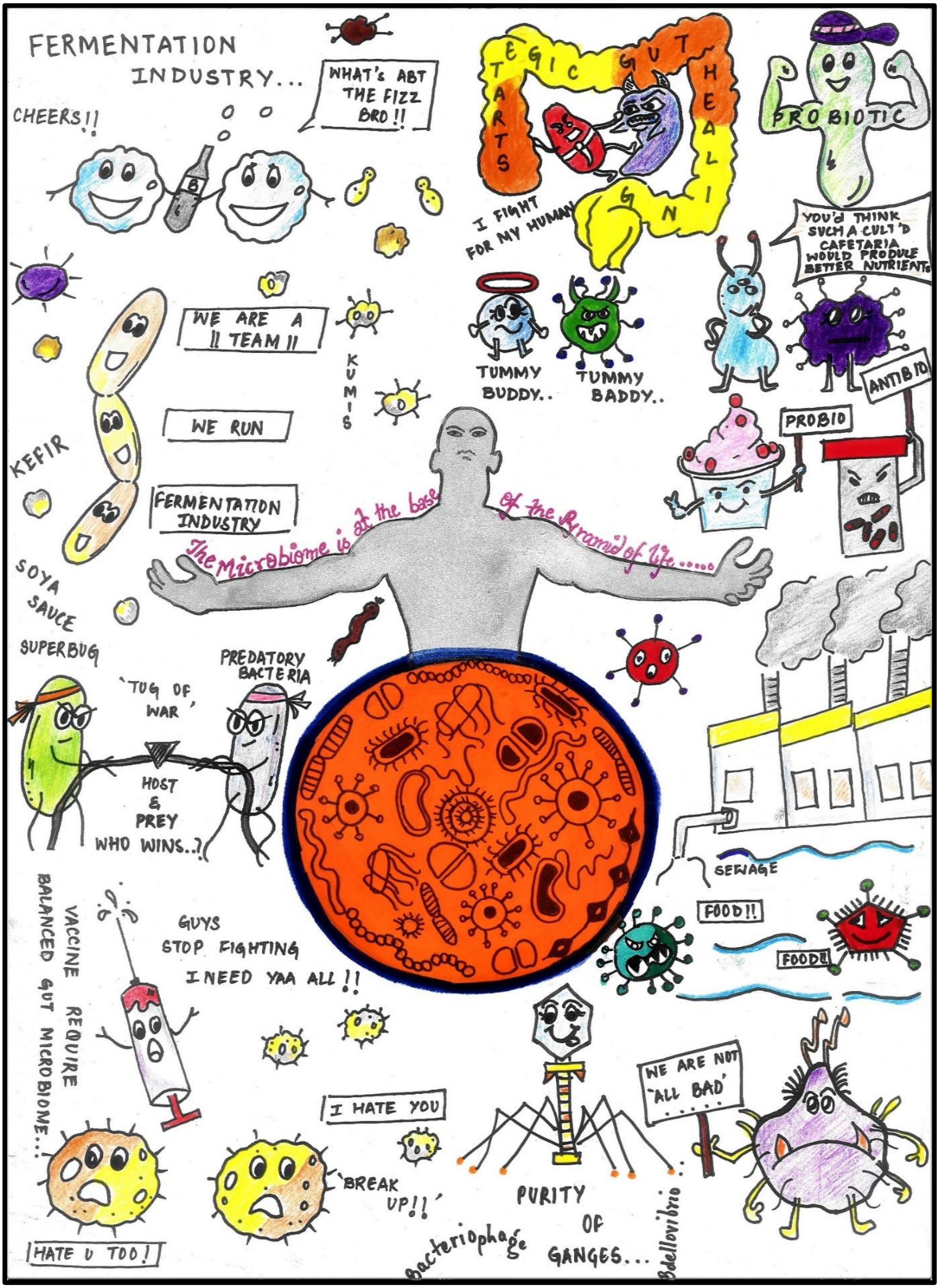
Hence, pathogenicity and immunity grow and develop as a result of co-evolution. The more complex and sophisticated our immune system becomes, more would be the probability for microbes to find some breakthrough for it. It's greatly remarkable that how these microscopic organisms have been able to detect the loop holes and deceive our immune system. Who knows by these method of co-evolution, we will be able to resist and develop immunity to some of the most fatal infectious diseases that claims lives today.

Some chosen entries from Doodle Making Competition...



Doodle by Riya Kashyap (II Year)

Doodle by Abhishek Behera, Aman Jaiswal and Sukamal Kundu (II Year)



Doodle by Amit Bhatt and Bhawna Sharma (III Year)

Doodle by Deepanshi Koul (III Year)

| How our Microbiome changes with seasons?

Himanshi Upadhyay (I Year)

Our microbiome has been shown to be influenced by change in seasons. The human microbiome includes microbes found on or in the human body. The bacterial community in our gut is not a static entity. In fact, just as we go about our daily lives within an evolving, dynamic, and interrelated environment, our gut bacteria do too. It is now being recognized that beyond the organs and systems in the body, external factors including seasonal variations, what we eat, the animals that we get exposed to, our social interactions, the weather experienced, our work-life balance, and even changes in the seasons can have an effect on the microbiome.

A longitudinal study on the gut microbiome of Hadza people of Tanzania, a tribe of hunter gatherers, has reported that the natural seasonal variations much influenced their gut microbial population. The Hadza activities largely revolve around food acquisition and are subjected to two distinct seasons: wet and dry. The microbiome of the Hadza people showed a cyclic variation.

The gut microbial population found to be present in the dry seasons was indistinguishable in the subsequent dry seasons too, with the intermittent wet seasons characterized by a different microflora. In another study conducted to look at the seasonal variations in the microflora, Actinobacterial population, the microbes associated with processing fat increased in winters, because of the intake of high fat, low fiber food while the Bacteroidetes population became more abundant in the summer with the latter known to bring about digestion of complex carbohydrates present in fresh fruits and vegetables.

The idea that some bacteria are only present during a season substantiates the beliefs that our body naturally changes and adapts with weather and temperature fluctuations. To seasonally support our gut, it is important to spend time doing outdoor activities, and eat seasonal food. This will expose our gut to seasonal microbes, boost immunity, and help reduce stress levels.

Finally, including prebiotic and probiotic-rich foods as well as frequent boost through a probiotic supplement help support our microbiome throughout the seasons. Our gut is one of the most important yet one of most easily overlooked components of our overall well-being and just like we see changes in our own mood, energy levels, appetite due to the changing of the seasons, our microbiome undergoes seasonal fluctuations too!

| Fecal Microbiota Transplant-food that goes out comes in!!

Siddharth Trigunayat (I Year)

The number of studies conducted on the human microbiome ad gut microbiome in particular have precipitated. The studies have helped us in understanding the role of gut microbiome to comprehend the therapeutic potential of its manipulation. Fecal microbiota transplant (FMT) is one such therapy which aims to change the microbial composition of the recipient and confer health benefits. It involves the administration of a solution of the fecal matter from a donor into the intestinal tract of a recipient. As gross as it may sound, but it is being recognized as a very essential therapy in cases of various chronic diseases.

It has become well established that the gut microbiome is vital to us. There are approximately 10^{14} microbial cells in the entire gastrointestinal tract, and all are involved in essential processes like enhancing the immune response of the host, metabolism, protecting against pathogens and maintaining homeostasis. There are cases when there are alterations in the gut microbiome, a condition called as ‘dysbiosis’, which leads to distortions of these important functions. Even though the gut microbiome shows resilience, continuous perturbations due to environmental factors etc. may cause it to lose its resilience. Fecal microbiota transplant seeks to restore this balance of the gut microbiome by introducing the fecal sample from a healthy donor. The first description of the use of feces as a therapy was given by Ge Hong in the fourth century in China to treat variety of conditions like diarrhoea. In 1958, Eiseman and colleagues also described the use of fecal enemas for the treatment of pseudomembranous colitis, marking the introduction of FMT into mainstream medicine. The process usually involves selecting a donor without a family history of autoimmune, metabolic and malignant diseases and, screening for any potential pathogens. The feces are then prepared by mixing with water or normal saline, followed by a filtration step to remove any particulate matter.

The mixture can be administered through a nasogastric tube, nasojejunal tube, esophagogastroduodenoscopy, colonoscopy, or retention enema. Fecal microbiota transplant is used in the treatment of diseases causing or caused by dysbiosis, like inflammatory bowel disease, obesity and *Clostridium difficile* infection (CDI), especially recurrent CDI (rCDI). The conventional treatment of CDI involves the use of the antibiotic vancomycin, a broad spectrum antibiotic that kills a number of microbes leading to dysbiosis and is therefore not very effective in treating rCDI.

Alternately, fidaxomicin which has a narrow spectrum and selectively targets *C. difficile* is used for the treatment. But, FMT is far more effective with a cure rate of 81% as compared to a low cure of 31% of vancomycin and fidaxomicin.

FMT is also quite effective in treating obesity amongst humans. It has been found that there is a marked difference in the microbiota of an obese individual and a lean individual. A study conducted by Turnbaugh and colleagues reported that colonization of a germ free mice with the obese microbiota lead to increased adiposity as compared to the mice colonized with lean microbiota. Moreover, when the obese-transplanted mice were co-housed with the lean-transplanted mice, the obese-transplanted mice were protected from developing the increased adiposity and body mass. This was found to occur through coprophagy (feeding on dung) and was associated with transfer of the lean microbiota (and Bacteroidetes, in particular) into the obese-transplanted mouse.

FMT has hardly any adverse affects, as stated in the experiments conducted in the past. The only few adverse effects are diarrhoea, constipation, post-FMT which lasted not more than 2 days. In the entire set of experiments conducted (total number of subject used is not given), there has been only one case of death and

2 cases of norovirus infection during colonoscopy. This makes FMT an efficient and safe treatment. However, it is not widely recognized by medical practitioners. In certain countries like USA and Canada the treatment can only be performed with the patients consent and the donor should either be known to the practitioner or the recipient. The US food and drug administration also requires the practitioner to obtain an investigational new drug application to administer FMT. FMT clearly highlights how important even the human excreta can be for the purpose of treating our own problems. Even though currently the treatment is not much in practice, but with advancement of technology, one can certainly hope that this would come up as a viable treatment strategy.

| The Curse of the Pharaoh

Ashmit Mittal (II Year)

Ancient Egypt is a land of mysteries. Archaeological surveys have uncovered remnants of arguably the greatest ancient civilizations. Ancient Egypt was a land of beliefs, strange practices, rituals, gods and spooky curses. It would be safe to say, there was never another civilization which lived so focused on the afterlife. Egyptians believed that a person departing to the afterlife requires all the basic necessities that he needs in the living world. These possessions according to their beliefs are necessary for him to survive and reach the heavens to finally reunite with the gods, or suffer in hell for eternity. This was no simple process. The burial chamber of Pharaoh Seti I reveals intricate details of the journey to the afterlife.

Pharaohs were the kings of Egypt. They built huge monuments known as Pyramids to house their mortal remains and possessions. The burial chambers were stashed with unimaginable amounts of gold and semi-precious stones which made these chambers very attractive to Tomb Raiders during the recession era. Most of the tombs were looted thousands of years ago, before archaeologists ever found them. It seemed like the fear of curses and gods were not enough to reason with the urge for survival. Most of the tombs uncovered to this day had very little wealth than recorded in ancient scriptures. However, the tomb of a boy king, Pharaoh Tutankhamun is the only exception. The tomb was unusual because it was left untouched for thousands of years and perhaps the only one tomb with an ancient seal intact. The discovery of this tomb by Howard Carter under the sponsorship of the George Edward Stanhope Molyneux Herbert, the 5th Earl of Carnarvon sparked a renewed interest in Egyptology. However, the fate of the team involved was not so good. Many of them met mysterious deaths beginning with Lord Carnarvon, who died of a mosquito bite on the cheek and his dog who died at the exact time thousands of miles away. It was later found that the Pharaoh had a similar lesion at exactly the same spot. Remains of DNA of malarial parasites were found on the mummy suggesting malarial parasite infections. These deaths, further fuelled by authors and media created ‘The Curse of the Pharaoh’.

But the question is ‘Was this a curse or a fateful accident’? Accounts of such curses are rare and there was no such curse inscribed anywhere in relation to Tutankhamun. Curses have been found in the tombs of the old kingdom era. Some such examples are that of Ankhtifi and Khentika Ikhekhi.

What was this curse that the high priests had put to protect the integrity of the tomb? Was it something elemental or something supernatural?

To analyze the matter logically we must take into consideration the possible conditions inside a stone room that has been devoid of fresh air for thousands of years. One feature that would attract eyes of any microbiologist would be the large amount of organic matter present within. The tombs did not only hold the mummified bodies, but also other foodstuffs like meat, fruits and vegetables. All these food stuffs are -

reportedly spoiled in the modern world by bacteria and fungi. Also the stone build and the dark interiors would have only provided a dark and moist chamber in the face of a desert. A heaven for microbial growth. Right??

In 1922, Lord Carnarvon, British sponsor of archaeology died after visiting the king Tutankhamun's tomb. It was later found that some tombs carry molds including two dangerous species *Aspergillus niger* and *Aspergillus flavus*. Some tombs may also have some species of *Psuedomonas* and *Staphylococcus*. Scientists also have detected ammonia gases, formaldehyde, and hydrogen sulfide inside the sarcophagi indicating microbial activity. The droppings of the bat inhabiting the tombs also contained fungal spores, which might have helped in inoculation.

The curse of the pharaoh might have been an instrument of keeping away the raiders. The curse might have a very simple explanation, but no matter what, the idea of a curse will never fail to attract public imagination and will thus always live on protecting the king in everlasting sleep.

| Human Skin Microbiome

Preetha Goswami (I Year)

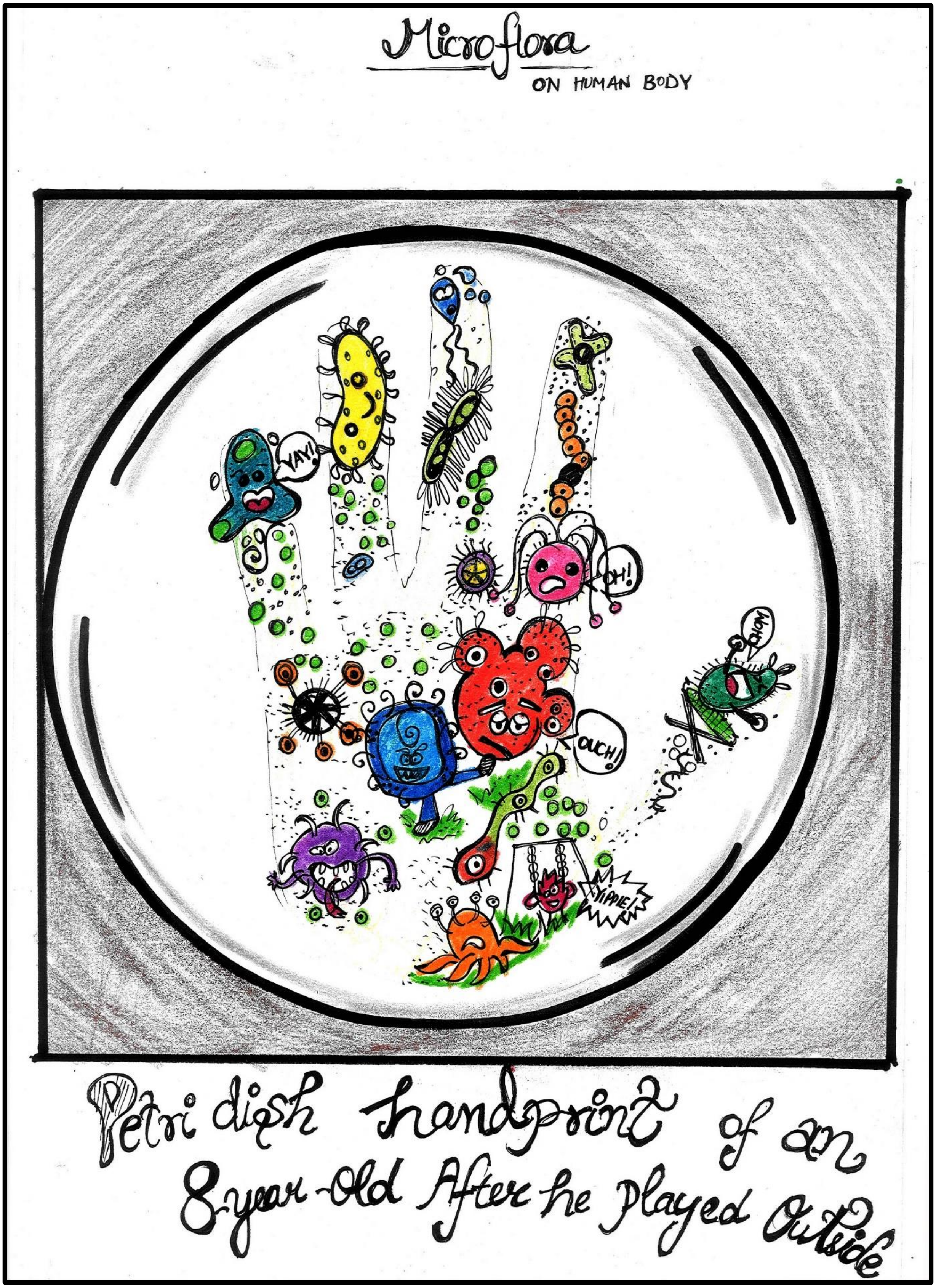
The skin is the largest organ of the human body and despite being poor in nutrients and being acidic, it is home to a variety of microorganisms like bacteria, fungi and viruses which constitutes the human skin microbiota. Skin microorganisms have adapted to utilize the limiting nutrients available on the skin. In a healthy adult, the skin microbiota remains stable over time, despite environmental perturbations. The primary taxonomic groups of skin microbial community include Actinobacteria, Firmicutes, Proteobacteria, and *Bacteroides*. The microorganisms present on the skin serve as a physical barrier to prevent the invasion by pathogens. When the skin barrier gets broken or when the balance between commensals and pathogens is disturbed, skin disease or even systemic disease can result.

Human skin sites can be categorized as sebaceous (oily), moist or dry based on their physiological characteristics. Different areas of the skin are colonized by different types of microbes depending upon their adaptability to a certain region. Sebaceous areas, such as the back, face, area behind the ears, tend to be colonized by the lipophilic bacteria, *Propionibacterium*. The moist skin areas tend to be colonized by bacteria such as *Staphylococcus* and *Corynebacterium*, the organisms which are known to be present in humid environments. Although dry areas of the skin have a lower bacterial load, the diversity of bacteria harbored is much higher than sebaceous and moist sites.

Drier areas contain greater amounts of Proteobacteria and Bacteroidetes, in comparison to moist and sebaceous sites. Certain species of bacteria are responsible for body odour. It is caused by bacteria which can break down sweat and is largely linked to the apocrine glands. In our day-to-day lives we tend to use certain cosmetics on our skin in the forms of lotions, creams or as means to enhance beauty. These cosmetics contain chemicals that interact with the skin microbiome. Many of these cosmetics contain agents that erode the microflora of the skin, and can cause diseases in the long run. The exposure of skin to twenty-first century cosmetics, soaps, antibiotics, steroids and showers,

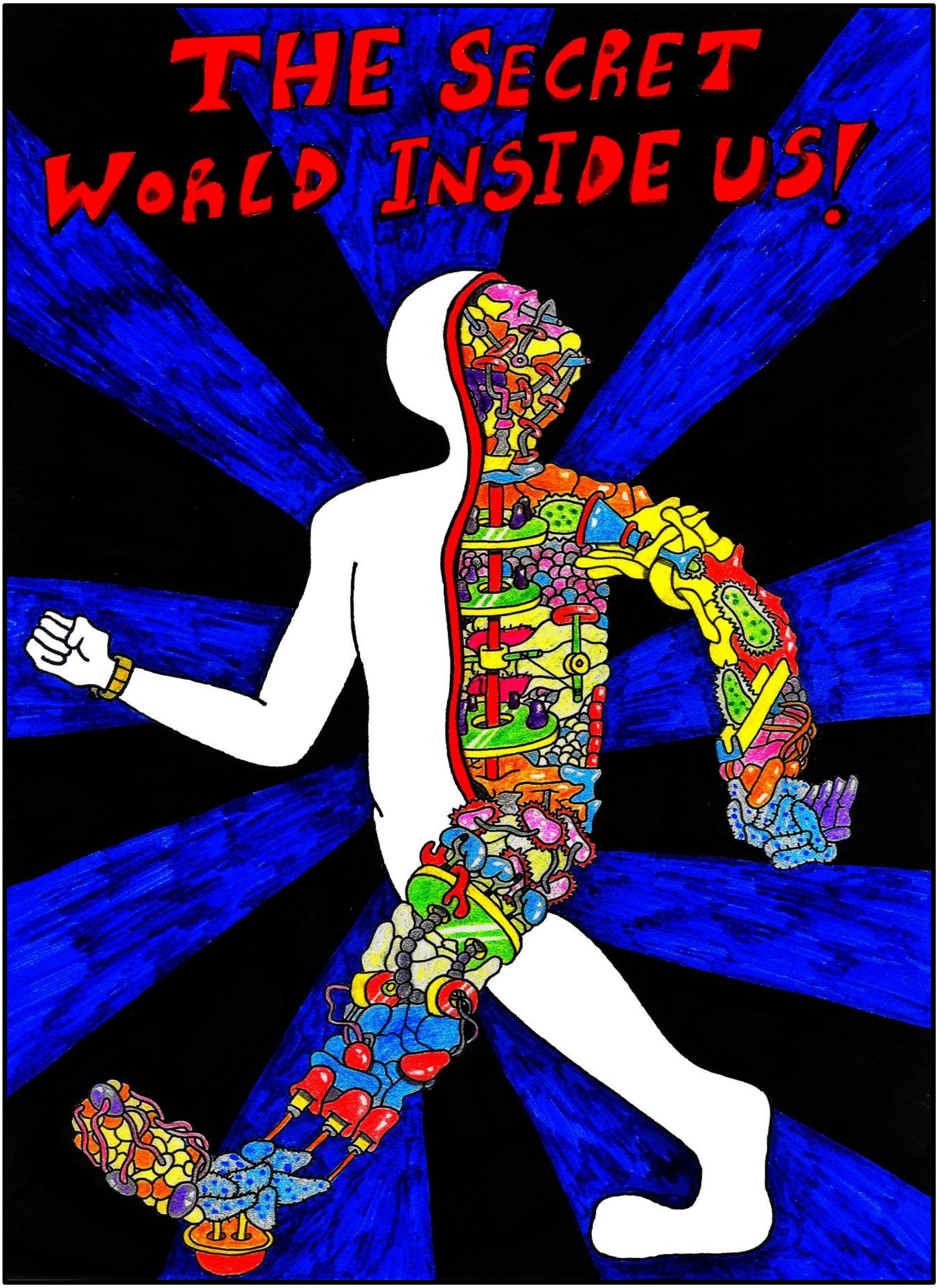
does appear to have altered the natural microflora of humans in the modern world. This alteration in a number of cases, has been a cause of increased susceptibility to diseases and infections.

“ Our Microbeprints”



Doodle by Riya Kashyap (II Year)

"Everyone has got a microbial side"



Doodle by Neelansh Kumar (III Year)

| Human Microbiome Project

Bhawna Sharma (III Year)

Microbiome refers to the totality of organisms, their hereditary elements (genome) and their environmental interactions in a particular environment. The human microbiota refers to the collective genomes of microorganisms inhabiting the human body residing within human tissues and biofluids, including the skin, mammary glands, placenta, seminal fluid, uterus, lung, saliva, oral and gastrointestinal tracts. The human microbiome makes about 1-2 % of the body mass of an adult. It includes bacteria, members of domain Archaea, yeasts, single-celled eukaryotes and various helminth, parasites and viruses, including bacteriophages. Microorganisms present under normal circumstances and that do not contribute to any disease, are sometimes deemed normal flora or normal microbiota. It was considered that there are about 10 times as many microbial cells and 100 times as many microbial genes in the human body as there are human cells, comprising around 100 trillion bacterial cells in human microbiome which are involved in human health and disease. A research initiative was launched by United States National Institutes of Health (NIH) known as the human microbiome project (HMP) and described as "a logical, conceptual and experimental extension of the Human Genome Project. Integral elements of the HMP were culture-independent methods of microbial community characterization, which includes metagenomics as well as extensive whole genome sequencing." Various institutions i.e., Stanford University, the Broad Institute, Virginia Commonwealth University, Washington University, Northeastern University, MIT, the Baylor College of Medicine, and many others are involved in HMP.

HMP was conducted in two phases, the first phase (HMP1) launched in 2007 mainly focused on identifying and characterizing human microbial flora in order to develop a reference set of microbial genome to conduct initial characterization of the human microbiome. The HMP1 examines the association between disease and changes in the human microbiome, helpful in designing new methods and tools for computational analysis and also for establishing a resource repository. The second phase, the Integrative Human Microbiome Project (iHMP) introduced in 2014 with the idea of generating resources to designate the microbiome and exemplify the roles of microbes in health and disease states. It was a 5 year project with a total budget of $115-$150 billion. HMP is a global and interdisciplinary project with many historical milestones and a variety of achievements characterizing the human microbiome project. A major milestone of the HMP was declared by the NIH director Francis Collins. The announcement included many coordinated articles published in Nature and several reputed journals including the Public Library of Science (PLoS) on 13 june 2012. Around 5,000 samples were collected from different tissues and their DNA analyzed. Using 16S rRNA sequencing, the microbial genome were sequenced and identified. The HMP project revealed some important facts that microbial genome in humans confers for their survival than their own genes and their metabolic activities seems to matter more. Some major work and development that were funded by HMP includes, database systems allowing systematic organization, storage, access, search and annotation of data. Databases/Methods such as the Integrated Microbial Genomes database, the Genomes OnLine Database (GOLD), CharProtDB, development of tools for comparative analysis, new methods and systems for assembly of massive sequence data sets are well included in the list.

Advancement in microbiome engineering is greatly linked to emergence of synthetic biology. Synthetic biology may lead to the engineering of smart microbes that can detect and treat disease. This approach could be potentially applied to selectively eradicate strains from microbiota for microbiome engineering. Some strains of *E. coli* has been engineered.

These *E. coli* sense, seek and specifically kill pathogenic *P. aeruginosa*. It interrupts signaling between microbes as a means to alter microbiota composition. For instance, *E. coli* was modified to overproduce AI-2 signaling molecules which can rebalance the Firmicutes/Bacteroidetes ratio caused by streptomycin-induced dysbiosis in mouse intestine.

Microbiome research has made great progress in the past decades. Consequently, despite being a relatively new field, microbiome engineering has been successfully employed to alter microbiota. With continuous efforts in understanding and manipulating microbiome, the microbiome engineering will be a mainstream strategy for improving human health and agriculture in the coming future.

HMP also lead to identify the distinctive adaptations of segmented filamentous bacteria (SFB), job of Verrucomicrobia in soil bacterial networks, a connection between oral microbiota and atherosclerosis, microbial identification of diseased and healthy gut.

Human microbiome project has been the go-to in numerous clinical and pharmaceutical applications, first it gives the database of data which serves as reference for future researches, recognizes the microbiota of healthy and diseased human body. Further, a total comprehension of the decent variety of organisms make up the human microbiome could prompt novel treatments. For instance, it is conceivable to treat a bacterial disease brought about by "awful" bacteria by advancement in the development of microscopic organisms. Microbiome transplants are as of now being utilized to battle certain sicknesses, for example, *Clostridium difficile* contaminations, to build up progressively refreshing bacterial populations. As per HMP information it was investigated that pregnant ladies have less species variety in vaginal microbiome during preparation of birth, likewise youngsters with unexplained fevers have high viral DNA load in the nasal microbiome. The HMP information and strategies clarifies the job of microbiome in the digestive tract, skin, regenerative organs and youth disorders.

The HMP has significantly improved our insight into the microorganisms in human populace, and gave a reference data of genomes; lab conventions, computational techniques, which at last empowers our knowledge in relationship to the human-related microbial networks and sickness. Further research would definitely allow us to alter the microbial genome more easily than host genome in order to maintain and improve human health.

| Aeromicroflora

Sreyashi Nath (II Year)

Aeromicroflora is the collection of microbes living and interacting with the aerosphere. There are countless microscopic organisms living in air. These are vegetative cells and spores of bacteria, fungi, actinomycetes and algae, viruses and protozoan cysts. Their population size is less than that found in oceans and soil. Aeromicrobiology is the branch of science that deals with the study of living microorganisms suspended in the air. It includes study of aerosolization, formation of aerosols and their transmission and deposition in soil and study of respiratory diseases. Microorganisms are suspended in air currents and travel long distances with them. They are observed to cause a wide range of airborne diseases. They contribute to indoor aeromicroflora which is responsible for biodeterioration of storage materials, equipments, library materials and pharmaceuticals.

Aeromicroflora plays a significant role in environment i.e., as cloud condensation nuclei and alteration of atmospheric chemistry. They are found in the cloud pockets, and are involved in the formation of rain water from clouds and also in the cloud formation. Tropospheric microorganisms were isolated from the clouds over France, with up to 8×10^4 CFU/mL of cloud water. These microorganisms generally grow at low temperatures.

According to Schnell, the bacteria attached to mineral particles are actually responsible for ice nucleation rather than mineral particles themselves. *Pseudomonas spp*. have been found to contain ice nucleation gene and the corresponding protein is present on the outer membrane which helps in ice crystallization.

Stratospheric isolates include two bacteria *Bacillus simplex* and *Staphylococcus pasteuri* and a fungus *Engyodontium album*. Partitioning between different vertical segments could result from thermal boundaries and thin buffer zones. The environmental parameters affecting their survival are oxygen stress, ionic stress, temperature stress, moisture stress, UV radiation etc. Sunlight with little water causes death of many micro-organisms. High levels of oxygen stress and its reactive forms causes damage to DNA, inactivates the proteins and also cause water shearing and ion displacement. Both high and low temperatures are damaging to microbes. Higher temperature causes denaturation of enzymes and proteins, and lower temperature causes ice crystal formation. High moisture causes death and low moisture damages the lipid bilayer. Short wavelength radiations and X-rays cause single strand and double strand breaks in DNA and also affect genomic expression. Spores are more abundant because of the ability to tolerate UV radiations, scarcity of nutrients and desiccation. Certain gases such as hydrogen sulfide, sulphur dioxide, carbon monoxide, chlorine, hydrogen fluoride also affect microflora. Some aero-microorganisms may be pathogenic to plants, animals and humans. Airborne particles are a major cause of respiratory ailments causing allergies, asthma and pathogenic infections of respiratory tract.

Fungal spores are important agents of plant diseases and dissemination of saprophytic fungi. During a sneeze, millions of tiny droplets of water and mucus are expelled out, dry rapidly to droplet nuclei of 1-4 micrometers containing viruses and bacteria, and this is a major cause of transition of several diseases in humans.

Mark Hayes and team used fingerprinting techniques to isolate microbes from air. Arguably, it is very important to perform routine air sampling to monitor the aeromicroflora for public awareness about the air quality. Air sampling is used in crop pathology for disease identification, so that farmers can apply fungicide as when required. Hospitals can also use air sampling methods to monitor the presence of specific allergens.

This elucidates that the aeromicroflora plays an important role in maintaining an ecosystem. The role played by aeromicroflora for dispersion of air-borne diseases is one of the most fatal one.

| Plant Microbiome

Priya Verma (I Year)

Plant microbiome is the microbial community that interacts extensively with a plant. Plant microbiome has received considerable attention in the recent years as it is a key determinant of plant health and productivity. The functional importance of the plant microbiome is the acquisition and mobilization of nutrients, out-competing the pathogens, plant stress alleviation, plant growth promotion, co-metabolism and degradation of toxins. Manipulation of the plant microbiome has the potential to reduce the cases of plant diseases, increase agricultural production, reduce chemical inputs and reduce emissions of greenhouse gases, making it a more sustainable agricultural practice. In fact it is increasingly being recognized as vital for sustaining the world's growing population. The focus of this panegyric are rhizosphere (narrow region of soil influenced directly by root secretions), phyllosphere (portion of plant above the ground) and endosphere (internal tissues). The plant microbiome can be present either inside (called endophytes) or on the outside of plant tissues (called epiphytes), performing various plant beneficial activities including bio-control of potential plant pathogens and promotion of plant growth. An extremely important component of the plant microbiome are plant growth-promoting bacteria (PGPB) that are frequently found in the rhizosphere, phyllosphere, and endosphere of the plant. The rhizosphere includes largely soil-derived microbial diversity, influenced by deposition of plant mucilage and root exudates. Much of the nutrient cycling and disease control required by plants occurs immediately adjacent to roots due to the root exudants and microbial communities present in the rhizosphere. Of particular interest in the rhizosphere are plant-growth-promoting rhizobacteria, which act through a variety of mechanisms. Other bacteria also act to defend the plant from various phytopathogens, for eg. *Pseudomonas fluorescens*, which produces the antifungal compound diacetylphloroglucinol (DAPG). Nitrogen-fixing bacteria, including the free-living (such as *Azotobacter spp.*) and symbiotic (such as root-nodulating *Rhizobium spp.*) nitrogen fixers provide fixed nitrogen to the plant. Also many bacteria are capable of solubilizing phosphorous-containing minerals, increasing its bioavailability. Microbial manipulation of plant hormones like auxins, gibberellins and ethylene can be used for promoting plant growth and increasing tolerance to stress too.

In contrast to rhizosphere, the phyllosphere is relatively nutrient deprived and subject to extreme fluxes in temperature, radiation and moisture. These abiotic factors also affect the phyllosphere microbiome through changes in plant metabolism. Endophytes are fungi or bacteria, which during all or part of their life cycle, invade the tissues of living plants and cause unapparent and asymptotic infections entirely within plant tissues. These are generally regarded as non-pathogenic as they do not cause any visible symptom of disease. Some of them can be latent pathogens that may cause a disease depending on the environmental conditions and/or host genotype. Endophytes are thought to be a sub-population of the rhizosphere microbiome, but they also have characteristics distinct from rhizospheric bacteria, implying that not all rhizospheric bacteria can enter plants, and/or that once inside their hosts, they may change their metabolism and become adapted to their internal environment.

Microbes in these niches may establish beneficial, neutral or disadvantageous associations of varying degrees with their host plants. Specific interactions between microbes and model plants, such as in Rhizobium-legume symbiosis, are well understood, but the majority of the plant microbiome, and its role in the phenotype of the host, remains largely unexplored.

The microbiome is strongly influenced by the plant genome and is sometimes considered as an extension to form a second genome. The plant genome and the microbiome together make up the pan-genome. Genetic amendment of plants with an aim to make it disease resistant may have unpredicted consequences for the rest of the microbiome. Given the pertinent role of plant microbiome in plant health, productivity and the biogeochemical cycles, it is important that their role be considered as much as the plant itself.

| Existence in desierto de Atacama

Ayush Upadhyay (II Year)

The desert of Atacama found in the great lands of Chile, is the true epitome of what we call “Heaven on Earth”. With its innately acidic and oligotrophic soil which undergoes great temperature and UV fluctuations, it is considered to be the closest analogue of Mar’s surface.

It mimics the low atmospheric pressure of Mars with elevations of more than 6000 m above the sea level. Even with such harsh conditions for survival, life has still found a way to exist in this perdition. This panegyric is dedicated to the undaunted microorganisms surviving the worst possible conditions on the planet. One of the strongest candidates among the existing microbiota of Atacama is a yeast belonging to the genus *Naganishia*. It eludes high levels of UV radiation and sub-zero temperatures. The genus is also famous for surviving the ozone hole in the Antarctic region.

Being stuck in such a nutritionally starved environment, these organisms are adapted to utilize the most unconventional sources of energy. These include H_2, CO and CH_4. At the elevation of 6030 m above the sea level, the lands are covered with dry tephra (soil) and are dominated by *Actinobacteria*. As we move to regions at higher altitudes, phylotypes of *Chloroflexi*, including the relatives of KT clade and B12-WMSP1 clade, take over the habitat.

The beacon of hope for these drylands is found near fumaroles, the openings near the volcanoes which are oozing with sulfurous gases and steam. It may seem counter intuitive, but these little scabs on the earth’s crust are also rich in carbon, nitrogen and water. As a matter of fact, the highest species richness has been observed in fumaroles at elevations of about 6049 m above sea level. These places had over 800 16S rRNA Operational taxonomic Units (OTUs) as opposed to just 61 in the nearby dry tephra. The presence of bryozoans (like the infamous Tardigrades) and vampyrellid amoeba in these areas indicate existence of established complex food webs. It is probably because of the stable warm temperature and consistent water supply, the fumaroles provide suitable microbial habitat comparable to that of the forests and agricultural soils.

The existence of fumaroles on Mars has not yet been confirmed, but it has been firmly acknowledged in the planet’s history. Fumaroles are a unique site in quest of the forms of life that may have roamed the red dunes of the Martian soil.

| Microorganisms living in Outer Space

Nitesh Kumar (I Year)

Microbial existence in outer space was not very well researched until recently Russian scientists have detected the presence of living bacteria from samples extracted from the international space station. They extracted these living materials from the Russian space station Mir and ISS with the help of cotton swabs and sent these samples on earth for further studies. During the launch of ISS module, these bacteria were absent indicating their presence in outer space. However studies suggested that they are of no danger for the humans living on the ISS. According to the recent research it has been found that over 250 different species of bacteria and fungi survive and thrive even in the harsh environment of outer space. The first evidence of the impact of space microbiology was retrieved from the orbital space station, Mir on which these microbes grew as a film over its window and reduces visibility. When this space station returned to earth the scientists were surprised to find numerous bacteria and fungi growing on the window surface. In fact the microorganisms not only produced a film of microbes, but also corroded the window.

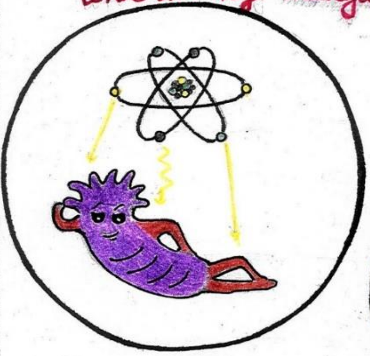
Further, when space station was again sent to the outer space it was thoroughly sterilized with toxic gases, but still colonies of bacteria and fungi were recovered. These colonies might have survived the toxic gases by hiding under the areas where the gases could not reach. Scientists found that these bacteria, initially hiding in such spaces, grew and increased in number. It was found that the cosmic radiation does not kill these microorganisms, in fact they caused mutations, allowing these microbes to divide at much faster rate than normal bacteria. Researchers also recovered both culturable and non culturable microorganisms from the stratospheric samples. With the help of fluorescence techniques, non culturable materials have been detected. Moreover, 16S rRNA of some culturable microorganisms have also been sequenced.

Some scientists believe that these small sized microbes of less than 1 micrometer may have been lifted from the ground, while others believe that these clumps of bio materials (bacteria /nanobacteria /viruses) are far too heavy to be lifted from the earth. In recent studies, it has been found that the microbiome of ISS mainly consists of human associated microorganisms such as *Corynebacterium* and *Propionibacterium* suggesting that the specific skin-associated microorganisms are the major contributors to the ISS microbiome.

Some bacteria failed to tolerate these harsh environments of outer space. A group of bacteria known as OU-20 which resembles the blue green algae genus *Gloeocapsa,* survived on the outer surface of ISS for about one and half year. Researchers now have the samples of these hardly survivors back on earth for further studies. In recent years, NASA performed many experiments in which the bacteria- laden rocks were installed on the outside of the international space station. These experiments helped scientists to see how the microorganisms react to the harsh environments of outer space i.e., extreme temperature, UV exposure and cosmic radiations.

“The Big Boys of the survival game”

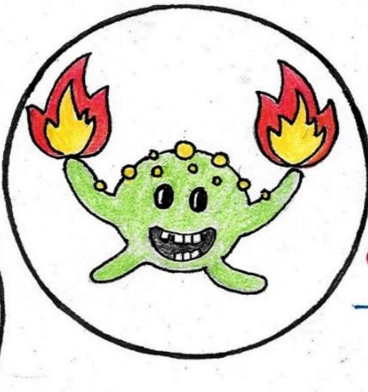
When radiation enters, I fight
Protect my DNA,
With all my manganese inside....
a *Deinococcus radiodurans*



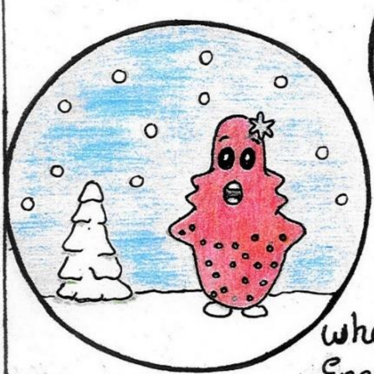
Deep under the sea
I am pressurised by thee
Still I survive
Not with my brain
But my tightly packed
Cell Membrane....
–a *Halomonas salasia*

Somewhere On The Planet EXTREMOPHILES Reign Too ...

In dark &
Vaccum
I survive &
Bloom....
a *Gloeocapsa*



When its too hot outside
I still replicate and transcribe
My enzymes and protien doesn't
easily denaturise....
–a *Sulfolobus acidocaldarius*



When temperature is low, I do not sleep
Enzymes and cell membrane, are my swords & shield....
– a *Psychrobacter urativorans*

Doddle by Arnab Kakati, Priyam Chopra and Nitesh Kumar (I Year)

“Strategic warfare”

Doodle by Bhawna Sharma (III Year)

|The Living Antibiotics: Treatment of Superbugs by Predatory Bacteria

Sweaksha Langoo (II Year)

Antibiotic resistance has become an extremely grave problem in today's world. Before the first antibiotic (penicillin) was discovered in 1928, millions of people lost their lives to relatively simple microbial infections. Therefore, the discovery of antibiotics revolutionised the field of medical science. A study by the World Health Organisation (WHO) estimates that antibiotics, on an average, may add upto 20 years to a person's life. However, the overuse of antibiotics has led the bacteria to develop resistance against these antibiotics, leading to the evolution of Superbugs which cannot be treated by antibiotics.

Presently, researchers at a South Korean Institute, Ulsan National Institute of Science and Technology (UNIST) have undertaken the problem of antibiotic resistance and are aiming to fight "fire with fire" by introducing Predatory Bacteria, bacteria that attack other bacteria and cause no harm to the human cells in the process. Professor Robert Mitchell, the team leader of UNIST researchers, prefers the term "Bacteria eating bacteria" for these predatory bacteria. Along with his colleagues, he is working to synthesize a natural compound called Violacein to tackle *Staphylococcus spp*. (a group of around 30 different bacteria known to cause skin infections, pneumonia and blood poisoning). Infections caused by some antibiotic resistant *Staphylococcus* bacteria like MRSA (methicillin-resistant *Staphylococcus aureus)* are hard to treat.

Violacein is a 'bisindole': a metabolite synthesized by bacteria from the condensation of two molecules of tryptophan (an essential amino acid used in many organisms to ensure normal functioning and avoid illness and death). The colour of 'violacein' is a vibrant shade of purple. It is of particular interest to researchers because of its anticancer, antifungal and antiviral properties. During their study on violacein, researchers observed its ability to stop bacteria from reproducing and when used in right doses, it could even kill the multidrug resistant *Staphylococcus aureus*. Violacein can also work well if conjugated with previously existing antibiotics.

The team of researchers are also studying the predatory properties of the bacterium *Bdellovibrio bacteriovorus*. This bacterium is normally found in river water or soil. It is an obligate predator of bacteria. It attacks the bacterial cell and enters inside it and carries out division. It must predate on other bacteria to survive, grow and divide. Once inside the host cell, it eats it from inside out, ruptures the host's cell membrane to exit and then finds the next host to attack. Until now, it has been found to be harmless to human cells and can attack over 100 different pathogenic types of bacteria.

Bdellovibrio and alike organisms (BALOs) are Deltaproteobacteria. They prey on other Gram-negative bacteria for their survival. Many scientists have found their use as possible biological control agents in environment and in medical microbiological settings. Their strong association with biofilms is being studied and these studies have shown the efficient way of predation of these naturally occurring bacterial communities.

Periodontal infections are emerging as interesting targets for application of BALOs as biological Gram-negative bacteria and therefore potentially susceptible to BALOs antimicrobial agents. The elimination of causative pathogens of these Periodontal diseases during the treatment will improve the clinical response. But, mechanical periodontal therapy alone was shown to be an unpredictable method of elimination of periodontal pathogens. Also, treatment of these diseases is complicated because of a number of factors like growing resistance to antibiotics and inefficiency of antimicrobial agent to penetrate dental biofilms. Therefore, it is important to think of alternatives with these factors in consideration.

Recently, it has been found that BALOs reduce the overall levels of Gram-negative pathogens significantly in the oral cavity. Following are some of the important advantages of using BALO's in treatment of oral infections:

- Favourable commensal periodontal microbiota show resistance to BALO predation,
- Easy attack on bacteria lacking resistance to predation,
- Strong immunological response is not produced.

These properties of BALOs complies almost all the necessary requirements for an oral biological antimicrobial agent.

There are also various drawbacks associated with the use of BALOs

- BALOs are not always successful in killing their prey even when present in much higher concentration as compared to their prey. The resistance, however is due to a plastic phenotype and is not genetically encoded and a completely resistant mutant prey has not been yet isolated. The fact that the resistance against BALOs is not stable and/or permanent suggests involvement of a cellular component present in prey which is necessary for their survival.
- They are unable to attack Gram-negative bacteria having an S-layer on their surface. The physiological status of their prey and the presence of other bacteria also affect their activity either in a positive or in a negative manner.
- These bacteria are strict aerobes. This property limits their use to an oxygen rich environment and restricting their potential use in oxygen-limited environments, such as gut, urinary tract or periodontal pockets.
- Indole, a well-known metabolite produced by *E. coli* and many other bacteria, was found to affect the predability of BALOs.

In conclusion, BALOs prove to be promising agents for treatment of disease-related biofilms and particularly, periodontal infections. Its extensive applications offer an exciting path for further research where *in vivo* studies should be the focus..

| Hospital Microbiome

Shreya Sharma (II Year)

Hospitals are the institutions for cure, but do they really live up to their responsibilities? Do the people seeking treatment really get cured or take home agents responsible for Hospital Acquired Infections? This is a blazing question that needs to be addressed by the authorities.

Indoor environment of a hospital. is a very intimate ecosystem for the microorganisms. There is a huge difference in the microbiome of a new hospital not under operation and that of a hospital where patients visit. In a functional hospital there is a significant increase in the relative abundance of the human-skin associated Genera *Corynebacterium*, *Staphylococcus*, and *Streptococcus*, and amount of 15 other genera that included *Enterococcus* and Enterobacteriaceae family, and in a un/pre-functional hospital there is dominance in the *Acinetobacter* and *Pseudomonas* species. A study was carried out to understand how microorganisms colonize and move through the hospital environment. The bacterial dynamics in hospital surfaces, patients and staff members was characterized over a period of one year after the hospital became operational. It was found that microbiome in patient rooms, especially on the bedrails, resembled the skin microbiome of the patients occupying the room and the two became increasingly similar over the course of stay.

Interestingly, while initially the patient seemed to acquire the room's microbiome, during the course of the stay, their own signature microbiomes began to influence the room's microbiota. Imagine, a patient suffering from infectious diseases could pass on the culprits to the patient who next stays in the room!

Even though hospitals are said to be efficiently disinfected, there are pathogenic bacteria which are commonly found in the hospital environment and equipment. It is therefore very likely to get Hospital-Acquired Infections (HAI's), and such infections are more fatal and life threatening than regular infections or disease. In fact HAI's is the 6th leading cause of death, in United States; thereby killing more people than diabetes or influenza could. Despite the stringent cleaning and disinfection procedures followed, there is a significant increases in the HAI's, indicating that the current procedures and measure are inadequate to protect the patients. Patients have weaker immune systems and presence of these infectious agents will only deteriorate their condition. It has been proposed that introduction of beneficial microorganisms may reinforce the beneficial microbial interactions and mitigate the harmful ones through the course of hospitalization, but much needs to be done before this comes to practice.

|The Gill-associated Microbiome of Mangrove Shipworm *Neoteredo reynei*

Abhishek Behera(II Year)

Teredinidae is a family of wood-feeding and wood-boring bivalves, called as shipworms, whose evolution linked to the attainment of cellulolytic gamma proteobacterial symbionts harbored in bacteriocytes within the gills. Metagenomics can be used to characterize microbiomes of the gills and digestive tract of *Neoteredo reynei*, a mangrove-adapted shipworm species found over a large range of the Brazilian coast. Comparative metagenomics assembles the gill symbiont community of different *N. reynei* specimens, indicating closely related bacterial types are shared.

The intestine and digestive gland communities were also characterized and were found to be more diverse. Annotation of assembled metagenomic contigs highlighted that the gill symbiotic community of *N. reynei* contains a plethora of plant cell wall polysaccharides degrading glycoside hydrolase encoding genes, and Biosynthetic Gene Clusters (BGCs). In contrast, the digestive tract microbiomes was found to have a little role in wood digestion and secondary metabolite biosynthesis. Metagenome binning showed almost the complete genome sequences of two symbiotic *Teredinibacter* strains from the gills, a representative of *Teredinibacter turnerae* "clade I" strain, and a yet to be cultivated *Teredinibacter sp.* type. These *Teredinibacter* genomes, as well as un-binned gill-derived gamma-proteobacteria contigs, also include an endo-β-1,4-xylanase/acetylxylan esterase multi-catalytic carbohydrate-active enzyme, and a trans-acyltransferasepolyketide synthase (trans-AT PKS) gene cluster with the gene cassette for generating β-branching on complex polyketides.

Finally, multivariate analyses was used to highlight that the secondary metabolome from the genomes of *Teredinibacter* representatives, including genomes binned from *N. reynei* gills' metagenomes stands out within the Cellvibrionaceae family by size, and enrichments for polyketide, nonribosomal peptide and hybrid BGCs. The characterization of symbiotic microbiomes of the shipworm has revealed the presence of gammaproteobacterial community, which is a prolific source of biotechnologically relevant enzymes for wood-digestion and bioactive compounds production.

In this they study applied metagenomics to characterize the microbial communities of the digestive gland, intestine and gill of the mangrove specialist shipworm *Neoteredo reynei*. They provided strong evidences that the *N. reynei* gill symbiont gammaproteobacterial community is a hot spot for biotechnologically relevant enzymes, such as Carbohydrate activating enzymes (CAZymes) involved on breaking down wood-derived complex polysaccharides, and biosynthetic gene clusters for production of potentially bioactive secondary metabolites such as complex polyketides, peptides and lipopeptides. Further, the discrete bacterial communities forming the microbiome of the digestive tract tissues seems to have little or no involvement in host nutritional support or chemical defense. Digestive gland and intestine datasets presented a simple repertoire of CAZymes, lacking GHs for digestion of woody material, and only one fragmented BGC with hits to a locus of the Yesso scallop bivalve mollusk genome.

Thus the characterization of gill associated microbiome of *N. reynei* has shown that the gill microbial community is a very rich source of biotechnologically relevant enzymes. More such interesting discoveries related to microbiomes are definitely in store.

| Probiotics

Disha Arora (I Year)

Probiotics are living micro-organisms which are considered to be good for our health and promotes life. They protect our digestive system from harmful bacteria. Bacteria are generally responsible for causing disease, thus the idea is that they can be useful for health. Not all probiotics are same, different strains of bacteria have different effects. Probiotics have been found useful in the prevention of many diseases such as diarrhoea, urinary tract infection etc. Probiotics provide immense benefits such as it boost up our immunity, improve digestive function and also prevent and treat urinary tract infections. The good bacteria prevents the bad ones from taking their spaces. Probiotics may give the body a healthy boost as they “travel through” the digestive tract by altering the structure of microbiome. When a prebiotic or probiotic is added to diet they improve your gut health. Kraut, Kvass, Kombucha are some of the natural probiotics.

Prebiotics provide food meant to promote the growth of beneficial bacteria in the gut while probotics are live good bacteria. One of the major bacterial strain present in milk is *Lactobacillus sp.* The gut flora performs many useful functions such as production of vitamin K and B. Probiotics can also fight *Helicobacter pylori* infections which can cause ulcers and stomach cancer. Probiotics are normally added to food as a part of the fermentation process. The emphasis for prolonged survival of probiotics in the food matrix would alter the functionality and efficiency of the food product. Different probiotics have different effects, if one *Lactobacillus sp.* prevents illness it does not mean that the other *Lactobacillus sp.* will perform the same function. Probiotic bacteria must remain viable in the food carriers and survive the harsh condition of gastro-intestinal tract with a minimum count of 10^6 CFU/gram. The dairy based products are considered to be the main carriers for the delivery of probiotics. Many of the micro-organism in probiotic products are the same as or similar to micro-organisms that naturally live in our bodies.

Another term called synbiotics represent when a probiotic and a prebiotic are combined. Fermented dairy products such as yoghurt and kefir are considered synbiotic because they contain live bacteria and the fuel they need to thrive.

| Dysbiosis and Aging

RomitaTrehan (I Year)

The microflora residing on or within any human tissue or fluid can be referred as microbiota. Most of these bacteria have a positive effect on our health and contribute to our body's natural processes. Dysbiosis typically occurs when the bacterial population balance in our gastrointestinal tract (stomach and intestines) is disturbed. It is characterized by the taxonomic categories of gut microbes i.e., using the 16S or 18S rRNA sequence. The taxonomic characterization or genetic make-up of the community is used to infer its functions based on data in the literature from studies using reference microbial strains. These microbes are studied i*n vitro* for more information and further to produce functional data.

A definitive disease-associated community structure has not been identified due to the large variation in gut microbial community composition among. The human gastrointestinal tract harbours about 1014 bacterial cells, which is ten times the number of cells in the human body.

Therefore, how to define dysbiosis and determine which microbial community is dysbiotic is unclear! The composition of microbial community and its behaviour is sensitive to the environment and host components. Changes in lifestyle, mobility, nutrition and physiological changes are some of the factors which can lead to dysbiosis. Poor dental health and less protein and fiber intake can also be included in these factors. An increasing amount of evidence suggests that the innumerable microorganisms that populate the mammalian gastrointestinal tract (gut microbiota) are tightly linked to the ageing process of their host. The microbial community, mostly comprises the bacteria that take part in important activities of the gut. The production of metabolites is crucial for many host functions and the mediation of chemical effects on the host. The main feature in the microbiota in older individuals is a change in the relative amount of the Firmicutes and the Bacteroidetes. The elder people have higher portion of Bacteroidetes while young adults have higher portions of Firmicutes. A noticeable reduction in the proportion of Lactobacilli, *Bacteroides/Prevotella* and *Faecalibacterium prausnitzii*, and a significant decrease in the proportion of *Ruminococcus*, *Atopobium*, and Enterobacteriaceae was observed in people with more infirmity scores.

The gut microbiota is linked with features of gut barrier integrity, intestinal pro- and anti-inflammatory balance, immune and cardio-metabolic health, and gut-brain axis. These clinical issues will contribute to the increased susceptibility to a variety of gut-associated diseases by causing alarming changes in the microbiome of the old people. These studies hint that the gut microbiome may be linked with inflammation and age-related chronic health disorders, and therefore alter the process of ageing.

The gut microbiota is dependent on the nutrient signaling pathways of the host for its beneficial effects on host health, lifespan. Gut dysbiosis might diminish the beneficial effects or even have reverse effects. Gut dysbiosis can stimulate the innate immune response and chronic low-grade inflammation, leading to many degenerative pathologies and unhealthy aging. The gut microbiome communicates with the host through biomolecules, nutrient signaling-independent pathways, and epigenetic mechanisms. Disturbance of these by age-related gut dysbiosis can affect the health and lifespan of the host.

| Microbiome Engineering

Priyam Chopra (I Year)

There is a unique microbiome in humans, animals, plants, soil and oceans. Different types of microorganism are found in different habitats which may or may not be interacting with each other. Any changes in microbial community that is different from that found naturally can disturb the balance of the ecosystem, resulting in disease and disorders. That is where microbiome engineering comes into play. Microbiome engineering attempts to mitigate these disturbances by modifying structure of the microbiota to restore ecological balance. Because of such reasons, microbiome engineering has played an important role in improving human health and agriculture productivity.

As mentioned above, all microbial communities interact with each other in an ecosystem as well as within a microbiome. The metabolites produced by microorganisms aid in the process of microbial interaction. Any deviation in microbial community has adverse effects like reduced soil fertility, diseases etc. By engineering of microbiomes, microbial composition can be altered to improve host phenotype and benefit the ecosystem.

Microbial engineering has been extensively used on human microbiome in order to treat various diseases. As gut microbiota plays an important role in our health and any change in the gut microbiota leads to gastrointestinal infection such as ulcerative colitis, *Clostridium difficile* infection (CDI) and inflammatory bowel disease (IBD). Fecal microbiota transplantation is used as a technique in microbiome engineering to establish healthy microbial composition in patients. In this technique fecal material is taken from a healthy donor, turned into a suspension and then injected into gastrointestinal tract of the affected patients. This method has been extensively used for treating recurrent CDI. Besides FMT, other strategies that can potentially alter the human gut microbiome have been devised and investigated in animal model studies. For example, antimicrobial peptides (AMPs), such as thuricin CD and pyocin S5 have been utilized for narrow-spectrum targeting of pathogens, thus reducing the chance of resistance and disturbance to the gut microbiota.

Microbiome engineering is used to administer prebiotics to remodel microbiota. Prebiotics such as galactooligosaccharide and soluble corn fibre have been used for selective fermentation by gut microbiota by increasing beneficial *Bifidobacterium* and decreasing pathogenic *C. histolyticum* to improve health. Probiotic *Lactobacillus* has been employed to promote growth of *Staphylococcus epidermidis* to inhibit the growth of pathogenic skin bacteria thereby helping in treatment of various skin diseases. Probiotics also find wide use in animal microbiome engineering to treat diseases and promote growth. The most common probiotic strains are *Lactobacillus*, *Bifidobacterium*, *Bacillus*, *Enterococcus* and *Saccharomyces boulardii*.

The role of microbiome engineering is not limited to animals, it has been used to improve plant microbiome which in turn helps to promote growth and provide resistance to various diseases and stress like droughts etc. Plant microbiome is mainly represented by root associated rhizospheric microorganisms. In order to fight plant diseases, the disease suppressive soil is mixed with disease conductive ones.

Advancement in microbiome engineering is greatly linked to emergence of synthetic biology. Synthetic biology may lead to the engineering of smart microbes that can detect and treat disease. This approach could be potentially applied to selectively eradicate strains from microbiota for microbiome engineering. Some strains of *E. coli* have been engineered. These *E. coli* sense, seek and specifically kill pathogenic *P. aeruginosa*. Signalling between microbes is interrupted as a means to alter microbiota composition. For instance, *E. coli* was modified to overproduce AI-2 signalling molecules which can rebalance the Firmicutes/Bacteroidetes ratio caused by streptomycin-induced dysbiosis in mouse intestine.

Microbiome research has made great progress in the past decades. Thus, despite being a relatively new field, microbiome engineering has been successfully employed to alter microbiota. With continuous efforts in understanding and manipulating microbiome, the microbiome engineering may become a mainstream strategy for improving human health and agriculture in the coming future.

| Is life within the Earth larger than life on top of it?

Amit Bhatt (III Year)

Have you ever thought about finding the limit beyond which life cannot exist? Or to which extent an organism can adapt to survive? The threshold point of 'existence of life' still remains a mystery, but recent advances in science and technology helps us to better understand how life and the Earth co-evolved. Life is incredibly resilient; can always find its way and this is backed by "deep life" studies that revealed the presence of a rich ecosystem underneath our feet that is virtually double the size of all the world's oceans. According to researchers, at the Deep Carbon Observatory, the underwater species diversity can be compared to the Amazon or the Galápagos Islands, but unlike those places the sub-terrestrial environment is still largely pristine because most of the subsurface life is still undiscovered. "It's like finding a whole new reservoir of life on Earth," said Karen Lloyd, an associate professor at the University of Tennessee in Knoxville.

The breakthrough discovery of underwater life is a consequence of extensive study conducted on samples taken from boreholes more than 5 km deep and undersea drilling sites by a research team encompassing 1,200 scientists from fifty two countries in disciplines varying from earth science and biology to chemistry and physics. Samples were examined and models of the ecosystem were constructed to estimate the quantity of carbon. Further the technical advances in tools including drills that can reach the interiors of Earth's crust and incredible improvements in microscopes that permit the detection of life at increasingly minute levels have made this research even more expedient. The results counsel that 70% of Earth's bacteria and archaea exist within the subterranean region, including barbed *Altiarchaeales* living in sulphuric springs and *Geogemmabarossii*, a single-celled organism found in hydrothermal vents. An organism was found deep below the surface are predicted to have buried for millions of years without receiving any energy from sun.

Quoting Lloyd "The strangest thing for me is that some organisms can exist for millennia. They are metabolically active, but in stasis, with less energy than we thought possible of supporting life."

These optimistic research outputs have attracted a lot of scientific interest and emphasis is being given on further exploring and development of more sophisticated instruments. Robert Hazen, a mineralogist at the Carnegie Institution for Science, said: "We must ask ourselves: if life on Earth can be this different from what experience has led us to expect, then what strangeness might await as we probe for life on other worlds?"

| The Countdown to Apocalypse

Anirban Adhikary (III Year)

Homo sapiens, the wisest of all living forms rules planet Earth. Unfortunately, they have built a civilization that has scarred the planet, decimated its ecological balance and is making it increasingly inhospitable for other life forms. Besides being so evolved, we still stand divided in our sense of responsibility in the face of challenges that might question our survival in the years to come. The 'Goldilock's Zone' in the Solar System that has facilitated evolution of life won't last forever. An ageing Sun would expand and eventually make temperatures inhospitable for life and leave the Blue planet not so blue. Life on Earth would come to an inevitable end. We can only slow down the approaching apocalypse, but not prevent it. Science fiction and imagination takes us to distant galaxies where human life would continue after the Earth is left unfit for life, but for now, this blue planet is our best chance for survival. Ironically, such challenges that we face today are largely due to irresponsible human activities and one such issue that require immediate attention is Antimicrobial Resistance.

In the late 1800s, Europe was jeopardised by lethal infectious diseases. The only treatment known was hope and prayers before the patient died from blood poisoning. In 1910, a ray of hope appeared with the synthesis of Arsphenamine, popularly known as Salvarsan by Paul Ehrlich. Salvarsan was effective against Syphilis and considered to be the first chemotherapeutic agent. Following Salvarsan in 1935, sulphonamides were developed by Domagk and other researchers. However, these chemically synthesized drugs have limitations in terms of safety and efficacy and we need better means to treat infections. Antiseptics of this nature often worsened injuries causing more deaths than injuries themselves.

Organisms have been battling for survival in their habitat since inception. Plants and microorganisms have the ability to produce certain bioactive molecules to counter invading life forms. Plant and mould extracts have been used historically in many cultures to treat cuts, wounds and injuries. It is only lately that we understand their mode of action. The earliest accounts of using a mould extract to treat infections dates back to Ancient Egypt. Egyptians applied poultice of moldy bread to infected wounds. The modern Antibiotic era began with the accidental discovery of benzylpenicillin (Penicillin G) from the mould *Penicillium notatum*. The drug was very effective to treat diseases like scarlet fever, pneumonia, gonorrhoea, meningitis and diphtheria. The drug gained huge popularity because of its effective action to cure diseases that were incurable before and was made publicly available. Flemming also made another significant discovery that bacteria could turn resistant to penicillin whenever it was used in sub-inhibitory concentrations or used for a period shorter than recommended dosage period. He cautioned not to use penicillin unless there was a properly diagnosed reason for it to be used and only to be used strictly following the required dosage pattern and period. Much alike his prediction, in the 1940s, there was emergence of a penicillinase-producing *Staphylococcus aureus*. The very same organism, against which penicillin activity was first discovered, had just turned resistant. Since Penicillin, the discovery and development of a new class of antibiotic drug has created an alternating pattern in timeline of history with emergence of drug-resistant bacteria.

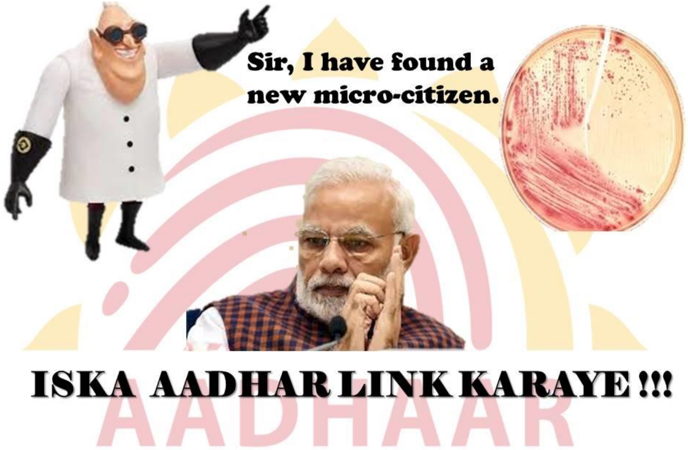
he subsequent decades witnessed discovery of new classes of antibiotics such as streptomycin, cephems, carbapenem, monobactams, aminoglycosides, chloramphenicol, tetracycline, macrolides, vancomycin and methicillin. In 1962, the first quinolone antimicrobial was synthesized.

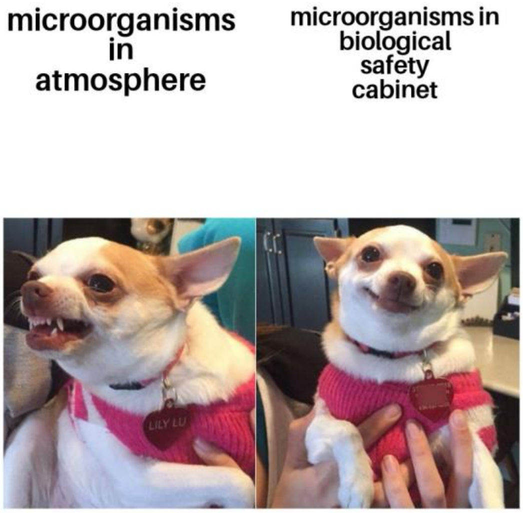
This era came to be known as 'Golden age of antimicicrobial chemotherapy'. Further improvements in each class of drugs to counter antimicrobial-resistance, higher antimicrobial activity, better pharmacodynamics and broader antimicrobial spectrum have been achieved. However, it seems that our innovations and inventions haven't outsmarted pathogens. In fact, the capacity of microorganisms to develop resistance even-against the latest antimicrobial agents has surpassed our imagination. It has appeared that they have always been a step ahead of us. This has been largely due to remarkable capacity of microorganisms to multiply and thus evolving faster than other life forms. Any survival stress can be countered by a bacteria through a plethora of metabolic choices. Bacterial transformation facilitating horizontal gene transfer through conjugative plasmids is a major cause of developing antimicrobial resistance across species. *Staphylococcus aureus* is the resistant bacterium most commonly encountered in clinical settings. It had shown the ability to produce penicillinases in 1950s. To counter penicillin-resistance, penicillinase stable Methicillin was developed in the 1960s. Unfortunately, the very following year of 1961, MRSA (Methicillin resistant *Staphylococcus aureus*) was isolated in the United Kingdom. In the 1990s, MRSA infections became a social problem. MRSA acquired resistance to all forms of beta-lactam antibiotics including second and third-generation cephems by acquisition of Penicillin Binding Protein. It is an enzyme involved in cell wall synthesis with low affinity for beta-lactam antibiotics. In Japan, a different strain of MRSA turned intermediate to vancomycin susceptibility. It is known as VISA. In the United States, it was reported that Vancomycin resistant *S. aureus* (VRSA) had acquired resistance genes horizontally from Vancomycin-resistant enterococci (VRE).

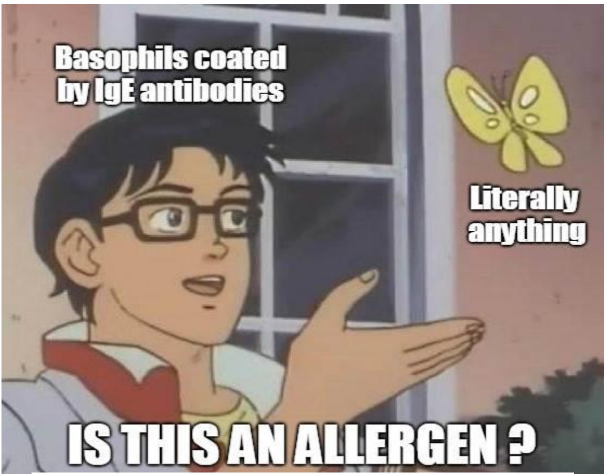
In the later half of 1960s, penicillin intermediate *Streptococcus pneumonia* was isolated and in the 1970s it turned resistant. *S. pneumoniae*, originally penicillin susceptible was believed to have turned resistant due to frequent use of cephem antibiotics. The same organism was found to have developed macrolide resistance. Ampicillin resistant *Haemophilus influezae* strains known as BLNAR are most common in Japan and western countries. *Pseudomonas aeruginosa* was found to be resistant to all three classes of antibiotics i.e., carbapenams, quinolones and aminoglycosides is a recent concern. MDRP (Multiple drug resistant *Pseudomonas aeruginosa*) has developed very complex mechanism of resistance. These include reduced membrane permeability due to decreased outer membrane protein, overexpression of efflux pumps, mutating quinolone targets in the DNA, production of aminoglycoside modification enzyme and production of metallo-beta-lactamase (carbapenem-hydrolysing enzyme). Gonococcal infections are no more treatable by quinolone-class of antibiotics. It would be safe to say that most of the antimicrobial agents from the 'golden age' are completely irrelevant or in the process now. These organisms are of major concern because they cause noscomical infections or Hospital Acquired infections and are very common in day to day life. Antibiotic resistance is a major concern because a small infection can turn out to be 'Achilles heel'. In the post-1990s, the use of third generation cephem, carbapenam, oral cephem and new quinolone antimicrobials has increased. Keeping pace with it, the number of MDRP and quinolone-resistant *E. coli* has increased significantly.

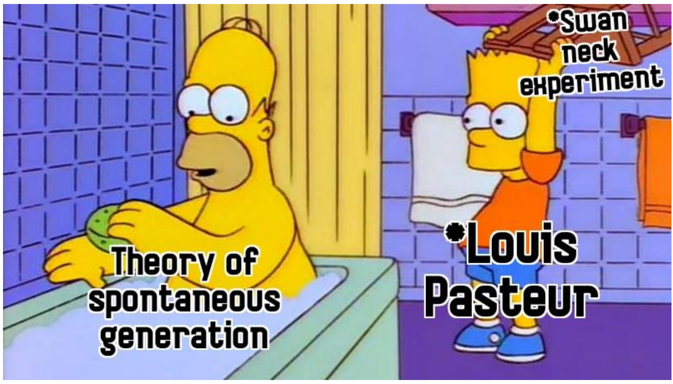
In the modern era, the number of newly discovered antibiotics has been very few. Antibiotics used today are mostly chemically modified forms or used in combinations. The major reason for this has been increased concerns of drug safety and stringent rules and regulation in place. After the discovery of penicillin, Alexander Flemming famously said, "the microbes are educated to resist penicillin and a host of penicillin-fast organisms is bred out…In such cases the thoughtless person playing with penicillin is morally responsible for the death of the man who finally succumbs to infection with the penicillin resistant organism." It is to our huge discredit that the human race is largely ignorant of the damages caused by the careless use of antibiotics. In developing countries, antibiotics are sold over the counter without prescriptions. Doctors prescribe drugs without performing proper diagnostic tests. Hospitals do not have proper infrastructures for sanitation and prevention of unwanted exposure of environmental microflora to sub-inhibitory concentrations of antibiotics. These problems are more prevalent in developing and underdeveloped countries and awareness among the common people is important to address the challenges of growing antimicrobial resistance.

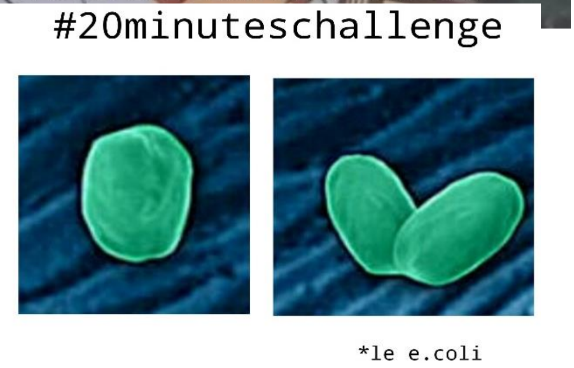
Some entries from Microbe-Meme Competition

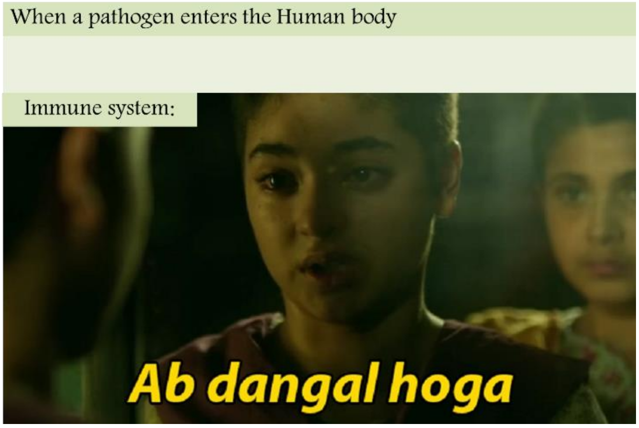


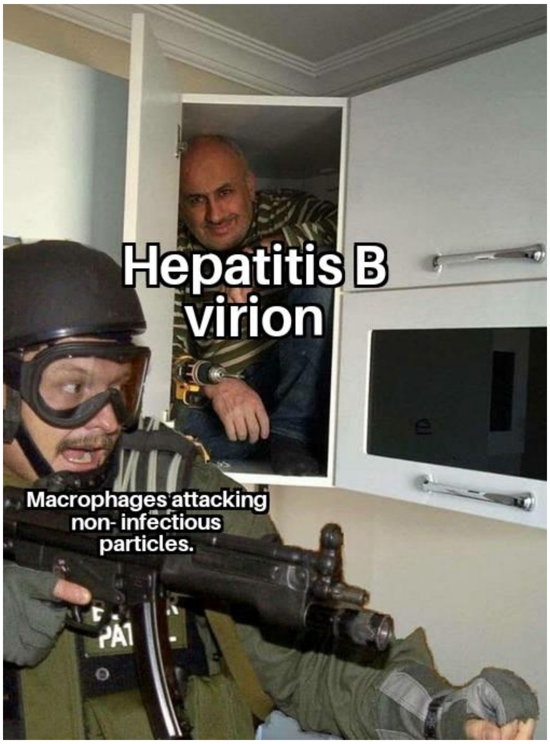






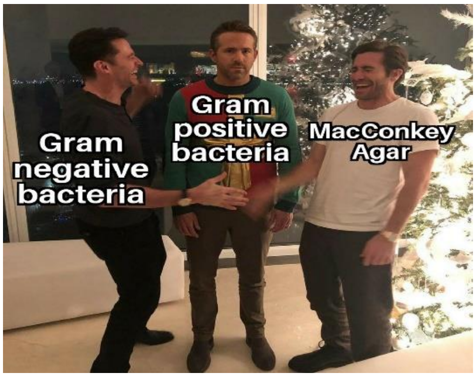


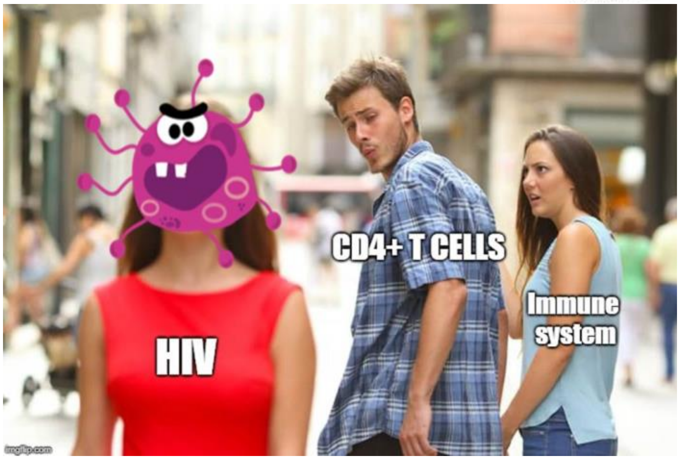




When you get those cool disposable inoculating loops

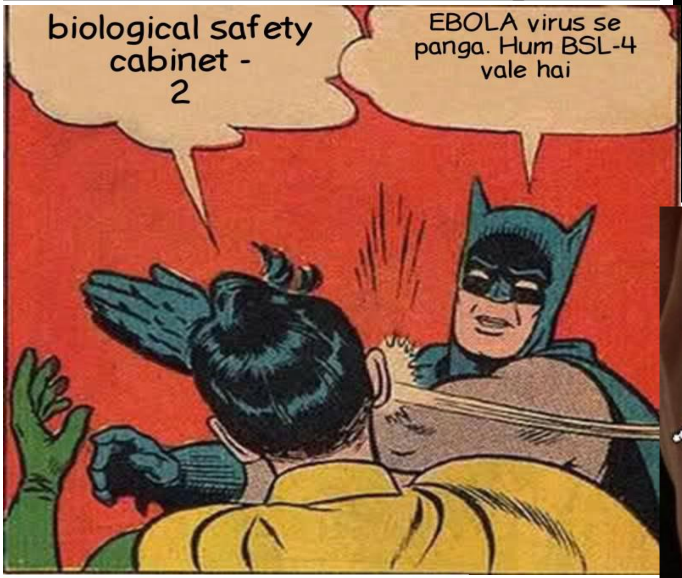
But then you start by heating it






Babu bhaiya hum dono ki Plate me Contamination aaya hai
Kaisi baat karta hai re Deva, Humne to Laminar Flow k andar kiya tha


ALEXANDER FLEMING
PENICILLIUM NOTATUM
STAPHYLOCOCCUS
imgflip.com


biological safety cabinet - 2
EBOLA virus se panga. Hum BSL-4 vale hai


MAN
WOMAN
WHITE
BLACK
POOR
RICH
ASIAN
KIDS WHO DON'T STERILIZE THEIR WORKPLACE

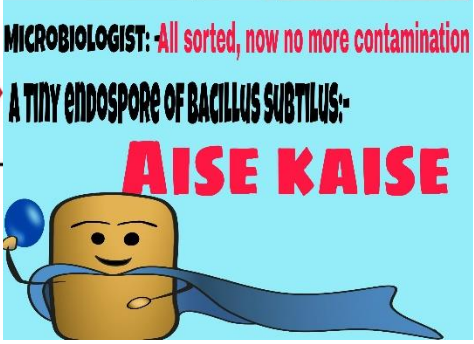

when you love street food
CHOLERA
DIARRHOEA
DYSENTERY
But you also have a weak immune system


do you love microbiology?
noooo....there is nothing except microbes

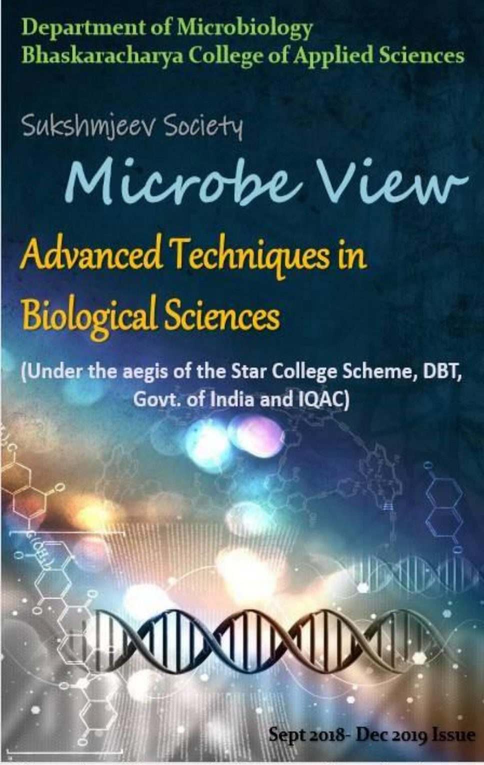

What does a RETROVIRUS cause?
SATURDAY NIGHT FEVER


110'C
10 -20 min


STOP
UAA
UAG
UGA


MICROBIOLOGIST: All sorted, now no more contamination
A TINY ENDOSPORE OF BACILLUS SUBTILUS:-
AISE KAISE

Cancer awareness programme



Department of Microbiology
Bhaskaracharya College of Applied Sciences

Sukshmjeev Society

Microbe View

Advanced Techniques in Biological Sciences

(Under the aegis of the Star College Scheme, DBT, Govt. of India and IQAC)

Sept 2018- Dec 2019 Issue

Microbe View: Advanced techniques in Biological Sciences

Debate Competition

The Sukshmjeev Society, Department of Microbiology
(under the aegis of the Star College Scheme, DBT, Govt. of India and IQAC)
is organising

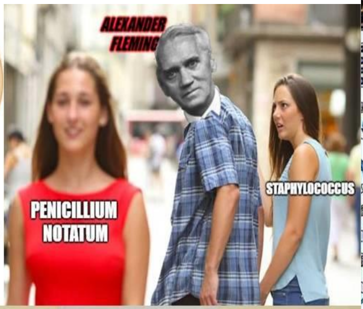
An Interdepartmental Essay Writing Competition
on the topic

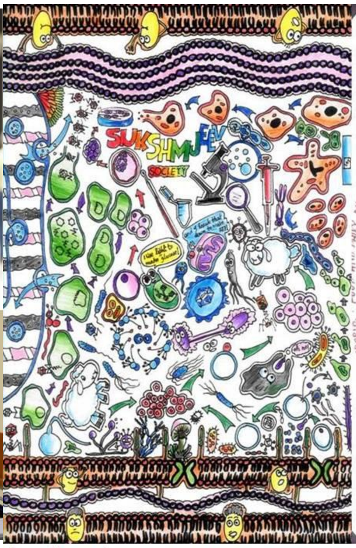
Advancement in computer and network technology: Driving progress in scientific fields

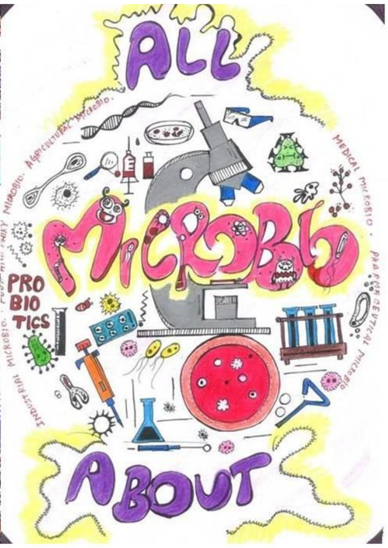
Date: 10th January, 2019 (Thursday)
Time: 11 AM to 12 PM
Venue: Microbiology Lab

Essay-writing Competition

Microbe-Meme







Doodle-making competition

National Conference 2018

Pathkind Lab Visit

Lecture series

Agar-Art competition

About the Sukshmjeev Society

The Sukshmjeev Society of the Department of Microbiology, Bhaskaracharya College of Applied Sciences was founded in 2007 by enterprising faculty members, to celebrate the passion that we all at the department share for Microbiology and its related fields of study. As an interactive platform that allows both the students and teachers to put forth their perspectives in discussing diverse ideas, the society has successfully organized and participated in various academic as well as co-curricular events since its inception, and only aims higher going forward.

At Sukshmjeev, we find ourselves in complete agreement with the American virologist Nathan Wolfe, who articulates quite simply a profound truth about microbial life:

"If an alien visited Earth, they would take some note of humans, but probably spend most of their time trying to understand the dominant form of life on our planet-microorganisms like bacteria and viruses."

Awarded 'Star Status' by the Department of Biotechnology, Government of India, under its Star College Scheme in June 2017

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