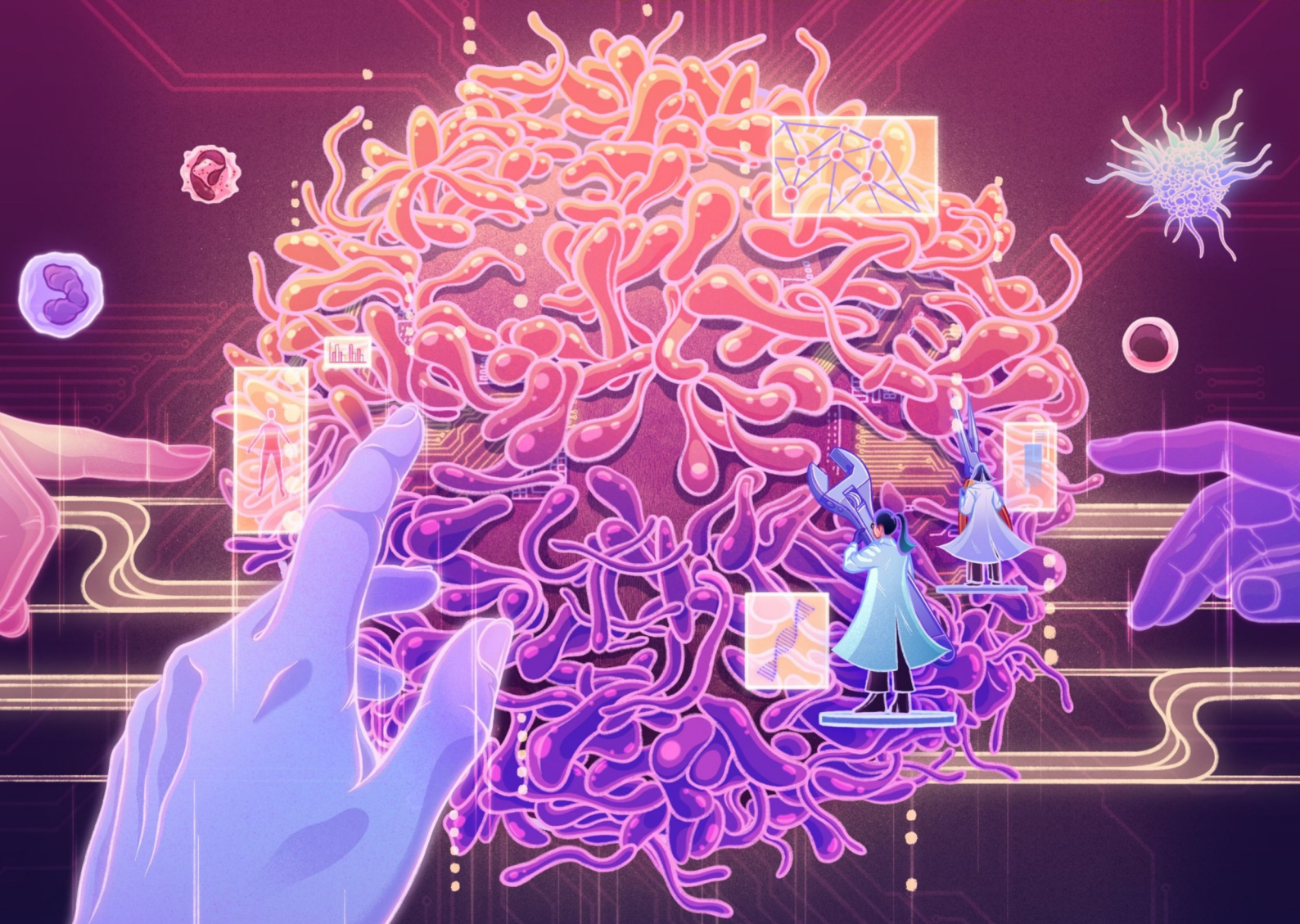
MICROBYTE

DISCOVER THE INVISIBLES



Bacterial Secondary Metabolites

Antimicrobial Resistance

Metagenomics

VOL-2

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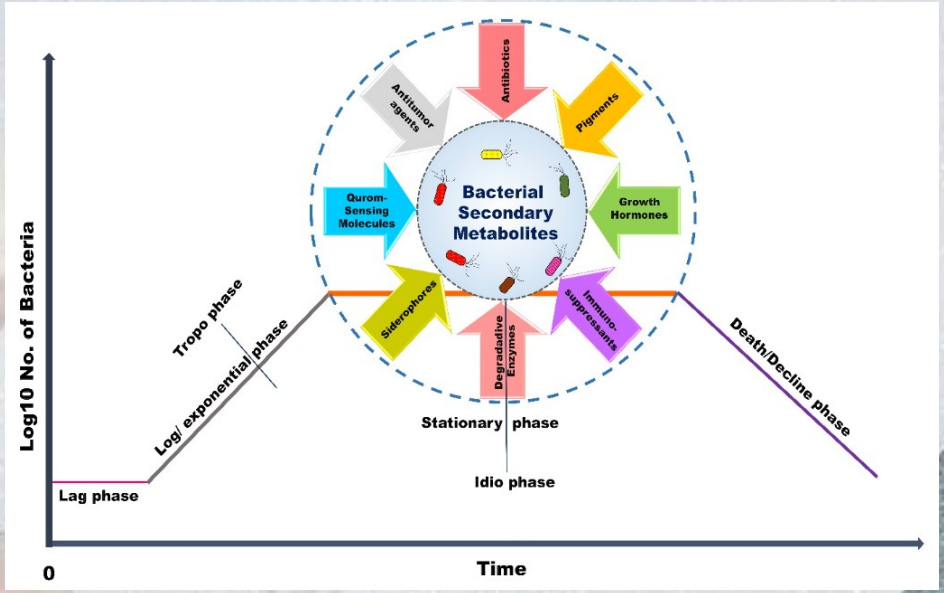
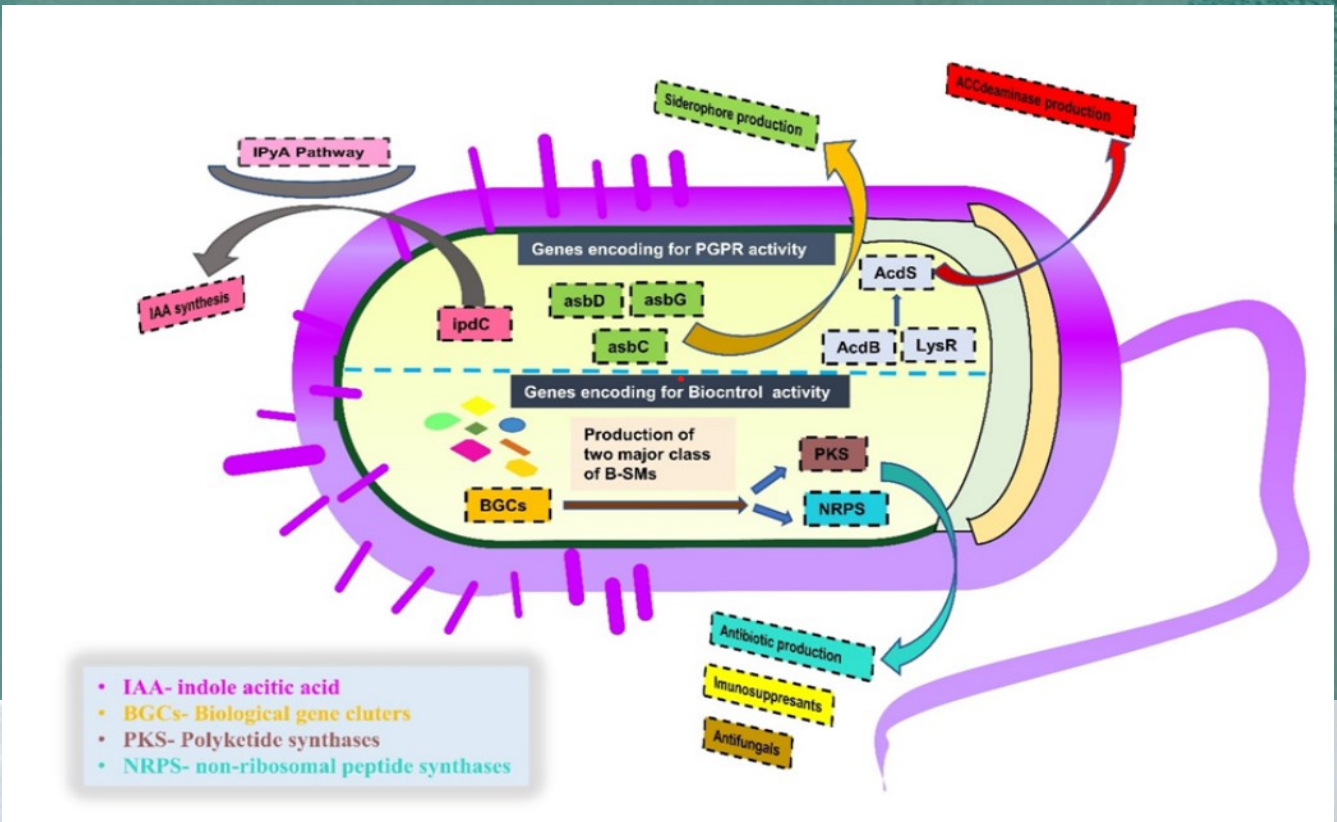
“Bacterial Secondary Metabolites (B-SMs) :

A Goldmine of Antifungal Agents”

Soil is an admirable niche for the growth of voluminous bacteria that can influence plant evolution. Metabolite production is the general property of microorganism's inhabitants in a natural environment, including eukaryotes and prokaryotes. Bacteria produce a variety of metabolites with diverse biotic stress management functionalities (Bérdy, 2005 ; Salazar et al., 2022). B-SMs (Bacterial secondary metabolites) are composites that are not essential for the growth or replication of bacteria; however, are formed to converse a selective advantage to the organism. B- SMs are low molecular mass products of secondary metabolism, having weight of 2.5 KDa and less (Pathma et al., 2011) and are produced from minor categories of microbes. These amalgams help to persist inter-species antagonism, offer self-protective mechanisms and simplify propagative practices (Vaishnav and Demain, 2011). Numerous secondary metabolites have recognized their role in plant stress management, including defence mechanism(s), by serving as an antibiotic and by producing pigments (Keswani et at., 2020).





Secondary metabolites, comprised of terpenes, phenolics, nitrogen (N) and sulphur (S) encompassing compounds, protects plants against several biotic stresses i.e. herbivores and pathogenic microorganisms especially fungi, bacteria, and other parasites. Along with biotic stress management, they also provide a shield against certain abiotic stresses (Mazid et al., 2011). These B-SMs act as defensive molecules against numerous disease stresses either by straight inhibition of phytopathogen growth and indirectly by stimulation of plant defences, or by boosting plant immunity (Keswani et al., 2019 a, 2019 b; Sansinenea and Ortiz, 2011). These bacteria trigger plant growth by produ ing secondary metabolites providing shield against biotic stress blended with other plant growth and endorsing features such as nitrogen fixation, Auxins production, phosphate solubilisation, siderophore production, HCN production and the production of various degradative enzymes that convert complex polymers to simple consumable form (Keswani et al., 2020; Mitra et al., 2022 ; Sansinenea, 2019 ; Sansinenea and Ortiz, 2011). B-SMs are chemically and functionally assorted with amazing antimicrobial, plant growth regulators, plant enzyme inhibitory, herbicidal, insecticidal and antiparasitic activities (Mitra et al., 2022). These amalgams mainly comprise phospholipids, peptides, polypeptides, quinols, polyketides, alkaloids, polyenes, phenazines, volatiles, amino sugars, macrolactone and aminoglycosides. Due to their noteworthy biotic deeds and striking defensive capabilities as antifungal, antibacterial, antiviral, antitumor and anti-algal assets, they are broadly used in the field of agronomy, treatment, and veterinary disciplines (Barrios-Gonzalez et al., 2005).

Antimicrobial Resistance

Antimicrobial resistance (AMR) is one of the top global public health and development threats. According to estimations of World Health Organization 1.2 million global deaths in 2019 and 4.95 million deaths in 2023.

WHAT IS ANTIMICROBIAL RESISTANCE (AMR) ?

AMR develops when microbes change over time and become resistant to medicines, making infections difficult to treat and raising the risk of disease spread due to microbes.

REASONS FOR AMR?

1. OVERUSE OF ANTIMICROBIALS

The misuse and overuse of antimicrobials mainly antibiotics are among the leading causes of emergence of drug resistant pathogens.

2. ANTIBIOTIC USE IN LIVESTOCK

Over three quarters of world's antibiotic are used in animal food to speed up their growth. As a result new strains of drug resistant bacteria can spill over from animals and make untreatable infections.

3. PATIENTS NOT FINISHING THE PRESCRIBED COURSE

Not completing the course can also make microbe resistant to that particular antibiotic.

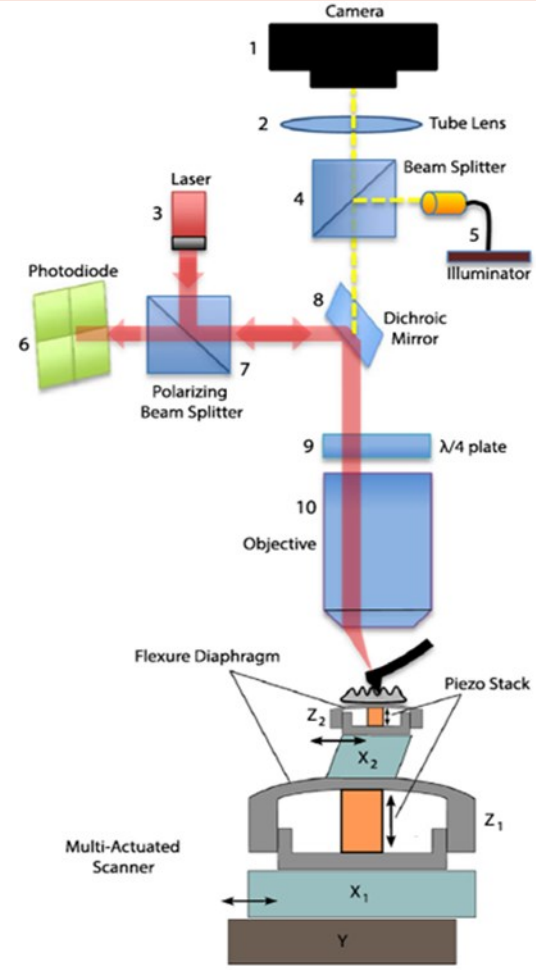
WHAT IS THE PRESENT SITUATION ?

The 2022 report of glass i.e global antimicrobial resistance and use surveillance system suggests 42% for third generation cephalosporin resistant e. coli and 35% for METHICILLIN RESISTANT Staphylococcus aureus are a major concern . Klebsiella pneumoniae , a common intestinal bacterium also showed elevated resistance levels against critical antibiotics. similar type of drug resistance is as well seen in HIV virus.

WHAT ARE COORDINATED GLOBAL ACTION TO ADDRESS AMR ?

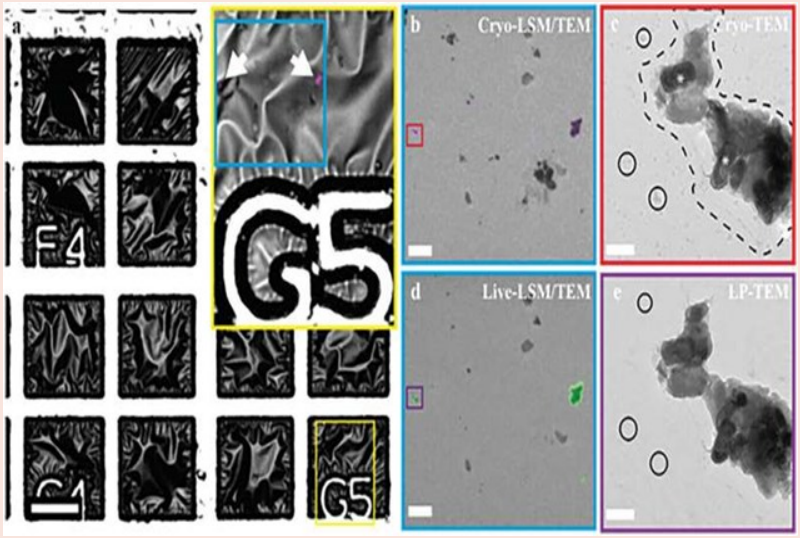
1. Global Action Plan (GAP) in 2015 was subsequently endorsed by Food And Agriculture Organization (FAO) And World Organization For Animal Health (WOAH) In United Nations.
2. World Amr Awareness Week (WAAW) Is Celebrated Across 18-24 November Every Year.

TANAY MANOJ DUBEY (FY SEM 2)



Next-Generation Microscopy: Watching Proteins Move in Real Time

Researchers at Radboud university medical center, led by Nico Sommerdijk, have developed a groundbreaking microscope that enables live imaging of biological processes, revealing intricate details such as moving protein complexes. Previously, high-resolution imaging was only possible with static samples, while observing living material required sacrificing detail. This new technique combines both capabilities by using graphene, a single-layer carbon material, to protect samples from electron beam damage during electron microscopy. However, applying the graphene layer often triggers the biological processes researchers aim to capture, requiring rapid preparation to observe the phenomenon before it concludes. Demonstrated by visualizing the onset of arterial calcification, this innovation opens possibilities for studying vaccine-cell interactions and early disease mechanisms. Published in *Advanced Functional Materials*, the technique represents a transformative advance in bioimaging, allowing real-time observation of living systems at the molecular level for the first time.



Arterial calcification

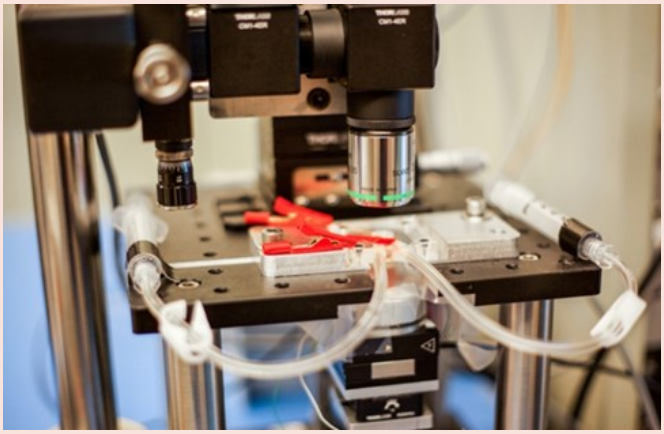
Sommerdijk's team developed a technique for live imaging by encasing tissue in graphene and freezing it to pause biological processes. After identifying the target area with a light microscope, the sample is warmed in a specialized electron microscope to reactivate processes for nanoscale visualization. This method revealed how calcium deposits form, potentially leading to arterial and aortic valve calcification. Ph.D. candidate Luco Rutten explained that proteins initially prevent calcium phosphate precipitation, but overgrowth of protein-calcium phosphate spheres can create calcified deposits that resist breakdown, contributing to calcification.

Heart valve on a chip

Currently, no treatment exists for calcified aortic valves other than complete valve replacement.

"We still don't fully understand what exactly happens with this type of calcification, which is why there are no medications yet," says Sommerdijk.

He aims to further study this with the new microscope. In this project, he plans to develop a "heart valve on a chip." Initially, this will be a model of a healthy valve, into which he will then introduce classification. This project will begin in 2025.

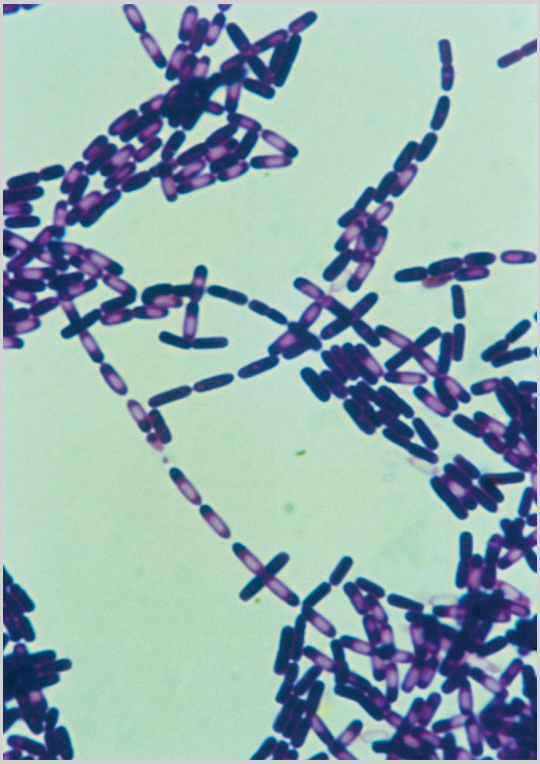


~AASHVI BHATT (SY, SEM-4)

Microbial Vessel for Long-Term DNA Data Storage

Hey Bacteria ! Save Your Data, Make Multiple Backups

Artificial DNA with encoded information can be added to the genome of common bacteria, thus preserving the data. The technique was developed at Keio University Institute for Advanced Biosciences and Keio University Shonan Fujisawa Campus. If you think flash thumb drives are small, check this data storage out. According to researchers, up to 100 bits of data can be attached to each organism. Scientists successfully encoded and attached the phrase "e=mc2 1905" to the DNA of *Bacillus subtilis*, a common soil bacteria.



One early use for the technique would be to create special markers to identify legitimate versions of pharmaceuticals. However, the bacillus itself creates new copies of the data every time it reproduces itself, thus making it an ideal archival storage system.

***Bacillus subtilis* also creates extra copies of the data, inserting it in different places in its genome, further safeguarding the data. That's "multiple back-up copies" for those of you who have lost data in the past.**

The first time I read about this idea was in an excellent series of fantasy novels by Barbara Hambly. In her 1982 Darwath trilogy, she writes about how wizards of several thousand years ago succeeded in tying information to the DNA of selected individuals. In the story, several people from 1980's California find themselves transported across the Void to another planet and the Realm of Darwath. They face a deadly species of queerly magical beings - the Dark - who destroyed civilization thousands of years ago. Everything that was made of paper (like books and records) were burned to stave off attacks by the Dark. Tying memories to a few suitable bloodlines was the only way to preserve a record of that period that would endure.

DNA data storage technology may supersede conventional chip or magnetic data storage medium, providing long-term stability, high density and sustainable storage. Due to its error-correcting capability, DNA data stored in living organisms exhibits high fidelity in information replication. Here, we report the development of a *Bacillus* chassis integrated with an inducible artificially assembled bacterial chromosome to facilitate random data access. We generated three sets of data in the form of DNA sequences using a rudimentary coding system accessible by the regulatory promoter. Sporulated *Bacillus* harbouring the genes were used for long-term storage, where viability assays of spores were subjected to harsh environmental stresses to evaluate the data storage stability. The data accuracy remained above 99% after high temperature and oxidative stress treatment, whereas UV irradiation treatment provided above 96% accuracy. The developed *Bacillus* chassis and artificial chromosome facilitate the long-term storage of larger datum volume by using other DNA digital encoding and decoding programs.

One of the main advantages is that storage and copying of data in living organisms is highly scalable since each living cell possesses machinery to replicate DNA and correct it in case of damage. There are also organisms that can maintain their DNA intact for years under harsh environmental conditions through sporulation, and that characteristic has been used to preserve data during the storage process. DNA holding digital data can be integrated into stable regions of the host genome or stored apart in synthetic chromosomes.

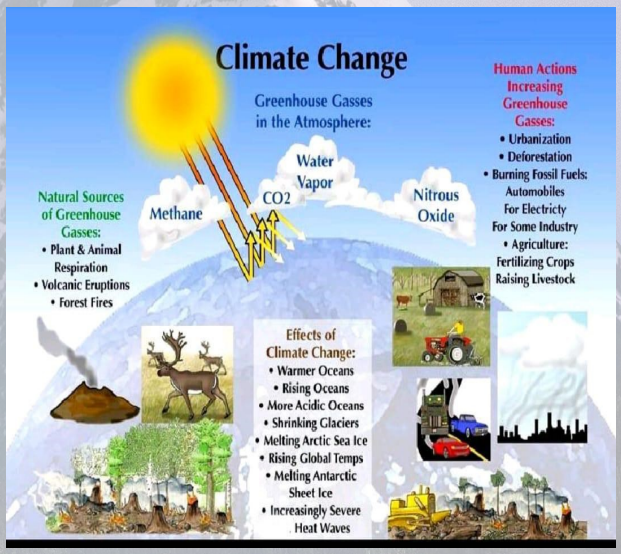
There are also organisms that can maintain their DNA intact for years under harsh environmental conditions through sporulation, and that characteristic has been used to preserve data during the storage process. DNA holding digital data can be integrated into stable regions of the host genome or stored apart in synthetic chromosomes. The method uses several molecular techniques including CRISPR-Cas9 and gene editing to manipulate the microbial genetic material.

~ ARPITA PATEL (T.Y. B.Sc. Sem-6)

The Role Of Microbes In Climate Change

Climate change refers to long-term shifts in temperatures and weather patterns, which can occur naturally due to change in the sun's activity or large volcanic eruptions. However, since the 1800s, Human activities, primarily the burning of fossil fuels like coal, oil and gas, have been the main drivers of climate change. This has led to an increase in average global temperatures due to the rising concentration of greenhouse gases. Climate change is one of the most serious challenges facing humanity, with a report from the Intergovernmental panel on Climate Change (IPCC) Stating that a quarter a quarter of the world's population is highly vulnerable to its effects.

Microbes play a significant role in climate change as they produce and consume the three dominant greenhouse gases responsible for 98% of global warming: carbon dioxide(CO_2), Methane (CH_4), and nitrous oxide(N_2O). Their activity depends on favorable growth conditions. Microbes responsible for producing and consuming these gases are found in various habitats, including terrestrial, oceanic and urban ecosystems. Each of these environments presents unique challenges in understanding microbial contributions to greenhouse gas emissions. Improved measurements and models are essential to accurately determine their impact on climate change.



Microbes contribute significantly to global warming with approximately 85% of the world's methane emissions resulting from microbial activity. In spongy bog soils, methane-releasing microbes thrive due to the presence of the enzyme methyl coenzyme M reductase, which transforms carbon dioxide into methane. The microbe *Methanoflorens stordalenmirensis* plays a crucial role in releasing trapped methane from Arctic Permafrost. Methane is a particularly potent green house gas, trapping about 20 times more heat than he same volume of carbon dioxide.

In conclusion, microbes play a vital and complex role In climate change, influencing the carbon cycle, greenhouse gas emissions and overall ecosystems resilience. Understanding microbial contributions is essential for developing effective mitigation and adaptation strategies. By harnessing microbial power through innovative technologies and sustainable practice, we can explore new solutions to reduce greenhouse gas emission, enhance carbon sequestration and promote ecosystems health. Ultimately, leveraging microbial processes can support a more resilient and sustainable future for our planet.

~ NIDHI NAYAK (M.Sc. Sem-1)

The Guest at the Banquet of Fish

Epulopiscium, meaning "a guest at a banquet of fish," is a fascinating microorganism found in the intestines of marine surgeonfish. In 1985, marine biologist Lev Fishelson discovered an unusually large microorganism in the gut of a brown surgeonfish from the Red Sea. Visible to the naked eye, this organism was named Epulopiscium fishelsoni in his honor. Due to its impressive size and complexity, scientists initially misclassified it as a protist.

Defying the Microscopic Norm:-

First discovered in the Red Sea, E. fishelsoni was later found in surgeonfish off the coast of Australia. Measuring over one-fiftieth of an inch—about the size of a hyphen in a newspaper—it remains one of the largest known bacteria.

Reclassifying the Giant:-

Advancements in molecular biology confirmed E. fishelsoni as a bacterium within the Firmicutes phylum, which includes other large bacteria like Clostridia. This reclassification reshaped our understanding of bacterial diversity, proving that size alone is not a defining trait.

A Symbiotic Relationship with Surgeonfish:-

Epulopiscium fishelsoni has a symbiotic relationship with its surgeonfish host. While details remain under study, it likely helps digest components of the fish's diet. In return, the bacterium thrives in the nutrient-rich environment of the fish's gut. Notably, it has never been successfully cultured outside its host, emphasizing its unique adaptation.

Life Cycle and Cellular Dynamics:-

The life cycle of E. fishelsoni involves notable changes in size and structure. Unlike most bacteria, which reproduce by binary fission, it forms multiple daughter cells internally. These cells develop inside the parent until they are fully mature and then released, setting it apart from typical bacterial reproduction.

Conclusion:-

Epulopiscium fishelsoni redefines bacterial limits in size and complexity. Its discovery expanded our understanding of microbial life, showing that bacteria can be far more diverse than previously thought. As one of the largest bacteria ever found, it continues to intrigue scientists and challenge conventional microbiology.

Deep Kanani (SY Sem-4)

Mycelium Mode:

Where Nature Wears the Trend

Fungi are eukaryotic organisms that include microorganisms such as yeasts, moulds and mushrooms. As we know, microorganisms don't just exist in the nature but they have a lot of applications which benefit the nature and us as human beings. They can boost the economy by turning into products. FUNGI are one such group of microbes which can be used to make a lot of products in various industries. The use of Fungi in the Fashion Industry is a very interesting discovery. It helps in the making of different types of materials used in the industry and they look beautiful too. There are various implications of the fungi in the industry, a few of them are as follows:

1

Mycelium Leather: It is the root structure of fungi which is used to create a sustainable leather-like material. It is main ly used to make bags, clothes, shoes, etc. REISHI and MYLO are some examples of the products. The market size in 2024 is calculated to be around 3-5 billion USD.

Advantages: These are biodegradable, doesn't need real leather and can be moulded into various shapes.

Disadvantages: These are not very water resistant, co2 production and can dry out very quickly.

2

Biodegradable Textile: These are the fabric materials made from Mycelium. This type of textile is used to make different types of clothes, accessories, surgical instruments, etc.

Advantages: These can be degraded into the soil without harming it. Also, these are better in material quality.

Disadvantages: A slightly expensive textile which is not as durable as the normal textiles. Also, has a slow degradable rate.

3

Closed Loop System: A cycle of fungi which makes the reuse of fungi in the fashion world to produce new materials. Waste materials made from fungi are fed to different lot of fungi to produce a new set of fungi.

Advantages: Waste recycling is done and new types of materials are made.

Disadvantages: The process can be lengthy and there's probability that the new material produced is not of the same quality.

The above main points justify the significance of FUNGI in the fashion world. But, there is more to it, yes the fungi is one of the most beautiful microorganism of all and it is one such type of it that is used in the production and making of many different types of materials. With all of this, there are many challenges which are to be focused on.

One big challenge is the scaling of production and number of units of materials produced with the help of fungi. The over exploitation of fungi for the sake of fashion industry is one of the major reasons of low-quality production. The other challenge is the low durability and simultaneously the low consumer education of how to maintain the products made from fungi. To avoid all these, we need a little revolution, how? - By offering innovative solutions to long-standing environmental issues.

~ PARAM BAXI (F.Y. Sem -2)

Metagenomics:

Unlocking the World of Unculturable Microbes

Microbes are essential for life on Earth, driving processes such as photosynthesis, nutrient cycling, and enzyme production. They hold immense potential for industrial, medical, and biotechnological applications. However, more than 99% of microbial diversity remains unexplored due to the limitations of traditional lab cultivation methods.

Metagenomics offers a solution by studying genetic material from entire microbial communities directly from their environment, bypassing the need for culturing microbes. This approach not only reveals microbial diversity but also uncovers novel genes and provides insights into biochemical pathways and ecosystem roles. Among the benefits of metagenomics are the discovery of novel genes and enzymes, understanding the roles of microbes in ecosystems, and identifying processes with applications in industry and medicine. By enabling the study of the vast majority of unculturable microbes, metagenomics is revolutionizing microbiology.

The key steps in metagenomics include DNA isolation from environmental samples, DNA manipulation to fragment the DNA and create libraries, library construction where DNA fragments are inserted into model organisms like *E. coli*, and DNA analysis to identify genes and study their functions. Advancements in technology, such as high throughput sequencing methods like pyrosequencing, have significantly enhanced the efficiency of analysing microbial communities.

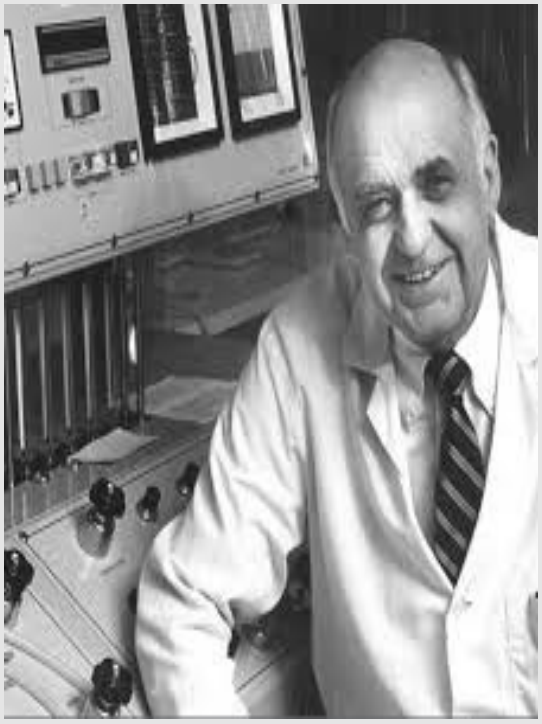
Metagenomics has wide-ranging applications, including mapping microbial diversity in marine ecosystems, studying the human microbiome to understand the impact of gut microbes on health, exploring termite gut enzymes for biofuel production, and analysing viral genes in environmental samples to uncover viral diversity. Recent projects in this field have yielded ground breaking results, such as studies of marine microbiota and global ocean sampling that have revealed microbial and viral diversity, as well as research on the human gut microbiome, highlighting its crucial role in health and digestion.

Metagenomics is driving transformative discoveries, positioning microbes as integrated systems critical to numerous processes. To advance this innovative field further, collaboration across disciplines is essential.

~PRIYANKA SOLANKI (T.Y. SEM - 6)

Maurice R. Hilleman

—A Forgotten Pioneer of Vaccines



"THERE'S NO GREATER TRIBUTE THAT ANYONE CAN PAY TO A SCIENTIST THAN TO GIVE APPROVAL TO A PEER"

Maurice Ralph Hilleman (1919–2005), a renowned microbiologist and vaccinologist, developed vaccines for Asian flu, Hong Kong flu, measles, mumps, hepatitis A and B, chickenpox, meningitis, and pneumonia. His six-decade career, mainly at Merck, revolutionized virology, immunology, and vaccine development, saving millions of lives worldwide.

Maurice R. Hilleman, born in 1919 in Miles City, Montana, was a pioneer in the field of microbiology. Raised by his uncle, he graduated from high school in 1937 amidst great depression. Inspired by his brother he won a full scholarship to Montana State University. After being offered scholarships at ten universities, he chose the University of Chicago for graduate studies. He received his PhD in 1944, focusing on Chlamydia. He then worked at E.R. Squibb & Sons, where he developed a vaccine against Japanese B encephalitis, which was crucial for World War II troops at the Pacific Front. In 1957, at age 38, Hilleman was recruited by the pharmaceutical company Merck & Company at West Point, Pennsylvania, to lead its virus and vaccination research programs for the next 47 years. From the 1950s to the 1990s, Hilleman and his team created more than 40 experimental and licensed human and animal vaccines, including those in use currently offering protection against measles, mumps, chickenpox, rubella, hepatitis A, hepatitis B, pneumococcal pneumonia, meningitis, pandemic influenza, and chlamydia.

Hilleman led the development of the Asian flu vaccine in 1957 which was important in alleviating the world-wide pandemic. In February 1957, a life-threatening wave of flu was spreading across China with reports of 20,000 cases in Hong Kong. Then a microbiologist at Walter Reed Army Medical Centre, Hilleman suspected this could become a pandemic threat and coined the term Asian flu. Hilleman took the sample from an ill US serviceman and discovered that most people lacked antibody protection for the new influenza virus. He initiated vaccine production by sending virus samples to manufacturers, producing 40 million doses and reducing the US epidemic, which caused 2 million deaths in the time span of two years (1957-1958).

He also worked on developing a vaccine for the Hong Kong pandemic in 1968. He worked with academic scientists, but was also responsible for the field work of collecting samples for vaccine development as well as administrative and scientific leadership, which resulted in field testing and the production of many new—or improved—vaccines. He characterized and isolated antigens, performed the basic- and process research as well as doing clinical studies, all the way through to the manufacturing process which resulted in fundamental breakthroughs in vaccine development.

~YUG PATEL (S.Y. SEM - 4)

Smart Antibiotics

A New Era Of Targeted Treatment

Researchers in the United States discovered Lolamicin, an antibiotics that selectively targets the lol lipoprotein transport system in the gram-negative bacteria. This antibiotic is effective against multidrug-resistant pathogens while sparing the beneficial gut microbiota which is crucial for gut immunity and structural integrity. Traditional antibiotics often disrupt the gut microbiome, leading to secondary infections like Clostridioides difficile. Lolamicin avoids this by specifically killing harmful bacteria without disturbing healthy gut bacteria. In mouse models, Lolamicin showed high efficacy against *E.coli*, *klebsiella pneumoniae* and *Enterobacter cloacae* with survival benefits for mice infected with septicemia and pneumonia. It also demonstrated the ability to prevent C. difficile infection, with mice treated with Lolamicin clearing the pathogen clearing the pathogen, unlike those treated with amoxicillin or clindamycin.

In 2023, Clovibactin was discovered by a team led by Kim Lewis from Northeastern University using a technique called the iChip. This method enables the culturing of previously unculturable bacteria, leading to the discovery of Clovibactin, produced by *Eleftheria terrae* subspecies Carolina, isolated from a soil sample in North Carolina. Clovibactin targets multiple precursors involved in cell wall synthesis, making it more difficult for bacteria to develop resistance. It has shown effectiveness against drug-resistant gram-positive bacteria, including *Staphylococcus aureus* (MRSA), offering an alternative to antibiotic that are losing efficacy.

Solanimycin, discovered by the University of Cambridge in 2023, Is an antifungal antibiotic produced by Dickeya Solani, a pathogen that infects potatoes. This compound disrupts fungal cell wall synthesis, causing cell death. Its unique structure, combining a polyketide and peptide likely contributes to its antifungal activity. Through initially found in a plant pathogen, Solanimycin has potential application for treating fungal infections in humans, especially those resistant to existing treatments.

These antibiotics Lolamicin, Clovibactin and Solanimycin represent important steps forward in combating antibiotic resistance. By targeting unique mechanisms in bacteria and fungi, these compounds offer new solution for treating resistant infections while minimizing collateral damage to beneficial microbiota. As resistance to current antibiotics to grow, these discoveries could be crucial in developing effective treatments.

~PURVA PATEL & HETAL ALGOTER (S.Y. SEM - 4)

BUGS AS DRUGS

Dr. William Coley, recognized as the "Father of immunotherapy" initiated the practice of administering bacterial injections to cancer patients in the late 19th century. His work established a connection between immune system stimulation and tumor regression. However, despite initial success, concerns regarding safety led to a decline in the utilization of this method.

Recent advancements in the fields of immunology, microbiology and synthetic biology have renewed the interest in utilizing bioengineered bacteria for cancer treatment. Researchers are actively developing probiotic bacteria capable of colonizing tumor sites and directing the activity of T cells, thereby highlighting the potential of bacteria as therapeutic agents.

Dr. Tal Danino observes that while certain bacteria can inhabit healthy organs, tumor-inhabiting bacteria exhibit a preference for environments that provide protection from the host's immune system. Dr. Danino's research focuses on harnessing the inherent properties of bacteria for tumor-specific diagnostic purposes. Researchers have engineered a strain of probiotic bacteria, *Escherichia Coli* Nissle 1917 which employs chimeric antigen receptor (CAR) therapy, a versatile approach that allows for customization with any antigen-binding domain. This CAR is designed to target green fluorescent protein (GFP) antigens, enabling tumor detection and facilitating recognition and attack by T cell. The initial In vivo testing Involved injecting the engineered bacteria into subcutaneous tumors in immunodeficient mice. The results demonstrated that the engineered probiotic CAR effectively inhibited tumor growth and enhanced T cell activation within 48 hours. Prior to initiating human trials, researchers must address the issue of the engineered bacteria's potential toxicity. The research team is currently developing a translation strain that will enable its transition to humans. This ongoing work exemplifies how engineered systems can effectively combine multiple functions, thereby advancing the field of microbiome engineering.

~JAHANVI PATEL & PRINSI YADAV (S.Y. SEM - 4)

NOBEL LAUREATES

The 2024 Nobel Prize in Physiology or Medicine was awarded jointly to Victor Ambros and Gary Ruvkun for their groundbreaking work on microRNA and its critical role in post-transcriptional gene regulation.

VICTOR AMBROS GARY RUVKUN

Their discovery, made in the early 1990s, revealed that microRNAs are small, non-coding RNA molecules that regulate gene expression by binding to messenger RNA (mRNA) and preventing translation into proteins. This finding revolutionized our understanding of genetic regulation and had profound implications for fields like molecular biology, disease research, and the development of new therapeutic strategies.

MicroRNAs are small RNA molecules that do not code for proteins but instead regulate gene expression by interacting with messenger RNA (mRNA) to either degrade it or inhibit its translation. This discovery uncovered an entirely new layer of regulation, which plays a fundamental role in how cells differentiate and specialize in multicellular organisms.

The recognition of over a thousand microRNAs in the human genome further emphasizes their significance, not only in development and differentiation but also in diseases like cancer, where gene regulation can go awry. Ambros and Ruvkun 's discovery has opened up exciting possibilities for therapeutic applications, especially in the fields of genetics and medicine. Before their work, scientists believed that transcription factors, which bind to DNA and control which genes are turned on or off, were the primary means of regulating gene expression. However, **Ambros and Ruvkun 's** research introduced a surprising twist to this understanding. They discovered that microRNAs, tiny RNA molecules that do not code for proteins, can also regulate gene expression. These microRNAs don't directly bind to DNA like transcription factors but instead control gene activity by binding to mRNA, the intermediary between DNA and protein. By binding to specific regions of mRNA, microRNAs can prevent mRNA from being translated into protein, thus adding an entirely new layer of regulation.

Ambros and Ruvkun 's work essentially expanded our view of how genes are regulated, revealing that gene expression is influenced not only by what is "on" or "off" in the DNA but also by complex interactions involving non-coding RNA molecules. Specifically, they focused on two mutant strains of ***C. elegans***, lin-4 and lin-14, which showed defects in the timing of activation of specific genetic programs.

These defects were crucial for the proper development of various cell types, such as nerve and muscle cells, in the roundworm.Lin-14 is a gene that plays a role in the development of ***C. elegans*** by controlling the timing of certain cell processes. lin-4 was a gene that appeared to negatively regulate the lin-14 gene, essentially acting as a "brake" on lin-14's activity. However, what was unclear at the time was how lin-4 regulated lin-14. Ambros had already observed that lin-4 seemed to suppress lin-14 activity, but the exact mechanism was a mystery. They discovered that the lin-4 gene did not produce a traditional protein, as had been expected for a regulatory gene. Instead, it produced a small non-coding RNA molecule, which did not encode a protein but instead acted directly on lin-14 mRNA. The lin-4 RNA molecule binds to the lin-14 mRNA and blocks its translation into protein, thus downregulating its activity.

MicroRNAs are vital for normal cell function. Without them, cells and tissues fail to develop properly. For instance, embryonic development and the specialization of cell types are tightly regulated by microRNAs. These small RNA molecules help ensure that the right genes are turned on and off at the correct times during development. Furthermore, mutations in genes coding for microRNAs or the proteins involved in their production can lead to several genetic disorders in humans.

Ambros and Ruvkun 's unexpected discovery in the tiny worm ***C. elegans*** opened the door to a whole new dimension of gene regulation. Their work not only changed how scientists understand the regulation of gene activity but also paved the way for exploring how microRNAs contribute to health and disease. This discovery has had profound implications for genetics, molecular biology, and medical research, with applications ranging from understanding

~DHWANI PATEL (T.Y. SEM - 6)

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GUJARAT CANCER RESEARCH INSTITUTE (GCRI)

INTRODUCTION

Ahmedabad, a city celebrated for its culture and progress, is home to the prestigious Gujarat Cancer and Research Institute (GCRI) which was established by Dr. Karsanbhai K. Patel, a prominent industrialist and philanthropist from Gujarat. The institute was founded in 1972. Located within the Civil Hospital Campus, GCRI is one of the largest cancer care centres in the region and a key contributor to microbiology and biotechnology. Its NABL-accredited Microbiology Department is a cornerstone of its research and diagnostic excellence.

WHY GCRI IS SIGNIFICANT?

GCRI is not just a cancer care center; it is a hub of scientific innovation and education. Its presence elevates Ahmedabad's stature as a center for advanced medical research, attracting researchers, clinicians, and students from across the nation. The institute's work directly impacts cancer care while contributing to the broader fields of microbiology and biotechnology.

COURSES THEY OFFER

The institute offers medical and para- medical courses specializing in oncology. Super-specialty (M. Ch., DM, FNB) and MD programs cover fields like Medical, Surgical, Gynecological Oncology, and Radiation Oncology. Fellowships provide advanced training in Surgical and Gyn Oncology, Radiotherapy, and related areas. Para-medical courses include M.Sc. in Cancer Biology, Medical Physics, PGDMLT, and CMRT. These programs are affiliated with reputed universities and focus on comprehensive oncology education.

NABL-ACCREDITED MICROBIOLOGY DEPARTMENT

The NABL-accredited Microbiology Department at GCRI plays a pivotal role in cancer care and research. It specializes in:

***Infection Diagnostics**: Identifying and managing infections in immunocompromised cancer patients, ensuring precise and timely treatments.*

***Antimicrobial Resistance Studies:** Monitoring and analyzing resistance patterns to guide effective therapeutic strategies.*

***Cancer-Related Microbial Research**: Investigating the role of microbiomes in cancer development and progression, as well as exploring microbial biomarkers for early cancer detection.*

~ADITI DUTT (S.Y. SEM - 4)

SCRATC

CROSSWORD

• ACROSS ➡

I. A Space, chamber or cavity forming the entryway to another cavity called as _____ . (9)

II. Penetrating _____ that ionize atoms & molecules causing errors in S-P backbone of DNA. (4)

III. The raised, rounded, most prominent part of a bivalve mollusk's shell; called as _____. (4)

IV. A symptom & the name of the disease on oats caused by ***DITYLENCHUS DIPSACI***; TULIP _____.(4)

• DOWN ⬇

I. In Diatoms one of the two major pieces of the frustule; the each cover one of the cell & are separated by the girdle.(5)

VI. A gene that inhibits progression towards neoplastic transformation called as TUMOR _____ .(10)

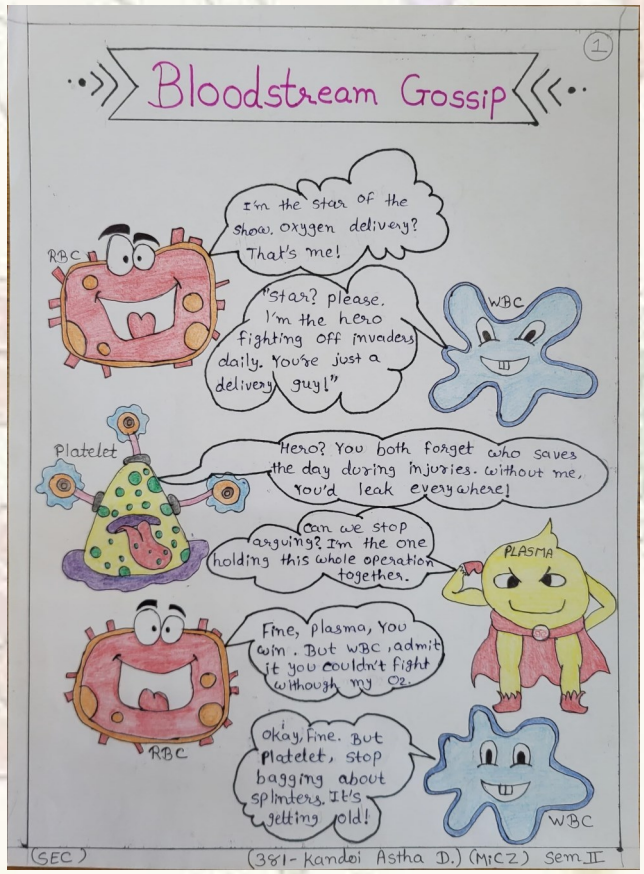
VII. An unidentified_____ is a substance in a drug that is limited by a general acceptance but not individually listed.(8)

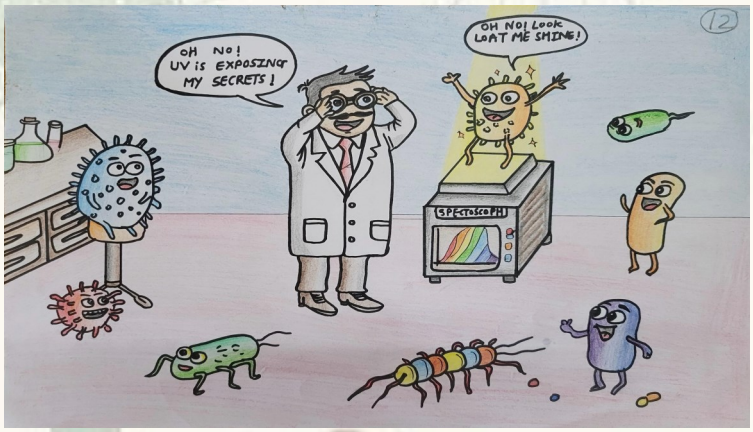
VIII. Which types of spores produced by unilocular organ(~an organ that has a single chamber).(9)

IX. The phenomenon where genetic variations, particularly alleles, are shared between different species ; called as _____ .(9)

Scan for answers

TINYTOON





H IT

Microzzles

I am a bacterium that causes tuberculosis and leprosy and have a thick, waxy cell wall. Who am I?

I am a virus that can integrate into the host genome and remain dormant as a provirus. Who am I?

I am a bacterium responsible for causing cholera, producing a toxin that induces watery diarrhea.

I am an antibiotic-resistant protein that binds to penicillin, deactivating it. Who am I?

MICROTIMES

● Microbial Ecology ● Infectious Diseases ● Biotechnology

14 February, 2025

For For More : @msmg_mgscience

THE MICROBIOLOGY REPORT: TRENDS & DISCOVERIES

Discovery of New Viruses on Common Household Items

A study from Northwestern University revealed that hundreds of previously unknown viruses, specifically bacteriophages, reside on everyday items like toothbrushes and shower heads. These viruses target bacteria rather than humans and offer promising potential for future biotechnological innovations, such as combating antibiotic-resistant bacterial pathogens through phage therapy.

Gut Bacteria Byproduct Protects Against Salmonella

Researchers at the Stanford University School of Medicine have identified a molecule that serves as natural protection against one of the most common intestinal pathogens.

Propionate, a byproduct of metabolism by a group of bacteria called the Bacteroides, inhibits the growth of Salmonella in the intestinal tract of mice, according to the researchers. The finding may help to explain why some people are better able to fight infection by Salmonella and other intestinal pathogens and lead to the development of better treatment strategies.

ACTIVITIES

Visit to Haster Bioscience —7th– Jan - 2025

Magazine launch— Microbyte (Vol-1) Dt:-Sept-2024

GiBioN State Level Competetion Dt:-9th-Feb-2025

ACHIVEMENTS

3rd prize in GiBioN Scitoon : Miral Raiyani

1st prize in GiBioN Article : Aditi Dutt

Runners up in Cricket Intercollege Sports
TY (Sem-5)

Science Manthan : Poster Making
SY(Sem-3)

FACULTY ACHIEVEMENTS:

Leena Patel, K R Shah, S Gondaliya, P M Patel, and R K Patel. (2024). Exploring Saline Desert Actinomycetes for Novel Anti-MRSA Antibiotic Production. *The Bioscan, 19*(Special-Issue-1)451–460.

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