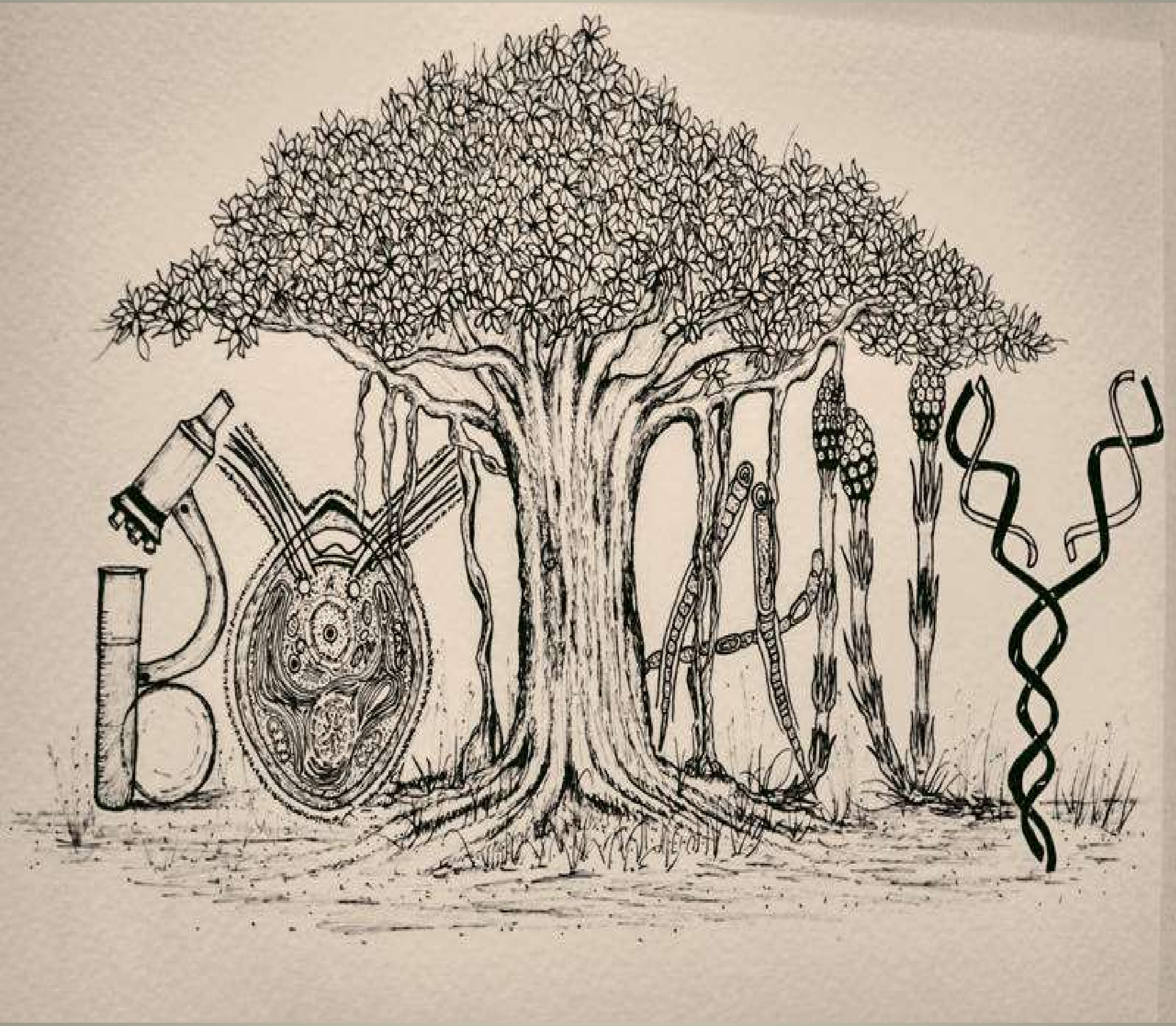
E - Magazine

LA FLOR

The Bloom of Hope



Post Graduate Department of Botany
Barasat Government College

2021

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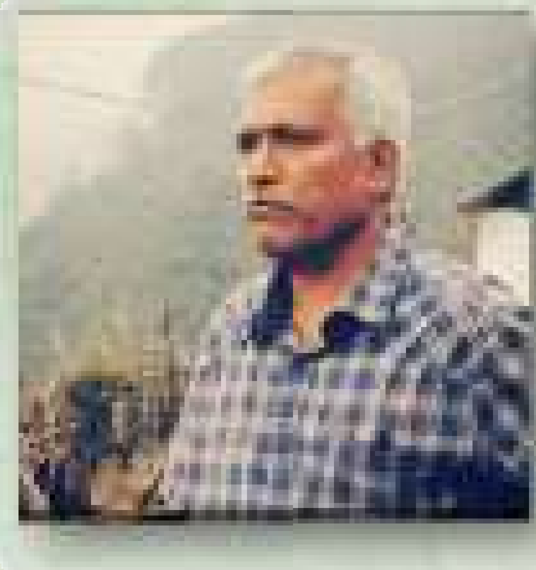

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‘From the Desk of Principal

BARASAT GOVERNMENT COLLEGE

The PG department of Botany, keeping its long standing standard and the tradition, is going to publish an e-Magazine and several Hard copies of that, in order to enrich the students and building their confidences for subsequent entrance in broader Canvas of Research and Academic arena. It also aims to provide impetus and enthusiasm to the young faculties of the particular subject and other subjects concerned with it, thus ultimately make a strong bridge in student teacher chemistry and relationship. The content is pedagogic, in broad spectrum, in depth and versatile in nature manifesting the subject Botany is also a thrilling one.

The Principal wishes it a grand success with far reaching impacts. Best wishes also to the students and to the members of the Editorial Board of the magazine and the Department of Botany as a whole.

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Dr. Samar Chattopadhyay, WBSES
Principal
Barasat Government College

'From the Desk of

Head of The Department

I feel enormous pleasure to see that the Department of Botany (UG & PG), Barasat Govt. College is going to publish one excellent E-Magazine in 2021 under the leadership of Dr. Nirmalendu Das (Associate Professor) where there is a real diversity can be marked from various articles, photos, literary and scientific works contributed by the students and some faculty members of this department.

I would like to congratulate all who are involved in this task even within the threat of Covid -19 pandemic. We know that any true effort can overcome all barriers. This is a simple example of it. I must express my gratitude and thanks to our Honourable Principal of this college for his constant encouragement and involvement in this event. I, finally, hope that this effort will be fruitful and persuade to our juvenile students for getting the pleasure of creativity. Best wishes to all.

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Dr. JuktaAdhikari

Professor & Head,
Department of Botany,
Barasat Govt. College

‘From the Editor’s Desk

Dr. Nirmalendu Das
Associate Professor
Department of Botany

‘All good things come to an end and then there’s always a new beginning’. Over the past one and half year, the COVID 19 pandemic has brought us call in an unprecedented situation and challenging times. We indeed, became jailbirds in our home, detached from all social activities. In an attempt to rejuvenate and be together once again, the students, faculties and staff members of Department of Botany, Barasat Government College have endeavored to publish e-magazine. College magazine is a forum where students, faculties and staff members can exhibit their creativity and thoughts. Every year, students of our department publish wall magazine. But in the present pandemic scenario, there was an urgent need to transform the form of display from conventional wall magazine to electronic version. The present volume of e-magazine, titled ‘La Flor’ meaning ‘The Flower’ in Spanish is a wonderful medley of creativity in various categories; from photography to art work, scientific poster designs to puzzles/ crosswords, stories, poetry, memoirs, and scientific articles contributed by undergraduate and post graduate students (alumni and present), invited guests, faculties and staff members.

Hopefully, this academic effort will be useful to enrich knowledge and give joy of reading to the readers. The students will be motivated to express their essence of talent, gain knowledge, and improve writing skill and thinking ability. It will also encourage imparting updated information and arousing social awareness to the community in general.

I would like to convey congratulations and appreciations to undergraduate and post graduate students (alumni & present) of our department for being as forefront worker of this gigantic task. I extend my gratitude and thanks to HOD sir and all faculties of this department for their constant cooperation and motivation to the students. I should express my utmost gratitude and sincere thanks to our Principal, Barasat Govt. College for his guidance and constant encouragement. Thanks are also due for the contributors who have made this e-magazine possible.

I am proud to present our readers the much anticipated e-magazine ‘La Flor’ in this festive season with heartiest wishes of merry Christmas and prosperous new year 2022.

আমাদের কথা....

দোতলা থেকে উপরে উঠতে, সিঁড়ি ঘুরতেই বড় বড় অক্ষরে লেখা মেন্ডেল ব্লক, ডিপার্টমেন্ট অফ বোটানি। এই সিঁড়ি পেরোলেই চোখে এক রঙিন চশমা এসে লাগে, চারদিকের প্রকৃতিকে অন্যরকম ভাবে দেখার, উপলব্ধি করার ইচ্ছা জাগে। যেই সালোকসংশ্লেষকে গাছের রান্না জেনে এসেছিলাম, তা থেকে উঠে আসে C_3, C_4, C_2, CAM। ঘাসের মধ্যে মিশে থাকা সাদা বা হলুদ ফুল হয়ে যায় ডেন্টেলা বা হারপেষ্টিস। মাননীয় শিক্ষক-শিক্ষিকাদের চক-ডাস্টারের জাদুতে ক্লাসরুমে জলবৎ তরলং হয় মাইক্রোবায়োলজি থেকে প্যাথলজি। কিন্তু হঠাৎই খেল দেখায় এক ভাইরাস। করোনার প্রভাবে বর্তমানে জেনেটিক্সের গল্প থেকে ব্যসিডিওমাইকোটিনার বুলার ড্রপের কার্যপ্রণালী সবই ইন্টারনেট, গুগল মিটের ভরসায়। কখনো কেটে কেটে যায় যোগাযোগ, কখনো বা খুবই মসৃণভাবে চলে। সহপাঠী থেকে স্যার ম্যাডাম - সবাই যেন অর্ধ-পরিচিত। সামনে দেখিনি, শুধুমাত্র ভিডিও ক্যামেরা আর গলার স্বরই অবলম্বন। কোথাও যেন এই প্রতিদিনের অনলাইন লিংক, স্ক্রিন প্রেসেন্টে হারিয়ে যায় শেষ মুহূর্তে ছুটতে ছুটতে ক্লাসে ঢোকা, সামনাসামনি ডাউট ক্লিয়ার, ফাঁকা সময় সহপাঠীদের সাথে গল্প, আলোচনা, তর্ক-বিতর্ক, কবিতা, প্রাকটিক্যাল আঁকা। সেই হারিয়ে যাওয়া ঘটনাগুলোর কিছুটা আভাস যেন পাওয়া গেল এই পত্রিকা প্রকাশের সময়। কেউ ধুলো ঝেড়ে বের করলো আঁকার সরঞ্জাম। গ্যালারি ঘেঁটে প্রতিযোগিতা ও ফটোগ্যালারির জন্য স্মৃতিমন্থন শুরু হল। লেখার জন্য অনেকে বেছে নিলেন বোটানির বিভিন্ন বিষয় । বিভিন্ন গবেষণা, নতুন নতুন আবিষ্কারের ওপর আর্টিকেল লেখার দিকে আগ্রহ দেখালেন আমাদের সহপাঠী, সিনিয়র, জুনিয়ররা। আবার কেউ পড়ার খাতা একটু দূরে রেখে গল্প, কবিতা, বেড়াতে যাবার ঘটনা লিখলেন। যেমন বর্তমান ছাত্র-ছাত্রীদের সৃষ্টিকে পত্রিকা সাদরে গ্রহণ করেছে, তেমনই পত্রিকা সমৃদ্ধ হয়েছে কলেজের সম্মানীয় প্রাক্তনীদের কলমে। বিজ্ঞান ও কৃষ্টির মেলবন্ধনে এমনই একএকটি পুষ্পে সজ্জিত হয়েছে আমাদের বিভাগীয় পত্রিকা LA FLOR।

আমরা আন্তরিক প্রণাম এবং ধন্যবাদ জানাই উদ্ভিদবিদ্যার ভিত্তিপ্রতিম শ্রদ্ধেয় শিক্ষক-শিক্ষিকাগণকে, যাদের অপরিসীম উৎসাহের ফসল এই পত্রিকা। শুভেচ্ছা জানাই আমাদের সকল সহপাঠী, ভাই-বোন এবং দাদা-দিদিদের যারা নিজেদের সৃষ্টি উপহার দিয়েছেন এই পত্রিকা সাজানোর জন্য।

শুভেচ্ছা এবং প্রণামান্তে,

প্রীতিকণা সিনহা,
অর্চা ভট্টাচার্য্য।

SCIENTIFIC
SECTION

Classification and Phylogeny of Algae Explained Through Endosymbiotic Theory

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Abstract

Heterogeneity of the informal taxonomic group "Algae" is established on the basis of wide range of diversification in morphology, modes of development, ultrastructure of cell and cellular organelles, biochemical pathways and genetic composition of the organisms that are placed into it. Consequent upon a series of research outputs, the parameters that have been identified for the recent classification of algal organisms into various divisions are – (i) fundamental structural organization of the cells (prokaryotic, mesokaryotic or eukaryotic), (ii) types of pigments in the vegetative cells and their relative amount, (iii) physical organization and chemical composition of the cell wall, (iv) chemical nature of the reserve food and their location in the cells, (v) types, number per cell, relative length and ultratsructure of flagella and basal bodies, (vi) ultrastructural features of plastids, mitochondria, (vii) types of mitosis and cytokinesis, (viii) cytoskeleton of zoospores, (ix) sequence analysis of rRNA molecules 16S rRNA and 23S rRNA for prokaryotic cyanobacteria and 18S, 28S rRNA or rDNA for eukaryotic algae, (x) modes of propagation, (xi) alternation of generations and life-cycles pattern. The major eukaryotic algal divisions created on the basis of above mentions parameters are - Glaucophyta, Chlorophyta, Rhodophyta, Heterokontophyta (Ochrophyta), Euglenophyta, Dinophyta, Prymnesiophyta, Cryptophyta, Chlorarachniophyta. This approach has revealed very fundamental differences between these divisions and established their phylogenetic relationship with other organisms and resulted in placement of algal organisms in different kingdoms or supergroups of the living world. Glaucophyta and Rhodophyta are placed in the subkingdom Biliphyta of kingdom Plantae; Chlorophyta is placed in the subkingdom Viridaeplantae of kingdom Plantae; Heterokontophyta, Dinophyta, Cryptophyta, Prymnesiophyta are placed in the kingdom Chromista. Euglenophyta is placed under the kingdom Protozoa; Chlorarachniophyta is placed under the

infrakingdom Rhizaria of kingdom Chromista. In tracing the origin of these diversified groups of organisms and tracing their phylogeny, endosymbiotic theory of origin of cellular organelles has played a significant role. Origin of plastids and the combination of features related to other cellular organelles is traced with the help of primary, secondary and tertiary endosymbiosis and endosymbiotic genetic transfer. This approach has clearly established the monophyletic and polyphyletic origin of various plastid types and the organisms containing those plastids. Molecular phylogenetic studies have revealed the following with regard to algal phylogeny – (i) the first group of photosynthetic protists to diverge from the eukaryotic line of descent well before crown group radiation is the Euglenophyta, (ii) the red algae form a distinct group with structural and genomic features where loss of flagella took place during the course of evolution, (iii) the heterokontophyta is a clearly defined monophyletic lineage characterized by the presence of synapomorphic character tubular, tripartite flagellar hair, (iv) the green algae form a natural division Chlorophyta which is divided into several classes on the basis of ultrastructural variations. It has been established that the charophycean green algae, which are put in Streptophyta are the progenitors of higher green plants, (v) the division Chlorarachniophyta characterized by CER and nucleomorph arose by secondary endosymbiosis involving green algae.

Encephalartos woodii : The Loneliest Plant in the World!

Dr. Sautrik Basu

Assistant Professor, P. G. Department of Botany, Barasat Govt. College

This is a story of a plant that long ago once ruled the world. The story is about *Encephalartos woodii*, a Cycad that today is the very last of its kind. Cycads are the survivors of a very ancient race of plants and are botanically remarkable because of their great antiquity, exceptional vitality and remarkable ornamental value. In many aspects cycads can be regarded as the **crocodiles of the plant world**. They have been around when the dinosaurs roamed the earth (~ 300 million yrs ago) and they often provided shade for Triceratops, a safe perch for Pterodactyls and a tasty snack for Brontnosaurases.

At one point during the Jurassic, Cycads made upto 20% of all the plants on earth and covered nearly every corner of the globe (from Greenland to Antarctica). However, as the dinosaurs went extinct, ice ages came and went and new modern plants (conifers and fruit trees) started pushing the cycads their number started dwindling alarmingly. At present 38% of the extant cycads are on the IUCN red list and are facing the risk of extinction.

Our story dates back to 1895 when British botanist and Curator of the Durban Botanic Gardens, John Medly Wood (1827-1915) [Fig:1 (A)] while walking through the Ngoya forest in Zululand came across a solitary, interesting looking palm like plant growing on a steep slope on the margin of Ngoya forest (Northen region of Kwa-Zulu Natal province) in South Africa. The plant was nearly 12 ft tall, had multiple trunks and was massive in appearance (diameter of 18 inches and approximate weight somewhere in between 590–680 kg]. Dr. Wood had some of the stems pulled down and sent one of them to London in a box.

After the initial discovery in 1895 Wood sent his deputy James Wylie in 1903 to fetch some of the smaller offsets from the original specimen. Wylie collected a few and three out of them were experimentally grown in the Durban Botanic garden [Fig: 1 (B)]. In a later expedition conducted in 1907 Wylie noticed that out of the 4 remaining trunks the largest one was badly mutilated. After witnessing this 2 of the existing unmutilated trunks were collected by Wylie (both of which are still to be seen in the Durban Botanic garden) [Fig: 1 (C)]. By 1912 there was only one 3 m tall trunk left in the wild, which was hastily removed and sent to the Government Conservatory located at Pretoria, where the plant eventually succumbed to death in 1964. There was a great deal of confusion regarding the botanical identity of the specimen. After its initial discovery, the plant was confused to be a cultivar of *Encephalartos altensteinii* and it was not until 1908, when English horticulturist Henry Sander described it as a new species and named it *Encephalartos woodii* after its discoverer J.M. Wood.

Meanwhile, portions of the original stem that were collected by J. M. Wood in 1895 landed up in the Palm house of Kew Gardens where it grew and turned out to be a male producing large colourful staminate cones [Fig:1 (D)]. This implied that all other plants collected and raised from the parent plant were males and shared the exact genes of the original specimen.

Like all other cycads *E. woodii* is also dioecious and it needs a female mate in order to reproduce. Hence, in absence of a suitable mate all captive grown *E. woodii* are incapable of producing offsprings naturally and are likely to have no successors. Thus, *E. woodii* is the most solitary organism in this world. Throughout the year multiple concerted efforts have been made by taxonomists, horticulturists and plant enthusiasts in order to find a suitable mate for the solitary male *E. woodii.* Unfortunately, all these efforts have proved fruitless as no plants were ever discovered in the wild. Although, this technically makes Wood's cycad the only one of its kind, the statement is not entirely accurate. The Wood's cycad has been fairly agreeable to cultivation and is well represented in few Botanic gardens and Cycad collections (there are only around 110 individual male plants in botanical gardens and private collections around the world). However, in spite of its availability in Botanical conservatories the plant can never be re introduced to the wild due to looming risk of theft.

In an effort to resurrect the species, plant scientists and horticulturists have been backcrossing *E. woodii* with *E. natalensis,* with which it forms fertile hybrids [Fig:1 (E)]. If the hybrid and the progenies in subsequent generations are repeatedly crossed to *E. woodii* the female offspring would be very close to a female *E. woodii*. Genetic analysis of Cp DNA of F_1 hybrids between *E. woodii* and *E. natalensis* however have clearly elucidated that the multigenerational hybrid offsprings possess *E. natalensis* chloroplast only, as a result of which they could never be pure *E. woodii.* There is also a faraway possibility that a spontaneous sex change will occur some day in one of the plants which in course of time will rescue the last surviving individual form extinction. Although cases of spontaneous sex reversal is not uncommon in Cycads. The process is rather obscure and chances of spontaneous sex change in *E. woodii* are rather remote.

E. woodii is an interesting and enigmatic plant which has attracted considerable scientific attention since the beginning of the 20th Century and a great debate still exists regarding its origin and true identity. Some workers believe that it is a natural hybrid between *E. natalensis* and *E. ferox* (due to its close resemblance with *E. natalensis)* others still believe that it is the last remaining relic of a bygone era. Like most other cycads which are already on the top of the list of endangered plants the future of *E. woodii* also does not look very bright. Although cycads live for thousands of years and are unlikely to die soon, they will not be able to reproduce If

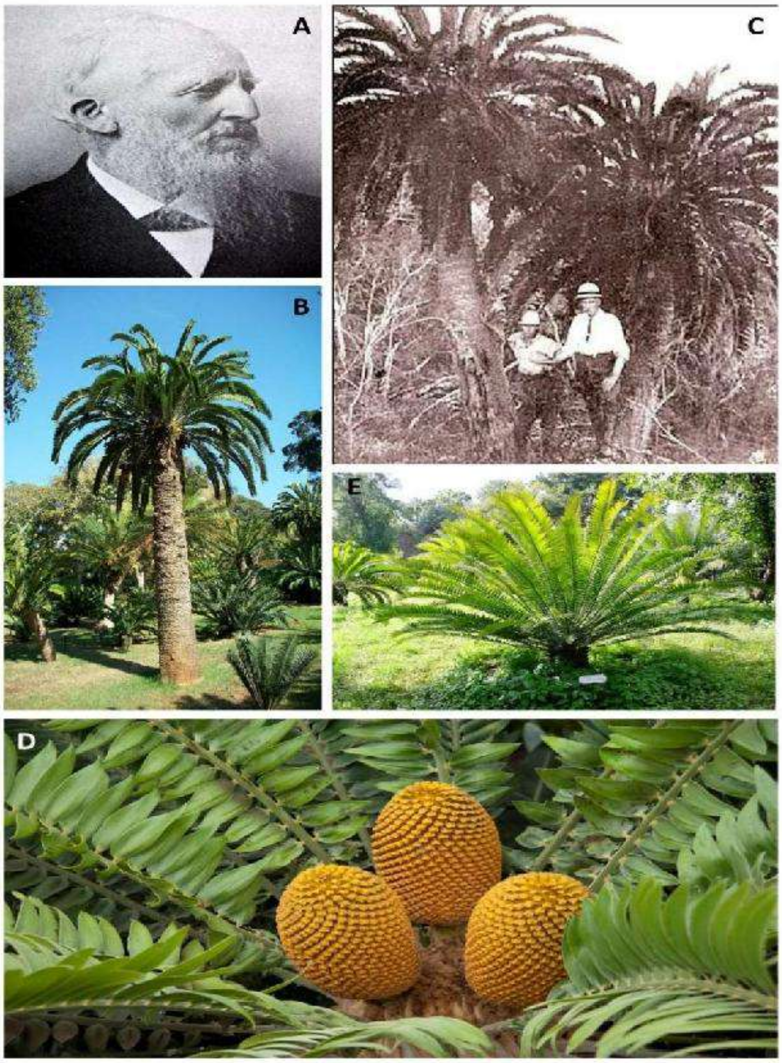

Figure 1: (A) John Medly Wood (1827-1915): The discoverer of *E. woodii,*

(B) Old specimen of *E. woodii* (collected in 1907) at the Durban Botanic Gardens,

(C) The last two stems of *E. woodii* at Nogoye in the early 1900s,

(D) *E. woodii* bearing male cones (At Kew Gardens),

(E) *E. natalensis* x *E. woodii* hybrid at Orto botanico di Palermo.

a female mate cannot be found. However, to this day researchers are still looking for a female mate for this 126 year old lonely bachelor!. After all, it's a big world there might just be a chance of an accidental discovery!!.

Further Reading

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Bioinformatics - A Quintessential Skill for Biologists

Sayak Ganguli (Ph.D.)

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PG Student (2003 - 2005)

Background

Bioinformatics, Computational Biology and its foster child System Biology have gradually emerged as significant players in the practice of both the knowledge and skill for a biology student and a teacher. A simple lecture on Protein Structure can be augmented by including the use and demonstration of an easy to use software such as Pymol or Rasmol, which provides the students with an insight as to how a protein looks in 3D and takes the visual quotient to a new level. This discipline has completed its golden jubilee last year amidst the pandemic after being coined in 1970 as the "the study of informatics processes in biotic systems" by Professor Paulien Hodgeweg a dutch scientist. Very few people know that probably the first computer program that dealt with solving a biological problem was designed to predict a simple primary protein structure by Dayhoff and colleagues in the year 1962. Realizing the need for spreading awareness and building up skilled manpower, the Department of Bio-technology, Government of India launched a program in early 2006 - 2007 under the BTIS Net platform where the onus was Biology Teaching through Bioinformatics (BTBI) and several Bioinformatics Infra-structure Facilities (BIF's) were initiated all around India, for promoting the subject. I believe that very few students and faculty are aware of the existence of such centres (For a complete list visit: http://www.btisnet.gov.in/bif.html). It is only recently that under-graduate and post graduate syllabi of different Universities in West Bengal have been augmented with some elements of this discipline; however, skilled faculties having suitable hands on experience are really handful and most rely on chauffeur knowledge, as a result the learning experience remains incomplete for the students. This article shall attempt to provide an agog biologist with the glimpse of some recent successful scientific achievements which would not have been possible without the intervention and efforts of computational biologists or bio-informaticians around the world. For the curious mind these are just the stepping stones for subsequent progress and an opportunity to explore this quintessential skill in their own terms.

Solving the Protein Folding Problem using Artificial Intelligence

The protein folding problem is one of the most important unsolved mysteries of modern biology (doi:10.1146/annurev.biophys.37.092707.153558). In the year 2019; Google's AI firm "Deep Mind" reported an algorithm called "Alpha Fold (doi: https://doi.org/10.1038/d41586-019-01357-6)," which was established by combining two emerging techniques involving deep neural networks which yielded a set of scores which were then optimized using gradient descent method (Figure 1).

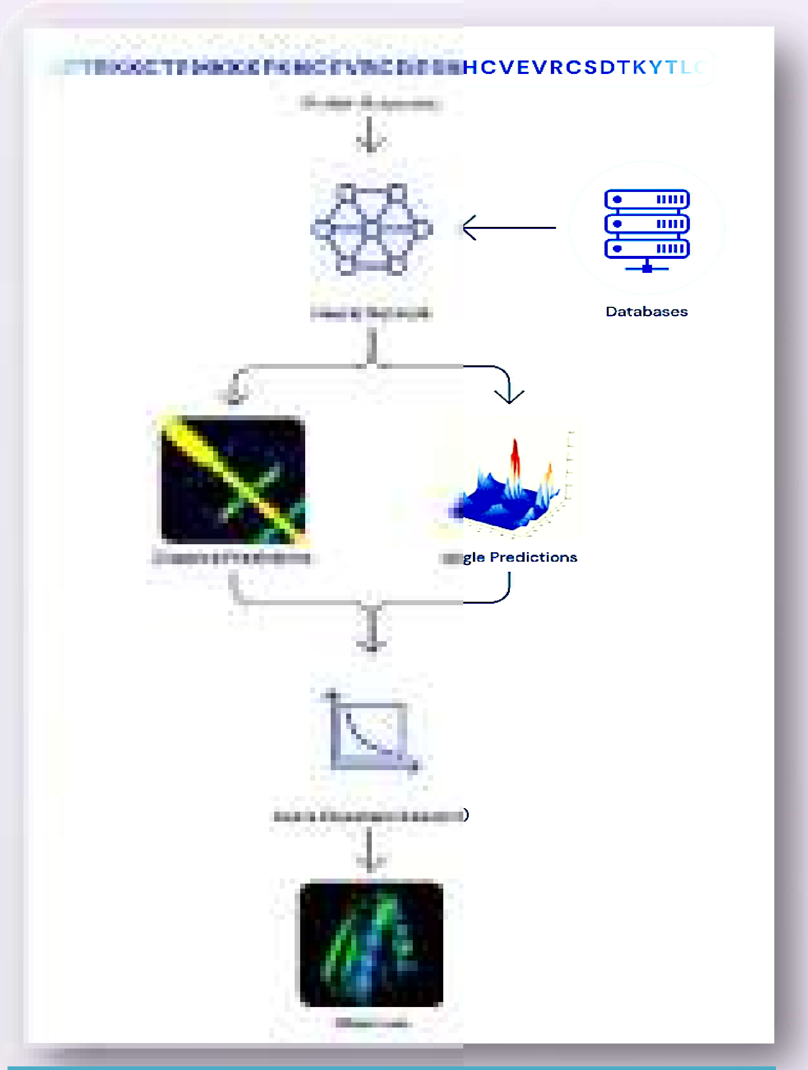

Figure 1: The background algorithm of Deep Minds Alpha Fold (modified from: https://deepmind.com/blog/article/AlphaFold-Using-AI-for-scientific-discovery)

The 3D models of proteins that are generated using Alpha Fold has been seen to generate, far more accurate structures. The Alpha Fold code used at CASP13 is available on Github (https://github.com/deepmind/deepmind-research/tree/master/alphafold_casp13) for anyone interested in learning or replicating the results obtained.

The Complete Human Genome - T2T Consortium using ONT and Hi Fi Sequencing

In 2020, almost 30 years after the launch of the Human Genome Project, the first “GAPLESS” assembly of the human genome was published by Miga, Koren and colleagues described as the telomere-to-telomere (T2T) assembly.

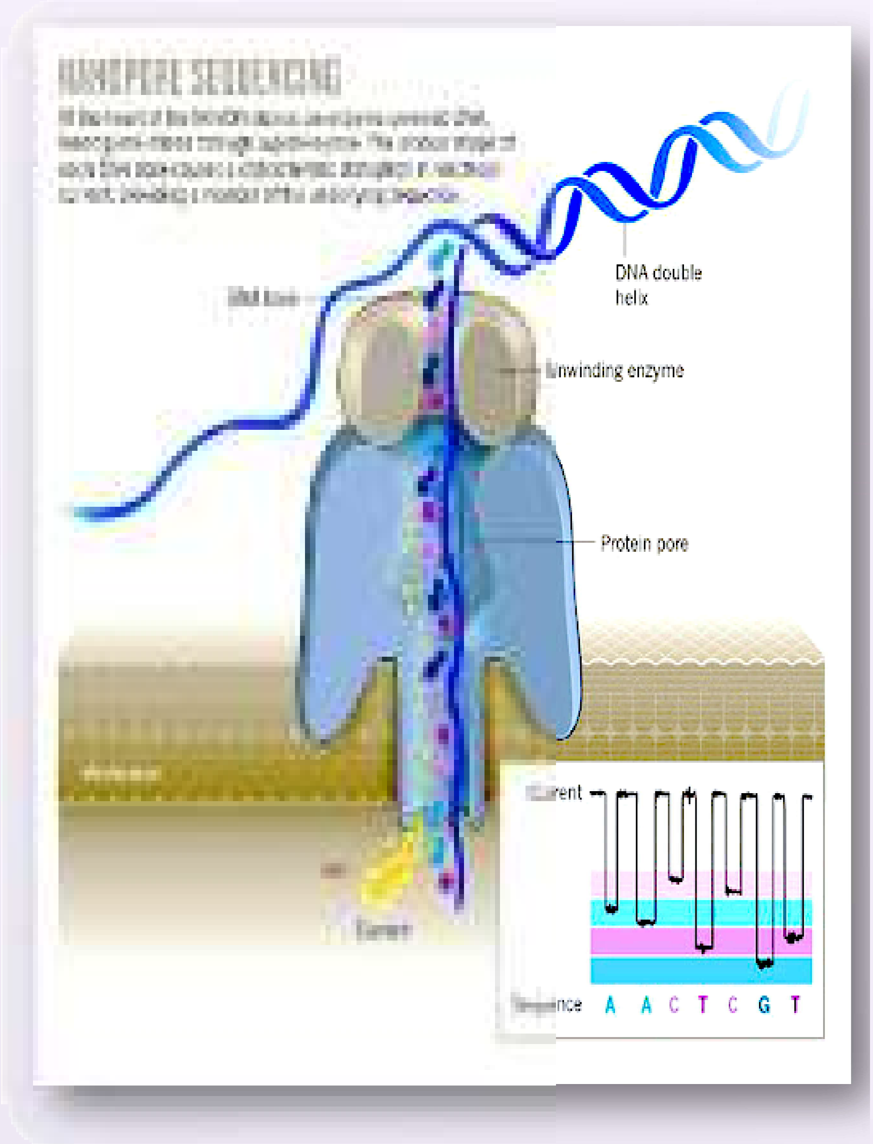

Figure 2: Highlights of ONT technology (Adapted from: http://blogs.nature.com/blog/tag/oxford-nanopore-technologies/)

The consortium used two advanced sequencing techniques - Oxford nanopore technology (ONT) method and PacBio Hi Fi sequencing. The ONT method (Figure 2) had been extremely useful during the EBOLA epidemic of 2014 where the Minion platform was used to detect infected patients easily (doi: 10.3201/eid2202.151796). However, the Hi-Fi platform was a more recent advancement which utilized the traditional Single Molecule, Real-Time (SMRT) Sequencing technology; producing long reads with the modification being the incorporation of circular consensus sequencing method (Figure 3) thus providing >99.9% accuracy. This breakthrough was the work of the T2T consortium and brought together sequencing technologies and bio-informatics algorithms that enabled the analysis and comparison of the generated data that had been developed in the preceding six years (https://www.nature.com/articles/d42859-020-00117-1).

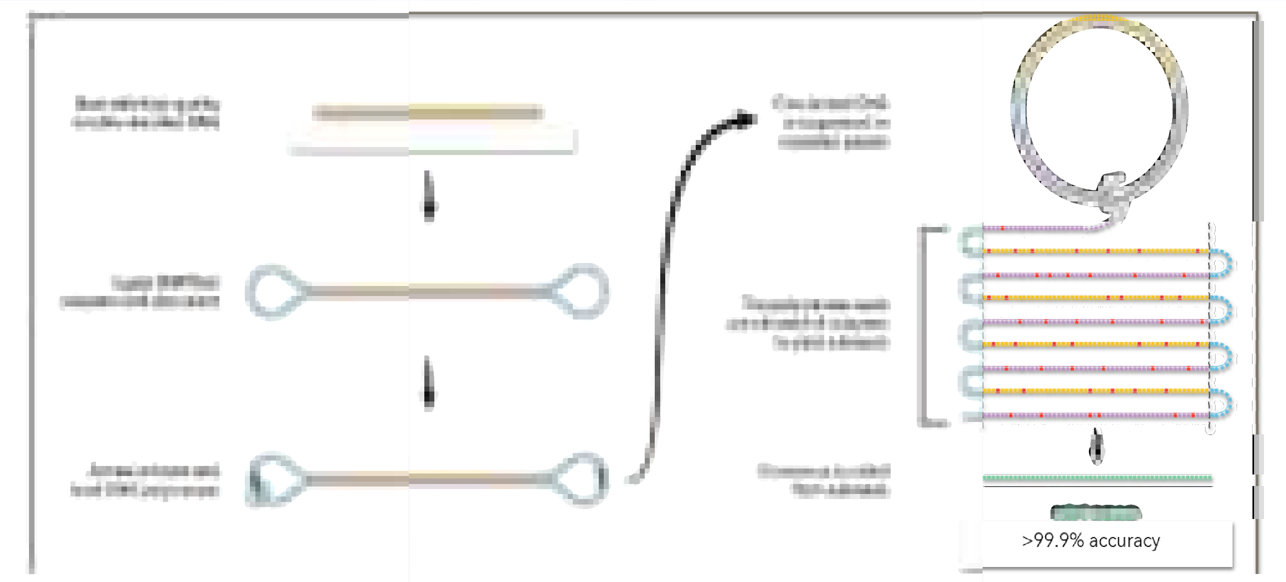

Figure 3: Outline of Hi Fi sequencing using circular consensus sequencing method (Adapted from https://www.pacb.com/smrt-science/smrt-sequencing/hifi-reads-for-highly-accurate-long-read-sequencing/)

SARS - COV2 and Vaccine Development

When the pandemic hit us in early 2020, the scientific community responded to the challenge by tackling the incessant waves of the virus using a two pronged approach - the first was to generate high quality complete genome sequences from all around the world made possible by advances in sequencing methodologies as discussed above. This resulted in the GISAID database [https://www.gisaid.org/] being populated with more than 10000 complete genome sequences of both ancestral (from the theoretical patient zero) and mutant strains. hCoV-19/Wuhan/WIV04/2019 (WIV04) was the official reference sequence employed by GISAID (EPI_ISL_402124). WIV04 was chosen because of its high-quality genome sequence and because it represented the consensus of a handful of early submissions for the beta corona virus responsible for COVID-19. (Pilailuk et al 2020). WIV04 is representative of an identical to the early outbreak sequences. WIV04 was isolated by the Wuhan Institute of Virology from a clinical sample of a broncho alveolar lavage fluid (BALF) collected at the Wuhan Jinyintan Hospital in Hubei Province on 30th December 2019 from a symptomatic patient, a retailer working at the Huanan Seafood Wholesale Market. BALF was used for RNA extraction and metagenomic next-generation sequencing (NGS). The consensus sequence was obtained by de-novo assembly. (Zheng-Li Shi et al 2020). The second approach was the elucidation of the structures of the encoded proteins of the SARS-COV2; specifically the Spike protein. A recent paper elucidates the impact of the spike protein variations in context of the structure (Fig. 4).

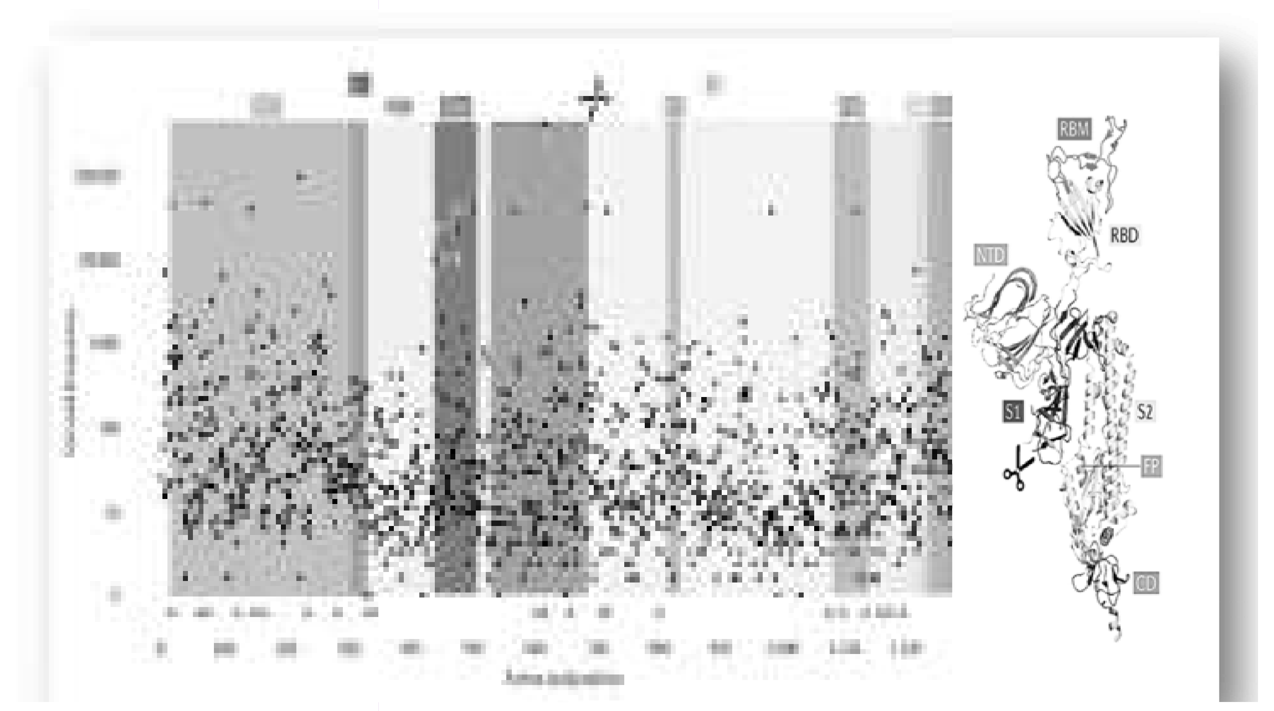

Figure 4: The domain organization of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike protein showing amino acid sequence variability (Adapted and Modified from: https://doi.org/10.1038/s41579-021-00573-0)

This was only made possible by the intervention of comparative modeling and ab initio modeling methods which allowed the elucidation of the structures until crystallographic structures were available. This humongous analysis effort was only made possible by the active involvement of Computational Biologists and Bioinformaticians from all around the world in unison with experimental biologists; which enabled us to formulate the different strategies of vaccines that has since been administered to millions of people worldwide.

Plant Pan Genomes, Machine Learning and Phenomics

Soon gone will be the days when you sit in a boring class of plant taxonomy and describe a supplied specimen using classical morpho-taxonomic approach and use Bengal Plants to identify the specimen up to the genus level. Machine Learning algorithms are being developed which will process images. A good quality image will be processed within minutes to reveal the true identity of the plants (Tang et al. 2019).

Similarly digitization and trait extraction followed by comparison with existing holotypes around the world would be achieved within a few moments. The latter will be made possible using Convolutional neural networks (Soltis et al 2020). NGS techniques described above has enabled a many fold advancement of plant genomics by tremendously increasing the number of sequenced genomes and identifying core and pan genomes which enables identification of genomic diversity (Bayer et al. 2020).

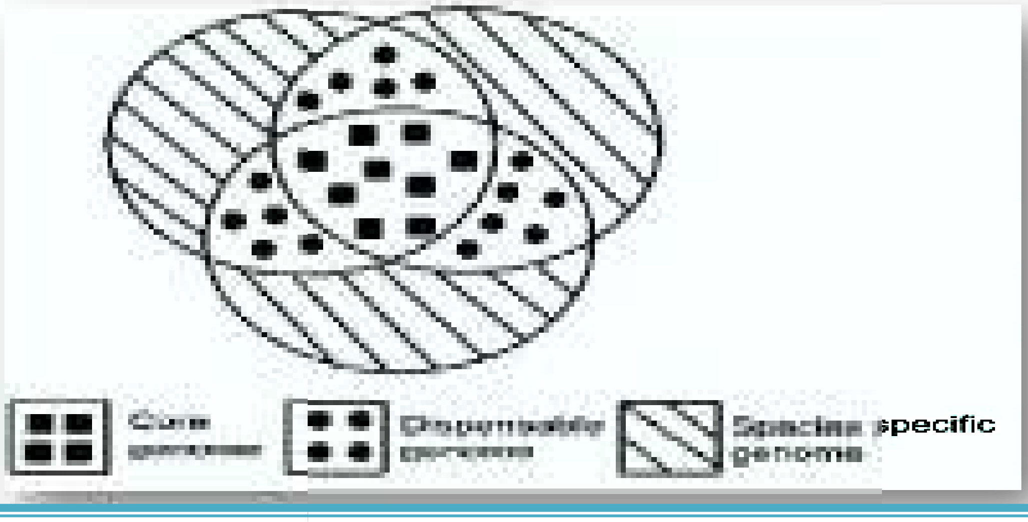

Figure 5: An overview of the concept of plant pangenome (Adapted and Modified from https://doi.org/10.1016/B978-0-12-817076-2.00014-7)

For those interested in the different data types that plant science has to offer in terms of diversity you can visit the repository of the Leibniz Institute of Plant Genetics and Crop Plant Research and the German Plant Phenotyping Network who have jointly initiated the Plant Genomics and Phenomics Research Data Repository (PGP) [https://edal-pgp.ipk-gatersleben.de/] as infrastructure to comprehensively publish plant research data. Here cross-domain datasets like image collections from plant phenotyping and microscopy, unfinished genomes, genotyping data, visualizations of morphological plant models, data from mass spectrometry as well software and documents are being gradually made available (Arend et al., 2016). These advances have only been made possible through active computational biology research.

The Way Forward

The above case studies should have provided the reader with the necessary insight as to the rapid and significant contributions that computational biology and bioinformatics is making in the entire biological science discipline. Within five years an individual is it faculty or research student who is unaccustomed with the nuances of computational biology or does not have strong collaborations with such researchers or scientists will become obsolete in the field of scientific research - that is the true reality however harsh it may appear. In the upcoming days the following essential elements need to be kept in mind for a successful career in biological research

1. Develop knowledge and skill in any programming language such as R or PERL or python would be mandatory if you want to succeed in cutting edge fields.
2. Access and listen to webinars, youtube channels for rich videos on essential topics and explore numerous journals through open access contents. Keeping abreast with such emerging methods, accessing blogs, podcasts and scientific articles should be a daily practice for researchers.

In conclusion, the desire to learn and adapt to the requirements of the era should be always inculcated from within since "change is inevitable"; otherwise soon people around you would evolve and you might find yourself being classified with a *Gingko* or a *Ornithorhynchus*.

Acknowledgement

I acknowledge all the faculty members namely Dr. Anadi Kumar Kundu; Dr. Kunal Sen, Dr. Sukumar Sarkar, Dr. Santanu Saha, Dr. Ashoke Das, Dr. Naim Uddin, Dr. Tulika Talukdar, Dr. Amal Kumar Mondal and Dr. Kalyan Kumar De; who took it upon themselves to carve out the first batch of Post Graduate students of Botany (2003 -2005) along with the esteemed members of the then Board of studies Prof. Amita Pal; Dr. Abhijit Banerjee and Prof. N.D. Paria, who supported and encouraged us during our course. I am proud to represent that batch of 22 students who faced numerous odds from different quarters and yet successfully went through to achieve their respective degrees. All my friends are successfully pursuing careers either in academics or in Government Administrative Services; which bears testimony to their resilience and indomitable spirit. Finally, I congratulate the current members of the Post Graduate Department of Botany who have worked really hard to make this e-magazine a reality.

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The Early Fungi on Earth

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The fungi are vital components of modern ecosystem. They do many unseen and unspectacular tasks. They are abundant in nature, where they break down numberless amounts of detritus and dead organic matters, playing key role in the recycling of minerals and carbon nutrients across the environment, without which the world would cease functioning. Fungi also induce plant life possible on planet earth. Vast networks of fungal mycelia stretching through soil function as nature's internet (www), transferring chemical signals, food, water and interconnecting plants. Not to mention their roles in our day to day life including fermenting alcohol, leavening bread, producing antibiotics, enzymes and causing diseases in plants and animals.

Scientists predicted that fungi might have an important role in the colonization of land by eukaryotes, and in appearance and succession of land plants and metazoans (Loron et al. 2019). But, much about the distant past of fungi remained a puzzle. While fungi and Animalia form monophyletic groups, branching off more than 1 billion years ago, making them more closely associated to us than plants, there is a wide gap in fossil records. However, recent research publications have provided insights about fungal existence before 400 million years ago, the age of oldest fungal fossils.

Previously, it was known that the specimens from Scotland (410 million years old) and spores of glomeromycotan fungi in Ordovician period (450 million years ago) from Wiscons into be the earliest fossil fungi. In May 2019, Palaeobiologist Corentin Loron at the University of Liège, Belgium, and his associates reported the discovery of minute fossils with filament like structures on 1 billion old rocks (Proterozoic era) from a region of Arctic Canada called the Grassy Bay Formation. These minuscule organisms were found in shallow estuarine water shale, a type of finely grained sedimentary rock, from a region south of Victoria Island on the edge of the Arctic Ocean in Northwest Territories.

Images of thin sections of fossils under electron microscope exposed branched filaments ending in round structures. The filaments were segmented by presence of septae, link walls found in some modern fungi. Thus scientists could identify the key features of fungus present in the fossil including spherical spores, the branched filaments connecting the spores, and their smooth unornamented bi-layered cell walls. The presence of chitinas observed after chemical analysis, in the specimens further convinced the investigators that they were conserved fungal specimens that died a billion years ago. Scientists named the fungus *Ourasphaira giraldae*. Spores of the fungus measured less than a tenth of a millimetre long and connected to one another by branched slender filaments. Scientist reported that SEM images exposed the presence of well-preserved, intertwined microfibrils (approximately 15–20-nm thick), making up the walls. Ultra-structural analyses by TEM showed that flattened microfossils are hollow, bilayered wall consisting of an electron-dense thick inner layer and a thin electron-weak outer layer. Thus the combined characteristics of complex morphology, comparatively large size, perpendicular branching, multicellular, double layered wall ultra-structure, and presence of chitin permits *Ourasphaira giraldae* to be placed among eukaryotes.

As stated by Loron, billion years old tiny fossils, found from the mud rocks are the remnants of the oldest known fungus on Earth. As preserved in estuarine shale of the Grassy Bay Formation, *Ourasphaira giraldae* probably lived in estuarine environment, and probably had transported from land or marine niches. The fungal colonization in terrestrial habitat may have preceded and facilitated the colonization of first land plants 470m years ago, through symbiotic association and soil processing. This would have provided better ecological niches, enriched substrate, nutrient uptake and enhanced aboveground productivity. The authors suggested that this may have implications for history of other lives on earth. Since fungi and Animalia are monophyletic group existed on the same branch of evolutionary tree before diverging, there must be a probability of existence of primitive animals like sponges similar to fungi.

But there have been controversy to this discovery. Loron claimed that the remnants contained chitin and other organic compounds and indicated the presence of chitin like fibres and chemo-signalling on the fossil surface. The ‘molecular clock’ analyses placed the fungal origin back to about a billion years. But palaeobiologist Christine Strullu-Derrien from Natural History Museum in London opined that single test cannot be conclusive on presence chitin in such a primitive fossil. Moreover, previous

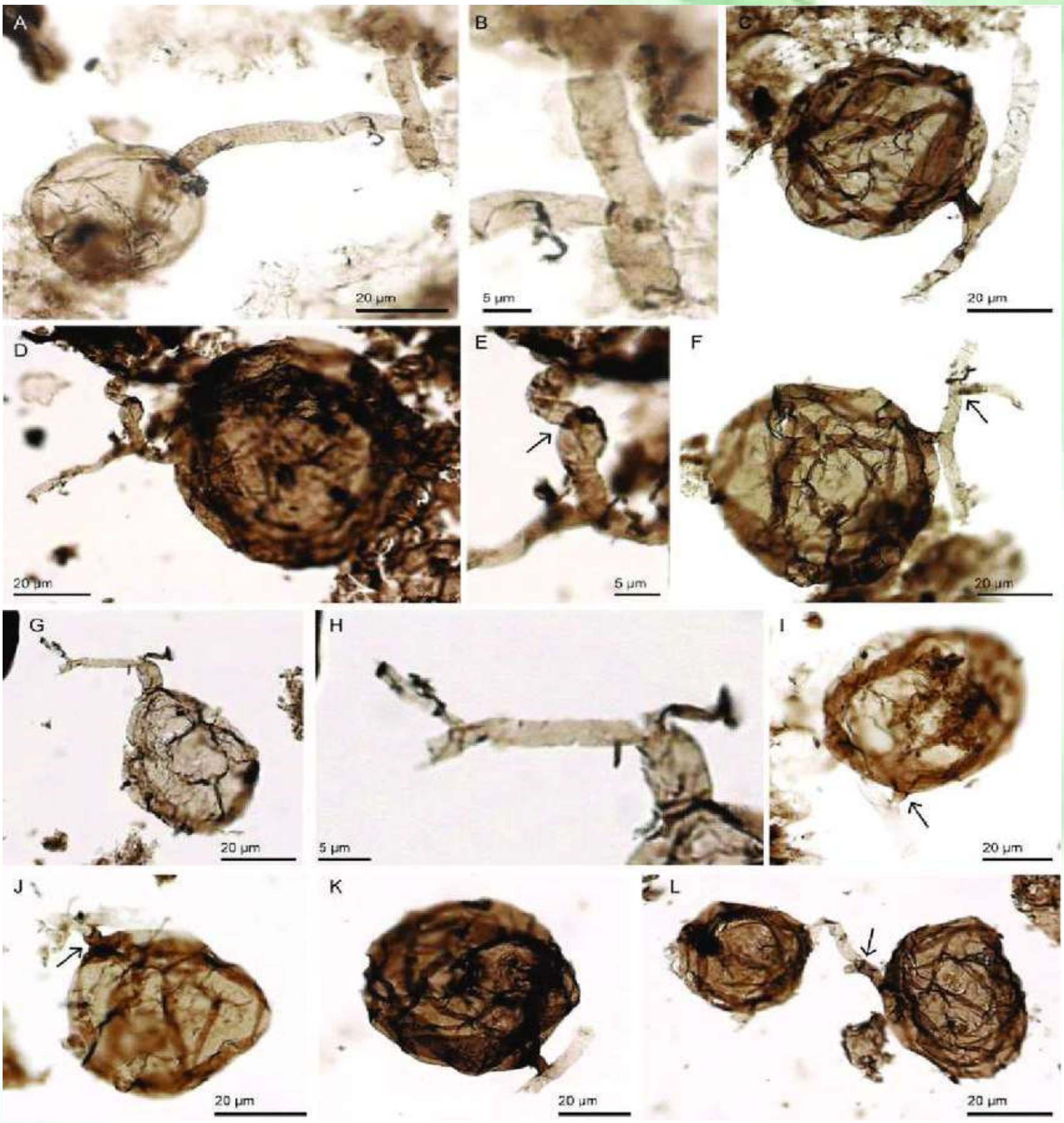

Figure 1: *Ourasphaira giraldae* new genus, new species. (A) Holotype; 74639-W46,3. (B) Detail from (A) showing the process branching. (C) 74710-Q52,2. (D) 74639Q43,1. (E) Detail of from (D). (F) 75309-G49,2. (G) Paratype; 74640-G29,2. (H) Detail of the process of (G) showing second and third order branching and septa between segments. (I) 74639-M30. (J) 74639-L27. (K) 74639-Z30. (L) Vesicles connecting through their processes; 74641-T31,4. Arrows in (E) and (F) show second and third order branching of the process; arrows in (I) and (J) show bulbous protrusions of the process base; arrow in (L) shows septate connection between processes. All specimens from 15RAT-021A1. (Reference: Organic-walled microfossils from the late Mesoproterozoic to early Neoproterozoic lower ShalerSupergroup (Arctic Canada): Diversity and biostratigraphic significance - Scientific Figure on ResearchGate. (Source: https://www.researchgate.net/figure/Ourasphaira-giraldae-new-genus-new-species-A-Holotype-74639-W46-3-B-Detail-from_fig7_329839018 [accessed 10 Dec, 2021]

molecular clock analyses suggested the presence of only a single celled simple fungi one billion years ago rather than complex filamented structure as found in fossils.

In another paper, Steeve Bonneville and his associates from Universitélibre de Bruxelles scanned a fossil from a piece of shale originating in the Democratic Republic of the Congo dated between 715 and 810 million years ago. Bonneville used three techniques to show that the filaments which extended like a woven mesh throughout, containing chitin on their exterior, thus showing clear signs of a fungus. One detection technique employed a fluorescent dye binding to chitin.

Figure 2: Researchers recently found a one-billion-year-old fossil fungus in the Northern Territories of Canada. Image: Robert Rainbird, Geological Survey of Canada. (Source: https://www.weforum.org/agenda/2019/05/scientists-found-a-billion-year-old-fungus-and-it-could-change-our-understanding-of-how-life-migrated-to-land/)

The other two involved the use of synchotron, a particle accelerator, bombarding material with fast-moving atoms to study more about chemical makeup of the sample. All the tests provided clear evidence of chitin in the fossil's filamentous network. Christine Strullu-Derrien found the results convincing, as a combination of three tests to analysis the chemical components of the fossil, converged to the same result, the chitin.

Figure 3: Fossilized fungal filaments are visible in the shale, found in the Democratic Republic of the Congo. (Source: https://www.science.org/doi/10.1126/sciadv.aax7599#)

In accordance with Bonneville et al. 2020, this weft of fungi lived in Neoproterozoic era, when the land was comparatively bare. Probably, only bacteria lived coating the ground forming biofilms. Land plants didn't evolve until 300 million years later. On the supercontinent Rodinia, this ancient fungal matt lived in sediments probably along edge of a lake or just under water, feeding on decaying organic matters of cyanobacteria and green algae. It is not even impossible that fungi behaved symbiotically with photosynthetic bacteria, though Strullu-Derrien clarified that the fungi would not have been the similar type which now symbiotically associate with land plants in soil. This may teach us about the evolution of fungi and algae as well as lichen that survived in primitive earth's extreme environment. Apart from symbiotic association, early fungi could also breakdown the detritus and acquire nutrition for land plants, thus paving ways for establishment of land plants on earth. Therefore, fungi played vital role to this evolutionary transition.

Figure 4: Aggregate of Type A filaments associated with small spheres. Microscopic image of the fungus-like microfossils. (Image credit: Andrew Czaja of University of Cincinnati; Source: https://www.livescience.com/fungi-fossil-oldest-terrestrial-life.html)

In a recent publication, oldest evidence of terrestrial fungus with filaments was found in a microfossil in sedimentary rocks from China's Doushantuo Formation in Guizhou Province, dating back Ediacaran period (635 million- 541 million years ago) (Gan et al. 2021).The authors assumed that the minute fossils belong to a period known as 'snowball earth' when the planet was locked in ice 750-580 million years ago. The land fungus by its presence at this key point may have helped in transition of earth from ice to a planet with a diverse ecosystem that could host various life-forms. With the breaking down of minerals, organic matter and recycling nutrients into soil, ocean and atmosphere, the ancient fungus had a role in reshaping geochemistry of the planet, thus paving ways for land plants and animals to appear and flourish eventually.

Therefore, the discovery of primitive fungi give an insight about a primitive earth, with different continents and atmosphere, much different from today's world and might be more advanced than we thought.

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A Brief Account of ROS Responses and Signal Transduction During The Drought and Biotic Stresses in Plants

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Plants while exposed to individual or combined biotic and abiotic stresses show unique complex responses to identify and resist the same. Biotic and/or abiotic stress initiates a cascade of immune response pathways to minimize damages and protect plant origin valuable resources against a host of factors during their developmental phases and growth under own habitats. These are biotic (mostly viruses, bacteria, fungi and insects) and abiotic (primarily cold, drought and salinity). This impact adversely on productivity of the crops also generates scarcity in global food supply. When a stress mechanism is identified within plant system defence mechanisms are activated. Pathogen associated molecular pattern (PAMPs) have been reported as the first line of defence response generates primary responses against biotic and abiotic stresses. Production of ROS, specific ion channels activation, kinase cascades are included as major responses. In addition to this accumulation of hormones are also reported. These are abscisic acid (ABA), salicylic acids (SA), Jasmonic acid (JA) and Ethylene (ET). It was noted that PAMPs immunity generates a similar molecular pattern while encountered with closely related biotic and abiotic stresses. The other line of defence comprises Resistance (R) gene activation where effector molecule triggered immunity specific to pathogen infection. Here in, proteins generated during defence mechanism confers programmed cell death. Combined stresses however generate a unique and specific way of responses varying from the stresses applied alone. Earlier reports suggest that simultaneously occurring multiple stress factors can mutually interact in an either antagonistic or synergistic manner depending upon the field conditions. Also the developmental stages, intensity and combination of the stress factors, geographical origin, and species specifications are responsible for differential responses. Combined drought-biotic stresses are most commonly encountered phenomenon affecting the plant health negatively.

These dual stresses in combination can have the following results such as: plant growth and development can be affected negatively; there could be an increased resistance against pathogen or pathogens augmenting plant's tolerance to drought stress; an efficient modulation of the prevailing defence mechanisms occurs in a unique manner which ultimately incurs tolerance towards combined stresses (Ramegowda and Senthil-Kumar 2015)

Plant Responses During Combined Stress

During drought stress, plants can become prone towards infection by pathogenic organisms. Common beans while subjected to drought stress become easily susceptible to a fungus *Macrophomina phaseolina* causing a charcoal rot. Another instance reportedly caused intense scorch symptoms while *Parthenocissus quinquefolia* was grown under drought condition. These were compared with plants showing infections, developed under well irrigated field conditions (McElrone et al. 2003).This augmented the infestations by pests and transformed minor pest to a devastating one. However on the contrary, drought-stricken plants could combat those pathogens which proliferated in saturated climatic conditions. Reportedly Drought stress helped to reduce *Botrytis cinerea* infection commonly known as gray mold, by half in tomato (Achuo et al. 2006). *Nicotiana benthamiana* when grown under drought condition, showed speck disease caused by a bacteria *P. syringae* pv. Tomato at a much lower intensity compared with non-infected plants (Ramegowda et al. 2015).

Crop improvement has been successfully implied against drought and other biotic stress tolerance in an individual manner. However, these programmes failed to exhibit effective tolerance to simultaneous biotic and abiotic stresses. It has been reported that rice cultivars showing drought tolerance were susceptible to nematode attack due to presence of deeply penetrating roots (Kreye et al. 2009). It was proposed that proper in depth studies of plant responses towards differential more than one stresses could be measured by implying simultaneous stress-factors and further research for individual set should be carried out.

Transcriptome Studies of Combined Stress Responses

During biotic and abiotic stress conditions complex signaling pathways were triggered. In one report, chickpea was infected with a fungal pathogen, *Ascochyta rabiei* in combination with stresses like drought, cold and high salinity. Further Transcriptome study was performed and the response was analyzed to the above mentioned stresses. The combinatorial effect of *A. rabie* with high salinity stress in chickpea generated differentially expressed transcripts in highest number, while compared with same pathogen in combination with cold or drought stress individually. Differential Transcriptomics play a significant role in deducing stress factors induced during signal transduction pathways subjected to multiple stress (Zhang et al. 2016). Improvement of crops against various stresses can be performed with the help of this study. Minimum investigations have been done so far on transcriptomic changes as per global data during combined biotic and abiotic stresses.

Induction of Signalling Pathways

Several interacting factors interactive in a complicated sequences resulted in biotic and abiotic stress signal transduction. Certain crucial gene products controlled combinatorial stress factors and thereby particular responses were elicited during combined biotic and abiotic stresses. A molecular characterization of events contributed towards our understanding of various stress tolerance in light of signal transduction pathways.

The internal regulatory pathways were mediated by MAPK cascades, while the transducing stimuli were supplied from environment (Rodriguez et al. 2010).According to a report by Andreasson and Ellis 2010, after activation of MAPK reactions; several transcription factors that belonged to WRKY family were generated. Another group ETHYLENE INSENSITIVE3 was also induced (EIN3).However expression of PR gene and production of PR specific proteins have been reported through pathogen-induced MAPK cascades. Particularly in *Arabidopsis* a protein namely virE2 interacting protein 1 (VIP1) was transferred into the nucleus that was subsequently phosphorylated by MPK3. These reactions are again induced by a natural growth regulator salicylic acid. Five *MAPK* genes were also induced in rice plant during both the stresses applied individually, among these; few MAPKs were responsible for inducing both types of stress responses (Purohit et. al., 2019).

MAPK cascades were influenced by ROS, and also regulated generation of ROS. In addition to this, reportedly both MAPK and ABA signaling interacted, which provided betterment of plant defence mechanism and initiated tolerance when dual stresses are applied in combination (Zhou et al. 2014).

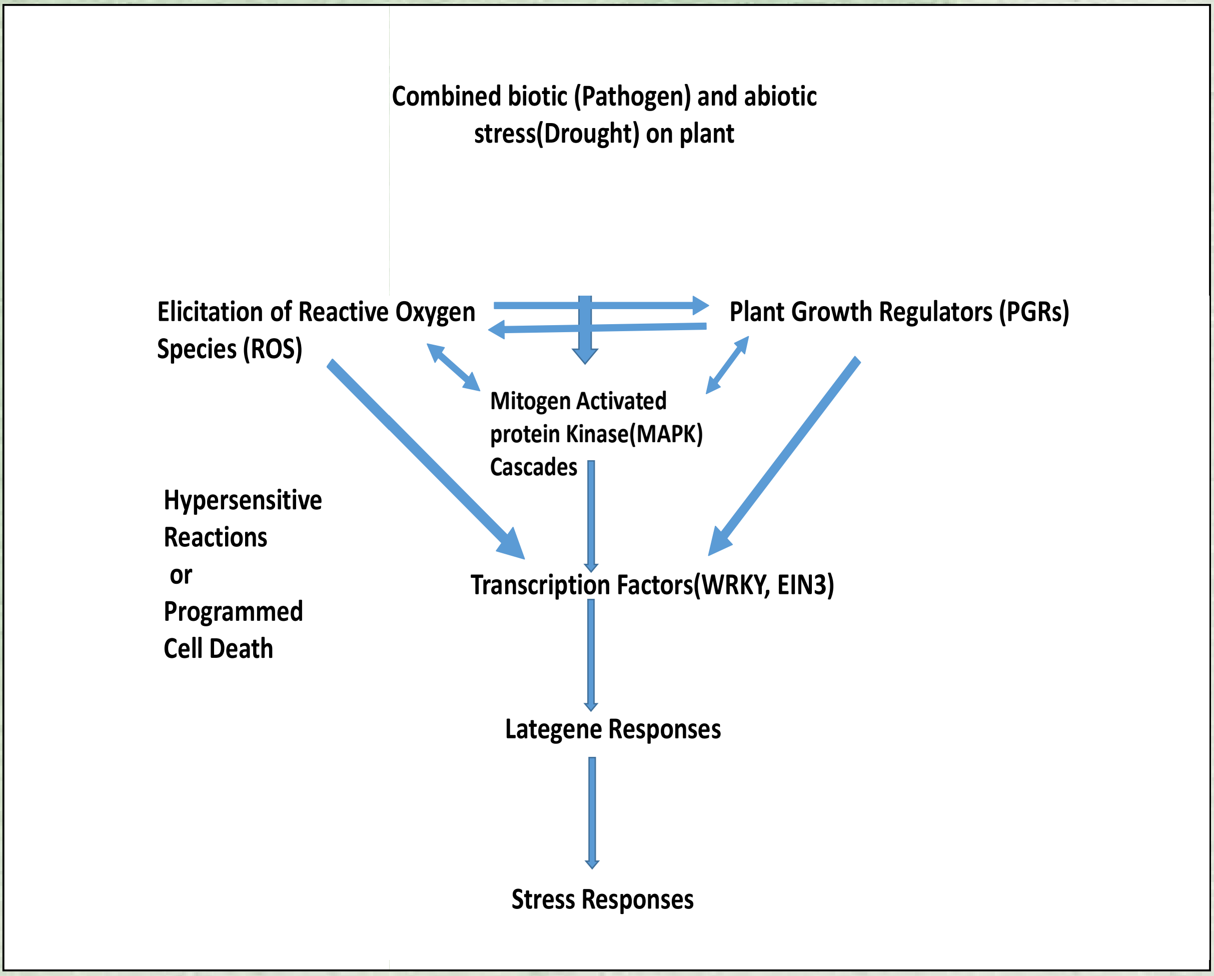

Figure 1: Primarysignaling pathway elicited during plant's response to combined drought–biotic stresses (after Purohit et al., 2019)

ROS Mediated Hormonal Regulation and Transcription Factor Induction

It has been well demonstrated that ROS performed a primary role during biotic and abiotic stresses. Various stresses, primarily drought, salinity and osmotic stress including high light fluence effectively increased concentration of ROS. These harmful radicals were mitigated by synergistic actions of antioxidants as well as ROS-scavenging enzymes produced by plants to diminish physiological damages (Purohit et al., 2019). However production of ROS was also found during oxidative burst when plants encountered pathogens. This restricted proliferation of pathogens through implication of hypersensitive response and ROS were found to trigger a regulatory mechanism that initiated cross-tolerance to abiotic and biotic stress response pathways. Further some transcription factors were identified as 'ROS-sensitive'. These could perceive the generation of ROS in *Arabidopsis* (Miller et al. 2008) and further stress tolerance or resistance was attributed to ROS. These in turn produced transcription factors (TFs) involved in stress responses, mitogen-activated protein kinases (MAPKs), and scavenging enzymes related to antioxidants. Also heat shock proteins (HSPs) and pathogenesis-related (PR) proteins were generated. Immediately after wounding by pathogen, H_2O_2 was produced by NADPH oxidases present in membrane. Hydrogen Peroxide then diffused into plant tissues and activated various defence mechanisms. Hyper-sensitive reactions, phytoalexins were elicited including various hydrolytic enzyme biosynthetic pathways. Lignin, salicylic acid biosynthesis was also initiated (Purohit et. al., 2019).

The positive effect of ROS development was demonstrated by ABA-induced closing of stomata. ABA also induced various enzymes, NADPH oxidases including two Respiratory Burst Oxidase Homologues D and F both reported from *Arabidopsis*. These together generated ROS in guard cells which acted as signal molecules (Atkinson and Urwin 2012). On the contrary, ABA also acted as negative regulator of pathogen defence mechanism mediated by ROS. It was considered that the above mentioned response towards defence was due to profound accumulation of ABA-precursors in tomato mutants (*sitiens* plants) that caused disruption in redox equilibrium and effected production of ROS in high level (Ton et al. 2009).

In *Arabidopsis*, during abiotic and biotic stress another transcription factor (zinc-finger, i.e., ZAT12) was produced due to increased H_2O_2. Reportedly genes like ROS scavenging ascorbate peroxidase (APX1) were upregulated by ZAT12, in turn.APX1,a well-known stress responsive enzyme, was accumulated in *Arabidopsis* while subjected to multiple stresses (Koussevitzky et al. 2008). Such accumulation was not observed during a single stress application. Simultaneously it was reported that *APX1* knockout mutants survived at a much low rate, under combined stress when compared with wild-type plants. It was noted that they survived at much higher rate under single stress.

However as a conclusion, the above studies confer upon that different stress responses are achieved while a complex signaling exists. Understanding of transcriptomes, and ROS and hormone mediated signaling pathways as well as identification of key controlling elements is likely to generate stress related knowledge that will be helpful for development of multiple stress-tolerant plants.

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DNA Has Four Bases. Some Viruses Replace In a Fifth

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Alien' genomes can be found on Universe. Recently, some viruses (mainly Phage's) that infect bacteria use a different genetic symbol that's distinct from the universal code used by nearly all other organisms in the universe. The studies show how these bacteriophages draw their genomes using a chemical base called 2-aminoadenine (Z for short), instead of using adenine (the A in the A, T, G, C bases of genetics toolbox).

Researchers have long been involved by the likelihood that evolution could have gone in an alternate direction with DNA's four bases: adenine (A), thymine (T), guanine (G) and cytosine (C). Perhaps they could have had very different chemical or binding abilities, or they could have used a different rule to represent information in genetical studies. Synthetic biologists, Romesberg have investigated this principal by engineering artificial base pairs and additional amino acids to produce new proteins. As we know, organism's survival depends on keeping its genetic materials and code intact; the precise ingredients in DNA's composition are thought to have been conserved in by evolution for billions of years — making them "frozen accidents," in the **words of Francis Crick.**

Early History

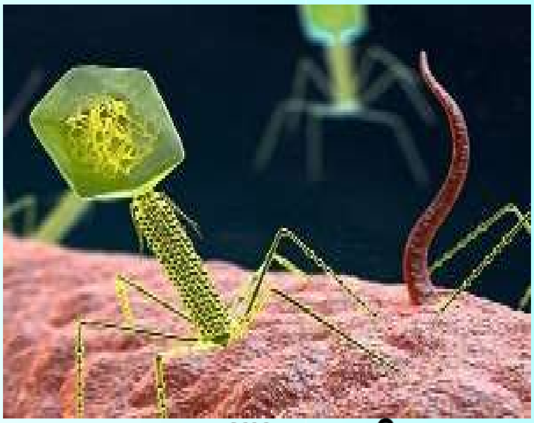
Scientists in the Soviet Union were the first to discover Z-DNA, in the late 1970s, in a phage called S-2L, which infects photosynthetic bacteria. They found that the phage DNA behaved peculiarly when its two helical strands were melted and separate from each other. The triple hydrogen bond that forms between G and C bases have higher melting temperature (Tm) than the A and T joining bases, and the phage's DNA behaved as if it was made mainly from G and C. Interestingly, analysis showed that the phage had replaced its A with Z, which forms a stronger bond with T(During gene transcription).

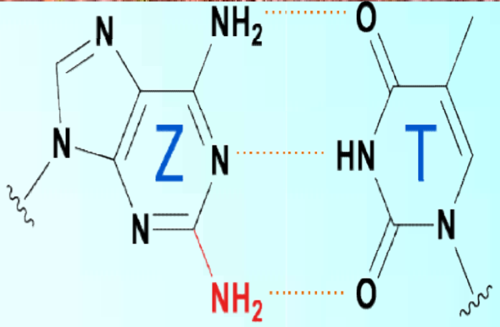
The Z base looks like a chemical modification of A; it's an adenine nucleotide with an extra attachment of hydrogen bond. But that humble change allows Z to form a triple hydrogen bond with T, which is more stable than the double bond that holds together A-T. “It looked like something offensive,” says Philippe Marlière, an inventor and geneticist at the University of Evry in France.

The genome of the bacteriophage was sequenced in the early 2000s by Marliere and his colleagues that the Russian team had studied, and they recognize a genetic sequence associated with production of the novel Z base. For the next 15 years, they searched for matches in existing databases of other viral genomes. Another group, led by researchers in Illinois and China, also independently joined the effort.

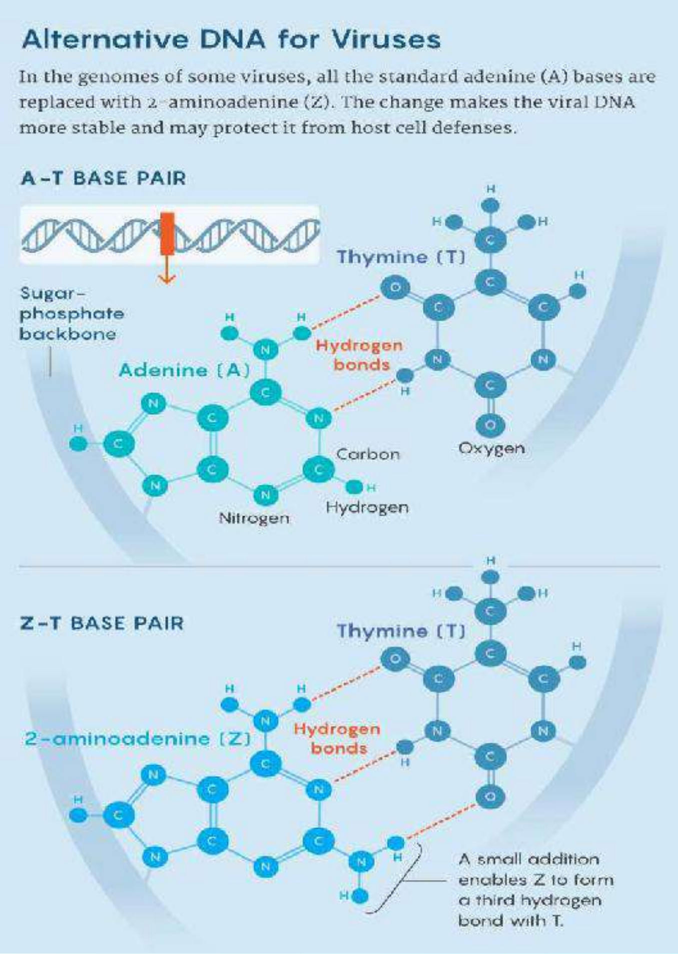
Alternative DNA for Viruses

Recently, the scientists have reported finding the Z substitution in more than 200 phages. Further analysis by various scientists of the viral genomes allowed the research groups to expose a key enzyme for constructing Z base, as well as an enzyme that destroy free-floating A nucleotides, helping Z base more likely to be taken up during DNA synthesis. But the biggest surprise was that the viruses can synthesized a polymerase enzyme dedicated to pairing Z bases with





2-aminoadenine : thymine



Alternative DNA for Viruses

In the genomes of some viruses, all the standard adenine (A) bases are replaced with 2-aminoadenine (Z). The change makes the viral DNA more stable and may protect it from host cell defenses.

T's during DNA replication machinery. "It was like a fairy tale," said Marliere, who had been expecting to find such a polymerase. "Our uncivilized dreams come true."

Advantages

1. Z base and other modified DNA bases have evolved to help viruses the defences with which bacteria degrade foreign genetic materials. The eternal conflict between bacteriophages and their host cells probably provides huge selection pressure to affect something as apparently "defended" as DNA.

2. Right now, everyone thinks the modifications are just protecting the DNA. But something more may be at work.

3. The triple bond of Z, for instance, might add to DNA's stability and rigidity, and perhaps influence some of its other physical and biochemical properties.

4. Those changes could carry advantages beyond hiding from bacterial defences and could make such modifications more broadly significant.

It's still unsettled how hosts keep this Z out of their DNA or how cellular machinery that explains DNA to make proteins copes with Z-DNA. It's also not fully understood how Z-DNA is copied. The functionality of host key enzymes could be improved when properly working on Z-DNA, says David Dunlap, a biophysicist at Emory University in Atlanta, Georgia, who has found that an *Escherichia coli* enzyme fights to coil the exotic double helix. The discovery of more phages with Z-DNA, and of genes involved in making it, should help researchers to understand how phages profit from using it. On the applications of Z-DNA's hardiness could make the novel technique of DNA data storage more stable and long-lasting. Other techniques called Nano machines known as DNA origami might fold into unique shape faster when made of Z-DNA.

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Application of Stem Cells in Parkinson's Disease

Reba Rani Pandit (M. Sc. Semester IV)

Stem cell biology has attracted tremendous interest recently. It is hoped that it will play a major role in the treatment of a number of incurable diseases via transplantation therapy. Several varieties of stem cells have been isolated and identified in vivo and in vitro. Very broadly they comprise of two major classes: embryonic/fetal stem cells and adult stem cells. Some scientists wish to pursue research on embryonic/fetal stem cells because of their versatility and pluripotentiality, while others prefer to pursue research on adult stem cells because of the controversial ethical sensitivities behind embryonic/fetal stem cells. However, both embryonic/fetal and adult stem cells are equally important and research on both types must be enthusiastically pursued since the final objective is the application of this technology for the treatment of a variety of diseases that plague mankind. It is very possible that the findings from one stem cell type may complement that of the other.

The word "stem cell" has also been loosely used by some scientists without the demonstration of stem cell markers or confirmation of stemness via transcriptome profiling. It is their ability to self-renew and differentiate that certain cells are termed stem cells both in vivo and in vitro. It is very crucial that the correct definition and proof of stemness through proper and accepted characterization tests be addressed before a particular cell type is classified as a stem cell. Stem cell therapy has already reached the bedside in some hospitals through the transplantation of donor bone marrow stem cells into the circulatory system of leukemic patients and the transfer of umbilical cord stem cells into the circulatory system of leukemic children or their siblings produced from the same mother who had previously stored her umbilical cord cells. However, the more challenging and impactful use of stem cells would come from the directed differentiation or trans-differentiation of stem cells into other cell types and tissues to help cure a plethora of incurable diseases. It would be tremendously useful if embryonic, fetal, adult or umbilical cord stem cells could be coaxed to produce islets cells for the treatment of diabetes or neurons for neurodegenerative diseases, cardiomyocytes for heart disease, and so on. This chapter attempts to define, classify and describe the sources of the various types of stem cells that have been isolated to date.

Definition of Stem Cells

Stem cells are unspecialized cells in the human body that are capable of becoming specialized cells, each with new specialized cell functions. The best example of a stem cell is the bone marrow stem cell that is unspecialized and able to specialize into blood cells, such as white blood cells and red blood cells, and these new cell types have special functions, such as being able to produce antibodies, act as scavengers to combat infection and transport gases. Thus one cell type stems from the other and hence the term "stem cell." Basically, a stem cell remains uncommitted until it receives a signal to develop into a specialized cell. Stem cells have the remarkable properties of developing into a variety of cell types in the human body. They serve as a repair system by being able to divide without limit to replenish other cells. When stem cells divides, each new cell has the potential to either remain as a stem cell or become another cell type with new special functions, such as blood cells, brain cells, etc.

Classification and Sources of Stem Cells

Stem cells can be classified into four broad types based on their origin, viz. stem cells from embryos; stem cells from the fetus; stem cells from the umbilical cord; and stem cells from the adult. Each of these can be grouped into subtypes (Fig. 1). Some believe that adult and fetal stem cells evolved from embryonic stem cells and the few stem cells observed in adult organs are the remnants of original embryonic stem cells that gave up in the race to differentiate into developing organs or remained in cell niches in the organs which are called upon for repair during tissue injury.

Present Scenario in Stem Cell Therapy

Following types of stem cell therapy is possible in present scenario:

- Allogenic stem cell therapy: matched or unmatched.
- Syngenic stem cell transplant: Identical twin.
- Autologous stem cell transplant.
- Cord blood stem cell transplant.
- Nonmyeloablative stem cell transplant.

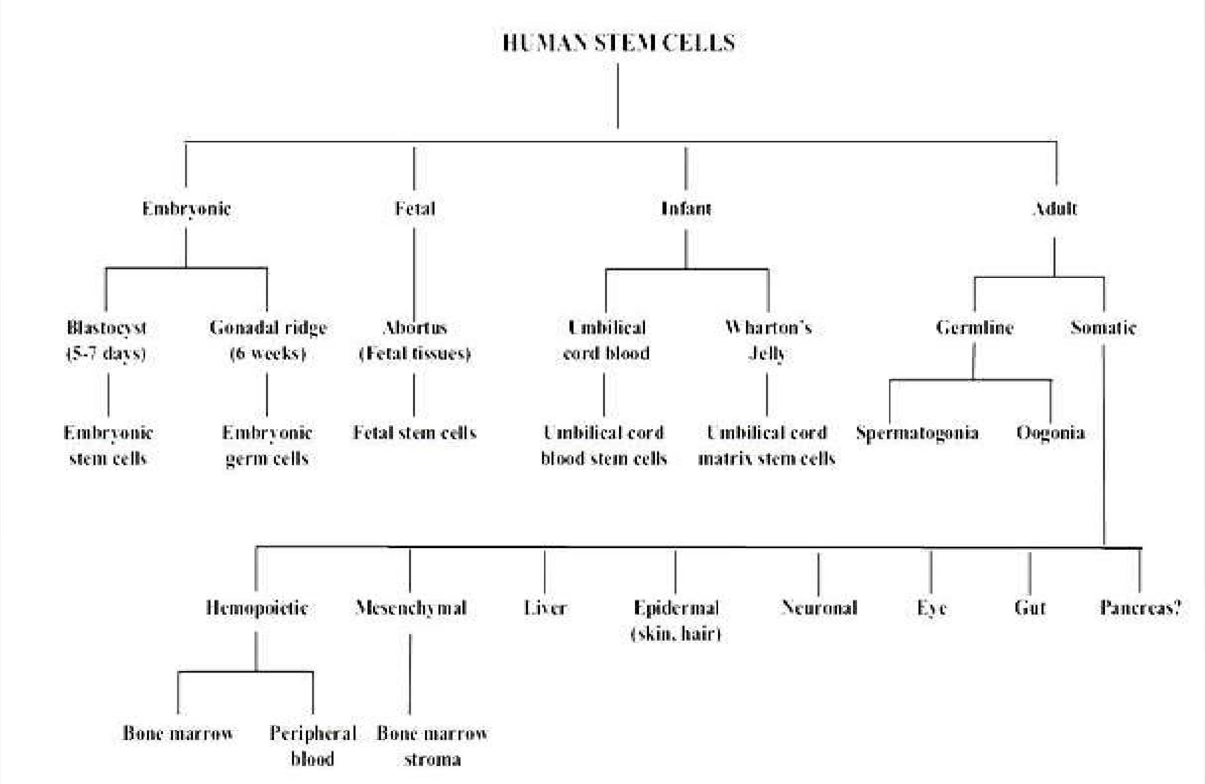

Figure 1: Classification of Human Stem Cells

Parkinson's Disease

Parkinson's disease (PD) is a common neurodegenerative disorder—a synucleinopathy—with a prevalence of 160/100 000 in Western Europe rising to 4% of the population over 80.1 With an ageing population, the management of PD is likely to prove an increasingly important and challenging aspect of medical practice for neurologists and general physicians. Our understanding of the pathogenesis of the disease has been advanced in the last decade with the identification of several gene mutations which may shed light on the mechanisms of pathogenesis in sporadic cases of PD.

Stem Cell Use for Parkinson's Disease

Parkinson's disease (PD) is characterized by motor symptoms, which include prominent akinesia, rigidity, tremor and postural instability. The degeneration of dopamine (DA) neurons in the substantianigra pars compacta, with consequent reduction of DA in the striatum, plays a central role for these motor symptoms. In later stages of the disease some patients also develop dementia, depression, disturbed sleep and signs of autonomic nervous system impairment. These symptoms, known as 'non-dopaminergic' symptoms are caused by the degeneration of other neuronal systems, such as noradrenergic, serotonergic and cholinergic. Thus, today the neuropathology of PD is viewed as being more complex than previously thought, involving not merely the nigrostriatal DA pathway, but also several other brain systems.

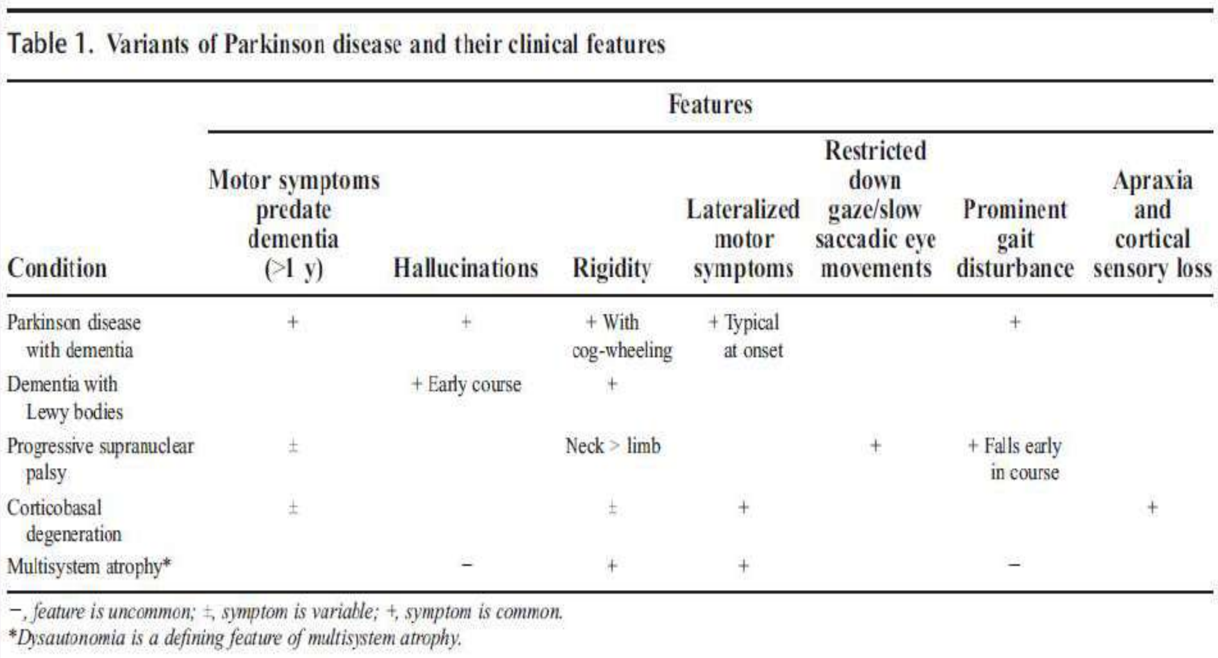

Table 1. Variants of Parkinson disease and their clinical features

	Features					
Condition	Motor symptoms predate dementia (>1 y)	Hallucinations	Rigidity	Lateralized motor symptoms	Restricted down gaze/slow saccadic eye movements	Prominent gait disturbance	Apraxia and cortical sensory loss
Parkinson disease with dementia	+	+	+ With cog-wheeling	+ Typical at onset		+	
Dementia with Lewy bodies		+ Early course	+				
Progressive supranuclear palsy	±		Neck > limb		+	+ Falls early in course	
Corticobasal degeneration	±		±	+			+
Multisystem atrophy*		−	+	+		−	

−, *feature is uncommon;* ±, *symptom is variable;* +, *symptom is common.*
**Dysautonomia is a defining feature of multisystem atrophy.*

The DA precursor L-3,4-dihydroxyphenylalanine (L-DOPA) remains the key treatment for PD, providing excellent symptomatic relief during the first years after start of the therapy. Invariably, the vast majority of patients develop motor fluctuations, known as the 'on–off' phenomenon, after about 5 to 10 years of treatment. Thus, despite careful administration of multiple daily doses of L-DOPA the patients oscillate between a severely akinetic state and a condition when they exhibit disabling abnormal involuntary movement, called dyskinesia. Besides this, with the progression of the disease the benefits of L-DOPA treatment gradually diminish and the time spent in 'on' phase gradually declines. Recently, several DA agonists, inhibitors of DA breakdown and novel surgical approaches (e.g. deep brain stimulation) have been shown to partially ameliorate these problems. These therapies do not, however, prevent disease progression and, furthermore, existing pharmacological treatments do not really improve symptoms believed to be due to non-dopaminergic pathology. There is little doubt that other therapeutic strategies are still needed for advanced PD. In Figure 2 are represented the alternative sources of stem cells for a cell-based therapy for Parkinson's disease.

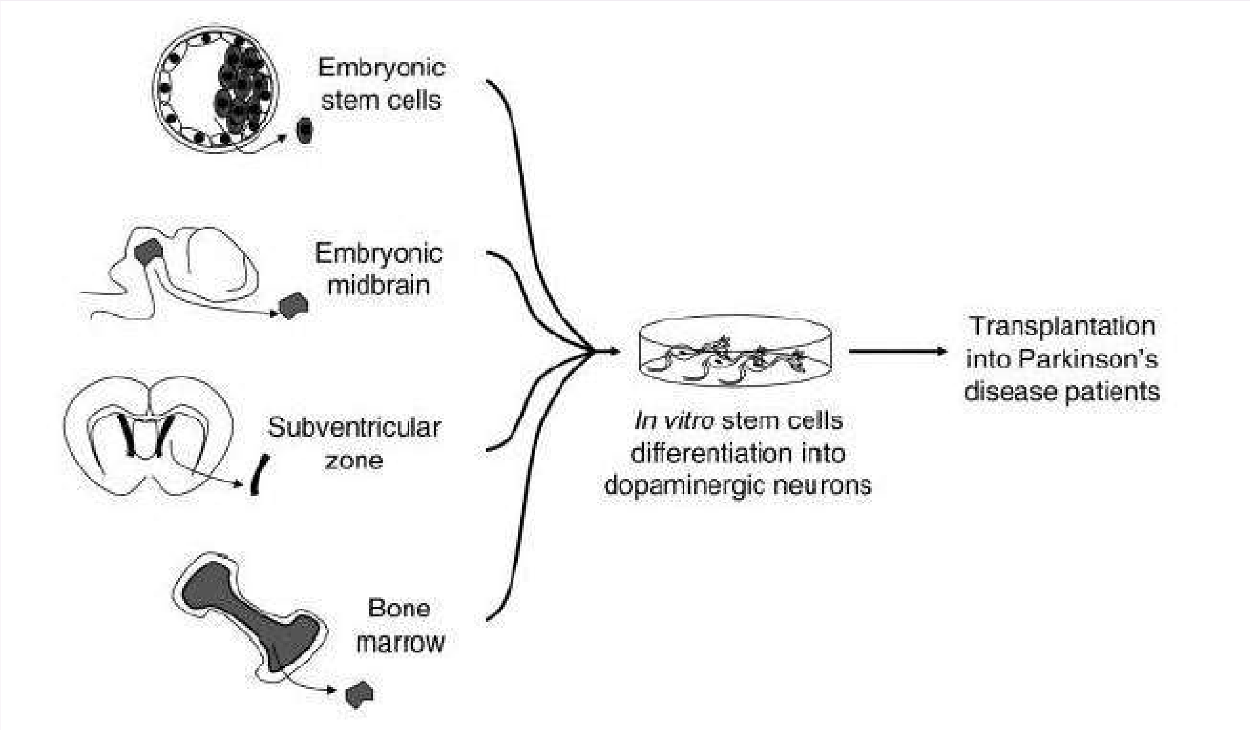

Figure 2: The alternative sources of stem cells for a cell-based therapy for Parkinson's disease.

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Caterpillar Fungus - *Cordyceps*

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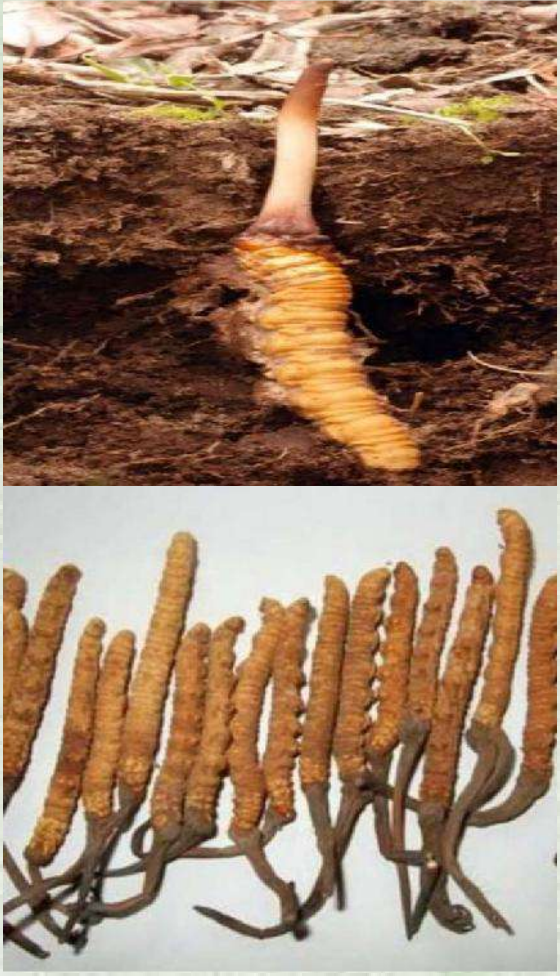
Cordyceps is a genus of ascomycete fungi that includes about 600 species that have been described from Nepal, China, Bhutan, India, Thailand and few other Asian countries. Most of them are parasitic on insects and other arthropods. The species of *Cordyceps* are especially valued for their medicinal importance.

Greek word 'kordyle', meaning 'club' and 'cephali', meaning 'head' from which the fungal genus got its name.

Cordyceps sinensis, popularly known as caterpillar fungus, is a parasite of caterpillars and is naturally distributed in the Tibetan Plateau of China and surrounding high-altitude grasslands of Nepal, Bhutan, and India. This fungus lives primarily on the head of the larva of one particular species of moth, *Hepialus armoricanus*, but is also occasionally found growing on other moth species. The fungus first parasitizes the larva of Hepiaidae. The larvae are infected by fungi in the summer and autumn seasons. These caterpillars then bury themselves down a couple inches into the soil. Meanwhile the fungus consumed the larva and turned it into 'stiff worms' in winter.



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In the spring and summer season of the following year, the fungal tissue emerges from the ground, growing from the head of the larva.

Importances

It has been used for medicinal purposes for centuries particularly in China, Japan and other Asian countries. *C. sinensis* contains many bioactive components such as 30-deoxyadenosine, cordycepic acid, cordycepin, cordyceps polysaccharides, ergosterol, crude fats, proteins, fibre, and a series of vitamins, etc. It is commonly used to replenish the kidney and soothe the lung, and for the treatment of fatigue. It also can be used to treat conditions such as night sweating, hypo-sexuality, hyper-glycaemia, hyper-lipidaemia, asthenia after severe illness, respiratory disease, renal dysfunction, renal failure, arrhythmias and other heart disease and liver disease. Because of its rarity and outstanding curative effects, several mycelial strains have been isolated from natural *Cordyceps* and manufactured by fermentation technology. The bioactive components in *Cordyceps* have anti-tumour activity.

❖ They stimulate or suppress specific components of the immune system. Thus immune-modulators can be effective agents for treating or preventing diseases and illnesses that arise from certain immune-deficiencies.

❖ These showed protective effects on human organs such as kidney, heart and liver; *Cordyceps* showed protective effect in liver patients, including those with viral hepatitis A, chronic hepatitis B, chronic hepatitis C, hepatic fibrosis, etc. and improves liver function. It also has obvious effects on other organ systems. For example, on the central nervous system, *C. sinensis* has sedative, anticonvulsant and cooling effects. On the respiratory system, it has a significant relaxant role in the bronchi, markedly increases adrenaline secretion from the adrenal glands and also has a role in tracheal contraction caused by histamine; it also has an antitussive, expectorant and anti-asthmatic action and prevents pulmonary emphysema. On the endocrine system, *C. sinensis* has effects as a male hormone.

Health food

There has been some *C. militaris* (substituent of *C. Sinensis* but not as efficient as *C. sinensis*) health food on the market, such as oral liquid Cordyceps tonic, Cordyceps wine, etc.

A parasitic Cordyceps fungus, such as *Cordyceps sinensis*, is a parasitic complex of fungus and caterpillar, which has been used for medicinal purposes for centuries particularly in China, Japan and other Asian countries. This article gives a general idea of the latest developments in *C. Sinensis* research, with regard to the active chemical components, the pharmacological effects and the research and development of products in recent years. Since *Cordyceps* is involved in so many pharmacological actions, it has immense prospects as ingredient of modern medicine. But the natural *Cordyceps* i.e. wild *C. sinensis*is is rare and expensive in market. Moreover the over exploitation of this fungus is one of the root causes of its rarity.

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Astrobiology: Possibility of Life Beyond The Earth

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Astrobiology, previously known as exobiology is the study of origin, evolution, distribution and future of life on earth and in the universe. According to NASA Astrobiology Institute (NAI) astrobiology is the study of living universe. Astrobiology consists of molecular biology (the branch of biology that concerns the molecular basis of biological activity in and between cells, including molecular synthesis, modification, mechanisms and interactions), biophysics (an interdisciplinary science that applies approaches and methods traditionally used in physics to study biological phenomena), biochemistry (the study of chemical processes within and relating to living organisms), chemistry, astronomy, physical cosmology (branch of cosmology concerned with the study of cosmological models. A cosmological model, or simply cosmology, provides a description of the largest-scale structures and dynamics of the universe and allows study of fundamental questions about its origin), exoplanetology (an integrated field of astronomical science dedicated to the search for and study of exoplanets), geology, paleontology (the scientific study of life that existed prior to, and sometimes including, the start of the Holocene epoch, the current geological epoch, began approximately 11,650 years before present, after the last glacial period. It includes the study of fossils to classify organisms and study their interactions with each other and their environments), and ichnology (a fossil record of biological activity but not the preserved remains of the plant or animal itself), which helps to investigate the life possibility in the universe. The term astrobiology was first proposed by GavriilTikhov, a Russian astronomer in the year 1953 and used by another astronomer Otto Struve (1955), later adopted by NASA in 1995. In this context, astrobiology is about much more than just the search for life on Mars or Europa (one of Jupiter's moons). Although some people might expect to find evidence for current or past life on these two planetary bodies, failure to find evidence of life there does not mean that the US astrobiology programme has failed. On the contrary, it is an important scientific result that tells us much about the planetary conditions that allow life to originate or exist and those that are detrimental to life.

A concerted effort (a) to study the origin of life through early evolutionary studies and (b) to explore the surface of life, based on the fact that life forms can support multiple extremities, are two principles that govern the field of astronomy. Over the past 100 years, the conditions in which life can thrive have been pushed in all directions, including extreme heat, pH, pressure, radiation, salt, energy, and nutrient depletion. Microorganisms not only thrive under such vast expanses of Earth's atmosphere, but they can also survive the harsh conditions of space, extremely radioactive environments, mechanical pressure, extremely high temperatures, and gravity. Separate systems of classification have been published to describe the planetary bodies based on their ‘habitat’. Numerous studies have also shown the growth of microorganisms under laboratory-simulated planetary conditions, including conditions such as Mars and Enceladus. In this context, defining the boundaries of life on Earth is an important step in identifying conditions that may arise or support life on other planetary bodies. Therefore, research into the limits of health is important to understand four areas: (1) the potential for panspermia (the hypothesis that life exists throughout the Universe), (2) forward contamination due to human exploration ventures, (3) planetary colonization by humans, and (4) the exploration of extinct and extant life.

Similar to the Earth, some planets may have different environments for each parameter. Since our knowledge of their habitats is very limited for other planets, we consider the extent of each parameter (temperature, salt, pH, and pressure) in three layers: (1) atmosphere, (2) surface, and (3) the base. Many of the planets that have been studied so far have the potential to survive or exist, according to our knowledge of life on Earth. Depending on the planetary bodies, various extremophiles may persist. For example, halo-psychrophiles can persist on the Titan, Ceres, and Europa, which have a saline water sources, and on Mars that may have clusters of Cl-rich brines. These life forms will also need to withstand high pressure. For example, the hydrostatic pressure of the Titan ocean ranges from 140 to 800 MPa. While such pressures are higher than the Earth's most widely grown piezophile (*Thermococcus piezophilus*, Pmax = 125 MPa), micro-organisms have been successfully detected at pressures up to 2,000 MPA and have been found to be effective enough for fluid inclusions within type IV ice. Based on these observations it is possible that some of the planet's corpses may be accessible to life based on Earth.

The atmosphere other planetary bodies can also be supports life. In particular, the upper and middle layers of the Venus (0-60° C; pH~0) may be suitable for thermo- or acidophilic microbes. Titan is also airy, but extremely cold (-183 to -78° C) and life on Earth can only process temperatures above -20°C. Microorganisms, especially psychrophiles, are capable of biofilm formation, clumping, and repair systems are more likely to tolerate earth's atmospheric conditions. Similar techniques may be needed for other planetary corpses.

The faces of other planetary bodies, such as Ceres, Europa, and Mars, receive high levels of radiation, so they may not be ready to support life. UV radiation is detrimental to Earth-based health, and numerous studies have shown that there is a 99% reduction in the activity of bacteria placed under Earth's conditions such as Mars, with UV-C as the most dangerous source. However, protection from UV-C radiation increases the chances of survival and includes protection from atmospheric dust or burial. Protection is also required from charged particle radiation and can be obtained by hiding at a depth of only an inch below the surface.

Serpentinization is a process consists of water-rock interactions involving the hydration of Fe^{+2}-rich minerals, resulting in alkaline pH, production of H_2 and potentially low-molecular weight organic carbon (e.g., formate, methane and a wide variety of other organic compounds). Thus, serpentinization may have played a role in the origins of life on Earth and perhaps on icy worlds as well. Several planetary bodies could have ongoing serpentinization in a subsurface ocean, including Enceladus, Titan, Ceres, and Europa, and serpentinization reactions could be widespread in the cosmos. Mars might also have serpentinization occurring in the subsurface or had serpentinization occurring millions of years ago, as indicated by the observation of hydrated minerals, such as serpentine phases, on the surface of Mars. Serpentinite hosted sites on planetary bodies could likely support chemo-autotrophic life, such as methanogens. In contrast to serpentinization, radiolysis contains decomposition of radionuclides, such as uranium, thorium, and radioactive potassium, which decomposes water molecules into oxidizing radicals and then reacts with oxidizable substrates, such as pyrite, produce the chemical energy needed for life. For example, the sulfide-reducing bacterium *Candidatus desulforudisaudaxviator* is the only type of liquid known at a depth of> 1.5 km (Mponeng Mine, Johannesburg, South Africa) and may be influenced by the production of radiolytic chemicals such as H2 and sulfate. It is possible that radiolysis could support such life on other planetary bodies, including the Europan ocean and the martian subsurface.

Extremophiles have pushed our understanding of the boundaries of life in all directions since it was first discovered. Apart from this, there is a fundamental lack of studies that address the tolerance of microorganisms to excess, which can impede our understanding of the limits of the life. In the last 50 years of extremophile research has become clear that the limit for life varies when living organisms experience extreme extremes. For example, the upper extremity is raised above 100° C where high pressure was present. Future research will need to focus more on the link between multiple parameters. While considering the possibility that life may have originated and existed on other planetary bodies, it is important that you consider the differences in the geographical conditions of the Earth in relation to the definition of a planet. Most of the parameters considered in this article may not exceed the entire planet, and local or temporary conditions may still support life. Therefore, it is unlikely that a limited, superficial timing of any extraterrestrial space would be sufficient to determine with certainty the existence of life or conditions within the Earth's boundary of life, at least temporarily

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Pathogenic Induction of Plant Hypersensitive Responses

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Almost all higher plants show hypersensitive defense response by a rapid cell death after pathogenic invasion. It is associated with susceptibility of pathogen, growth retardation, and speciation during evolution. It is an enormously effective component and a rapid localized cell associated disease resistance mechanism in the infection site, a part of initial plant immune system. The term 'hypersensitive' implies rapid plant cell death followed by elicitation of diverse metabolite involved in pathogenesis. Thereof, cell lyses due to membrane damage leads necrosis of the distorted cells and sometimes it helps to suppress disease. Hypersensitive responses (HRs) are induced by viruses, bacteria, fungi, oomycetes, insects and nematodes through interactions with the host plants. It is beneficial to necrotrophs which require dead host tissue to complete their life cycle but complicated for hemibiotrophs, which initially interact as biotroph but subsequently change to a necrotroph such as *Phytophthora infestans*.

"Gene-For-Gene" Concept

'Gene for gene' concept determined establishment of disease or resistance/HR, in plant-pathogen interaction. Each dominant resistance gene (R-gene) in the host plant paralleled with a dominant avirulence gene (Avr gene) in the respective pathogen. Resistance was conferred only, if both the R-gene and the subsequent Avr gene were present in the same interaction. R-gene-mediated resistance is associated with HR, encodes for NBS-LRR proteins or NLRs (NOD like Reporters), performed as regulating the activity containing cytoplasmic proteins possessing both a nucleotide-binding site (NBS) and leucine-rich repeat (LRR) domains. NLRs either contained coiled coil (CC) or toll-interleukin receptor (TIR) domains at their N-terminal region which are mainly responsible for activating cell death.

Pattern Recognition Receptors

Pattern recognition receptors (PRRs), another class of proteins similar to NBS-LLR,are membrane-bound proteins.

MAMP/PAMP-triggered immunity (MTI/PTI) is able to recognize specific pathogen-associated molecular patterns (MAMPs or PAMPs).Some earliest ancestors of photosynthetic plants as well as all the land plants have NLRs but functions of most of them have not been defined except R-protein. All R-proteins are not NLRs because some R-protein classes do not have NLR structure. In most of the cases the R- and Avr proteins interact directly where as in some cases Avr protein interacts with guardee or decoy to activate the R-protein.

In very early defense responses, nitric oxide (NO) and reactive oxygen species (ROS) usually produced during initiation of HR and it also causes transcriptional reprogramming, lipid peroxidation, ion fluxes and cell wall strengthening etc. These interactions tend to evolve arms races in rapid rate. In some cases, NLR activated as a result of similar effector proteins produced by related pathogens or through mutation which leads the cell death. The detrimental effects on host plant causes growth reduction rather than resistance.

A small class of R-genes called ‘executor R-genes’ are active at the transcriptional level by a group of effectors identified as transcription activator-like effectors (TALEs). All executor genes are not related to NLRs; two encode flavin mono-oxygenase and four encode proteins containing predicted trans-membrane domains. There are few auto-active NLRs that interact inappropriately due to mutations in auto-inhibitory cascade, may show lesions or accelerated cell deaths in plants. Leaf spots of dead cells in patches are referred to as LES, have been found in a number of species like *Arabidopsis*, maize and rice. LES phenotypes are definitely linked with HR and the defense response.

HR generally tightly regulated, otherwise spontaneous cell death may be very detrimental to plant growth at the same time it needs to be quickly activated when required. Multiple layers of control are needed at the transcript level; NLR expression is generally low and sometimes tissue-specific. Different level of regulation cascade such as chromatin structure, transcription factors, alternative splicing, post-transcriptional regulation by small RNAs and possibly by alternative polyadenylation, and nonsense-mediated decay etc. found to be there. Chaperone HSP90 and other two interacting co-chaperones RAR1 and SGT1 form a complex and interacts with NLRs and stabilize them.

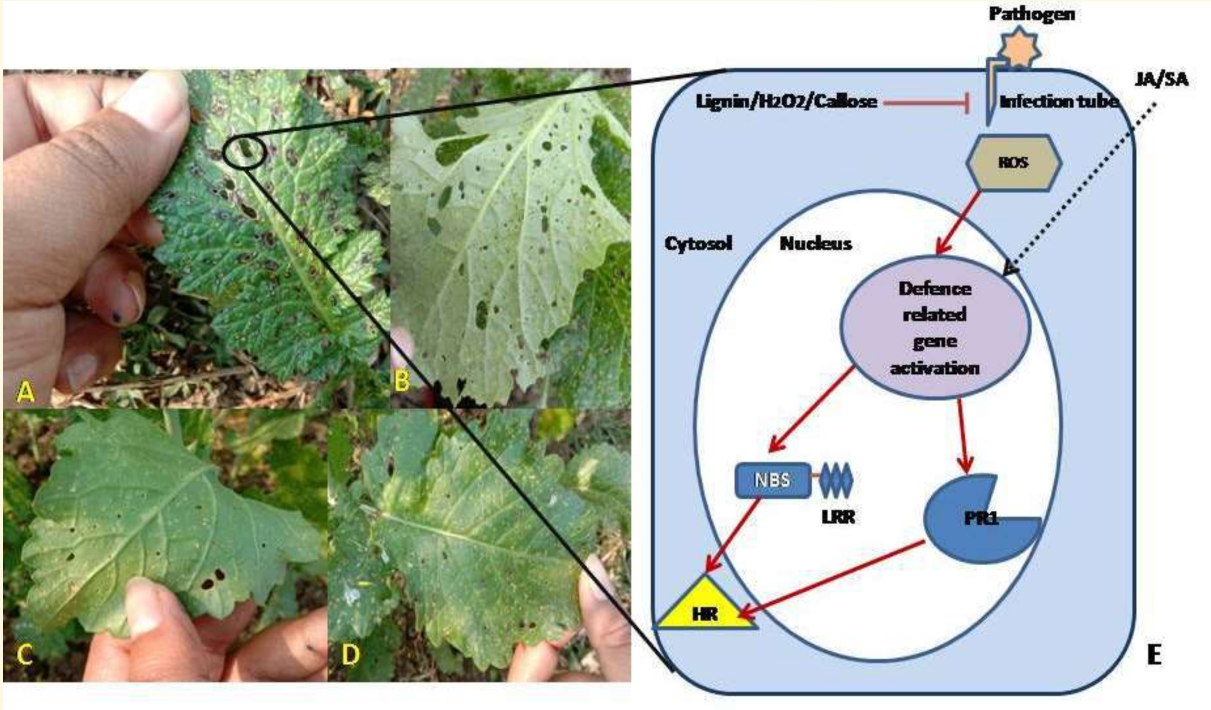

Figure 1: Hypersensitive reaction in *Brassica* sp. (A, B, C & D); General signaling cascade of plant HRs (E).

Role of SGT1

SGT1 recruits the NLR and interacts with the E3 ubiquitin ligase which has important roles in ubiquitin-mediated protein degradation with subunit Skp1. It is evidenced that specific NLRs has specific E3 ligases. Loss of function of any one of RAR1, SGT1 or HSP90 leads elimination of HR and causes the reduction of NLR protein levels whereas the role of SGT1 is still not completely understood.

In *Arabidopsis thaliana*, SGT1 (Suppressor of the G2 allele of SKP1) gene silencing leads to increase in accumulation of the RPS5. NBS-LRR R-protein, reflects that SGT1 somehow antagonized RAR1 (Required for MLA2A resistance) and also reduced levels of NLR proteins.

In *Nicotiana benthamiana*, silencing of SGT1 caused a reduction in the levels of the R-protein. This is exactly opposite to *Arabidopsis thaliana*. So, the role of SGT1 may vary depending on the species and the particular NLR or its activation state. These contradictory results have urged for further study to derive any conclusion.

Environmental Factor Influencing HRs

HRs are generally temperature sensitive and not stimulated above 30 °C as evidenced in *Puccinia graminis* (wheat), *P. coronata* (oat), *Glycine max* (soybean), *Nicotiana tabacum* (tobacco),and *Solanum lycopersicum* (tomato). Some mutated versions of NLRs,show leaf yellowing and cell death below 16 °C, are called chilling sensitive phenotypes. Mitochondria are the main source of ROS in the cell, particularly electron transport chain linked to HR has been proved in a number of studies. Some researchers also claimed that light dependent HR is chloroplast mediated. High humidity in climate represses or delayed HR possibly due to delayed dehydration of the cells.

Early History HR Causes Positive and Negative Effect On Host Plant

PR1 (Pathogenesis related protein 1), PR2 and PR5 proteins are related to pathogenesis and produced by salicylic acid (SA) associated pathway. NPR1 (Nonexpressor of pathogenesis related gene 1), NPR3 and NPR4 acting as SA receptors increased SA mediated responses. Transgenic disease resistance plants must be broad spectrum in order to be economically valuable as a commercial product and the approaches have focused on inducing HR and Systemic Acquired Resistance (SAR). Endogenous effectors used to induce pathogen-inducible promoters to auto activate HR**.** Disease resistance provided insufficient yield penalties both mild and extreme leaf flecking; milder flecking generally does not affect yield. Low activation of HR may activate SAR, useful for generating disease resistance without any yield penalties. One approach might be effective to development-specific promoters that can direct expression when the majority of growth has been completed.

Visible cell death in plants sometime referred to HR caused by biotic/abiotic factors and genetic factors mostly by mutations resulted auto induced HR. Multiple mechanisms are being operated by plants to suppress inappropriate HRs and to restrict its over activation. In higher plants, it is an extremely active component of the plant immune system and generally associated with pathogen resistance, however, in specific situations it may have other consequences such as pathogen susceptibility and growth retardation. The above mechanisms prove the fact that plants regulate huge genetic machinery to control the lethal effects during pathogenesis.

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A Sneak Peek on the Gene Editor: The Story of CRISPR

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Yes, you heard it right! Just like the video editor in your smart phone, CRISPR can cleave a specific DNA region of an organism. Thus CRISPR can be termed as a gene editor. The term CRISPR stands for clustered regularly interspaced short palindromic repeats which are types of DNA sequences found in Bacteria and Archaea. The idea of using this tool arises when scientists were trying to understand the mechanism by which a bacteria fight against viral infections (e.g. Bacteriophage infection). Many bacteria have come across with the adaptive immune system CRISPR-Cas9, which can target the viral DNA and destroy them. This Cas9 endonuclease protein generates a blunt double-strand DNA cleavage of the virus. The scientists realized that this bacterial defense mechanism could be utilized to delete or insert a specific portion of DNA into the cells of other organisms. Till now, this technology has already been used to edit the DNA of various organisms. A group of scientist from Philadelphia had successfully edited the DNA of HIV virus from infected human cells. Since then, after almost 8 years Emmanuelle Charpentier and Jennifer Doudna were awarded the 2020 Nobel Prize in Chemistry for the breathtaking discovery of gene editing CRISPR-Cas9 system.

Figure 1: Emmanuelle Charpentier and Jennifer Doudna

Application of CRISPR Editing

- Antimicrobial and antiviral applications are mainly focused on HIV therapy and HPV therapy. Most recently a group of researcher designed a specific CRISPR system named CRISPR-Cas13b which can suppress SARS-CoV-2 replication. This might be a big lead for a potent covid therapy.
- CRISPR system is having an impact on agriculture also. Various stress tolerant and disease tolerant food crops have been developed. This technology can also be harnessed to combat various pathogens of food crop.
- It is also likely to be used to edit the genome of microbes for green synthesis, synthesis of biofuel, biochemical and other industrial products.
- It has already been used in various pest control applications.

Figure 2: Results of CRISPR editing: dumpier nematodes (a), fruit flies with dark eyes (b) and zebrafish embryos with excess of ventral tissue (c) (adopted from The CRISPR Craze by Elizabeth Pennisi)

CRISPR in Cancer Therapy

A huge number of pre-clinical studies based on CRISPR mediated editing are going on with the aim of targeting various oncogenic proteins including HER2, EGFR and NRF2. Although the most interesting part of CRISPR mediated cancer therapy is the development of genetically engineered immune T cell which is also termed as CAR-T cell. T cells are the main pioneer of our immune system and has a critical role in killing the pathogen infected cells of our body. In the CAR-T cell therapy, the normal healthy T cells of cancer patients are isolated and edited with CRISPR-Cas9 tool so that the T-cells produce chimeric antigen receptor (CAR) on their surface.

This particular receptor can recognize and attach to a specific protein on cancer cells and kill them. These engineered T cells are then cultured and expanded in number and finally infused into cancer patients. A number of clinical trials are already completed with CRISPR mediated CAR-T cell therapy. Recently in this year, Government of India has allocated 19.15 crores to conduct first human phase-I/ II trials of CAR-T cell therapy through the collaboration of Tata Memorial Hospital and IIT Bombay.

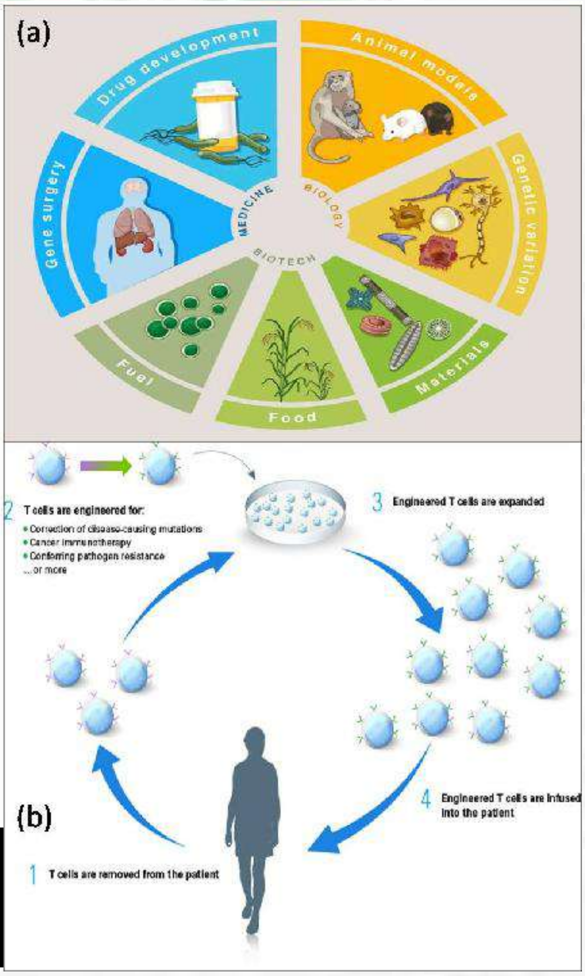

Figure 3: Applications of CRISPR editing

Source: https://doi.org/10.1016/j.cell.2014.05.010

Ethical Concern

Though the whole mechanism and applications of CRISPR sound very crispy, over the years it has raised some ethical issues because this gene editing technology can be used to edit human embryo also. In 2018, a Chinese researcher named He Jiankui claimed that he had created first ever genetically edited human babies (known by Lulu and Nana) by eliminating CCR5 gene that will make them resistant against HIV. After that news the Chinese court sentenced him for 3 years imprisonment and banned him for performing any further research. Another very important but less discussed ethical concern is the use of CRISPR technology in military applications. These studies are focused on increasing the tolerance of soldiers against chemical and biological warfare. Researchers also edited dog embryo with higher muscle mass which further can be applied to make the soldiers physically stronger. In this type of study the off target mutations can give rise to very fatal diseases and other undesirable conditions.

As there is a well-known say, every findings has its two sides of the coin. Similar is with this new piece of invention.

The negative and the accidental upshot can be devastating creating menace for the entire society and the mankind. So, the scientific community should be very much aware and with having full understanding should proceed to this technology bringing out any novel entity which will prove advantageous and welcoming in the field of science.

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The Relationship Between Autophagy and DNA Damage with Its Responses

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For maintaining cellular homeostasis and normal development process of an organism autophagy play a crucial role. Autophagy can be induced in response to several stresses such as oxidative stress, nutritional depletion stress or in response to pathogen attack. Recently, one of most emerging topics is autophagy induction in response to DNA damage. Although exact pathway of autophagy activation through DNA damage response is unclear but we gather some published data to support that there is a relationship between autophagy and DNA damage with its response.

Autophagy

Autophagy is a conserved biological process that occurs when cells challenged by oxidative stress nutrition starvation (1) etc. It is essential for cellular homeostasis and many development processes. At the time of autophagy, bulk protein degradation takes place with the assistance of lysosome within the cell. Autophagy can be divided into three classes : microautophagy (the direct degradation of cytoplasm through the invagination of lysosomal membrane), chaperone mediated autophagy (CMA) where cytoplasmic protein degraded by lysosome with the help of Cheperones Hsc 70 and co-chaperones and another one is macroautophagy (during macroautophagy cytoplasmic protein content enclosed within a double membrane structure, called autophagosome which subsequently attached with lysosome and protein degradation takes place) (2).

Autophagy–related genes (Atg) are responsible for autophagy. In the budding Yeast (*Saccharomyces cerevisiae*), first autophagy genes were reported (3). At the initial stage of autophagy, a double membrane structure, known as phagophore is formed through the phosphorylation of Unc-51 like Kinases ULK 1 and ULK 2. The activated ULK consist of ATG 13, ATG101 and FIP200; in its turn activate Beclin-1 complex consist of p150, ATG 14L and the class III phosphatidylinositol 3- phosphate kinase (PI3K). PI3K contains a catalytic subunit, known as Vps34. This is a step that operates the nucleation stage of autophagy. In this step cytoplasmic protein content is engulfed by the elongating vesicle. Activated Vps34 promote the binding of an E3 like protein complex member, known as ATG16L which is an ubiquitin like conjugation system (4). It plays an essential role in autophagy. It covalently conjugates with ATG12 to ATG5 ubiqutin like protein which promotes the covalent conjugation of LC3 protein to the phosphatidyl ethanolamine (PE) (5). This final complex matures the autophagosome structure. Then autophagosome engulfing cytoplasmic material and further degraded by the subsequent attachment with lysosome.

Autophagy can be triggered by nutritional deprivation condition, internally produced reactive oxygen species, superoxide molecule, DNA damage and many other stress conditions. Actually, autophagy is a stress related response. Here TORC1 and AMPK regulatory complexes play essential role in autophagosome formation. During normal condition ULK1 activation inhibited because TORC1 remain activated but during starved condition ULK1 activation takes place through AMPK activation (6).

DNA Damage and Its Response

DNA is the most important component of a cell but it can be damaged by both external factors such as ultraviolet ray, several genotoxic chemical and internal factors such as byproducts of many metabolic reactions which include ROS, RNS (reactive nitrogen species) (7). This component can affect mitochondrial DNA as well as nuclear DNA. However, mitochondrial DNA comparatively much accessible to DNA damage than nuclear DNA. Because unlike nuclear DNA; mitochondrial DNA does not possess histones and non-histone proteins (8).

However, for avoiding mutation, chromosomal instability and finally for cell survival damaged part of the DNA must be repaired. There are many types of DNA repair system. Among them mismatch repair (MMR), base pair excision repair (BER), nucleotide excision repair (NER), homologous recombination (HR), non-homologous end joining (NHEJ) play crucial role. Single strand breaks mainly repaired through MMR, NER and BER. Another repaired mechanism is direct protein-mediated reversal where O-(6)-methylguanine-DNA methyltransferase help to repaired methylated bases. However, homologous recombination and non-homologous end joining pathways mainly take part in double strand break repair.

For successful DNA repairing DNA damage signal and series of reaction occur, where phosphatidylinositol 3-kinase like protein kinases (PIKKS), poly (ADP- ribose) polymerase (PARP) family member, ataxia telangiectasia mutated (ATM), ATR (ATM and Rad3 related protein), replication factor C (RFC), Rad17, 9-1-1 complex (heterotrimeric complex of Rad9, Rad1 and Hus1) have crucial role (9). Firstly, ATM and ATR interact with double strand breakage site. MreII-Rad50-Nbs1 (MRN) complex helps ATM activation and binds with damage site and after that it reacts with p53, checkpoint kinase 1 and 2 (CHK1 and CHK2), histone deacetylases 1 and 2 (HDARC1 and HDARC2) and other proteins. A ring like structure are formed which has similarity with proliferating cell nuclear antigen (PCNA) by 9-1-1 complex. This ring like structure placed at the damage site through Rad17 which has a similarity with replication factor C. This 9-1-1 and Rad17 has crucial role in DNA damage response. The members of poly (ADP- ribose) polymerase protein family engaged with repairing of single strand break (10).

Relation between Autophagy and DNA Damage Response

According to many evidence autophagy can be correlated with DNA damage response. Mainly some major components such as ATM, PARP-1, p53, FIP200 play the crucial role for maintaining the relation. ATM is one of the major components that take part in autophagy induction in response to DNA damage, which can be raised through oxidative and nitrosative stress. 5’ adenosine monophosphate activated protein kinase (AMPK) which is activated through active ATM, phosphorylates ULK1 and induced autophagy by enhancing autophagosome formation. AMPK also phosphorylates tuberous sclerosis complex 1 and 2 (TSC 1/2) that deactivate TORC1 effect which promote autophagy. ATM can be activated by MRN complex and FOXO3, a transcriptional factor (11).

PARP1 also engaged with autophagy regulation in response to DNA damage. PARP1 has dual effect. It can induce necrotic cell death and autophagy (12). DNA damage induced PRAP1 is activated depending on NAD+ and ATP depletion. In the next step AMPK activate that recognized the energy reduction and ascendant AMP level. Then AMPK in its turn induced autophagy by repressing mTOR. When PARP1 hyper activated due to DNA damage stress, it causes cellular energy failure which leads to cell death. p53 is also an essential DNA damage response protein that regulate autophagy through up regulate PTEN (phosphatidylinositol-phosphate), transcription level of TSC2, transcription of DRAM (damage regulated autophagy modulator) (13). The up regulation of this above-mentioned component induces autophagy.

Autophagy can have induced in a cell by DNA damage like many other stress and autophagy increase the time to repair those damage. There is evidence that FIP200, a 200 KDa Fak- family interacting protein play essential role in autophagy (1). The same study suggested that in FIP200 lack mouse embryonic fibroblast (MEF), autophagy was suppressed which leads to reduced efficiency in DNA damage repairing(1). Another component c-jun-N-terminal kinase (JNK) also takes part in autophagy inducing in response to DNA damage. There is a study that shows Bcl 2 phosphorylate through JNK 1 that cause break up of Bcl 2 Beclin 1 complex and promote autophagy (14).

A recent study explains a new pathway of autophagy induction by DNA damage, known as genotoxin induced targeted autophagy (GTA) (15). The central DDR kinase Mec1/ATR, Tel1/ATM and Rad53/CHEK2 action has the main role in GTA. Here Rad53 suppress Rph1/KDM4 which is transcriptional repressor that leads to the up regulation of several autophagy genes at the transcriptional level. The overall relationship between DNA damage response and autophagy was schematically represented in figure 1.

DNA can be damaged through several internal and external stimuli but repairing of this damage is essential for avoiding mutation, maintaining genome stability and finally for cell survival. Under severe DNA damage condition which is impossible to overcome the damage, apoptotic cell death occurs for eliminating damaged cell but cell also induce autophagy to overcome the damage. Autophagy enhanced DNA repairing efficiency. So, it can be said that there is an internal relationship between autophagy and DNA damage response but further research is essential for gathering information about the exact and molecular pathway of autophagy induction through DNA damage response.

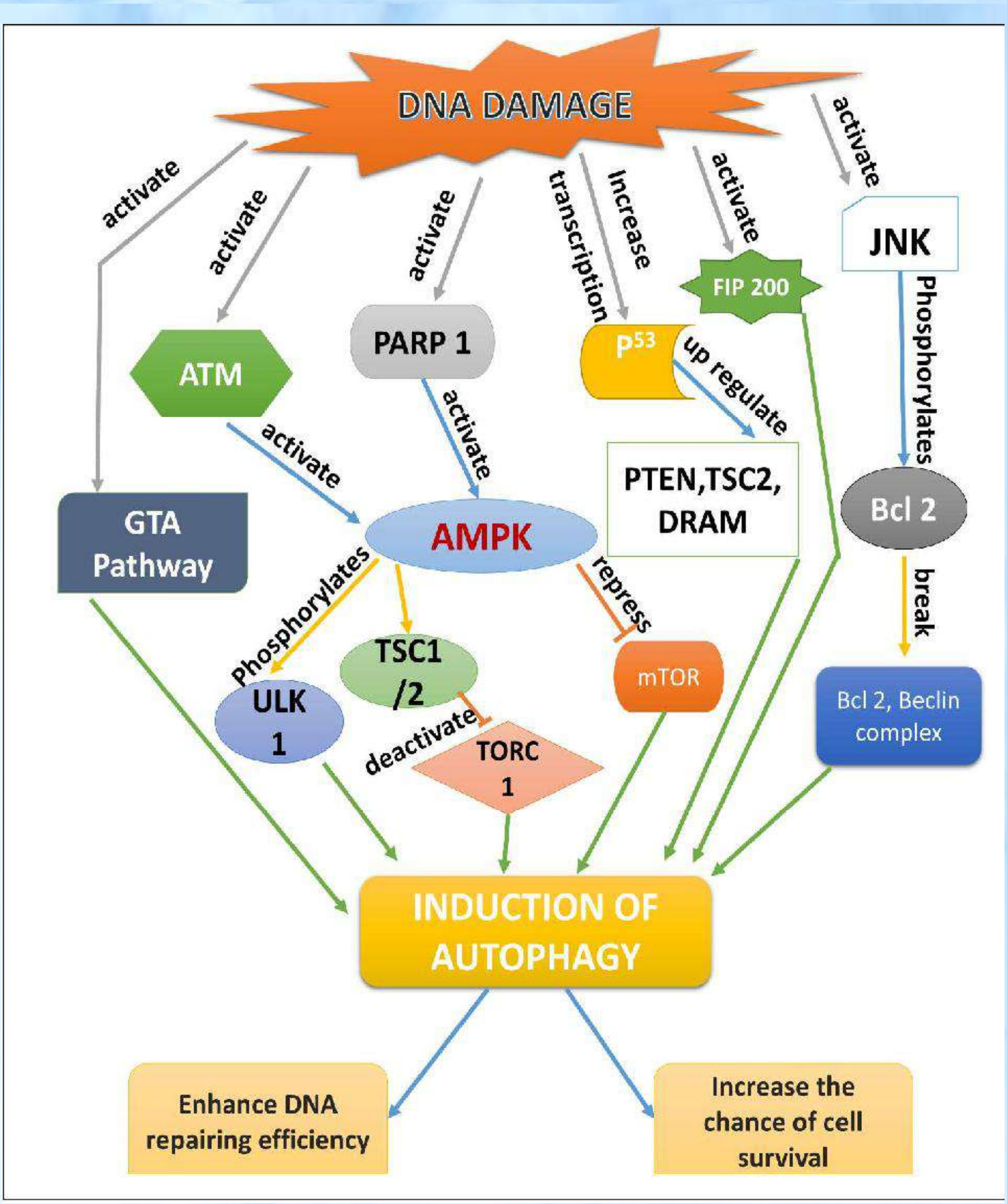

Figure 1: Schematic representation of the relationship between autophagy and DNA damage response

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Is Mucormycosis Black Fungus?

Ashima Biswas (M. Sc. Semester-IV)

The disease named 'Mucormycosis' has recently been observed in a number of COVID-19 patients in India. It is a rare but serious fungal infection and colloquially known as 'Black Fungus'. Numbers of mucormycosis cases are detected in Delhi, Maharashtra and Gujrat. A 2021 study found that more than 47000 cases of mucormycosis were reported in just three months in India. The novel coronavirus has recently been linked to two serious fungal infections: COVID-19 associated pulmonary aspergillosis (CAPA) and COVID-19 associated mucormycosis (CAM). Though the disease Mucormycosis is focused recently due to the frequent association with Covid-19 patients but existed long before the appearance of COVID-19.

The term "Black Fungus" has been used by the public to describe mucormycosis, but "black fungus" is actually a different category of fungus. Black fungus caused the disease named Chromoblastomycosis and Phaeohyphomycosis. But mucormycosis is caused by the fungi belonging to the group mucormycetes. The mucormycosis clinically manifested as the formation of "black crust" on the skin or inside the nasal cavity or inside the mouth. Because of these black crust people may wrongly called Mucormycosis as "Black fungus".

Mucormycosis is a serious but rare fungal infection caused by a group of mold called Mucormycetes. These molds can found throughout the environment. Mucormycosis mainly infects the immune-compromised patients. People who consume medicines, steroids that lower the body's immunity can be infected by these fungi. Mucormycetes are present in environment and they enter human body either through artificial oxygen that is given to the patient suffering from COVID-19 or in some cases other environmental factors *viz* use of contaminated water during production of medical oxygen. They are found throughout the nature, in soil, or decaying organic matter, decaying vegetation etc.

The disease transmitted through air by the fungal spore present in the environment. These spores are hit resistant and water resistant and are not easily infection occurred after someone inhales the spores from the air. Skin infection can occur after the fungus enters the skin through a scrape, burn, or other type of skin injury. It is not a contagious disease, cannot be spread from person to person. It mainly affects people who are immune-compromised. Use of steroids to treat COVID-19 patients is also a prominent reason why COVID-19 survivors are complaining of black fungus. Patient with low immunity level or have compromising health condition like diabetes, HIV, cancer have the maximum chance to be infected from this disease. Currently, this infection has created much havoc nationwide, until much recently this was considered to be rare, but is now showing devastation effects.

Causal Organism

Fungi belonging to the group mucormycetes caused the disease. They are opportunistic pathogen i.e. generally the fungi are not harmful for human but when it founds a immune-compromised body then it causes disease like mucormycosis. The most common fungi that cause mucormycosis are *Rhizopus sp., Mucor sp*. Other example includes *Rhizomucor sp.*

Mortality/Morbidity

Mucormycosis has a very high mortality rate reaching 50% to 80% even with treatment. Pulmonary and gastrointestinal disease have higher mortality rate due to late diagnosis. Due to extensive facial surgery during treatment, Rhinocerebral disease caused significant morbidity in patients after survival.

Figure 1: *Mucor* sp.

(https://mycology.adelaide.edu.au/images/mucor-sporang.jpg)

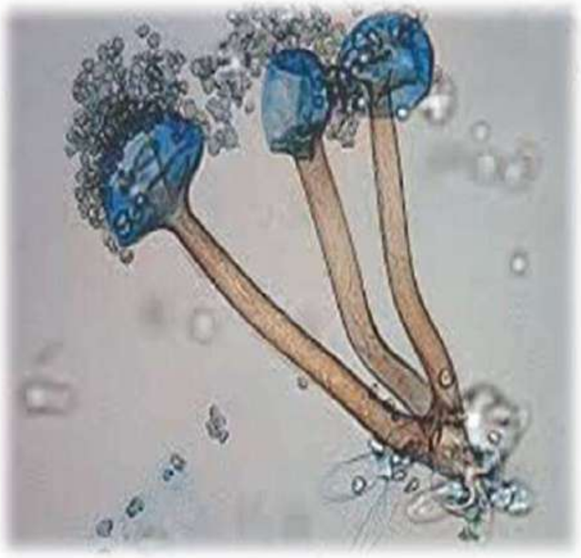

Figure 2: *Rhizopus* sp.

(https://mycology.adelaide.edu.au/images/rhizo-micro.jpg)

WHO MAY GET MUCORMYCOSIS?

The people who are suffering from

- Diabetes,
- Organ transplant
- Long term corticosteriod use
- Too much iron in body
- Post COVID patient
- Cancer
- Stem cell transplant
- Injection drug use
- Prematurity and low birth weight.
- Neutropenia (low number of white blood cells)
- Injured skin due to wounds, burns or surgery

Frequency

Mucormycosis is very rare, one report showed that it was present in 0.7% of patients at autopsy. Rhinopcerebral disease is the most common form, hence the name zygomycosis, others include pulmonary, cutaneous, gastrointestinal and disseminated diseases. Very rare cases occur in immunocompetent patients, usually after traumatic inoculation. Mucormycosis is found in patients of a wide age range. There is equal sex distribution except pulmonary mucormycosis which shows a male to female ratio 3:1.

Types of Mucormycosis:

Mucormycosis can be of different types, Rhinocerebral (sinus and brain) mucormycosis, Pulmonary (lung) mucormycosis, Gastrointestinal mucormycosis, Cutaneous (skin) mucormycosis, Disseminated mucormycosis.

(A) Rhinocerebral (Sinus and Brain) Mucormycosis:

It is the infection of sinus and can be spread into brain. 50% cases occur in patients with diabetes. Approx 50% cases of total case of mucormycosis are of this type.

Site of Infection: Nose, Paranasal sinuses, brain

Figure 3: Rhonocerebral mucormycosis

Symptoms: Onset with nasal stuffiness, epitaxixs and facial pain. Later, proptosis, chemosis and ophthalmoplegia, fever, black lessions on nasal bridge or upper inside of mouth that quickly becomes more severe. One sided facial swelling.

(B) Pulmonary (Lung) Mucormycosis:

Seen most commonly in Neutropenia patients, or people suffering from cancer.

Symptoms: Fever, cough, dyspnoea, chest pain

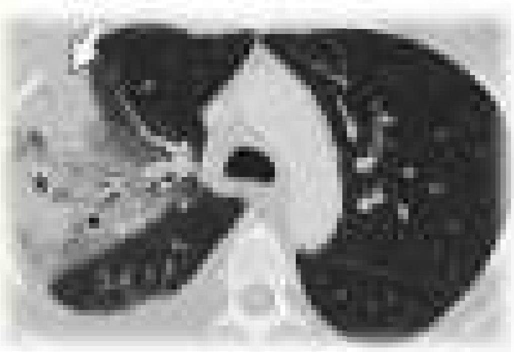

Figure 4: Pulmonary Mucormycosis (Hammer et al. 2018)

(C) Gastrointestinal Mucormucosis:

Commonly found among young children**.** Children who have to consume antibiotics, surgery, medicines that lower the body ability to fight against germs. Transmission through inhalation of spores.

Site of Infection: Stomach, colon, ileum.

Symptoms: Abdominal pain, Bowel obstruction, Vomiting, Bloody Diarrhea, Dyspepsia.

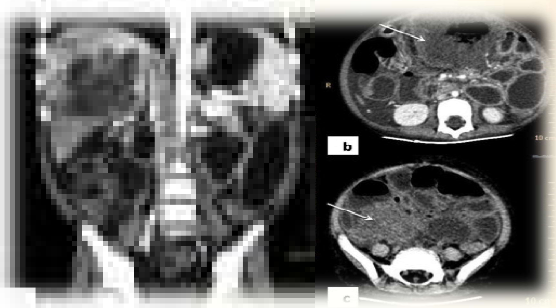

Figure 5: Gastrointestinal mucormycosis in a 2 years old child

(https://images.app.goo.gl/Zqg513v6moDqyJHm6)

(D) Cutaneous (Skin) Mucormycosis:

Most common form of mucormycosis among people who don't have weak immune system. It is frequent in poorly controlled diabetic patient. The fungal spore can be entered in the skin through a scrape, burn, or other type of skin injury.

Symptoms: Reddish and swollen skin, skin trauma, ulcer, painful patches of skin. The infected area may turn into black. Other symptoms include pain, warmth, excessive redness, or swelling around a wound.

Figure 6: Cutaneous mucormycosis

(https://images.app.goo.gl/PbHU88ZDKrHiD1vx8)

(E) Disemminated Mucormycosis:

This type of disease occurs when the infection spreads through the bloodstream to affect another part of the body. The infection most commonly affects the brain, but also can affect other organs such as the spleen, heart, and skin.

Accounts for 9% cases of mucormucosis and it carries high mortality. It occurs after organ transplantation. It happenes to those patients whose body is totally being compromised with many different other diseases. It is a rare, fatal complication disease. It may leads to coma.

Symptoms: Mental status changes.

Figure 7: Disemminated mucormycosis (https: //images.app.goo.gl/BNgwg7bNQvJfzf3h7

Pathogenesis of Mucormycosis

Diagnosis

Healthcare personnel consider the medical history, symptoms, physical examinations, and laboratory tests during diagnosing mucormycosis. Collection of sample or fluid will be done from the respiratory system from suspected person who have mucormycosis in the lungs or sinuses for laboratory diagnosis. A tissue biopsy also may require where a small sample of affected tissue is analyzed for evidence of mucormycosis under a microscope or in a fungal culture. They do sample microscopy, culture, culture microscopy in laboratory. In culture microscopy the fungi are identified. The suspected patient may also need imaging tests such as a CT scan of lungs, sinuses, or other body parts, depending on the position of the suspected infection.

Treatment

Mucormycosis is a serious infection and needs to be treated with antifungal medicine, usually amphotericin B, posaconazole, or isavuconazole. These medicines are given either intravenously (amphotericin B, posaconazole, isavuconazole) or orally (posaconazole, isavuconazole). Other medicines, including voricon-azole, fluconazole, and echinocandins, do not effective against fungi that causing mucormycosis. In general, mucormycosis necessitate surgery to incise away the infected tissue.

Prevention

- Strict control of diabetes
- Avoid contact with soil and dacaying matter.
- Stop corticosteriods and immune-compromised drugs.
- Treat neutropenia.

Use of mask and avoid contact with dead deacying matter, avoid of using cooler can reduce the chance of the disease.

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Plants Can Talk Too: A Glimpse of Plant Bioacoustics

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Tall brown trunk, standing straight above the ground, branches and sub-branches roofed with green leaves, multi petal colorful flower with sweet aroma; this is what we imagine whenever we hear the term “Plants”. The rustle of leaves in the cool spring breeze, or the rattling of the monsoon rain on the fronds, always have mesmerized poetic minds creating soulful wordplay works of literature. Different fictional writers have created talking plants and used them as a vital character in their stories. But in real life do they really talk? Plant bioacoustics is all about it. Photosynthates constitute the edible resource foundation for the animal kingdom, comprising about 80% of the earth's total biomass sequestering more than 100 billion tons of carbon every year (Thode, 2019). With the help of chlorophyll, they can absorb light waves and can converts light energy to chemical energy. But do plants radiate and respond to audiowaves? If yes then how? These are the questions plant researchers are asking now.

Making sound is a simple and common way of communication in animals. From, calling partners for mating to warn fellow animals from predators, animals have developed characteristic vocal frequencies that have become basic survival instincts in course of evolution. The animal bio-acoustic studies have become an integral part of behavioral biology in present time as it gives shape to the diversity of life. It might sound strange but plants have also been found to create and respond to recordable audio waves. In the past few years, studies and reports on plant bioacoustics are gaining acceleration globally.

In the early 1900s, Sir J.C. Bose pioneered bioacoustics studies claiming the plants do response against music. Later other scientists have also confirmed alike response from plants (Appel & Cocroft, 2014). In his writing, Sir J.C. Bose strongly believed that plants have a nervous system like system that help plants to respond in the availability of audio frequencies (BOSE, 1925), although anatomical and molecular studies denied the presence of such system. Detailed studies on the effect of plant bioacoustics in their physiology began in 1966 when researchers observed the ultrasonic frequencies of cavitation in dehydrating plants (Milburn & Johnson, 1966). Later on, studies have continued to demonstrate the priming effect of frequency-selective sensitivity on plant defense, stress endurance, and growth promotion (fig. 1).

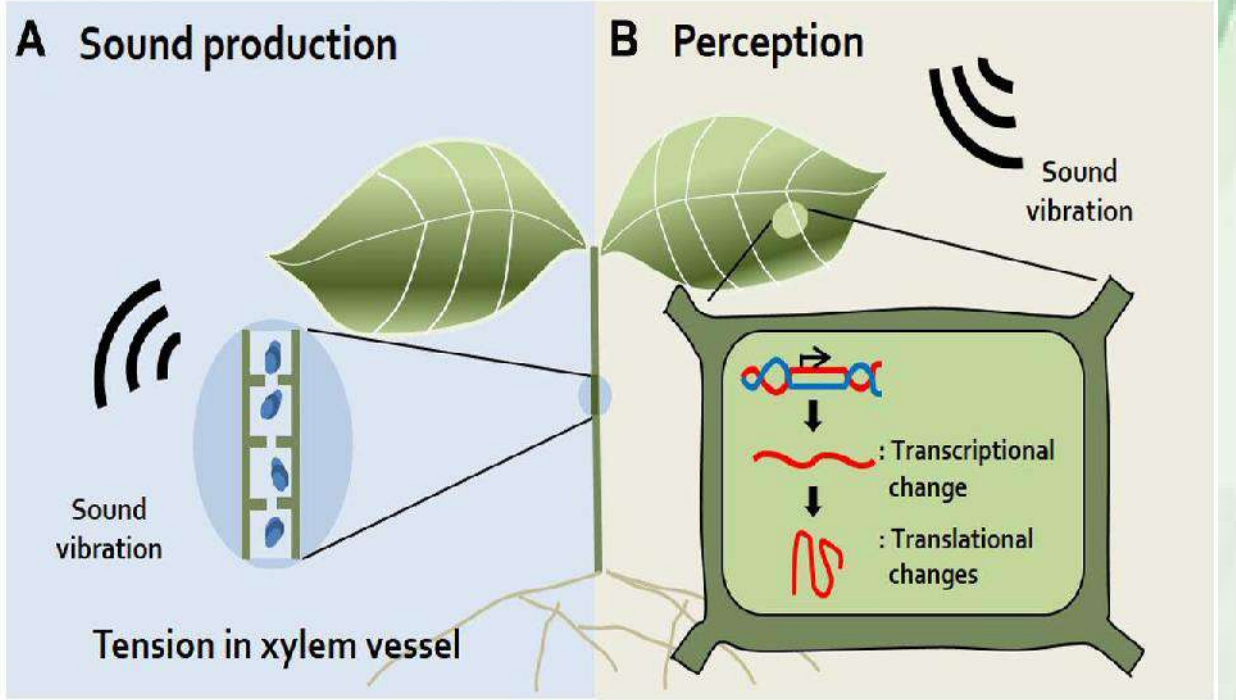

Figure 1: Sound production and perception in plants.
(A) Sound production. Plants produce sound vibrations in their xylem via the generation of tension in the xylem vessel when its diameter decreases. Additionally, gas bubbles produced in xylem vessels during transpiration may produce sound
(B) Sound Perception. Although there are no visible alterations, transcriptional and translational changes occur in plants exposed to sound vibrations. Levels of mechano-stimulus responsive, signalling-related, redox homeostasis, and defence-related transcripts are changed in sound-exposed plants However, the specific organs or proteins used for sound perception have not yet been identified (Jung et al., 2018) .

In many plants, flowers produce sweeter nectar and set loose the pollens as the buzzing sound of suitable pollinators hits the flower petals (Hedsén & Hedsén, 2019). M. Gagliano and her colleagues detected that the root of *Zea mays* plantlets can perceive the audio vibration of 200 Hz and bend towards the source of the sound. The seedling uses the audio frequency as a cue for the reorientation of the rhizo-system. In another experiment, they found that the sound of inaccessible flowing water attracts the root of the garden pea toward the audio source even in the absence of water. At a state when both soil moisture and audio frequency were available equally, root starts to choose soil moisture over the audio & which serves as evidence of positive root phonotrophism (Gagliano et al., 2012; Gagliano et al., 2017). These all are few experimental results that conclude the audio receiving and response capabilities of plants.

But can plants radiate sound? Plants that are under certain stress, produces various kinds of ultrasonic frequencies that help other plants for better tolerance of that stress. For example, audio (recorded from the desiccating plant) treated *Arabidopsis* were found with better tolerance to desiccation than untreated plants. The changes in gene expression and presence of stress tolerance strategies have concreted the role of plant audio emission in stress tolerance (Hedsén & Hedsén, 2019).

Figure 2: Experimental laboratory setup of Biophonic Garden routed: corn seeds are arranged on a grid which is situated in a container filled with water. The acoustic environment beneath the seeds is picked up by underwater microphones, which allows visitors to listen to the dialogue between the young corn plants. While the roots of the plants are submerged in the water, a constant sine tone of 220 hertz is played into the water which has an influence on the growing process of the roots, they bend towards the sound source. The phenomena of plants reacting to acoustic stimuli originated from scientific research into plant bioacoustics and is used in the work to raise questions about the communication of plants and the acoustic environment we humans live in. (source: Studio Freshmaniahttps://freshmania.at/portfolio/biophonic-garden/)

Several other noises are being recorded and termed as “Clicks” but their purposes are still unknown in the study of plant bioacoustics (Beloff, 2020). In experimental laboratory setups like Biophonic Garden (fig. 2) is used to display the possibility of making a dialogue between young plants perceivable for human ears. With upcoming technologies and advanced science these “raw audio data” may open a new horizon in plant-to-plant communication. There are more and more reports on audio induce physiological changes like change in hormone level, change in seed germination, change in genetic expression, etc. but the proper signalling pathways are still unknown to us (Mishra et al., 2016). We have to find those pathways for a better understanding of plant audio communication.

So, do plants talk to each other? The answer is yes, they do. They can radiate, receive and respond to audio vibration coming from other plants or organisms, but we have to find out how. Detailed anatomical studies have denied the presence of any auditory organs that can serve the plant bioacoustic communication, even no physical evidences of memory in plants were found till date that can help them to distinguish different audio waves for proper physiological actions. Then how do the plants radiate, receive and respond to different sound frequencies is still a mystery of plant science. Phonotrophism or plant bioacoustic is a promising and emerging sector of plant science that may provide a possible explanation to many unsolved questions of plant behavioural biology.

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Plant Based Vaccine –An Emerging Technology

Sudarshan Roy (M. Sc., Semester IV)

Vaccine is an immuno-biological material intended to produce specific defense against a particular disease. A vaccine is "antigenic" but not "pathogenic". Vaccines are now extensively regarded as an efficient and cost-effective device for improving health. There are several different types of vaccines. Each type is designed to enhance the immune system and avert serious, life-threatening diseases. Following types of vaccines are currently available: live, attenuated, inactivated, toxoid, polysaccharide & polypeptide (subunit), recombinant and conjugate vaccines. Quite a few plant-based biological products have attained clinical trials, with a few commercially accessible as medical appliances and pharmaceuticals for the management of chronic and infectious diseases. The drug ZMapp exercised first against the Ebola virus, obtained from the tobacco plant. It is combination of different antibodies that presented protection against the Ebola virus. The appearance of SARS-CoV-2 in late 2019 and its rapid spread in 2020 has created several global challenges that claimed new solutions in public healthcare and the pharmaceutical research ecosystem (Webb et al. 2020). In this present scenario it is better to diversify our research on plant based vaccine which has an immense potentiality against a number of diseases.

Production of Plant Based Vaccine

The production of plant-based vaccine requires the incorporation of transgene (gene of interest) into the plant cells. At first the target sequence of antigen is selected, cut and integrated within the vector then transferred it into the expression system. After a stable transformation or a transient transformation, the transgene expressed in the plants based on the location of their insertion in the cell. Stable transgenic plant cells may produce subunit antigen, in a range of 0.01 to 0.30% of overall soluble plant protein.

Recombinant Technologies

Due to the absence of live pathogen, recombinant subunit vaccines are safe and sound than traditional vaccines. A number of plants *viz*. tobacco, maize, rice, tomato, potato, lettuce, carrot, peanut, soybean alfalfa are used as hosts for *in vitro* transfer of gene using protoplast, cell or hairy root culture. Now plants can be used as bioreactors for production of commercial vaccines following these requirements: (a) quick and easy identification and design of target sequence of new antigens (b) high expression level of recombinant genes and (c) ascertain the safety of resultant proteins for consumption of humans or animals.

Agrobacterium-mediated Gene Transfer

Agrobacterium tumefaciens

Agrobacterium tumefaciens and *A. rhizogenes* are common gram-negative soil borne bacteria causing induction of ‘crown gall' and ‘hairy root' diseases, respectively. These bacteria naturally insert their genes into the genome of higher plants. In response to phenolic compound like acetosyringone, *A. tumefaciens* moved to the wound site via chemotaxis,. Infected plant cells (tumorous) were found to contain a segment of DNA of bacterial origin integrated in their genome. This transferred DNA (named T-DNA) was originally part of a small molecule of DNA located outside the chromosome of the bacterium. This DNA molecule is called as Ti (tumor-inducing) plasmid.

The steps involved in T-DNA transfer and integration in to the plant genome are explained in the following Figure 1. vir -protein (3); vir D1 and vir D2 are involved in ssT-DNA

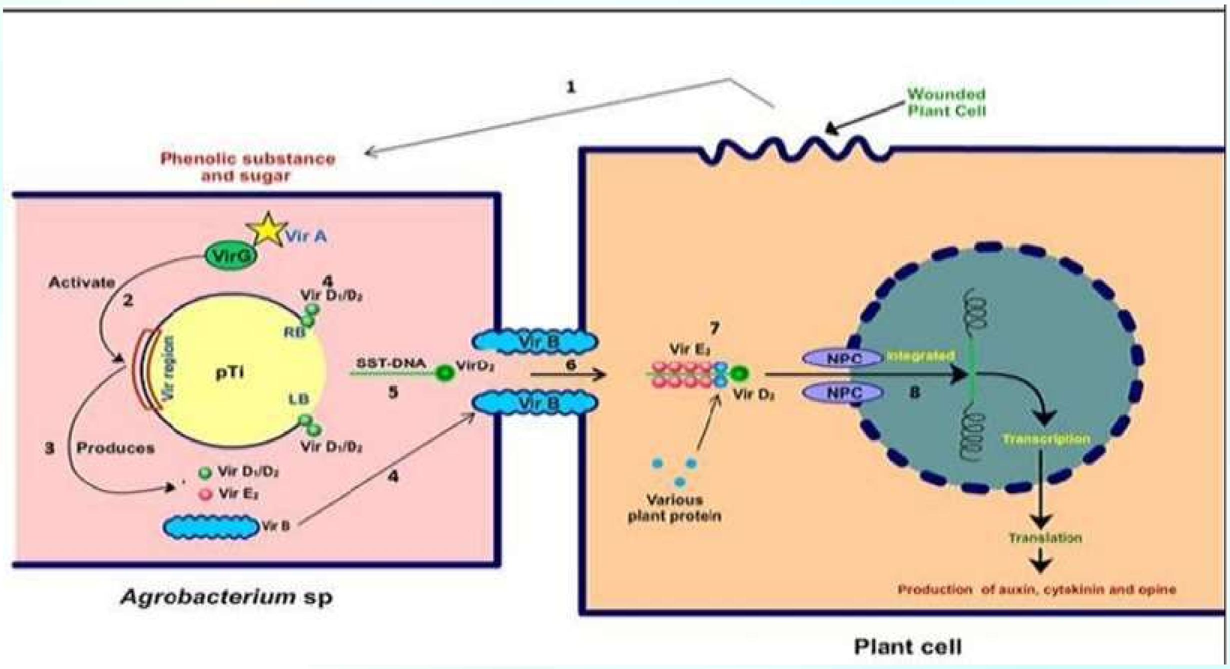

Figure 1: T DNA transfer and integration (Waghmare S. T., Belge S. A., Yeole P.T., Kharade S. S., Chavan N. S. (2017) *Agrobacterium* Mediated Gene Transfer: an Overview)

production from Ti-plasmid and its export (4) and (5); the ssT-DNA (with associated vir D1 and vir D2) with vir E2 are exported through transfer apparatus vir B (6); in plant cell, T-DNA coated with vir E2 (7); various plant proteins influence the transfer of T-DNA + vir D1 + vir D2 + vir E2 complex and integration of TDNA to plant nuclear DNA (8). (LB= left border; RB= Right border; pTi = Ti plasmid, NPC = nuclear pore complex).

The benefit of *Agrobacterium*-mediated transformation include the transfer of DNA segment with defined ends and nominal rearrangement, the incorporation of small copies of genes into plant chromosomes, the transfer of relatively large piece of DNA and the improved quality of transgenic plants.

Hairy Roots Technology

With the help of plant genetic engineering, hairy root production is carried out by plant tissue culture to manufacture valuable secondary metabolites or recombinant proteins as well as to study plant metabolic processes. Hairy root culture is also called as transformed root culture from naturally occurring Gram negative soil bacterium *Agrobacterium rhizogenes* that contains root inducing plasmids (Ri plasmids). It infects roots of dicot and some monocot and produce some unusual amino acids called opines (octopine, agropine, nopaline, mannopine, cucumopine etc.). The opines are utilized by the bacterium as the source of carbon, nitrogen and energy and helps to grow abnormally. Transformed roots are morphologically different from normal roots in that they are much more branched and have much lateral meristematic growth that leads to higher biomass.

Human Vaccines in Clinical Trials

Clinical study was conducted with oral HBsAg produced in transgenic potato . The registered volunteers received three doses of HBV injection-type vaccine within 15 years. The placebo group was given non-transgenic potato, the two-dose group was vaccinated at 0 and 28 days with 100 g of transgenic potato (850±210μg of antigen), and the three-dose group was vaccinated with the same doses at 14 days interval. It was found that 52.9% of contributors in the two-dose group and 62.5% of contributors in the three-dose group had superior HBsAg antibody titers in a 70-day follow-up period after the first immunization.

Development of veterinary vaccines

The low cost Plant-based vaccines can also be used against animals also. Edible vaccines require little effort for administration. Glycoprotein gene of different animal viruses expressed in different plants. Glycoprotein of Newcastle disease virus has been introduced in tobacco, potato, rice and maize. Likewise glycoprotein gene of infectious bronchitis virus (IBV) has been expressed in potato. Both can protect the chicken from respective diseases. FMDV VP1 and the structural polyprotein P1 defended mice and guinea pigs against Foot and Mouth Disease Virus (FMDV), were successfully produced in tomato tobacco, potato and alfalfa.

Plant-Based Vaccine Technology Fight against COVID-19

The coronaviruses (CoVs) are enveloped viruses having a positive-sense, single-stranded genomic RNA and are grouped into four genera: α-CoVs, β-CoVs, γ-CoVs, and δ-CoVs. Mammals are affected by α- and β-CoVs, while the other two genera infect both mammals as well as birds. Immunization is the most efficient approach to manage and eventually eradicate any infectious diseases. Since SARS-CoV-2 have elevated transmissibility (asymptomatic and presymptomatic virus shedding that results in a high percentage of patients with mild symptoms), the development of vaccines is a vital objective to combat against this pathogen. A vaccine formulated on live-attenuated virus is another promising approach. The cross protection of SARS-CoV-1 and MERS experimental vaccines remain to be explored. Thus far, there is indication that some SARS-CoV-1 neutralizing antibodies cross react with SARS-CoV-2, however, extensive research regarding this is required. The conserved epitopes among SARS-CoV-1 and SARS-CoV-2 have been identified and propose designed for vaccine development.

A key model for this field is the vaccine candidates already accounted for SARS-CoV-1 and MERS, which are both closely related to SARS-CoV-2. The N-terminal segment of the SARS-CoV-1 S protein (S1) was introduced in low-nicotine tobacco and potato plants through an *Agrobacterium*-mediated approach. Mice immunized orally with this transgenic tomato disclosed significantly increased levels of SARS-CoV-1-specific IgA. Sera of mice parentally primed with the transgenic tobacco showed the presence of anti-SARS-CoV-1- IgG.

Challenges:-

- Selection of Antigen and Plant Expression Host.
- Consistency of Dosage.
- Manufacturing of Vaccines according to GMP Procedures.

Importance of Plant Based Vaccine

- Plants that have engineered with genes encoding antigenic proteins of various pathogenic virus and bacterial organisms express the proteins that being out production of antibodies in mammalian hosts.
- When produced in edible parts of the plant, such as grains fruits or even leaves, sub unit vaccines may not require purification.

The Advantages of Plant Based Vaccine

Plant vaccines possess several advantages over conventional vaccines. They are highly cost effective with regard to production, storage and transportation. As these vaccines are produced in transgenic plants, simple agricultural techniques are needed for their production and processing, thus expenditure of equipment and technology etc. are reduced. Vaccines from plants are usually delivered by oral route consequently decreasing the necessity of a medical professional to deliver the same.

The Disadvantages of Plant Based Vaccine

- Development Immuno-tolerance to vaccine.
- Variation of dosage from plant to plant, fruit to fruit and generation-to-generation.
- The stability of the vaccine in fruit/seed is not known.
- Dosage of vaccine would be variable.

Plant-based vaccines are recently flourishing type of vaccines which have a higher remedial value to treat several human and veterinary diseases.. Due to the utilization of bacteria and virus as the vectors, the pathogens might be reactivated and infect other organisms that consume them. So, serious attention should be given in this respect.

The appearance of COVID-19 has created an emergency throughout the globe that insists the development of new medicines, particularly vaccines, to combat against this threat. In this scenario, a plant-based vaccine might be a feasible approach to respond to this need. The existing expression technologies suggest applicable corridors for production of anti-COVID-19 vaccines in plants. As the COVID-19 outbreak progresses, the development of plant-based vaccines might give an assurance to generate the simple, cost-effective, safe and successful vaccines to fight against this pandemic. The coming days will be crucial to visualize the actual potential of this emerging green technology.

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Potentiality of Mushrooms in Bioremediation

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Contamination of soil, air and water by industrial by products and utilization of unwarranted chemical fertilizer and pesticides in agriculture are the major concern of environmental scientists.. Though incineration is the most common and effective remediation practice but it is costly in terms of money and energy used. A cost effective and ecologically sustainable method of clean-up is 'bioremediation' that utilizes micro-organisms to completely degrade the toxic chemicals or at least convert into less harmful forms. Although, bioremediation by bacterial agents has received attention of workers, the role of fungi has been inadequately studied. Fungi are also able to transform a wide variety of harmful chemicals thus arouse the interest of their use in bioremediation. Fungi-based remediation technology i.e, mycoremediation is the application of fungi in the remediation of environmental pollutants from soil and aqueous effluents. According to Stamets (1999), mycoremediation is an aspect of remediation which is defined as the biological process that involves the decomposition of hydrocarbon based contaminants, filtration of agricultural /industrial water runoff, concentration/ removal of heavy metals from soil and other substrates by a living organism.

Mechanism of Biodegradation Process

Filamentous fungi including mushrooms are the powerful decomposers in nature that secrete an array of extra cellular enzymes as they grow and produced biomass aggressively. The white-rot fungal ligninolytic system is considered to contain a pool of enzymes, particularly lignin peroxidase (LiP), manganese peroxidase (MnP) and laccase (Lac), which are highly effective in oxidising and cleaving wood and lignin (natural components of the ecosystem), as well as various intractable xenobiotic pollutants structurally similar to lignin. The lignin-degrading system is triggered by the absence of any single nutrient, and the extracellular oxidative enzymes are not dependent upon the concentration of the pollutants (Del Pilar Castillo 1997). As the system is not specific, it allows the mineralisation of a broad range of persistent organic pollutants as opposed to bacterial systems which may require separate enzymes to catalyse the breakage of each bond type (Lonergan 1992).White rot fungi have been used to degrade petroleum hydrocarbons, biotransform pesticides, and also used to degrade lignocellulolytic wastes in the pulp and paper industry. Among many mushrooms *Pleurotus ostreatus*, *Phanerochaete chrysosporium*, *Trametes versicolor*, and *Agaricus bisporus*, have been reported in the decontamination of polluted sites.

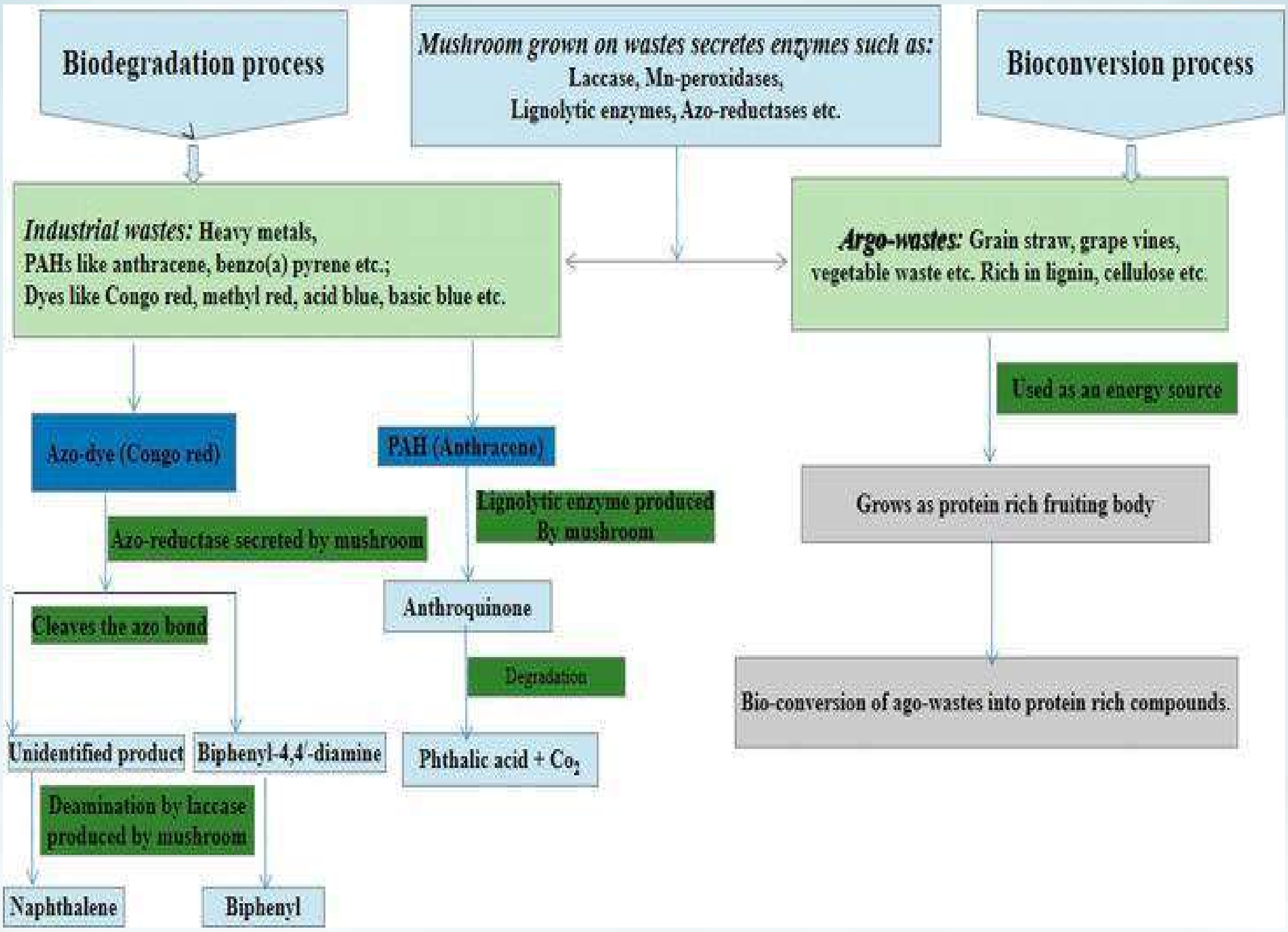

Figure1: Biodegradation process of Mushroom (Gulzar et al, 2020)

Mushrooms in Bioremediation

White-rot fungi are so called because their degradation processes result in a bleaching of wood substrates (Kirk et al., 1992). In contrast to brown rot fungi they digest wood lignin by enzyme secretions giving wood a bleached appearance. The degrading technology of white-rot fungi is quite different from other well-established methods of bioremediation (for example, bacterial systems). The differences are due to the unusual mechanisms which nature has provided them with several advantages for pollutant degradation (Asamudo et al., 2005). These fungi have a distinct advantage over bacterial systems as they do not require precondition for the particular pollutant. Usually bacteria must be pre-exposed to a pollutant to allow the enzymes that degrade the pollutant to be induced. The pollutant must also be in a significant concentration, otherwise induction of enzyme synthesis cannot occur. Barr and Aust (1994) reported degradation of aromatic compounds by a number of white-rot fungi.

According to Lang et al. (1995) lignin degrading white-rot fungi have the extraordinary abilities to transform recalcitrant pollutants such as polycyclic aromatic hydrocarbons (PAH's). This unique capability of these fungi may be used for the decontamination of oil-polluted soils although lignocellulosic substrates must be supplied for the survival of fungal species in the soil. These fungi have been used for the accumulation of heavy metals and bioremediation of polluted soils also. Bennet et al. (2002) reported that these fungi have the capability to be used for bio-deterioration, mineralization, bio-degradation, co-metabolism and transormation.

The main mechanism of bio-degradation employed by white-rot fungi is the enzymatic machinery of lignin degradation system. According to Hattaka (1994) a lot of species of this group are able to degrade lignin, a naturally occurring polymer. This capacity of lignin degradation is assumed to the result of extracellular secretion of oxidases and laccases (Glenn and Gold, 1983). These enzymes are nonspecific and capable to oxidize a wide range of xenobiotics (Barr and Aust, 1994; Martens et al., 1996). Loske et al., 1990 reported that these fungi have been proposed for the biodegradation of polluted sites containing complex mixtures of PAH's such as occurring in crude oil, coal tar and creosote.

White-rot fungi, *Phanerochaete chrysosporium* is used as a model system for bioremediation. *P. chrysosporium* degrade lignin macro molecules as well as also able to degrade many types of organopollutants such as chlorophenols, polycyclic aromatic hydrocarbons (PAH's nitrocranditics, polychlorinated biphenyls and dioxines, chlorolignins, different pesticides and synthetic dyes etc.. Nigam et al. (1995) reported that *P. chrysosporium* is capable for bioleaching of organic dyes. The first extracellular enzyme (ligninase) discovered to deploymerize lignin, and lignin sub-structured compounds *in vitro* were produced by this organism (Aitken and Irvine, 1989). *Phanerochaete flavido-alba* has been able to decolorize olive oil mill wastewater (OMW), a major waste product of olive oil extraction for subsequent use in bioremediation assays. *Trametes versicolor* produced three ligninolytic enzymes with efficient degradation capacity on lignin, polychlorinated biphenyl mixture, polycyclic aromatic hydrocarbons and also a number of synthetic dyes (Tanaka et al., 1999; Novotny et al., 2004). *T. versicolor* and its enzymes have been reported to delignify and to bleach kraft pulp (Gamelas et al., 2005) and also efficiently dechlorinate and decolorize bleach kraft pulp effluents (Selvam et al., 2002). Recent studies have shown that *Pleurotus ostreatus,* a member of edible oyster mushroom have the ability to degrade a variety of polycyclic aromatic hydrocarbons (PAH) (Sack and Gunthen, 1993). It can degrade PAH in non-sterile soil even in the presence of mercury and cadmium. Isikhuemhen et al. (2003) reported that *P. tuber-regium* has the ability to ameliorate crude oil polluted soil and the resulting soil sample supported seed germination and seedling growth of *Vigna unguiculata*.

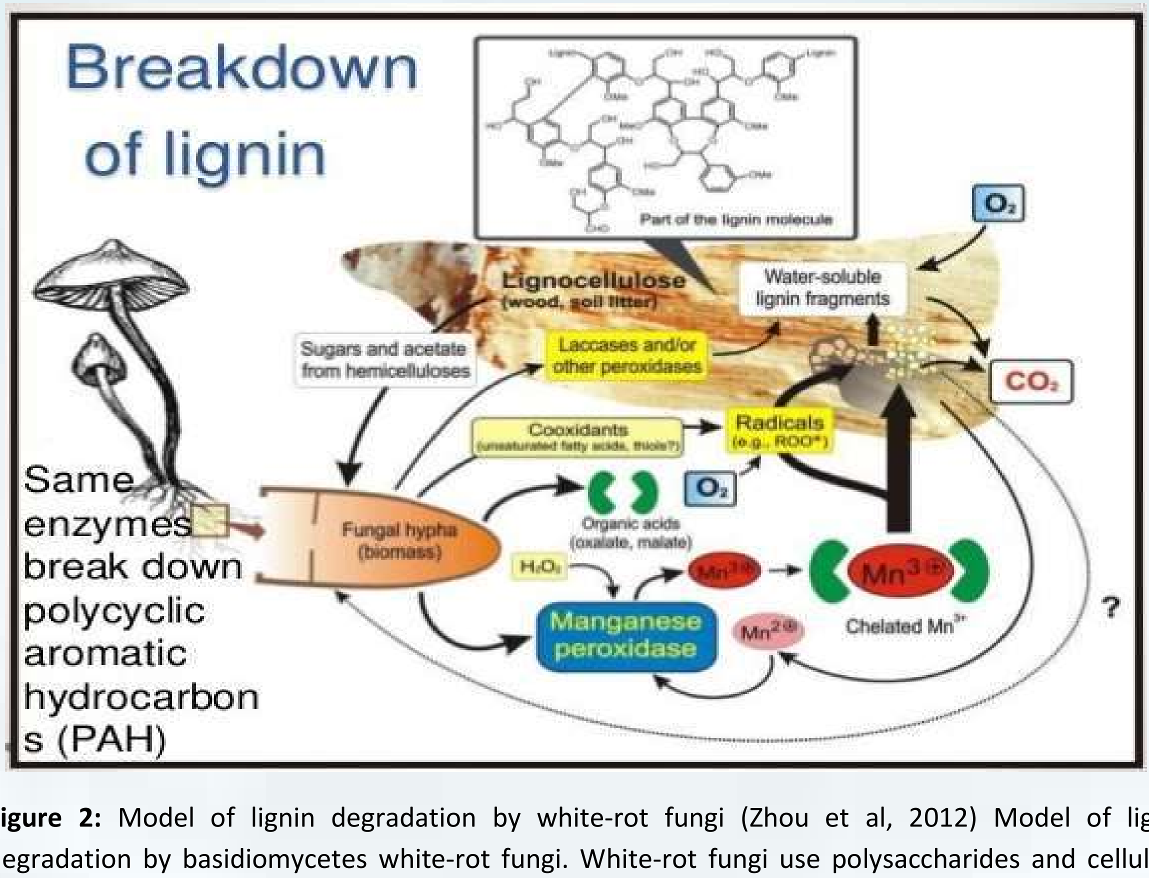

Figure 2: Model of lignin degradation by white-rot fungi (Zhou et al, 2012) Model of lignin degradation by basidiomycetes white-rot fungi. White-rot fungi use polysaccharides and cellulose acetate derived from hemicellulose as a source of carbon and energy, while at the same time the lignin is degraded (enzymatic combustion). Model of lignin degradation by basidiomycetes white-rot fungi. White-rot fungi use polysaccharides and cellulose acetate derived from hemicellulose as a source of carbon and energy, while at the same time the lignin is degraded (enzymatic combustion).

They reported a significant improvement in germination percentage, plant height and root elongation. Ogbo and Okhuoya (2009) investigated the effect of crude oil on the yield and chemical composition of *P. tuber-regium* (Fr.) Singer on soils to which sawdust, shredded banana leaves, NPK fertilizer and poultry litter were added. The study showed that the contamination of crude oil improves the overall well being of the fungus. *Lentinus squarrosulus,* another edible mushroom has the ability to mineralize the crude oil contaminated soil at different concentrations. Adenipekun and Fasidi (2005) reported that *L. squarrosulus* is able to mineralize soil contaminated with various concentrations of crude oil (1 to 40%). They also found that nutrient contents were generally higher after 6 months of incubation but potassium levels were not increased. The rate of biodegradation was *20*% after 3 months and 40% after 6 months of incubation (Adenipekun and Fasidi, 2005). Adenipekun et al. (2011) also worked on the management of *cement* and battery polluted soils by using *Pleurotus pulmonarius*. Since these mushrooms are member of white rot fungi, they have been used in the remediation of polluted soil in recent years. Research has shown that mushroom species such as *P. chrysosoporium* and *P. ostreatus* have emerged as model systems for studying degradation of a number of xenobiotics.

Figure 3: Oyster mushrooms producing on oil contaminated soil (Thomas et al, 1999)

Use of mushrooms and other white rot fungi in bioremediation is expected to be economical as they can be grown on a number of low cost agro-waste materials such as rice straw, sawdust, corn cobs etc.. Mycoremediation is not only efficient and cost effective but also very good technique for the environmental remediation and sustainable practices.

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Lampenflora – Plants Growing Without Sunlight

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Sunlight is the source of energy for every living organism on this planet earth. Green plants convert light energy to chemical energy, use it and also transfer it to heterotrophic organisms. But, there is a plant community which does not need sunlight to grow. They are called Lampenflora. In this article, I shall discuss about this unique plant community.

What is Lampenflora?

Lampenflora designates the phenomenon of proliferation of principally phototrophic organisms near artificial light sources at sites where under natural circumstances they would not appear. They are completely dependent on artificial lighting (Mulec, 2019).

This phenomenon was initially studied by Austrian and French scientists (Baquedano Estevez *et al*., 2019). In 1963, the word "lampenflora" (a German word which means "plants of the lamp") was first introduced by Dobàt (1963) and is presently adopted everywhere in the world to identify any kind of plants growing in the vicinity of lamps (Cigna, 2012).

Figure 1: The presence of lampenflora - 1.1-1.3 Lampenflora in Gong (1.1 Phycophyta, 1.2 Bryophyta, 1.3 Pteridophyta), 1.4 lampenflora in Tabuhan (Kurniawan et al., 2018)

Where is Lampenflora Observed?

Generally, the show caves which are the sites of greatest interest to tourists for their prehistoric cave paintings or high-value geological formations are the main locations to observe Lampenflora (Baquedano Estevez *et al*., 2019). Most of such caves particularly those intended for mass visitation are equipped with artificial lighting and are well illuminated to present them to the public, and consequently they become the prime sites for development of lampenflora (Mulec, 2019). Lampenflora proliferate in the vicinity of the light sources (Illuminated areas such as rocky surfaces, sediments and artificial materials around lamps) thanks to the energy released by the lamps (Cigna, 2012). Mass visitation and artificially induced air circulation enhance further expansion of lampenflora (Mulec, 2019).

Composition of Lampenflora Community

In general the lampenflora is firstly composed by algae at the beginning of its development, to be followed by mosses, ferns and sometimes by vascular plants (Cigna, 2012).

Prokaryotic cyanobacteria together with eukaryotic green (Chlorophyta) and golden (Chrysophyta) algae (mostly diatoms) are the most common micro-organisms identified in lampenflora communities, but their abundance varies from one cave to another (Baquedano Estevez *et al*., 2019). Other groups, such as Cryptophyta, Euglenophyta, Eustigmatophyta and Rhodophyta, are usually represented by only a few specimens. Among cyanobacteria the following genera are frequently encountered: *Aphanocapsa* sp., *Chroococcus* sp., *Gloeocapsa* sp., *Leptolyngbya* sp. and *Phormidium* sp. Chlorophytes often include *Chlorella* sp., *Scenedesmus* sp., and *Stichococcus* sp. These two groups give predominantly greenish colour of the biofilm. With the increase in abundance of diatoms (*Achnanthes* sp., *Cymbella* sp., *Fragilaria* sp., *Hantzschia* sp., *Navicula* sp. and *Nitzschia* sp.) lampenflora can adopt more brownish appearance (Mulec, 2019).

A common dweller in caves is tufa-forming moss *Eucladium verticillatum* which has high ecological tolerance based on the photosynthetic photon flux density (PPFD) span, ranging from poorly (e.g., 1.4µmol photons/m2/s) to powerful lighted places (e.g., 530µmolphotons/m^2/s) (Mulec, 2019). Bryophytes can complete their life cycle by longer exposure to light irradiance even at low PPFDs. Such an example is *Cratoneuron filicinum* which lives in a mine where lights are on nonstop with PPFD between 2.1 and 2.4µmolphotons/m2/s. Inspection of lampenflora also confirms the presence of moss protonemata (Mulec, 2019).

Ferns are also sometimes part of lampenflora community, but their diversity is low, and they are frequently found only as prothalli. Vascular plants are even rarer in this community, but if they appear, they are almost exclusively in form of germinating shoots (Mulec, 2019).

Heterotrophic bacteria, fungi, and protozoa are also largely found in lampenflora community, although their diversity and role are yet to be properly evaluated. The major bacterial phyla are Proteobacteria, Actinobacteria, Bacteroidetes, Chloroflexi, Gemmatimonadetes and other unclassified bacterial groups. Interestingly, *Chlorobium* sp., a representative of green sulfur bacteria was found in lampenflora biofilm in lighted aquarium in the Frasassi Caves, Italy (Mulec, 2019).

Fungi are less dominant in lampenflora, but mainly represented by Ascomycota and Zygomycota and to a lesser extent by Basidiomycota and Rozellomycota (Mulec, 2019).

Growth and Development of Lampenflora

In the early phases of colonization, cyanobacteria and eukaryotic algae play the most important role in the processes of forming biofilm and are considered as pioneering species in the ecological succession (Baquedano Estevez *et al.*, 2019). The presence of cyanobacteria in lampenflora communities is very important because these photosynthetic microorganisms grow most successfully in illuminated underground environments (Baquedano Estevez *et al.*, 2019). They require no organic matter and are capable of absorbing a wide spectrum of light radiation thanks to the presence of accessory pigments (phycobilins i.e. phyco-erythrin, phycocyanin and allophycocyanin) in addition to chlorophyll. These qualities confer a significant advantage for the colonisation of new areas (Baquedano Estevez *et al.*, 2019). Some cyanobacteria can even use fermentative pathways to obtain energy and such physiological capability allows these organisms to survive periods with no available light (Mulec, 2019). Although this group of algae may live independently in nature, most of the microorganisms tend to form multicellular communities known as “biofilms” in which cyanobacteria and algae coexist with bacteria, fungi and yeasts. Chemically, biofilms are composed mainly of water (~70-90%), organisms with a diverse metabolism and a hydrated matrix of extracellular polymeric substances (EPS) composed of polysaccharides, lipopoly-saccharides, proteins, glycoproteins, lipids, glycolipids, fatty acids and enzymes (Baquedano Estevez *et al*., 2019). This matrix confers a number of advantages favouring the survival of the lampenflora community in hostile environments by enhancing the resistance of its members to external agents or other organisms. Some of these benefits are: greater protection against sources of environmental stress (desiccation processes or exposure to UV rays, heavy metals and atmospheric contaminants), greater water retention and enhanced concentration and circulation of nutrients within the biofilm (Baquedano Estevez *et al*., 2019). It has also been observed that these single-cell microorganisms use a process of intracellular communication through chemical signals known as "quorum sensing", which helps them to act in a coordinated way as multicellular organisms (Baquedano Estevez *et al*., 2019).

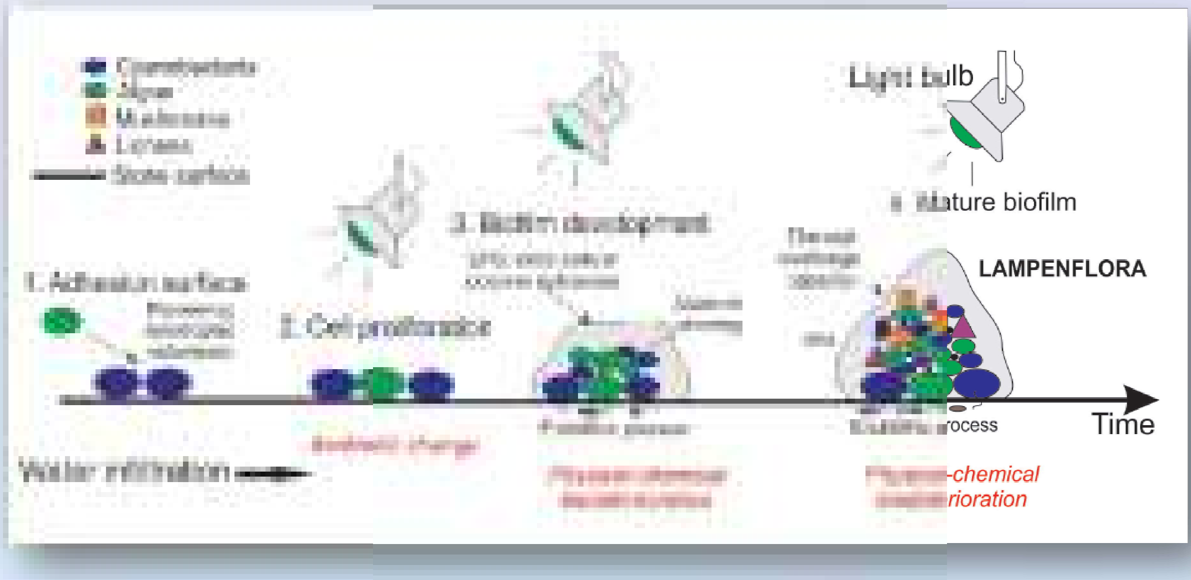

Figure 2: Diagram of the process of formation and evolution of biofilm of lampenflora community in show caves (Baquedano Estevez *et al.*, 2019)

The species' succession process of the early colonising microscopic community of the lampenflora (cyanobacteria and algae) is quite dynamic (Baquedano Estevez *et al*., 2019). They grow rapidly before being slowly displaced by more persistent organisms (Baquedano Estevez *et al*., 2019).

Thanks to early algal community's photosynthetic capacity and their nitrogen and CO_2 fixing ability, biofilms promote the occurrence of mosses and ferns in the sites around them (Baquedano Estevez *et al*., 2019). They get benefited from their nutrient rich environment in turn inducing the proliferation of some heterotrophic microorganisms (bacteria and fungi) (Baquedano Estevez *et al*., 2019).The final successional phase may also include vascular plants, although almost always in the form of germinating shoots (Baquedano Estevez *et al*., 2019).

Among all the microorganisms found in a cave, fungi are one of the reasons of greatest concern because of their huge rate of spore production and dispersion in the atmosphere (Baquedano Estevez *et al*., 2019). Moreover, fungi do not need light for their growth and can proliferate in the areas of dim light as well as in total darkness of the caves at some distances from the position of lamps (Baquedano Estevez *et al*., 2019).

The most critical environmental factors affecting the development and composition of photosynthetic micro-organisms in underground environments are availability of light, moisture, temperature and nutrients (Baquedano Estevez *et al*., 2019).

Regions with poor illumination are occupied by heterotrophic organisms and regions with strong illumination are colonised primarily by photosynthetic microorganisms (Baquedano Estevez *et al*., 2019). 85% of the lampenflora population can proliferate with an approximate minimum value of 40 lux, but an established lampenflora community may live for a long of time period with much lower amount of light (Baquedano Estevez *et al*., 2019). Certain algae and cyanobacteria can live and reproduce even at light intensities much below the "photosynthetic compensation point" (Baquedano Estevez *et al*., 2019). In low light, mosses may show a physiological adaptation called etiolation where they expose a greater surface area of their plant body to the light to capture the few available photons (Baquedano Estevez *et al*., 2019).

The microorganisms initiating the lampenflora communities get access inside the cave due to their mobility or by air currents, water flows, and gravitational sedimentation through cracks and small cavities in the rock or by the movement of cave fauna and tourists (Baquedano Estevez *et al*., 2019).

Another important factor in the proliferation of lampenflora is the local air currents caused by the warm air developed near the powerful lamps particularly halogen lamps (500-1000 W) (Baquedano Estevez *et al*., 2019). The development of lampenflora has even been found at distances of over 10 m from this type of artificial lights (Baquedano Estevez *et al*., 2019).

Is Lampenflora a blessing or curse?

A unique community structure and new taxa like *Timaviella circinata* and *T. karstica* may be discovered here but one has to always remember that this alien flora does not develop in underground environments naturally. Its occurrence is directly linked to human interference in natural environment (Mulec, 2019).

Moreover, the negative impacts of lampenflora should not be ignored because plants of this community may synthesize weak organic acids which in time can erode both limestone and other important geological formations in the show caves and can also damage significant paintings of the prehistoric caves as occurred in Lascaux cave in France (Cigna, 2012).

Control Measures Adapted for Lampenflora

Various measures that have been taken to restrict lampenflora growth in show caves of different parts of the world are: (a) usage of brushes and water jets for mechanical removal, (b) adoption of limited lighting regime, low light intensity and short illumination time in individual areas, (c) avoidance of illumination of damp surfaces and areas filled with sediments, (d) change of emission spectra of the artificial lights to avoid absorption maxima of the chlorophyll a (main photosynthetic pigment of oxygenic phototrophs) and (e) application of UV lamps when tourists are absent (Mulec, 2019).

Using water jet to remove lampenflora is not an acceptable approach as there are many delicate unique formations in the show caves and they can be destroyed during this procedure (Mulec, 2019). UV-C irradiation (255–280 nm) of areas occupied by lampenflora was a successful measure for their restriction, but it leads to the development of thymine-thymine dimers i.e. mutations of DNA and other dangerous changes in the cave ecosystem which is in the range of irradiation (Mulec, 2019).

Several chemicals Dichlorophenyl dimethyl urea (DCMU), formalin and cupric ammoniac solutions and herbicides (atrazine and simazine) have been used in caves for bringing back the pre-lampenflora state of the colonized surfaces, but most of them are very toxic and should not be introduced into the cave environment (Mulec, 2019).

Usage of bleach or other oxidizing compounds for restricting lampenflora growth damages significant art collections like prehistoric paintings, frescoes, stuccoes and mosaics of the show caves and thus should be avoided for managing such areas (Mulec, 2019).

An important step in controlling lampenflora problem should be the initiation of its treatment as early as possible and sometimes even before they are visible by a naked eye (Mulec, 2019). In future management of lampenflora community should definitely be done by adoption of a very limited (low PPFDs) lighting regime and short-time lighting and also development of a treatment which would limit lampenflora growth with zero or least impact on caves and its ecosystem (Mulec, 2019).

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অক্সিজেনের উৎস সন্ধানে

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প্রাক্তনী, স্নাতকোত্তর উদ্ভিদবিদ্যা বিভাগ
(বর্তমানে ইন্ডিয়ান স্ট্যাটিসটিক্যাল ইনস্টিটিউট এর জীববিজ্ঞান বিভাগে গবেষণারত)

ইদানিং যে ঘটনা আমাদের একসময়ের অলীক কল্পনাকে একেবারে সজ্ঞান বাস্তবের দিকে পা বাড়াতে সাহায্য করেছে সেটি হল মঙ্গল গ্রহে বসবাসের উদ্যোগ! এই বছরের গোড়ার দিকেই নাসার পার্সিভরেন্স রোভার লালগ্রহের মাটিতে সফল অবতরণের পর থেকে কি কি অসাধ্যসাধন যে করে চলেছে সে কথা কে না জানে। তবে মূল উদ্দেশ্য সফল হওয়ার অর্থাৎ মঙ্গলকে মানবজাতির বাসযোগ্য করে তোলার মাঝে বড় কাঁটা দুটিই। এক - সেখানকার অতি শীতল আবহাওয়া, আর দুই – তার স্বল্প বায়ুমণ্ডলের আস্তরণে কার্বন ডাই অক্সাইড এর আধিক্য তথা অক্সিজেনের অভাব। যা পৃথিবীর বায়ুমণ্ডলের চেহারার ঠিক উল্টো। তবে একথা বলার অপেক্ষা রাখে না যে পৃথিবীর বায়ুমণ্ডলও চিরকাল এরকম ছিল না। সৃষ্টির শুরু থেকে আজকের এই শস্যশ্যামলা বসুন্ধরা হয়ে ওঠার মাঝে কেটে গেছে কোটি কোটি বছর। আর এই সময়ে ঘটেছে একাধিক চমকপ্রদ ঘটনা যা আমূল পরিবর্তন করেছে পৃথিবীর পরিবেশকে।

যেমন, জীবনধারণের গুরুত্বপূর্ণ উপাদান অক্সিজেনের যোগান যে আসে গাছপালা থেকেই এ তো সবার জানা।মজার ব্যাপার এই যে পৃথিবীর বায়ুমণ্ডলের এই বিপুল পরিমাণ অক্সিজেন এর অর্ধেকের বেশি কিন্তু আসে সমুদ্রে বসবাসকারী উদ্ভিদগোষ্ঠীও অনুজীবদের থেকে। এখন, যে প্রক্রিয়ার মাধ্যমে তারা আলোর উপস্থিতিতে জলকণা থেকে অক্সিজেন অনুদের আলাদা করে সেগুলিকে গ্যাসীয় আকারে বায়ুমণ্ডলের নিক্ষেপ করে অর্থাৎ সেই সালোকসংশ্লেষের ক্ষমতা তারা ঠিক কিভাবে রপ্ত করলো সে বিষয়ে একটু আলোকপাত করা যাক। পৃথিবীর জন্ম প্রায় ৪৬০ কোটি বছর আগে হলেও বায়ুমন্ডলে এবং অগভীর সমুদ্রে বিপুল পরিমাণ অক্সিজেন জমা হতে শুরু করে ২৪০ কোটি থেকে ২০০ কোটি বছর আগে। বিজ্ঞানের পরিভাষায় যাকে বলা হয় 'বৃহৎ জারণ ঘটনা' বা Great Oxidation Event (GOE)। ইতিমধ্যে, ভূতাত্ত্বিক এবং রাসায়নিক গবেষণালব্ধ ফলাফল থেকে অনুমান করা গেছে যেতার কিছুকাল আগে থেকেই জৈব-উৎসগত আণবিক অক্সিজেন পৃথিবীর বায়ুমণ্ডলে সঞ্চিত হতে শুরু করে এবং ধীরে ধীরে বায়ুমণ্ডলকে বিজারক থেকে জারক অবস্থায় নিয়ে আসে। অতি সাম্প্রতিক গবেষণায় এর বেশ কিছু নিদর্শনও মিলেছে। যেমন, সদ্য প্রকাশিত হওয়া এক তত্ব অনুযায়ী– GOE এর চেয়ে প্রায় ৫-১০ কোটি বছর আগে ঘটতে থাকা কিছু আগ্নেয়গিরির অগ্ন্যুৎপাত পৃথিবীর উপরিভাগে এবং সংলগ্ন জলাশয়ে প্রচুর পরিমাণে লাভা ও ছাই নির্গমন করে, যা সম্ভবত সেখানে বসবাসকারী বিশেষ কিছু শ্রেণীর অনুজীবদের নানাবিধ পুষ্টি প্রদান

করে ছিল। ফলস্বরূপ সেগুলি প্রকারন্তরে ওই অণুজীবদের সংখ্যা বৃদ্ধিতে সহায়তা করে এবং তারাই পরবর্তীকালে বায়ুমণ্ডলীয় অক্সিজেন সৃষ্টিতে মুখ্য ভূমিকা পালন করে। মূলত, এই সব প্রাগৈতিহাসিক আগ্নেয়গিরি থেকে নির্গমন হওয়া ফসফরাস এবং তা থেকে বেড়ে ওঠা ওই বিশেষ প্রজাতির অণুজীবদের কার্যকলাপই ২৫০ কোটি বছর আগে বায়ুমণ্ডলে অক্সিজেনের অস্তিত্ব নিয়ে আসে। পৃথিবীর প্রথম আগ্নেয়গিরির অগ্ন্যুৎপাত কোথায় হয়েছিল সে সম্পর্কে পর্যাপ্ত তথ্য যদিও নেই, তবুও, কানাডা এবং ভারতের কিছু অংশে পাওয়া ভূতাত্ত্বিক নিদর্শন তাদের সম্ভাব্য অবস্থানের কথা জানান দেয়।

অপর দিকে ক্যালিফোর্নিয়া বিশ্ববিদ্যালয়ের অধ্যাপক ও স্বনামধন্য ভূতত্ত্ববিদ ডন সামনার এবং তার সহযোগী গবেষকরা অ্যান্টার্কটিকার ফ্রাইক্সেল হ্রদে গবেষণা কালে আবিষ্কার করেছেন অতি প্রাচীন কিছু নীলাভ সবুজ শৈবাল (Cyanobacteria), যারা বরফস্তরের নিচে একেবারে অক্সিজেন বিহীন পরিবেশেও টিকে থাকতে পারে। এমনকি এও দেখা গেছে যে স্বল্প পরিমাণ আলোর উপস্থিতিতে তারা কিছু অক্সিজেন তৈরিও করতে পারে। এ থেকে আন্দাজ করা যায় যে বায়ুমণ্ডলে উল্লেখযোগ্য পরিমাণে অক্সিজেন প্রবেশ করার আগেই এধরনের অনুজীবগুলো ওই পরিবেশের জন্য অভিযোজিত হয়েছিল এবং এই সময় থেকেই আণবিক অক্সিজেন মুক্ত হয়ে বায়ুমণ্ডলের অন্যতম গুরুত্বপূর্ণ উপাদানে পরিণত হয়েছে।

ওই গবেষক দলই আন্টার্কটিকার অন্য একটি লেক (Lake Vanda) থেকে আবিষ্কার করেছেন আরো এক প্রজাতির অনুজীব যারা ওই অক্সিজেন উৎপাদনে সক্ষম নীলাভ সবুজ শৈবাল এবং তার থেকেও প্রাচীন অক্সিজেন উৎপাদনে অক্ষম অনুজীবদের মাঝামাঝি পর্যায়ভুক্ত। মেরু প্রদেশ থেকে পাওয়া নতুন এই জীবের নামকরণ করা হয়েছে *Aurora vandensis*, যা বর্তমানে একাধিক গুরুত্বপূর্ণ গবেষণার কেন্দ্রবিন্দু। ওই নীলাভ সবুজ শৈবালরা কিভাবে সালোকসংশ্লেষ তথা অক্সিজেন উৎপাদনের কৌশল আয়ত্ত করল তা অনুধাবন করতে শুরু হয়েছে এই সব শ্রেণীর জীবদের ডিএনএ বিশ্লেষণ। পরীক্ষা-নিরীক্ষার মাধ্যমে জানার চেষ্টা চলছে অক্সিজেন তৈরি করার এক এবং অদ্বিতীয় ক্ষমতা যেই সব জিনের কারসাজিতে ঘটে -তারা পৃথিবীর ইতিহাসে কখন, কিভাবে এবং কোন পূর্বপুরুষদের থেকে এইসব নীলাভ সবুজ শৈবাল শ্রেণীর উদ্ভিদের কাছে এলো।

(বিঃ দ্রঃ খ্যাতনামা ভূতত্ত্ববিদ এবং অধ্যাপক ডন সামনার (Dawn Yvonne Sumner) এর একটি সেমিনারে অংশগ্রহণ করার সৌভাগ্য হয়েছিল লেখকের। এই নিবন্ধে উল্লেখিত কিছু তথ্য তাঁর বক্তৃতা থেকে সংগৃহীত।)

Viruses: An Enigmatic Entity of Life

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Viruses have existed in nature since the origin of life, but the evidence of their existence before human civilizations are recently discovered by series of scientific expedition on some undiscovered terrain of earth. The word "virus" originated from the Greek word 'ios', and was first used in English in 1599. However, the Greek word 'ios' actually originated from the Sanskrit word '*visha*', meaning poison. We know very well that viruses are obligate pathogens and require living hosts for their own survival. Earlier archaeological evidences suggest that as most of the human population began to expand in different parts of the world after the great tectonic plate separation, the invasion of viral infections within the migratory population increases rapidly. The evolution of viruses is very much fascinating topic for virologists. Due to large number of diversity biologists have struggled to classify the viruses in perfect group and draw a evolutionary relationship with the existing prokaryotic domains. It is still mysterious to the scientific community that how their genetic fragments gained the ability to move between cells and shows parasitic behaviour yet they don't have any proper cellular organization like other existing pathogens.

Origin of Viruses

Determination of the origin of viruses is one of the challenges for evolutionary biology. Viruses are intriguing entities that are border line between inanimate and living organisms. They have RNA/DNA-based genomes with single- and double-stranded configuration but cannot synthesis protein as they lack proper translational machinery, including ribo-somes. The main difference between a virus and any living organisms is that nor they have any metabolic activity, neither viruses are able to translate any functional protein outside a living host. Since several decades many debates are circulating among the virologists for finding the origin of Viruses. There are three possible theories of viral evolution which has been widely accepted. These are discussed here.

The Progressive Hypothesis (Escaped Gene Theory)

According to this theory, the origination of viruses processed through a progressive evolution viruses are genetic fragments that gained the ability to get inserted within a particular cell and move from one place to other. This mobile genetic fragments are mainly DNA or RNA and capable to move within multiple cells.

This hypothesis strongly supports the origin of specific type of RNA viruses When a RNA virus enters within the host cell, reverse transcriptase, a viral encoded enzyme converts RNA into DNA. The newly formed viral DNA gets inserted into the host cell's genome by another viral enzyme, integrase. When the RNA polymerase starts to produce cellular mRNA, simultaneously new copies of the virus's single-stranded RNA genome also being transcribed. As a result, multiple copies of viral progeny assemble.

This process is very rare and closely observed in a eukaryotic organism known as retrotransposons, in which a particular segment of genetic material tried to copy and paste themselves in different parts of the genome. It has also been found that 42% of the human genome has been made up of these mobile genetic elements (Lander *et al*. 2001).

The Regressive Hypothesis (Reduction Theory)

According to this hypothesis, it has been speculated that viruses are the remnant of a cellular organism and may have originated via a regressive process. One particular group of virus, Nucleo-Cytoplasmic large DNA Viruses (NCLDVs), best illustrates this hypothesis. These groups of viruses have significantly larger genome size as well as structurally they are highly complexes and contain different types of structural proteins which play various roles in viral pathogenicity.

Due to the genomic complexity of NCLDVs, some virologists have hypothesized that these viruses may be descendant of more complex ancestors. Theory suggests that, two organisms initially developed a symbiotic relationship but over time, one organism became more and more dependent on the other. Due to such dependency the dominating organism might lose some of the essential functional metabolic genes. Eventually that organism was unable to replicate independently, due to loss of some functional regulatory genes and becoming intracellular parasite termed as virus. Analysis of the genome organization of Mimivirus strongly support this hypothesis. It has been observed that Mimivirus contains a relatively large segment of genes which is assumed to be the remnants of a complete translation system which somehow lose its integrity due to course of evolution. Interestingly, phylogenetic analysis also revealed that Mimivirus does not differ much from parasitic bacteria, such as *Rickettsia prowazekii* in their genetic configuration (Raoult *et al*. 2004).

Origination of Viruses before Cellular Organization

The progressive and regressive hypotheses both assume that complete cellular organization existed before viruses but 'virus first hypothesis' suggests that viruses may have originated long before the origination of cell.

Some researchers postulated that viruses existed as a self-replicating unit in a pre-cellular world but they became more organized and complexly arranged due to course of evolution. Eventually, membranes and cell walls evolved as well as several protein complexes also developed for the formation of initial cellular organization. (Koonin, E. *et al 2005)*.

Others have strongly believed that precursors of today's NCLDVs led to the emergence of eukaryotic cells. It has also been hypothesized that, nuclear organization of eukaryotic cells arose from an endosymbiotic-association in which DNA virus became a permanent resident of an emerging eukaryotic cell which later form different eukaryotic cellular organizations like mitochondria, chloroplast etc. (Bell, P *et al,* 2001)

Evidences of Viral Outbreak

When human civilization started to expand on different geographic locations after the great tectonic plate separation, different socio-dynamic features started to influence viral infections within the populations. At the end of Neolithic age (at around 9500 BC), when agricultural revolution occurred there was a rapid spread of plant viruses emerged in Mediterranean area (Zeder MA., 2008). About 11,000 years ago when humans began to domesticate wild animals, several zoonotic viral transmission occurred from animal to humans. Most of those infections were so rare and posed no serious threat to the civilization although a notable exception such as influenza virus. At around 10,000 years ago smallpox was the first viral outbreak in India. The earliest documented records of poliovirus infection was found in 18th dynasty Egyptian stele (1580–1350 BC) thought to be an Egyptian priest with the deformity in foot. Not only that the sarcophagus of Ramesses V a ruler on 19th dynasty also showed the evidences of smallpox infections. The oldest evidence of smallpox pandemic was reported in Roman dynasty of about 3000 years ago which wiped out approximately five million civilian in the Roman dynasty.

In the mediaeval time period (late 15th century), European continent was largely effected by periodic invasion of smallpox and influenza which drained out most of the populations in several highly populated areas of Great Britain, France and many other countries. In England between 1557 and 1559, five per cent of the total population died from the epidemic caused by influenza. (Potter CW., 2001).

Existence of Yellow fever caused by a Flavivirus was first appeared over 3,000 years ago. *Aedes aegypti* is the vector responsible for transmitting the virus within the human host. At the middle of 16th century the brutality of yellow fever epidemic was reported on Barbados termed as “Barbados distemper" which infected the majority of the island population and North America. The earlier report of dengue fever occurred 17th century in Asia and Egypt. It was believed that this disease brought to the US by different trading ships carrying severely dengue infected sailors, and causes epidemic in the beginning of 18th century.

All these records are clearly indicating that viruses were co-existed with different types of organisms and by periodic invasions of such viruses in the human populations help them to evolve as well.

Quest for Viruses in Extreme Environment

Most of the viral research has focused on pathogenic viruses to humans, animals and plants, which deal only a fraction of viral community and the role of most viral genes and their coevolution with their host and environment beyond pathogenicity, still remain poorly understood. It has been proved that as the viruses are most abundant entities on the planet, most of the organisms might be infected with multiple type of viruses in their lifespan. Moreover, it has also been established that different extremophiles are severely infected with viruses, are responsible for maintaining the population diversity in different environmental conditions (Krupovic, M.*et al.,* 2019). Various ecological observations indicate that viruses predominantly infecting large number of extremophiles and can also outnumber their hosts (Danovaro, R. *et al* 2017). So, documenting the diversity and impact of viruses on extremophiles will provide us valuable information about the origination of virus.

Most of the Archaea are considered to be extremophiles which thrive in extreme environments, being infected with different types of viruses which have an important role in influencing global biogeochemical cycles; these viruses are responsible for the production of tones of carbon per year, by lysis of archaeal cells in the surface of deep-sea sediments (Danovaro, R. *et al,* 2016). Recent studies revealed that some viruses of *Rudiviridae* family are found to be infecting acidophilic archaeon *Sulfolobus islandicus* at temperature of 80^0C with high salinity level (above 36%) at deep sea hydrothermal vent which were completely undiscovered till last decade.

In the case of cryophilic environments, the most prevailing viral families are *Myoviridae* and *Siphoviridae,* infecting large number of bacteria within the genera *Shewanella*, *Flavobacterium* and *Colwellia*., Some species of *Acidithiobacillus* has been found to be infected with viruses from the *Myoviridae* family in acidic environment. Recent expedition on Glacier of Tibetan continent revealed the existence of multiple virus of unknown origins which are thought to be at least 14000-15000 years old. Only a few members of this viral pool has been identified belonging to *Myoviridae* family. Metagenomic analysis also indicates that there are unique viral communities, preserved in the glacier ice compared to modern environments. No explanation has drawn yet whether these viruses within ice glaciers are completely new to origin or ancestor to any already identified existing pathogenic viral strain.

Future of Mankind Will Be Regulated By Viruses

From several decades the scientific community tried to understand the route map of viral evolution, specially focusing on the pathogenic viral entities. Recent outbreak of SARS-CoV-2 strongly represent that the evolution and adaptation of viruses are quite impressive and highly destructive to the mankind. When a virus transmitting by crossing the intra-host barrier, it will pass through different type of environmental selection pressure which ultimately leads to mutation of that particular strain. From recent improvement of scientific knowledge, we are able to decipher the potentiality of viruses as a genome editing tools and also used them as drug delivery system in synthetic biology. Several recombinant viral vector based vaccines are showing promising new aged therapeutic strategies against various life threatening diseases including COVID-19 caused by SARS-Cov-2. In recent years, the biopharmaceutical industries are focusing on manufacturing several recombinant viruses which encodes different bacterial cell wall degrading enzymes which have been identified using different sequenced-based screening. These viral encoded enzymes are targeted to be integrated within the late responsive genes of the viral vectors which will be able to hydrolyse the cell wall of antibiotic resistant bacteria after the successful completion of a single virus replication cycle. A very limited number of viral communities is currently discovered by the researchers till date. Virologist are very much cautiously investigating the evolutionary lineages and the genetic constituents of the newly discovered ancient viruses from arctic area as well as from the hydrothermal vents because these viruses may also possess some serious threat to mankind if accidentally exposed to our environment by any natural disaster. As different types of pathogenic and non-pathogenic viruses show interactive relations to humans and due to continuous evolution these viruses are repeatedly mutating their genetic makeup by different type of external physical and environmental influences. Due to such unpredictability of viral biology we can say that day is no longer far from us when severe life threatening viral pandemic will be introduced to our civilization in near future from unpredictable viral origins and our civilizations must have to pass through that situation to up-regulate our immune system by directly interacting with that invasive viral pathogens rather than any successful permanent medicinal therapy.

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A Review on Regenerative Medicine and Translational Science with Special Emphasis on Retinitis Pigmentosa (RP)

Chetana Mukherjee (M. Sc., SEM IV)

Regenerative medicine (RM) is one of the most promising disciplines for advancements in modern medicine, and regenerative ophthalmology (RO) is one of the most dynamic fields of regenerative medicine. Regenerative ophthalmology combines and integrates these three areas of research: A. developing natural and synthetic biomaterials in order to provide physical support; B. applying primary (particularly autologous) or stem cells to improve functionality; C. discovering precise drugs, genes, and proteins necessary to construct a favourable microenvironment that regulates cell fate and accelerates tissue renewal (Aramwit et al., 2017)

Stem Cells

Human stem cells from a wide variety of sources are being explored for eye disease transplantation therapies. Cells, in particular, stem cells, are critical components required to reconstruct and rebuild tissues. There are significant, ongoing research efforts by a number of groups to elucidate the identity and function of stem cells in practically all tissues of the body, including the many tissue compartments of the eye. Stem cells are undifferentiated cells with unlimited proliferative ability of self-renewal, differentiating into differentiated cells. On the basis of trans-differentiation potential, stem cells are of four types, that is, (1) unipotent, (2) multipotent, (3) pluripotent, and (4) totipotent. Cells from inner cells mass (ICM) of the embryo are pluripotent in their nature and can differentiate into cells representing three germ layers, but do not differentiate into cells of extraembryonic tissue. Stem cell progenitors play a chief role in replenishing degenerated cells, despite being present in low quantity and quiescence in our body. Unlike other tissues and cells, regeneration of new optic cells accountable for visual function is rarely observed. Stemness and trans-differentiation potential of the embryonic, extraembryonic, foetal, or adult stem cells depend on functional status of pluripotency factors like OCT4, cMYC, KLF44, NANOG, SOX2, and so forth. On the basis of regenerative applications, stem cells can be categorized as embryonic stem cells (ESCs), tissue specific progenitor stem cells (TSPSCs), mesenchymal stem cells (MSCs), umbilical cord stem cells (UCSCs), bone marrow stem cells (BMSCs), and iPSCs. Following types of stem cell therapy is promising in present development:

- Allogenic stem cell therapy: matched or unmatched
- Syngenic stem cell transplant: Identical twin
- Autologous stem cell transplant
- Cord blood stem cell transplant
- Non-myeloablative stem cell transplant

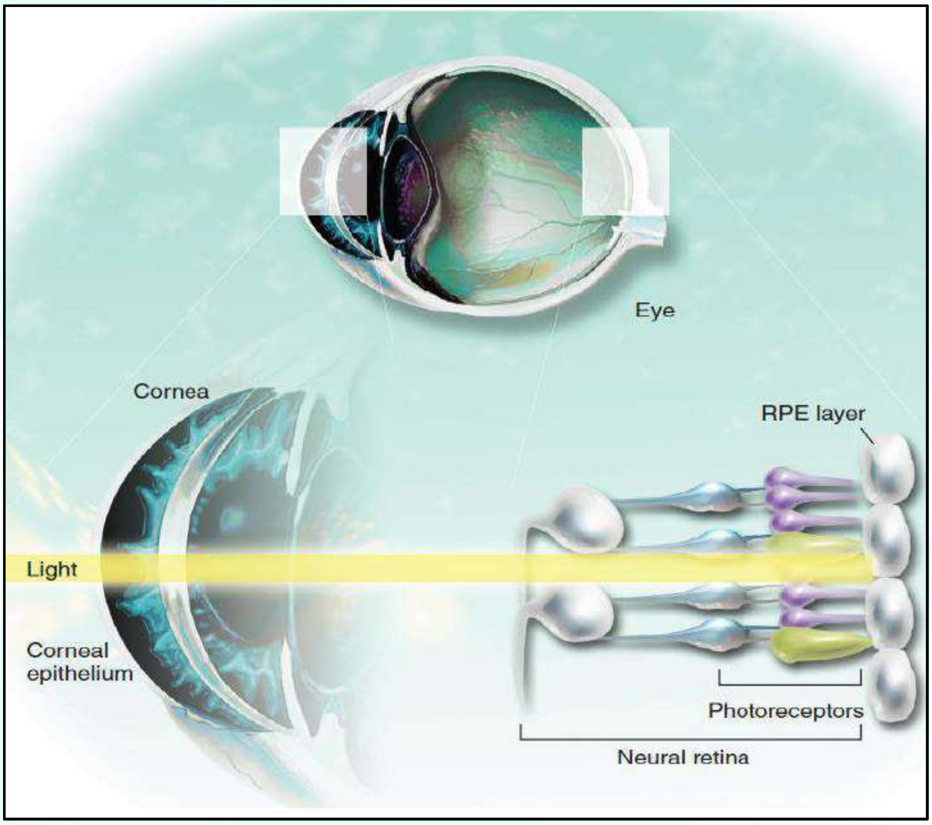

Figure1: Several tissues in the eye are being targeted for stem cell replacement. (Blenkinsop, Corneo; 2012)

Ophthalmology and CB Cells

Cord blood also contains stem cell populations able of giving rise to epithelial tissue, making CB agreeable for use in regenerative medicine applications for the eye (cornea), skin (wound healing) and other such tissues (e.g., gut and lung). When it's about the human eye, the cornea appears to have the most straight and routine clinical application. The external most layer of the eye is made up of the central cornea, the limbus and the sclera. The cornea epithelium is a quickly self-renewing tissue; concerned to have its own source of stem cells (the limbus) specialized for this purpose. Corneal epithelial stem cell shortage is an important cause of visual disability, which can be a result of alkali injury, Stevens-Johnson syndrome, ocular cicatricial pemphigoid, aniridia, chronic rosacea kerato-conjunctivitis and iatrogenic causes. Autologous corneal epithelial stem cell grafts have been flourishing for patients with unilateral disease. However, harvesting cells from the functional eye places the healthy eye at risk for vision loss. Additionally, in bilateral conditions, autologous grafts are not available. The optimum present solution for bilateral disease is a corneal epithelial stem cell allograft. Allografts require chronic anti-rejection therapy with possible systemic side effects. In addition, the average survival of allografted corneal stem cells is two years. Severe corneal wounds requiring intervention are not unusual. In fact, corneal wounds formulate up 37% of all visual disabilities and almost a one fourth section of all medical visits for ocular problems in North America Work from the group of Nichols et al. have used CB stem cells as a viable therapeutic alternative for ocular surface disease, as human CB stem cells could represent an unlimited source of tissue for ocular surface reconstruction. Preliminary laboratory and animal data is supportive of this hypothesis. Histology and immunohistochemistry of in vitro differentiated CB stem cells revealed that the consequential cell.

Umbilical cord serum contains a high concentration of many growths and neural factors and essential tear components, such as EGF, vitamin A, TGF-b, substance P, IGF-1, and NGF, and that umbilical cord serum eye drops can be used safely and effectively for the treatment of severe dry eye with or without Sjögren’s syndrome, GVHD, persistent epithelial defects, and neurotrophic keratopathy. (Yoon, K. C.; 2014)

Generating Photoreceptors from Stem Cells

Stem cells, with their superior plasticity and migratory capacity, have been anticipated as an ideal candidate donor cell. Embryonic stem cells are defined as a cell that can both renew itself by repeated division and can give rise to any one of the 200 or more adult cell types in the human body. An ESC cell arises from the eight-cell stage morula (Figure.2). Apart from the normal development, ESCs have been differentiated in vitro into neural cell types and even pigmented epithelium. (Haruta, M et al.; 2004)

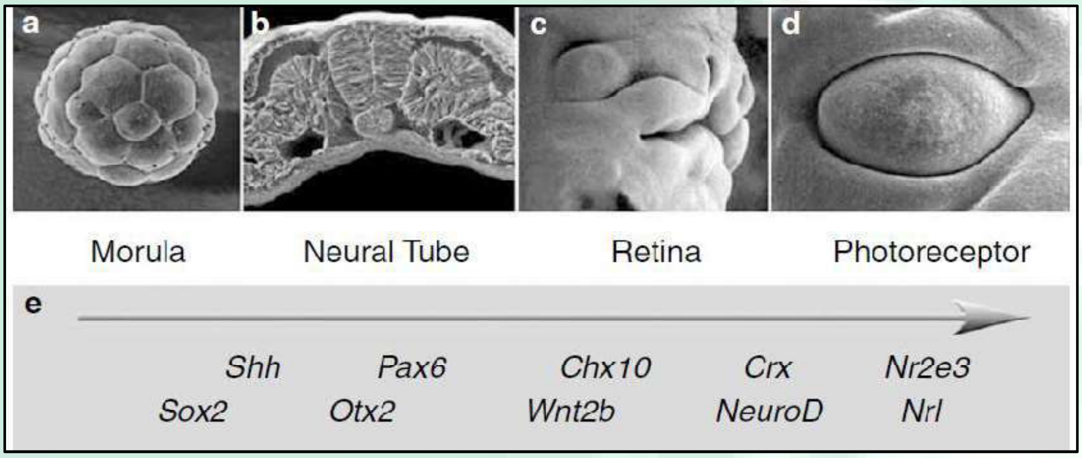

Figure 2: From stem cell to photoreceptor: transcription factors regulate development of the eye. (a) Embryonic stem cells are harvested from the morula each cell at this stage would have the potential to form a whole embryo. (b) Neurulation at the end of the third week of human development, specification of neural tube and neural crest progenitors. (c) At 5 weeks the primitive eye structures including retinal progenitor cells have formed. (d) By 10 weeks the outer retinal cells are undergoing terminal mitosis to differentiate into cones (and later rods). (e) Some of the transcription factors identified in relation to photoreceptor development and their approximate equivalent expression profile in humans. (MacLaren, R. E., & Pearson, R. A.; 2007)

Retinitis pigmentosa (RP)

Retinitis pigmentosa is the term specified to a set of hereditary retinal diseases that attribute degeneration of rod and cone photoreceptors. The worldwide prevalence of retinitis pigmentosa is about 1 in 4000 for a total of more than 1 million affected individuals. The disease can be inherited as an autosomal-dominant (about 30–40% of cases), autosomal-recessive (50–60%), or X-linked (5–15%) trait. In a multicentred study from Japan including 29 vision rehabilitation centres, retinitis pigmentosa was the major cause of visual handicap or blindness, accounting for 25% of patients (Hartong, D et al; 2006).

Symptoms

Retinitis pigmentosa is a very much unpredictable disorder; some patients build up symptomatic visual loss in childhood whereas others remain asymptomatic until mid-adulthood. Many patients fall into a classic pattern of complex with dark adaptation and night blindness in adolescence and loss of mid-peripheral visual field in young adulthood. As the disease progresses, they lose far peripheral vision, sooner or later develop tunnel vision, and finally lose central vision, usually by age 60 years. Visual symptoms indicate the gradual loss of the two photoreceptor types (fig. 4): rods, which mediate achromatic vision in starlight or moonlight; and cones, which are important for colour vision and fine acuity in daylight (Hartong, D et al; 2006)

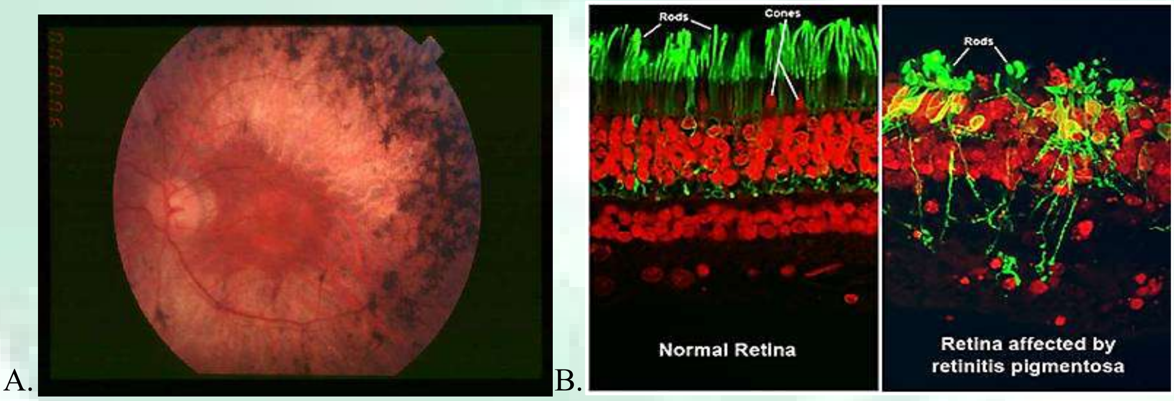

Figure 3: A. Fundus of patient with retinitis pigmentosa, mid stage (Bone spicule-shaped pigment deposits are present in the mid periphery along with retinal atrophy, while the macula is preserved although with a peripheral ring of depigmentation. Retinal vessels are attenuated.) (Hamel, C. 2006) B. Image courtesy of Robert N. Fariss, Ph.D., chief of the NEI Biological Imaging Core, and Ann H. Milam, Ph.D., former professor in the Department of Ophthalmology at the University of Washington.

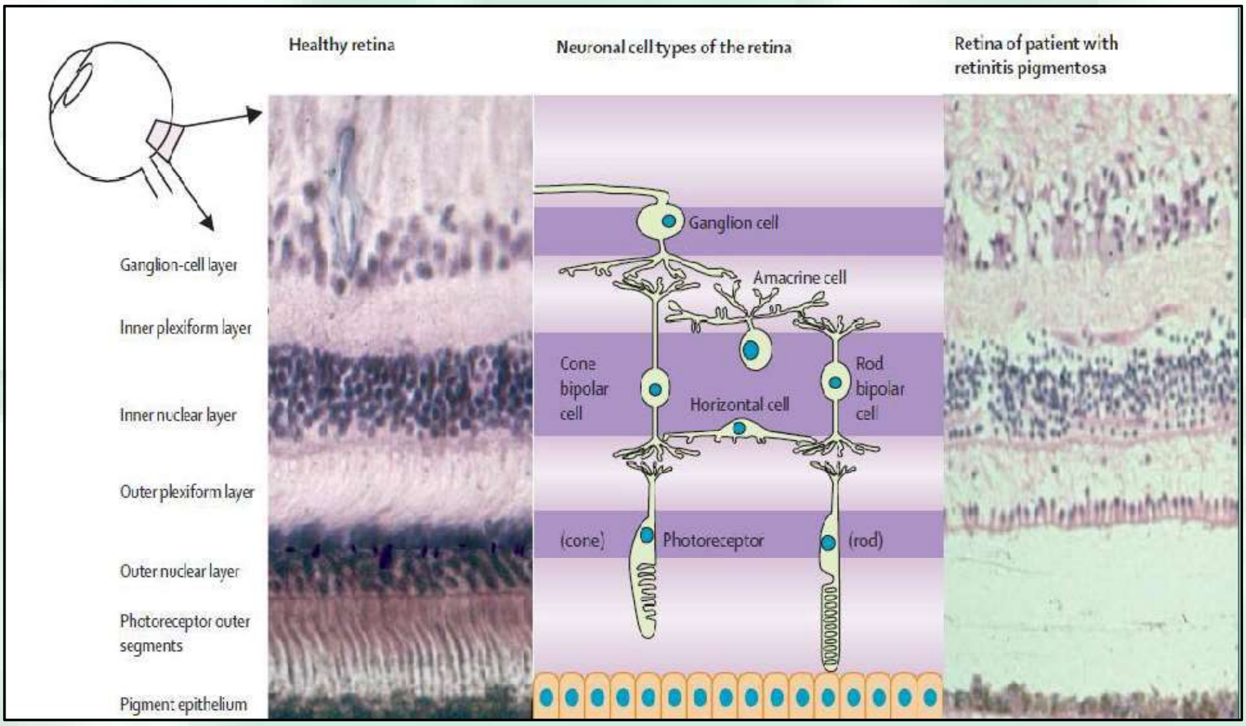

Figure 4: Histological appearance of healthy human retina (left) and retina of a patient with retinitis pigmentosa at a mid-stage of disease (right) the space between the retinal pigment epithelium and the outer nuclear layer in the diseased retina is a processing artifact. (Hartong, D et al; 2006)

Causal genes

The majority cases of retinitis pigmentosa are monogenic, but the disease is nevertheless incredibly heterogeneous genetically. Investigators have identified at least 45 loci so far at which mutations cause the disorder, and these genes together account for disease in a little over half of all patients. Most genes for retinitis pigmentosa cause only a small percentage of cases, exceptions being the rhodopsin gene (RHO), which leads to about 25% of dominant retinitis pigmentosa, the USH2A gene, which might cause about 20% of recessive disease (including many with Usher's syndrome type II), and the RPGR gene that accounts for about 70% of X-linked retinitis pigmentosa. In total, mutations in RHO, USH2A, and RPGR genes cause about 30% of all cases of retinitis pigmentosa. (Hartong, D et al; 2006)

Treatments

Some common treatments of this degenerative eye disorder are,

- Acetazolamide:This medication can ease swelling and improve your vision.
- Vitamin A supplements
- Retinal implant
- Replacement of damaged cells or tissues with healthy ones.
- Gene therapy to put healthy genes into the retina.

The studies using stem cells in animal models and clinical trials have established promising results and provide encouraging groundwork on which to continue explore in the pursuit of optimal cellular therapies for the treatment of RP. (Fig. 5) Clinical trials suggest that stem cell injection is technically feasible and has no detectable structural or functional toxicity in the long term. With the progress of study, more and more treatment methods are constantly improved. The present treatment methods and means are mainly through the inhibition of apoptosis, and protection, replenishment or repair of the RPE and photoreceptor cells. Mouse embryonic stem (ES) cells also can differentiate into RPE-like cells in vitro and then re-establish retinal function in a mouse model for retinitis pigmentosa by transplanting the cells into the sub-retinal space. On the basis of this finding, it was proved that ES cells can differentiate, morphologically and functionally, into RPE-like cells. Colozza and his colleagues proved that after transplantation of progenitor stem cells, the cells can be inspired to become replacement photoreceptors and supportive outer retina cells can theoretically lead to treatments that restore visual function. (Colozza et al. 2012). Many studies showed that stem cells have the potential for differentiation into retinal cells in vitro or in vivo and even participate in signal pathways, and additional improve retinal function (He et al. 2014).

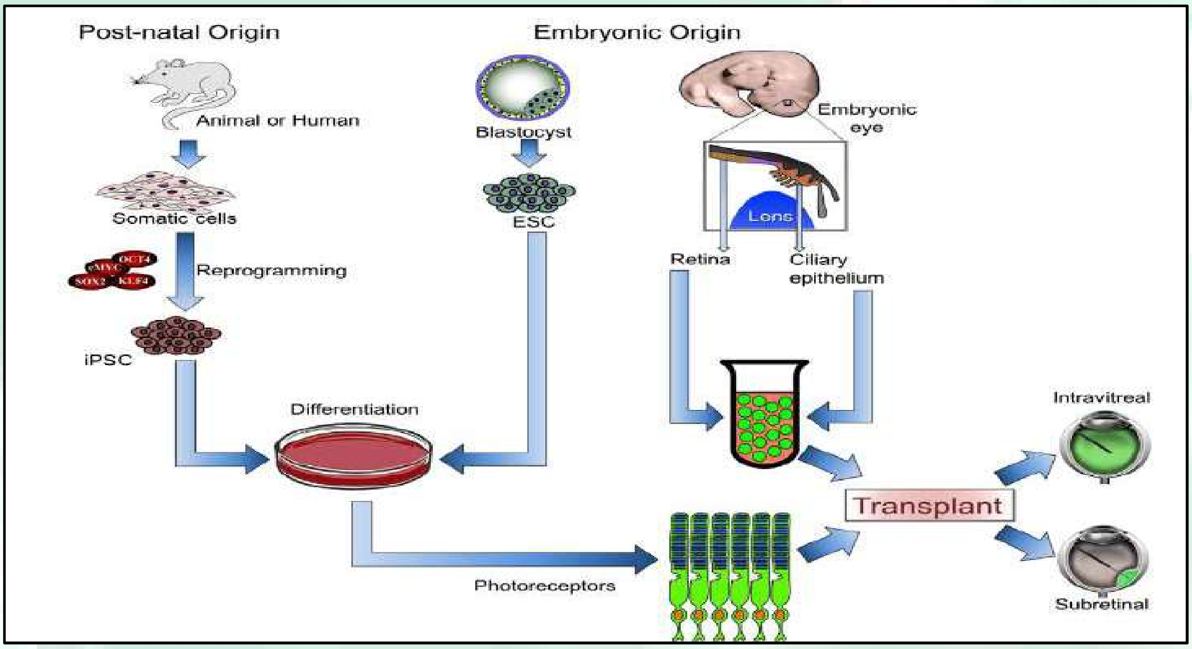

Figure 5: A diagram of the origins of numerous stem cells. Adult somatic cells can be reprogrammed into iPSC with some transcriptional factors, which differentiate into photoreceptors. ESC isolated from a blastocyst can also differentiate into photoreceptors. Embryonic retinal cells, as well as ciliary epithelial cells, have also been used to replenish photoreceptor populations. (Kaplan & de Castro 2012)

Conclusion

Restoration of vision is a vital objective, which is accomplished by using various types of stem cells. Although a numerous ethical and scientific risks are slowing the progressions of use of stem cells. Some problems like production of adequate cellular material or tissue for clinical use presents an ongoing challenge. Slow regulatory processes create another major barrier to the rapid development of RO technologies. Ethical problems including the use of human embryonic tissue continue to provoke controversy. Most of the treatments with the stem cells are on trial and have not received any authorization by FDA and others so they are getting performed on the other organisms like mice. But on those cases the treatment prognosis cannot be properly determined. Common problems like cost, efficiency, graft versus host disease and tumour progression due to uncontrolled growth of stem cell are the obstacles of the employment of stem cell-based treatments in human diseases. Among the various type of stem cell, embryonic stem cells and umbilical cord stem cells have capability to avoid graft versus host diseases; that is why the application of these two types of pluripotent stem cell and their applications are mainly focused in this review. Regenerative ophthalmology is a challenging but promising and fast-growing medical specialty, which will eventually bring the next revolution in ophthalmology.

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Ancient DNA

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DNA is one of the most marvelous things in nature. Although invisible to the naked eye, it contains all the necessary information needed to create a living creature from a single cell and to maintain its biological processes. 'Ancient DNA' is a term which covers any trace of DNA from a dead organism or parts of it. Therefore any DNA that has undergone autolytic process or any kind of fixation is considered to be ancient DNA (aDNA). After death DNA is degraded by various biotic and abiotic processes. It has been reported earlier that dry or low O_2 environments are beneficial for the survival of DNA. The two most daunting challenges encountered by aDNA researchers are: rapid degradation of DNA in deceased tissues and contamination by high-quality modern DNA. The field of ancient DNA research is full of surprises. Past few years an increasing interest has been observed among scientists for the retrieval of aDNA sequences from museum collections and archaeological artifacts. The advent of next generation sequencing (NGS) technologies has substantially expanded the range of studies possible, enabling the analysis of full chloroplast, mitochondrial and nuclear genomes. Future research on ancient DNA has the potential to reconstruct many of the key evolutionary processes that have shaped wild and domesticated plants.

Brief History

The major work in the field of ancient DNA research started in the early 1980s. In 1981, Anderson and his colleagues published the fully sequenced human mitochondrial genome. In 1984, Higuchi et al. succeeded in the extraction of DNA from quagga, an extinct member of the horse family and Johnson et al.(1985) investigated the DNA they had extracted from mammoth remains. Pääbo (1984) demonstrated that DNA was present in a mummified infant from an Egyptian dynasty, while Rogers and Bendich (1985) found DNA to be present in century old herbarium specimens.

Sources of aDNA

There are many sources of ancient DNA like archaeological microfossils, archaeological macrofossils, sediments, herbaria, mummified specimens, hair, amber, teeth and bones. In the archaeological record, plant remains are preserved, charred, waterlogged, desiccated or mineralized. In case of plants Seeds are the most common plant material used in ancient DNA studies because they are well adapted to protect the embryo and remain in dormancy before germination. This feature makes seeds a very important repository to preserve DNA under unfavorable conditions. Similarly, pollen grains phytoliths are also common sources utilized in this type of study. There are also some unusual sources like pipe stem and coprolites which also provide it also provide valuable information.

Pattern of aDNA Damage

Under favorable conditions DNA can survive for thousands of years in the remains of dead organisms. In living cells, DNA molecules continuously suffer chemical insults, which are countered by enzymatic repair mechanisms. On death, these cellular mechanism cease to function, the genome becomes exposed to the unmitigated effects of numerous factors that threaten its stability. These factors include intracellular nucleases as well as DNA degrading microorganisms. However, when tissues are frozen or they become desiccated quickly after death, these destructive processes are inhibited. When DNA is extracted and analyzed from ancient samples these destructive factors manifest themselves in three different ways: a reduction in DNA fragment size, lesions that block the replication of the DNA molecules by polymerases, thus impeding many forms of analysis and lesions that cause incorrect nucleotides to be incorporated when the DNA is replicated.

Contamination

In addition to getting degraded in course of time, aDNA often coexists with abundant environmental DNA, mostly from microbes, fungi and plants that had colonized the remains, resulting in extremely small proportion of endogenous DNA in an extract. Another source of non-endogenous DNA is contaminants from the present day environment. Taking these facts into consideration all operations and protocols related to aDNA research is carried out in a clean room.

Methodology

Plants have three genomic compartments: nucleus, mitochondria and chloroplasts, each differing in mutation rates and have complex modes of inheritance. In case of plants a great deal of variability exista in terms of ploidy level, genome complexity and modes of reproduction. Different related species can also hybridize among themselves and their spatial dispersal is mediated through different vectors such as wind, insects, birds or mammals—all of which influences the gene flow. All these plant-specific features must be taken into account in plant aDNA studies. The procedure for aDNA analysis in plants involve the following steps: excavation, morphological description, external cleaning (if possible) and powdering, amplification of the chosen target region within the organism's genome by polymerase chain reaction (PCR), gel electrophoresis to detect the presence of correct product, its size determination, cloning sequencing and verification. Depending of the type of tissue, the homogenization steps can be conducted by using dental drill, pestle & mortar or cryogenic mill. For lysis mainly EDTA buffer and proteinase K is extensively used. As aDNA is surely contaminated by various contaminants, purification is the crucial step which determines the recovery rate of aDNA. Phenol-chloroform based method and spin column based method are the two methods that are used for purification. CTAB and PVP are mainly used to remove secondary bi-products and phenolic compounds.

The main concern here is to compare the living specimens with ancient ones. Hence, choosing of an ideal marker is very much essential here. An ideal marker should be low mutation rate, low number of repeats and should be evenly distributed throughout the genome. For plants chloroplast DNA marker and for animal mitochondrial DNA markers are used. Chloroplast DNA marker has similar organization in all plants, have low mutation rates and they provide valuable information at order and family level and mitochondrial DNA markers on the other hand are present in high copy numbers, they mutate more than ten times slower than cp DNA & 100 times slower than animal mitochondrial DNA.

Next Generation Sequencing (NGS) made it possible to increase number of bases sequenced pen run due to technological improvements. The most important platform used in this field are Roche 454 & Illumina genome analyzer. The key steps of generating reads are—library preparation, library amplification, sequencing, data analysis. In the Roche 454, firstly a DNA fragment is chosen and then cut into shorter random fragments by physical shearing. The Second stage involves the ligation of adaptors, adap A & adap B. So the ss-DNA with the two adaptors ligated at both the ends it has taken and uses this to attach to the beads. The role of the adapter A is to attach with the sequence present in the bead. Because the nucleotide present in the bead is complementary to the adapter A sequence. Now adapter A sequence bind and rest the sequence has bind. Next step is amplification and then do the pyrosequencing method. Thus the pyrophosphate release during the DNA synthesis can be detected by the emission of the light and that is what the CCD camera picks up and converts it into a graph to analyze the data. The amount of light generated is proportional to the number of the nucleotides that are incorporated.

Major Applications

There are few application of ancient DNA studies. It has ability to relate extinct species with extant species. It has advantage to enhance the phenotypic evolution and genome diversity of species. There are several evidences obtained from extracted ancient DNA, eg. *Franklinia alatamaha*, which was obtained from 1803 in the form of a herbarium specimen. *Malvaciphyllum macondicus* an extinct member of Malvaceae, it was recovered from fossil leaves from Miocene and Pliocene of Argentina and Brazil. It has similarity with the leaf compression of *Abutilon* and several fruit compressions with *Hibiscus* & *Malva*. The coprolites provide information about environmental conditions and animals diet patterns. There are two cases of genome evolution from reconstructed ancestors Researchers of California took a sample of extinct quagga & compared it to other DNA fragment of living animals & concluded that quagga is very closely related to zebra. DNA from Y chromosome & mt-DNA also provide heritable genetic markers. Y chromosome data is extensively used to trace paternal history & mt-DNA is used to detect maternal history.

Studies of ancient DNA have provided several new insights into the evolutionary history of both species and populations. Ancient DNA holds tremendous potential for addressing questions of phylogeny and evolution.

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Micropropagation Industry in India- A Review

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Micropropagation is a process by which a large number of uniform, disease and pest free, true-to-the type of the mother plant are produced in *in vitro* condition (within bottles or tubes in sterile artificial culture medium) throughout the year by bypassing the normal sexual cycle. In broader sense, micropropagation is popularly known as plant tissue culture. Haberlandt (1902), the father of plant tissue culture put forward the idea of *in vitro* plant culture after his discovery on cellular totipotency of plant, i.e., each cell of a plant is capable to regenerate into a whole plant. Micropropagation is more advantageous over conventional propagation because it can produce millions of plants from a single clone within a short span of time.

Micropropagation industries have the following advantages in product development, product enhancement and market ability. Under product development section, the tissue culture industries are mainly engaged in rapid multiplication of valuable germplasms by maintaining their uniformity. The tissue culture generated plants are free from any diseases and viruses and generally show improved phenotype in their respective field. The success of any industry depends on the marketability of their products. The tissue cultured plants can be sold in different forms such as ex-agar, primary or secondary hardened stage, therefore the movement of product will be easier. If they are exported in foreign countries the ex-agar plants are preferred, whereas for inter-state and intra-state marketing primary and secondary hardened plants are more acceptable.

Plant tissue culture technique is not only used for large scale propagation of plants; but it is also involved in various types of plant breeding activities for exploring naturally existing genetic variability as well as to create artificial genetic variations. This *in vitro* technology in association with molecular marker are used for the selection of better germplasm, domestication, introduction of new germplasms, somatic hybridization, somaclonal variation and genetic engineering of plants. This technology is very popular for *ex vitro* conservation of valuable germplasm by using slow growing culture technique and cryopreservation. Recently the propagules are entrapped in sodium alginate which is popularly known as synthetic seeds and efforts are made to implant them in artificial soil mixture to get the full grown plants. These artificial seeds can easily be transported to the abroad without any quarantine and phyto-sanitary certificate and therefore it is very useful for germplasm exchange.

On the above background, we are now discussing the commercialization of plant tissue culture technology in industrial scale.

International Scenario of Micropropagation Industry

In 1965 George Morel, a French botanist, discovered the technique of plant tissue culture, while he was trying to develop virus-free orchid plants, and then after 1970, commercialization of this technology was popularized in USA mainly for the propagation of orchids. Since then, the industry expanded globally as the demands of different fruit plants, florist plants as well as medicinal and house plants increased day by day.

A recent report gives an overview that only agricultural biotechnology business is contributing approximately 75-80 billion USD through-out the world with a 10% expansion of the market at every year. In the world scenario, there was a huge jump of plant tissue culture industries since 1990s and it was estimated that during this period the total production increased from 130 to 500 million plants per annum. Simultaneously, the business was also expanded in the western European countries and now they can produce approximately 212 million plants per annum, from their 37 technologically advanced production units.

Among them, the Netherlands, the flower power of the world, has set up 67 commercial tissue culture units which can produce approximately 62 million plants per annum. On the other hand, Germany also increased their production upto 8 million tissue cultured plants from their 21 functional units. But, due to high labour cost the tissue culture industries from advanced countries shifted to the developing countries having low production cost. India is the forerunner in this field.

History of Micropropagation Industry in India

In India, the first commercial plant tissue culture laboratory (PTC) A.V Thomas Company was established in Kerala, in the year 1984 and in the next eight years the number of commercial PTC laboratory raised to 50. Though the number raised to 105 but due to technological crisis, it decreased to 70 to 75, gradually. Majority of the commercial PTC laboratories are located in Maharashtra (25) and Karnataka (9).Some of the renowned commercial tissue culture laboratories in India are Harrisons Malayam Ltd., Indo-American Hybrid Seed (IAHS), Godrej Plant Biotech Ltd., A.V. Thomas & Co., SPIC-Agro Biotech Centre etc. having ultra-modern facility of micropropagation. A reengineered cardamom variety was introduced by A. V. Thomas that could yield 250 kg/ha (normal 70 kg/ha). They also developed tissue cultured vanilla plant which has early flowering and high glucovanillin content. Tissue cultured banana plants were produced by IAHS, Bangalore. These two commercial units also exported millions of micropropagated banana and cardamom plantlets to the western countries. They also released several thousands of plantlets to the farmers for cultivation. IAHS worked in several collaborations with Netherland, Denmark and UK for the development of new plant variety by endosperm culture, selection of somaclonal variants, *in vitro* pollination etc. KF Bioplants, Pune is another commercial unit which is renowned for micropropagation of ornamental plants. In 1997 KF Bioplants worked in collaboration with Florist de kwakel BV, Holland for gerbera production. In the year 2003, they first introduced tissue cultured derived mini-tuber potato seed in India.

Role of DBT on Quality Control of Micropropagation Industry

In the year 1986, Indian government has established a department named, ‘Department of Biotechnology’ (DBT), under the Ministry of Science and Technology. DBT plays a significant role in the research and development of PTC generated plants and its comer-cialization. For virus free plant production and quality testing, DBT build up a new network project in 1999 with IARI, New Delhi. IHBT (Palampur), IARI (New Delhi), IIHR (Bangalore) are the three research centers for virus testing, whereas TERI (New Delhi), NCL (Pune), and SPIC-SF (Chennai) are the organizations related with the genetic uniformity testing. Eventually, in 2005, DBT has evolved National Certification System for Tissue Culture Raised Plants (NCS-TCP) vide the Gazette Notification, dated 10th March 2006, under section 8 of the Seeds Act, 1966, with the objective to certify the production of disease free and quality checked tissue culture plants. Gradually, in the year 2006, this certification system has become mandatory for commercial tissue culture industry in India. This system became very useful for capacity building in tissue culture units and for production of quality controlled plant material. Recently, under this system, around 92 companies and 5 Test laboratories are recognized.

Present Scenario of Micropropagation Industry

The tissue culture industries in India are growing at 15% rate, per annum. The export of tissue cultured ornamental plants is growing very fast. From the DBT it is known that around 200 commercial PTC units having the production capacity of about 500 million plantlets per annum are operating in India. In India, the PTC market is estimated of Rs 500 crores. The major plants tissue cultured products in India are Banana, Sugarcane, Strawberry, Apple, Pineapple, Potato, Gerbera, *Lillium*, *Anthurium*, Orchids, Teak, Bamboo, Date Palm and pomegranate. Among these, the highest production occurs in Maharashtra (31 millions) and the lowest in Orissa and Rajasthan (1 millions). 52000 ha. Land in Maharashtra is used for cultivation, 50% of which are used by tissue culture derived plants. In case of sugar cane, production increases by micropropagation in Tamil Nadu, Uttar Pradesh and Maharashtra. IARI introduced a new variety of seedless grapes, named 'Arkaneelamani', and has the highest market potential. Besides, several medicinal plants are also now in focus of biotechnologists, to produce huge number of plants in limited space and short time as well as to increase the quality and quantity of the bioactive components of plants. Consequently, the rare and endangered species (according to IUCN) are also conserved. Special attention is being given to the plants of Western Ghats for the development of PTC protocol. India is now recognized as the "Flower Power" due to the improvement in the floriculture industry.

In 2020, India earns $1.5 billion by export of floriculture products, annually. West Bengal (33.1%), Karnataka (12.3%) and Maharashtra (10.3%) are leading cut flower production states. *Chrysanthemum, Geranium, Marigold, Pentas, Hibiscus, Petunia, Dracaena, Gerbera, Syngonium, Spathiphyllum, Philodendrons, Aglonema,* Ferns etc are produced by many PTC commercial unit of India.

Future Prospects of Micropropagation Industry in India

As India is enriched with numerous medicinal plants, plant-based drug production needed more attention due to its less side-effect. To mitigate this huge demand PTC is the only solution. Besides secondary metabolites, plant proteins also possess nutraceutical values. It will be beneficial to focus on these plant peptides by some genetic modifications. Apart from medicinal plants, several modifications can also be done in crop plants. In case of ornamental plants, the size, colour and number of flower and leaf can be changed in *in vitro* conditions. Some mutant varieties like, vernalization insensitive, salt tolerant, drought tolerant etc may be introduced in tissue cultured plants.

Conclusion

From the very beginning, research works are continuously improving the protocol followed in PTC in search of new variety, pathogen free and high yielding plants. The elevation of tissue culture industry was possible with the support of Indian Government by financially and technologically. Commercial production can be increased with the help of PTC by removing all the barriers like, financial crisis and marketing. Lastly, we can conclude that the discovery of micro-propagation technique is a blessing of the scientists for us, by the application of which we can improve the economy of India as well as the whole world.

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Some Challenges and Solution during Field Survey for Plants Collection

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Field survey plays a significant role in Plant taxonomy. We all know that Plant Taxonomy is the science that helps to identify, find and give names, and classify plants. Through field survey, we can explore different types of vegetation in different geographical or ecological areas. We gather primary data for the floristic composition as much as possible according to our needs. Sometimes we may get a new taxon or new record for one or more taxa. Field survey commonly involves collection of plants for characterization, identification and preservation. Different types of survey or collections can be held based upon requirements. It may be a particular group of plants or a genus or species from a particular area or sampling plants for the floristic composition.

Before going to field, firstly we need to gather knowledge about that particular area. We should consult previous literatures to figure out total composition of taxa recorded there. For fruitful collection, we need to know about habit, habitat, flowering & fruiting timing of plants. For this we can take help from herbarium specimens. We need to consult all previous collections deposited at different herbaria and noted down all the above mentioned information. Now the question is who are interested to do this boring job where one have to travel here and there like a mad and also take care of old, died plants glued on big white sheets!! Yes, only plant taxonomist can relish the variability of nature, the discovery of new individual from nature and also by naming that plant being its mother! Every plant has so many nicknames but only one official name known by World is determined only by a plant taxonomist. They also determine the ecological, ethno-botanical, economical impact of plants which are new to us.

If one have plant taxonomy subject then he/she needs a preliminary idea about field tours. During B.Sc. and M.Sc. courses, excursions i.e. plant collection tours are held under the guidance of teachers. A student has no headache about food, travel, accommodation and other managements. But going alone for plant collection is little terrified. Before going field trips, one must have a suitable camera, a GPS, a field note book, collection bags, lots of blotting sheets or newspapers, magnifying glass, essential medicines, some dry foods, safety boots, torch, candle, matches and obviously with great observation power! During collection, one should not take any specimens from population having less than 50 individuals.

Now coming to the problems which one can face during solo field trips in different parts of India specially Himalayas. As we know Himalayas have witnessed many landslides due to earthquake, heavy rainfall, anthropogenic activities etc. it is very difficult to go for collection due to road blockage. Though you have prepared a list of collection places of your desired plants by consulting herbarium specimens but field scenario may differ. Due to landslides, urbanization and other calamities, plant population may be destroyed or shifted their home. So you can't overlook any places. Soon of the big challenges is managing your food, accommodation and travel in interior areas. Another big issue for collectors is to get permission for collection in the interior areas. Due to bio-piracy of medicinal plants, some states of India have high security issues. It is very tough and time taking process to convince forest, military and police officials to get permission for survey of military controlled areas. While travelling in tribal areas for collection we have to keep in mind that most of the tribal people blindly believe that civilized people come to steal their resources and thus they may poison and kill the collectors by offering poisonous food to them. So it is better to carry proper food. Most of the tribal people use their own languages and that is difficult for us to communicate and understand any information about the collected specimens. Safety is a very important issue when a lady researcher travels alone to a new place for exploration. In that situation she needs to be aware enough and have good communication skills with local people.

Some suggestion during field trip that one can also follow:

- Take more newspapers to avoid rotting of collected specimens.
- Carry a map and try to collect information about that area.
- Keep essential collection tools.
- Always maintain good communication with local people.
- Carry as little luggage as possible.
- Try to keep those essential things that can be used for many purposes.
- Try to keep garlic, cloves to avoid mountain sickness and breathing problems.

- Always keep some dry fruits, chocolate and obviously medicines with you.
- Keep pepper spray for safety purpose.

There are several collection methods for different groups of plants. In general during collection time, some points may keep in mind. These are:

- Plant parts or whole plants with flowers and fruits preferable for preservation.
- For herbarium preparation, 4 – 5 samples should be collected.
- We should not collect endangered or threatened plants.
- All essential parts should be preserved for proper identification.
- Take good photographs and note all primary data.
- Carry digger, secateurs, collection bags, scale, news paper, press etc.

We may face lots of challenges during field survey but surely we can manage somehow and enjoy the beauty of Mother Nature. It is always an excitement for a taxonomist to go for field trips to explore vegetation new to world!

Evaluating The Repertoire of Traditional Medicinal Practices Using Pharmacogenomics

Purnima Chatterjee (M. Sc. Semester-IV)

The term "Ethno-medicine" is used to mean the traditional health care methods which are based on indigenous cultural beliefs and practices and are not derived from the conceptual framework of modern medicine. Nearly 80% of the world's populations depend on traditional medicine for their healthcare [World Health Organization (WHO)]. The word "Tribe" is taken from the Latin word "Tribus" which means "one third". The word originally referred to one of the three territorial groups which united to make Rome. Tribal population have some specific characteristics which are different from others tribes [1]. They are simple people with unique customs, traditions and practices. They live a life of geographical isolation (Fig. 1).

According to WHO, traditional medicine is *"the sum total of the knowledge, skills and practices based on the theories, beliefs and experiences indigenous to different cultures, whether explicable or not, used in the maintenance of health, as well as*

Figure 1: Ethnomedical practices. (A) Field trips for awareness and capacity building; (B) A tribal woman from the Nilgiri area preparing a traditional concoction and (C) the medical plants used for treating chronic kidney and liver disease [Source: http://www.oneearthfoundation.in/ethnobotanical-study-of-nilgiri-tribes/]

in the prevention, diagnosis, improvement or treatment of physical and mental illnesses." [15].

India is considered as one of the 12 mega-biodiversity countries of the world having rich vegetation of about 45,000 vascular plants, with concentrated hotspots in the regions of Eastern Himalayas, Western Ghats and Andaman & Nicobar Islands. Of these, the folk medicine system of India use about 5,000 plant species with about 25,000 formulations for treating a variety of ailments, whereas the tribal medicine involves the use of over 8,000 wild plants with about 1,75,000 specific preparations/applications. The classical indigenous systems of Indian medicine prescribe 10,000 designated formulations (Fig. 2).

Figure 2: some commonly used plants by tribes

Strategies for the Improvement of Indian Tribal Medicine

While making tribal medicine a tool for development, the Government must recognize the cultural, intellectual and commercial importance of tribal medicine. Safeguarding of the cultural heritage and background of the tribals and tribal medicine should be incorporated in policy along with the protection of the intellectual property right of the tribals. Government should tap the commercial potentiality of the trading of medicinal plants and the tourism aspects of the tribal surroundings. Appropriate health policy has to be formulated to integrate tribal medicine with modern medicine and this is exactly where pharmacogenomics studies have a very important role to play. This is precisely where the interventions using modern tools and techniques such as pharmacogenomics, need to be investigated so that, they can yield appropriate results.

Pharmacogenomics, originated from the terms pharmacology and genomics, deals with heredity and the effect of drug. Medicine provided therapeutic activities are the subjects of pharmacology and when its mode of action is described through its role in genes and proteins, it becomes the subject of genomics and proteomics, respectively. An individual's response to drugs due to the individual's genetic inheritance is the pharmacogenomics. It deals with the influence of acquired and inherited genetic variation on drug response in patients by correlating gene expression or single-nucleotide polymorphisms with pharmacokinetics (drug absorption, distribution, metabolism, and elimination) and pharmacodynamics (effects mediated through a drug's biological targets) [10].

Polymorphisms in genes encoding drug metabolizing enzymes, such as CYP2C9, CYP2C19, and CYP2D6, drug transporters, such as SLCO1B1, and pharmacological targets, such as voltage-gated potassium channels related to congenital long QT syndromes, may lead to the occurrence of Adverse Drug Reactions (ADRs) by the direct effect on a specific product or due to impact on drug-drug interactions. It is a legal obligation that an effective pharmacovigilance system is in place and in order to capture previously unidentified reactions related to specific genomic traits of individuals leading to idiosyncratic reactions [13]. In addition, pharmacogenetic influence on the

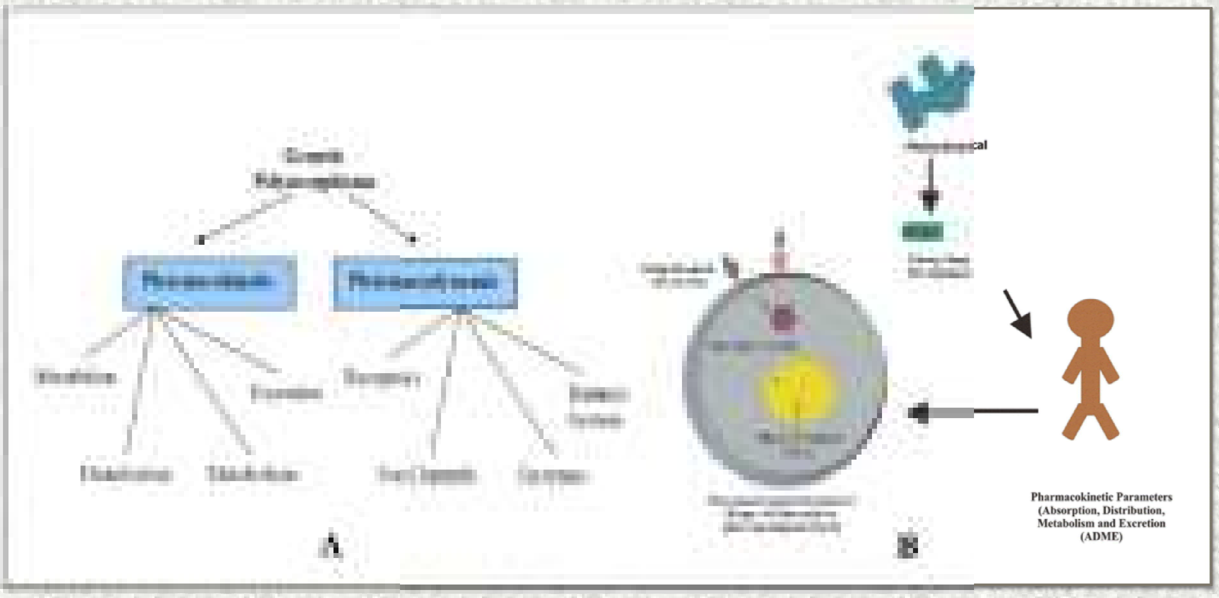

Figure 3: The steps of pharmacogenomic studies (A) The Components of a typical pharmacogenomic pipeline and (B) the steps of evaluation of a novel phytochemical.

occurrence of therapy failure can be investigated in the post-authorization period. For the successful adoption of genomic Biomarker (BM) testing into clinical practice and public health, clinical validity and utility of an identified BM and the corresponding test should be demonstrated.

Clinical validity refers to the accuracy with which a test detects or predicts a given phenotype, i.e. clinical disorder or outcome. Clinical utility refers to the net balance of risks and benefits associated with using a test in routine practice, including its ability to inform clinical decision making, prevent adverse health outcomes and predict outcomes considered important to patients and other stakeholders [11].

Correlation between Pharmacogenomics and Ethnomedicine

Drugs alter the genetic expression of their targets and present variable pharmacological effects in different individuals. Phytochemicals tend to follow similar pharmacokinetic, pharmaco-dynamics, and pharmaceutical profiles as other synthetically prepared formulations. Genetic variation in drug targets, transporters, and metabolism process cause significant changes in the pharmacological response to any drug. The CYP- 450 enzyme system, for example, is involved in the metabolism of a variety of plant products including alkaloids, terpenes, and essential oils. A number of different mutations have been identified in this enzyme system resulting in altered therapeutic responses. Administration of a crude drug affects the overall genotypic and phenotypic characteristics of an individual by the regulation of certain genes. The change in these properties is responsible for exhibiting the pharmacological properties of a drug. So Pharmacogenomics can be considered as a new age tool to analyze efficacy of traditional drugs. For example: Two of the commonly employed phytochemicals in both traditional and modern medicine are the vinca alkaloids, vincristine and vinblastine. They target the polymerization of microtubules by specifically targeting the β-tubulin subunit to specifically demonstrate their anticancer effects. Regulation of hypoxia induciblefactor-1 (HIF-1α) through various genetic routes is responsible for the induction of the therapeutic effects [12].

Role of Pharmacogenomics in the Field of Medicinal Practices

Manipulation of the responsible genes is the underlying basis of the mechanism of action of these drugs. Variation in the interindividual therapeutic responses is related to the genetic polymorphism in these genes. Personalized medicine or the concept of providing the most appropriate medicine in an accurate formulation and dose to an individual, based upon his/her genetic makeup, offers a solution to the problems of therapeutic failures and adverse drug reactions [5]. Genetic polymorphism has been associated with a number of disease presentations in susceptible individuals [14]. The pharmacogenomics approach can benefit the patients by detecting the candidate genes responsible, identifying the correct drug and dose for the individual, and monitoring of the pharmacological responses as a result of the drug. Personalized medicine, hence, incorporates the knowledge of a patient's genetic and ethnic variables in the drug selection process by a health care provider.

Disease Association in Plant Pharmacogenomics

Genetic polymorphism contributes to the difference in the pharmacological responses among individuals. Traditional healers, though not knowing the genetic basis, prescribe alternate drugs, dosage forms, and dose regimen to patients with distinctive physical characteristics and individual needs. Hence, the concept of personalized medicine owes its basis to the alternate medicine practitioners.

The Human Genome Project provided the scientific basis to strengthen this idea. Differences in therapeutic responses are attributable to the proteins regulating various pharmacokinetic and

Figure 4: Genetic control of drug metabolism processes (modified from Babar et al. 2015)

pharmacodynamics players of the drug-processing system. Artemisinin-based compounds are potent anti-malarial and anticancer agents.

They are thought to act by interacting with a number of different genes including those responsible for anti proliferative effects, apoptotic signals, oxidative stress, proto-oncogenes, and tumor suppressor genes [16].

Variation in any of these genes can cause a differential response to the artemisinin-based antitumor properties. Varying degrees of pharmacological responses are observed to herbs employed in Chinese, Korean, Ayurvedic, and African medicine, in individuals bearing genetic differences in the drug-processing enzymes. Plant-based remedies are, hence, subjected to similar pharmacological activities as the newer synthetic drugs are. However, lack of appropriate scientific data to establish correlation with the information from the health care practitioners hinders the incorporation of ethnomedicine in the mainstream of clinical practice [2].

Conclusion

Ethical issues are worth mentioning as key constraints. A patient's genetic information, including disease susceptibility and genetic background, has to be extracted and used in the decision-making process, which renders the additional need to safeguard this data. Additionally, as new and specific drugs would be targeted to a particular subpopulation of patients, the industry's economic concerns and profit margins would need to be addressed Regulatory authorities would have to devise newer protocols for drug analysis and testing. So, as a solution, a patient's genetic information, including disease susceptibility and genetic background (which is used in the decision making process) has to be safeguarded. The industry's economic concern and profit margins would need to be addressed and finally it is necessary to devise newer protocols for drug analysis and testing by the regulatory authorities. The scope of pharmacogenomics spreads from simple monogenic traits to complex pathways involving hundreds of alleles, influencing both pharmacokinetic and pharmacodynamics parameters, thus helping in the effective translation of molecular data into clinical findings. Once the correlation between the genetic makeup of an individual and the expected therapeutic response to a particular plant product is established, targeted, personalized pharmacotherapy can be developed.

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Life Story of Gregor Johann Mendel

Jyotipriya Mandal (B. Sc. Sem-II)

Gregor Johann Mendel, known as the "Father of Modern Genetics", was born in Austria in 1822. A monk, Mendel discovered the basic principles of heredity through experiments in his monastery's garden. His experiments showed that the inheritance of certain traits in pea plants follows particular patterns, subsequently becoming the foundation of modern genetics and leading to the study of heredity.

Gregor Johann Mendel

Early Life

Gregor Johann Mendel was born in 1822 in Morovia near Brunn in Austria, now Brno in Czechoslovakia, in the family of a poor family. He spent his early youth in rural setting, until age 11, when a local schoolmaster who was impressed with his aptitude for learning, recommended that he be sent to secondary school in Troppau to continue his education. The move was a financial strain on his family, but he excelled in his studies and in 1840, he graduated from the school with honours. In 1849, when his work in the community in Brno exhausted him to the point of illness, Mendel was sent to fill a temporary teaching position in Znaim. In 1851, he was sent to the University of Vienna, at the monastery's expense, to continue his studies in the sciences. While there, Mendel studied mathematics and physics under Christian Doppler, after whom the Doppler effect of wave frequency is named; he studied Botany under Franz Unger, who had begun using a microscope in his studies, and was a proponent of a pre-Darwinian version of evolutionary theory.

Experiments and Theories

Around 1854, Mendel began to research the transmission of hereditary traits in plant hybrids. At the time of Mendel studies, it was a generally accepted fact that the hereditary traits of the offspring of any species were merely the diluted blending of whatever traits were present in the "parents". It was also commonly accepted that, over generations, a hybrid would revert to its original form, the implication of which suggested that a hybrid could not create new forms. However, the results of such studies were often skewed by the relatively short period of time during which the experiments were conducted over as many as 8 years (between 1856 and 1863), and involved ten thousands of individual plants.

Mendel chose to use peas for his experiments due to their many distinct varieties, and because offspring could be quickly and easily produced. He cross-fertilized pea plants that had clearly opposite characteristics tall with short, smooth with wrinkled, those containing green seeds with those containing yellow seeds, etc. He had been working on genetic characters of pea (*Pisum sativum)* for 8 years. Mendel delivered two lectures to report his work at the meeting of the local scientific society in Brno on February 8 and March 8, 1865, then published his paper in the transactions of the society one year later (Mendel 1866).

The law of Segregation, which established that there are dominant and recessive traits passed on randomly from parents to offspring and the law of Independent Assortment, which established that traits were passed on independently of other traits from parent to offspring. He also proposed that this heredity followed basic statistical laws. Though Mendel's experiments had been conducted with pea plants, he put forth the theory that all living things had such traits.

Later Life, Death and Legacy

In 1868, Mendel was elected abbot of the school where he had been teaching for the previous 14 years, and both his resulting administrative duties and his gradually failing eyesight kept his from continuing any extensive scientific work.

Gregor Mendel died on January 6, 1884, at the age of 61. He was laid to rest in the monastery's burial plot and his funeral was well attended. His work, however, was still largely unknown.

It was not until decades later, when Mendel's research informed the work of several noted geneticists, botanists and biologists conducting research on heredity, that its significance was more fully appreciated, and his studies began to be referred to as Mendel's Laws. As Genetic theory continued to develop, the relevance of Mendel's work fell in and out of favor, but his research and theories are considered fundamental to any understanding of the field, and he is thus considered the "Father of Modern Genetics".

Transcriptome Analysis

Tilak Bhadra (M. Sc. Sem IV)

The concept of the transcriptome revolves around the complete set of transcripts present in a given cell type, tissue or organ and encompasses both coding and non-coding RNA molecules. Although we often assume that it consists only of messenger RNAs (mRNAs) because of their importance in encoding proteins. The transcriptome is influenced by the phase of the cell cycle, the organ concerned, exposure to drugs or physical agents, aging, diseases and a multitude of other variables, all of which must be considered at the time of its determination. Although transcriptomics is most commonly applied to the m-RNAs, it also provides important data regarding content of the cell's non coding RNAs including rRNAs, tRNA, lncRNA, siRNA and others. It describes the complete set of RNA transcripts that are produced by the genome, under specific circumstances or in a specific cell, using high throughput methods.

Techniques of Transcriptome Analysis

Two biological techniques are extensively used in transcriptome profiling, viz, DNA microarray (a hybridization-based technique) and sequence-based techniques.

DNA microarray is a laboratory tool used to detect the expression of thousands of genes at the same time. DNA microarrays are microscopic slides that are printed with thousands of tiny spots in defined positions, with each spot containing a known DNA sequence or gene. Often, these slides are referred to as gene chips or DNA chips. The DNA molecules attached to each slide act as probes to detect gene expression, which are also known as the transcriptome or the set of messenger RNA (mRNA) transcripts expressed by a group of genes. Thousands of reference genes can be immobilized, spotted or synthesized in situ on a small space of these glass slides. This technique works on principle of hybridization of mRNA of concerned cell with immobilized cDNA/oligonucleotide sequence present on array slide.

Next Generation Sequencing also known as high throughput sequencing. NGS is a general term used to describe a number of different modern sequencing technologies including- Illumina sequencing, Roche 454 sequencing, Ion torrent: proton/PGM sequencing , SOLID sequencing. Although the techniques differ slightly In spite of being different technologies the basic principle of next gen sequencing is almost the same in all of the stated procedure. We are going to see the overall overview of the next generation sequencing step by step. **Sample preparation→** Once we have isolated our DNA, we need to generate smaller fragments. Now all of these DNA fragments will be ligated to certain oligonucleotides. **Denaturation→**First our double stranded fragment is denatured, so in theory the whole genome should be in fragments. **Binding to chip→**All of the fragments have attached to different types of binding sited on each end, all fragments are now applied on a chip the so-called flow cell. The DNA fragments will at these ends hybridize with the flow cells applied to the plate. **DNA amplification by PCR→** By polymerase chain reaction the complementary sequence to our single stranded DNA fragment is synthesized. This process which we have seen here is done simultaneously for all DNA fragments on the whole flow cell. **Washing→** Now the DNA is denatured and the single strand which is not attached to the flow cells, oligonucleotides get washed away. **Bridge building and amplification→**We have two different types of oligonucleotides here and the second type of oligo will now also hybridize to one of these sticky oligonucleotides on the plate, this process is called bridge building. The DNA is now amplified again so a polymerase will synthesize the complementary sequence again. This whole process will repeat now. The DNA fragment will build a bridge again and again, so out of one DNA fragment generated multiple copies by PCR. **Reverse strands are cleaved→** Now the reverse strands are cleaved now and sequencing can begin. **Sequencing→** For sequencing we just look at one copy now as mentioned in the beginning a primer can bind to the oligonucleotides so this is a sequencing binding site here, sequencing is now done with specific nucleotides, these nucleotides in this case are fluorescently labelled. And fluorescent signal is obtained. **Data analysis→** Here informatics tools are required the whole process of next gent sequencing generated millions and billions of reads, these reads are now overlaid and compared to reference genome and by this overlay we can generate the whole genome. The differences between the different next gen sequencing platforms lie mainly in the technical details of the sequencing reaction and can be categorized in four groups: **Pyrosequencing Sequencing by**

synthesis, Sequencing by ligation, Ion semiconductor sequencing.

In **Pyrosequencing** the sequencing reaction is monitored through the release of a pyrophosphate during each nucleotide incorporation. The released pyrophosphate is used in a series of chemical reaction resulting in the generation of light. Light emission is detected by a camera which records the appropriate sequence of the cluster. The sequencing proceeds by incubating one base at a time measuring the light emission, degrading the unincorporated bases and then the addition of another base. This technology is capable of generating large read length much comparable to the read length of sanger sequencing, high reagent cost, high error rate over strings of 6 plus homopolymers.

Sequencing by synthesis: Sequencing by synthesis utilizes the step-by-step incorporation of reversibly fluorescent and terminated nucleotides for DNA sequencing and is used by the illumina NGS platforms. All four nucleotides are added to the sequencing chip at the same time and after nucleotide incorporation the remaining DNA based are washed away. The fluorescent signal is read at each cluster and recorded. Both the fluorescent molecule and the terminator group are then cleaved and washed away. This process is repeated until the sequencing reaction is complete.

Sequencing by ligation: Sequencing by ligation is different from the other two methods since it does not utilize a DNA polymerase to incorporate nucleotides. Instead, it relies on 16 octamer oligonucleotide probes each with one of the four fluorescents died and attached to its 5' end that are ligated to one another. Each octamer consists of two probe specific bases and six degenerate bases. The sequencing reaction commences by binding of the primer to the adapter sequence and then hybridization of the appropriate probe. This hybridization of the probe is guided by the two probe specific bases and upon annealing, is ligated to the primer sequence through DNA ligase. Unbound oligonucleotides are washed away and the signals are recorded. After that the fluorescent signal along with the last 3 bases of the octamer probe are cleaved and the next cycle commences. After approximately seven cycles of ligation the DNA strands is denatured and another sequencing primer, offset by the one base from the previous primer is used to repeat these steps. In total 5 sequencing primers are used.

Ion semiconductor sequencing: Ion semiconductor sequencing utilizes the release of hydrogen ions during the sequencing reaction, to detect the sequence of a cluster. Each cluster is located directly above a semiconductor transistor which is capable of detecting changes in the pH of the solution. During nucleotide incorporation, a single hydrogen ion is released into the solution and it is detected by the semiconductor. The sequencing reaction itself proceeds similarly to pyrosequencing, but at a fraction of the cost.

For understanding of interaction between protein and DNA we can study the following method- **ChIP Assay (Chromatin Immunoprecipitation)**: Chromatin Immunoprecipitation is a well established procedure to investigate interaction between protein and DNA. DNA-protein interactions play a key role in the regulation of Page 16 of 49 important cellular functions including gene transcription, DNA replication and recombination, repair, segregation, chromosomal stability, cell cycle progression, and epigenetic silencing. The 3- dimensional structure of chromatin is maintained by the binding of histones and other regulatory proteins to the DNA. It is vital to know how DNA-binding proteins affect the functioning of any particular gene and to identify which particular protein binds to a specific DNA sequence in vivo.

Expressed sequence tags (EST): Expressed sequence tag (EST) and complementary DNA (cDNA) sequences provide direct evidence for all the sampled transcripts and they are currently the most important resources for transcriptome exploration. ESTs are short (200–800 nucleotide bases in length), unedited, randomly selected single-pass sequence reads derived from cDNA libraries. High-throughput ESTs can be generated at a reasonably low cost from either the 5’ or 3’ end of a cDNA clone to get an insight into transcriptionally active regions in any organism.

Cap analysis of gene expression(CAGE): Transcripts abundance can be determined by various methods, including reverse transcription PCR, microarray analysis, sequencing of expressed sequence tags (EST), serial analysis of gene expression (SAGE), and massively parallel signature sequencing (MPSS), most of which rely on 3’ end related sequencing. But for the identification of start site of transcription and associ8ated promoters, 5’ end specific signature sequences are required for higher annotations of expression profiles. Therefore cloning of short sequence tags from the 5’ ends of cDNAs, using cap analysis gene expression (CAGE).

Data Analysis

RNA-Seq experiments generate a large volume of raw sequence reads, which have to be processed to yield useful information. Data analysis usually requires a combination of bioinformatics software tools that vary according to the experiment design and goals. The process can be broken down into the following four stages: a) **Quality control**- Sequence reads are not perfect, son the accuracy of each base in the sequence needs to be estimated for downstream analyses. Raw data are examined for high quality scores for base calls. b) **Alignment**- In order to link sequence read abundance to expression of a particular gene, transcript sequence are aligned to a reference genome, or de novo aligned to one another if no reference is available. c) **Quantification**- Quantification of sequence alignments may be performed at the gene, exon or transcript level. Typical outputs include a table of reads counts for each feature supplied to the software. Gene and exon read counts may be calculated easily using the HTSeq software. d) **Differential expression**- Once quantitative counts of each transcript are a varilable, differential gene expression is the measured by normalizing, modeling and statistically analyzing the data.

Applications

Transcriptome analysis have been performed in order to identify several transcripts and their key role in the metabolism of that particular plant. Few notable examples are: *Arabidopsis thaliana* [Disease resistance], 2) *Sellaginella sp* [Desiccation tolerance], 3) *Lotus Japonicus* [Mycorrhiza development], 4) *Zea mays* [resistance to *Fusarium graminearum*], 5) Conifers [shade avoidance and shade tolerance].

Conclusion

As the ability of sequencing platforms improve, production of longer reads has become a reality, new mapping methods are also required in order to accurately and efficiently align long reads. Because longer reads can span multiple exon–exon junctions, the identification and quantification of alternative isoforms will significantly improve in future with the extra information encoded in them.

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Covid-19 Infographic: Tracking the Variants

Subhasis Pal (M.Sc. Semester – IV)

The novel corona virus is a different strain that has not been previously identified in human being. Corona viruses are of large family which transmit between animals and humans causing illness, with symptoms ranging from common cold to more severe diseases like Middle East respiratory syndrome (MERS – CoV) and severe acute respiratory syndrome (SARS – CoV) . COVID-19 is a disease caused by a type of corona virus called "Sars-Cov2". The name corona virus is derived from the Latin term '*corona*', denoting crown or halo, referring to the typical resonant of a crown when viewed under electron microscope, due to the presence of club-shaped protein spikes covering the surface. SARS-CoV-2 responsible for coronavirus disease 2019 (COVID-19) was first discovered at Wuhan, China in December 2019. Since then, the disease has caused devastating pandemic around the world.

Coronaviruses are enveloped non segmented positive-sense RNA viruses belonging to the family Coronaviridae and the order Nidovirales. They are large pleomorphic spherical particles with surface projections. Like all viruses, SARS-CoV-2 also accrues mutations and changes in genetic code with time, as it replicates. The virus has inherent RNA repair mechanisms, thereby gathering mutations at comparatively slower rate than most RNA viruses. On an average, a genome from a virus collected In October 2020 has around 20 mutations compared to the first strain sequenced in January 2020.

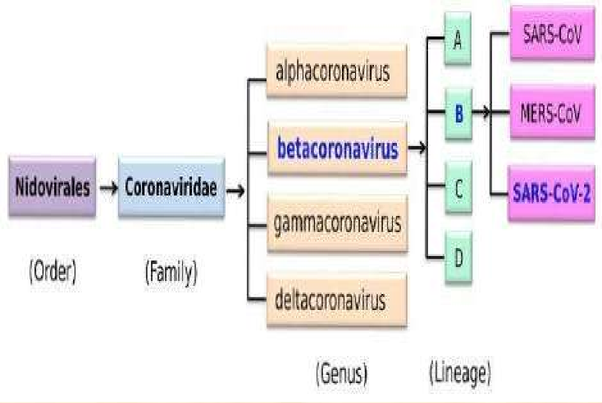

Figure 1: An Evolutionary tree of various coronavirus strains (Source Shutterstock.com).

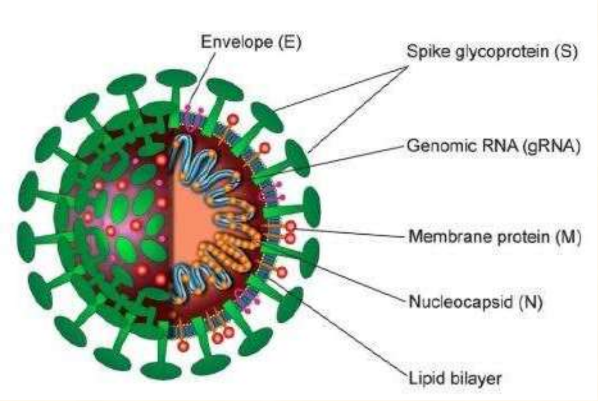

Figure 2: The schematic structure of SARS-COV-2 (Source Shutterstock.com)

The term **Variant** is used to classify a virus that has developed a "specific group of mutations" causing the variant to behave in a different way than that of the strain it originated from. A particular strain of virus is regarded as a variant when it has mutations to change a small portion of its genetic code. As the pandemic continued, variants have become the latest concern with several notable examples detected in South Africa , Brazil, UK and several other countries. Each one is made up of a collection of mutations, all of which have the potential to change the SARS-COV-2 virus in unexpected ways. Viruses multiply by copying their genome over and over, but like an old photocopier, these copies aren't always perfect. Each of these imperfect copies is a variant. Normally these imperfections or mutations don't change the behaviour of the virus much, often less successful than the original stain. But seldom, mutations can alter the virus in some critical forms. It could become more infectious, or more able to avoid the immune system. The more a virus is allowed to replicate unchecked, the more chance it has to accumulate these rare beneficial mutations. That can occur when viruses are allowed to spread quickly through a population, or if they encounter a host that's less able to fight them, such as people with compromised immune systems from medical treatment.

Types of variant- Scientists have classified certain variants as Variants Being Monitored, Variants of Concern (VOC), Variants of Interest (VOI) or Variants of High Consequence (VOHC) based on how easily they spread, how severe their symptoms are, and how they are treated. Some variants seem to spread more easily and quickly than other variants, which may lead to more cases of COVID-19, probably more severe spread.

WHO label: World Health Organization (WHO) proposed labels for global SARS-CoV-2 as variants of concern and variants of interest, which are to be used alongside the scientific nomenclature of the virus. WHO also released mandates outlining working definitions of VOC and VOI, and recommended actions for member states if a VOI or VOC is identified. A VOI is defined as an isolate of SARS-CoV-2 that has genotypic and/or phenotypic changes compared to the reference genome. A VOC is defined as a VOI which has a demonstrable increase in transmissibility, increase in virulence and/or is not being controlled effectively by existing public health measures.

Variant of Concern (VOC)

A variant for which there is evidence of increase in transmissibility, disease severity (e.g., hospitalizations or deaths), detrimental change in COVID-19 epidemiology, significant increase in virulence or pathogenicity, or neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or failures in diagnostic detection and therapeutics.

Variant of Interest (VOI)

A variant with definite genetic markers which are associated with changes to receptor binding reduce neutralization by antibodies generated against vaccination or previous infection. Therefore efficacy of diagnosis and treatment is reduced and enhanced transmissibility or disease severity.

Variant of High Consequence (VOHC)

A variant with established failure of diagnostics, a significant reduction in vaccine effectiveness, an unreasonably high number of infections among vaccinated persons, orvery low success in vaccine-induced protection against severe disease. These variants significantly reduced susceptibility to multiple Emergency Use Authorization (EUA) or approved therapeutic techniques. The variant causes more severe clinical disease and increased cases of hospitalizations. At present no SARS-CoV-2 variants are designated as VOHC.

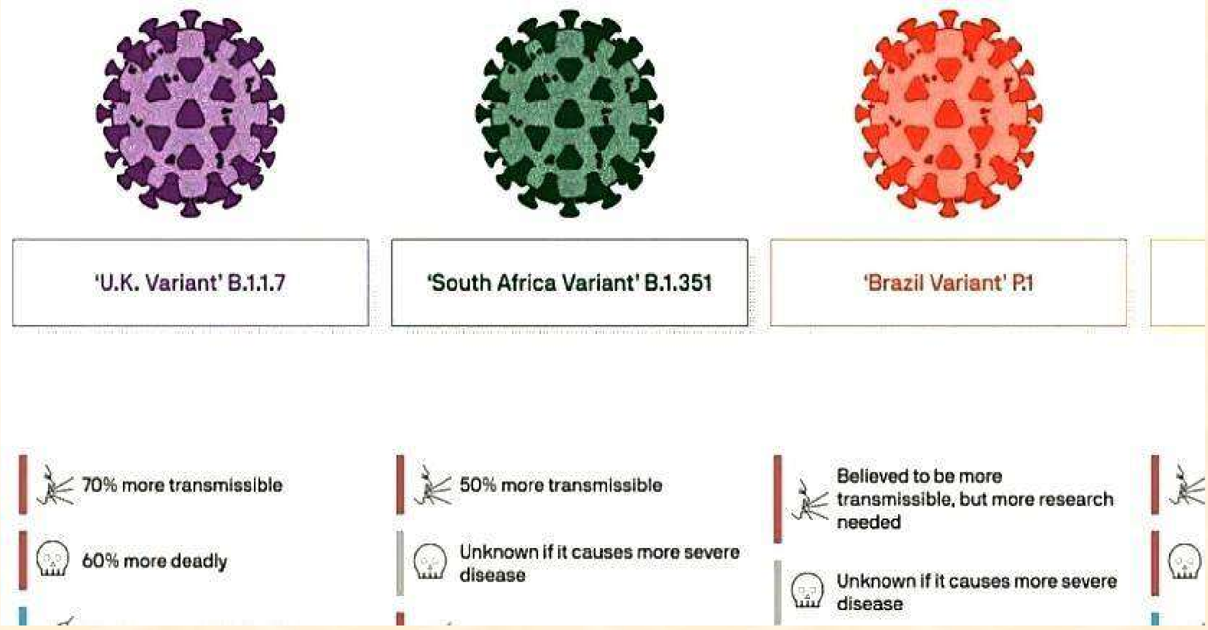

Figure 3: Tracking the Variant of Concern (Source from internet)

Table1: Variants of Cov-19 (Source https://www.cdc.gov/)

WHO level	**Lineage+ additional mutations**	**Country first detected (community)**	**Spike mutations of interest**	**Year and month first detected**
Alpha	B.1.1.7	United Kingdom	N501Y, D614G, P681H	September 2020
Not applicable	B.1.1.7+E484K	United Kingdom	E484K, N501Y, D614G, P681	December 2020
Beta	B.1.35	South Africa	K417N, E484K, N501Y, D614G, A701	September 2020
Gamma	P.1	Brazil	K417T, E484K, N501Y, D614G, H655	December 2020
Delta	B.1.617.2	India	L452R, T478K, D614G, P681R	December 2020
Eta	B.1.52	Nigeria	E484K, D614G, Q677	December 2020
Theta	P.3	The Philippines	E484K, N501Y, D614G, P681H	January 2021
Kappa	B.1.617.1	India	L452R, E484Q, D614G, P681R	December 2020
Not applicable	B.1.620	Colombia	S477N, E484K, D614G, P681H	February 2021
Not applicable	B.1.621	Unclear	R346K, E484K, N501Y, D614G, P681H	January 2021
Lambda	C.37	Peru	L452Q, F490S, D614G	December 2020

Infection Pathology of SARS-COV-2

The SARS-CoV-2 virus enters the human host, usually in the form of liquid droplets or aerosols from a cough or sneeze. The virus attaches by its surface S protein to the human ACE2 on cell surfaces, like a key fitting into a lock. ACE2 ``receptors" are present on virtually all human cell types. But they are especially common on cells of the human nose and throat. Cell entry is an essential component of cross-species transmission of coronavirus. Covs encode a surface glycoprotein (spike structures) and binds to the host-cell receptor. This starts the process of viral entry. Then a single region of the spike protein called the receptor-binding domain (RBD) interacts with the host-cell receptor. After binding the receptor, a nearby host protease cleaves the spike, releasing the spike fusion peptide. Thus the process of virus entry is completed.

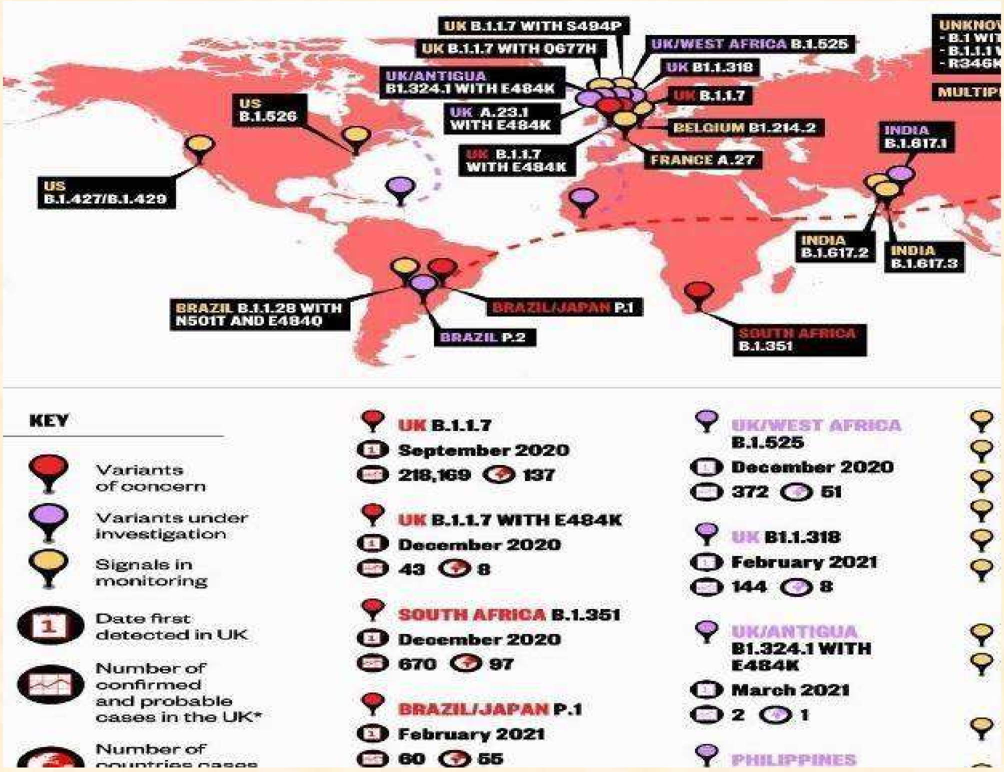

Figure 4: Current and future Variant of Concern. (Source from internet)

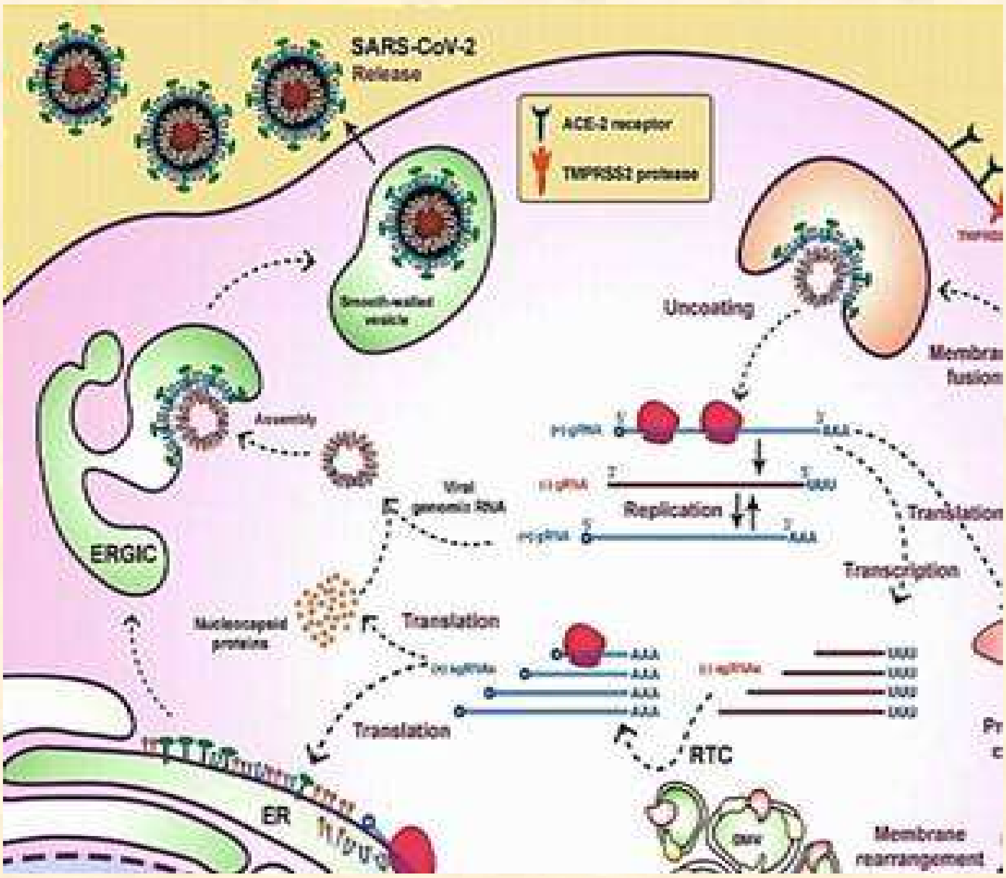

Figure 5: Life cycle of CoV in host cells. (Source from internet)

Types of Vaccine

All vaccine platforms are designed to train our immune system. There are two categories of COVID-19 Vaccines: I) Component Viral Vaccines-A) Protein Subunit, containing isolated and purified viral proteins. B) Virus-like Particles (VLP), containing viral proteins that mimic the structure of the virus, but not the genetic material. C) DNA-based and RNA-based, containing viral genetic material (such as mRNA) which provides the instructions for making viral proteins. D) Non-Replicated Viral Vector, containing viral genetic material packaged inside another harmless virus that cannot copy itself. E) Replicating Viral Vector, containing viral genetic material packaged inside another harmless virus that can copy itself. II) Whole Virus Vaccines-A) Inactivated, containing copies of the virus that have been killed (inactivated). B) Live-Attenuated, containing copies of the virus that have been weakened (attenuated).

Conclusion

Over the past several months, the emergence of new virus variants has become a new crucial point of interest in the ongoing COVID-19 pandemic. Many variants of SARS-CoV-2 have been discovered. However, the variants that have been recently identified in the UK, South Africa, Brazil and India are concern variants because of their critical characteristics of increased transmissibility, escaping immune responses triggered by previous infections, low vaccine efficacy, escalating disease severity, and increased hospitalization necessity. Furthermore, there are opinions relating to the British mutation, which is completely different from the origin and more contagious and deadlier, that the existing pandemic should be renamed the COVID-20 outbreak.

On 26 November, 2021, WHO designated the variant B.1.1.529 discovered from South Africa, a variant of concern, Omicron, on the advice of WHO's Technical Advisory Group on Virus Evolution (TAG-VE). This labelling was based on the evidences that Omicron has several mutations that might have an impact on its behaviour like on how easily it spreads, the disease severity, and neutralization of vaccine. At present, Omicron has spread in 52 countries worldwide including India. In India 23 cases of Omicron infection have been detected in patients till date.

Scientists are still investigating the emergence and origination of SARS-CoV-2. Characterization of the variants is essential to determine more precisely the roles of mutations, either individually or in combination, on virus biology. All the data suggests exactly that, the people who have been infected show symptoms that are consistent with the symptoms of any other lineage of SARS- CoV-2. So, the mutations may make the virus more transmissible, though not more lethal or more disease causing. But when a virus becomes more transmissible, that means it could generate more infection rates. Since this virus is spreading faster, it has great potential to cause more severe disease incidence in a population.

Acknowledgement

I would like to acknowledge my teacher Dr. Anuradha Bandopadhyay, P.G. Department of Botany, Barasat Govt. College for guidance to write the review.

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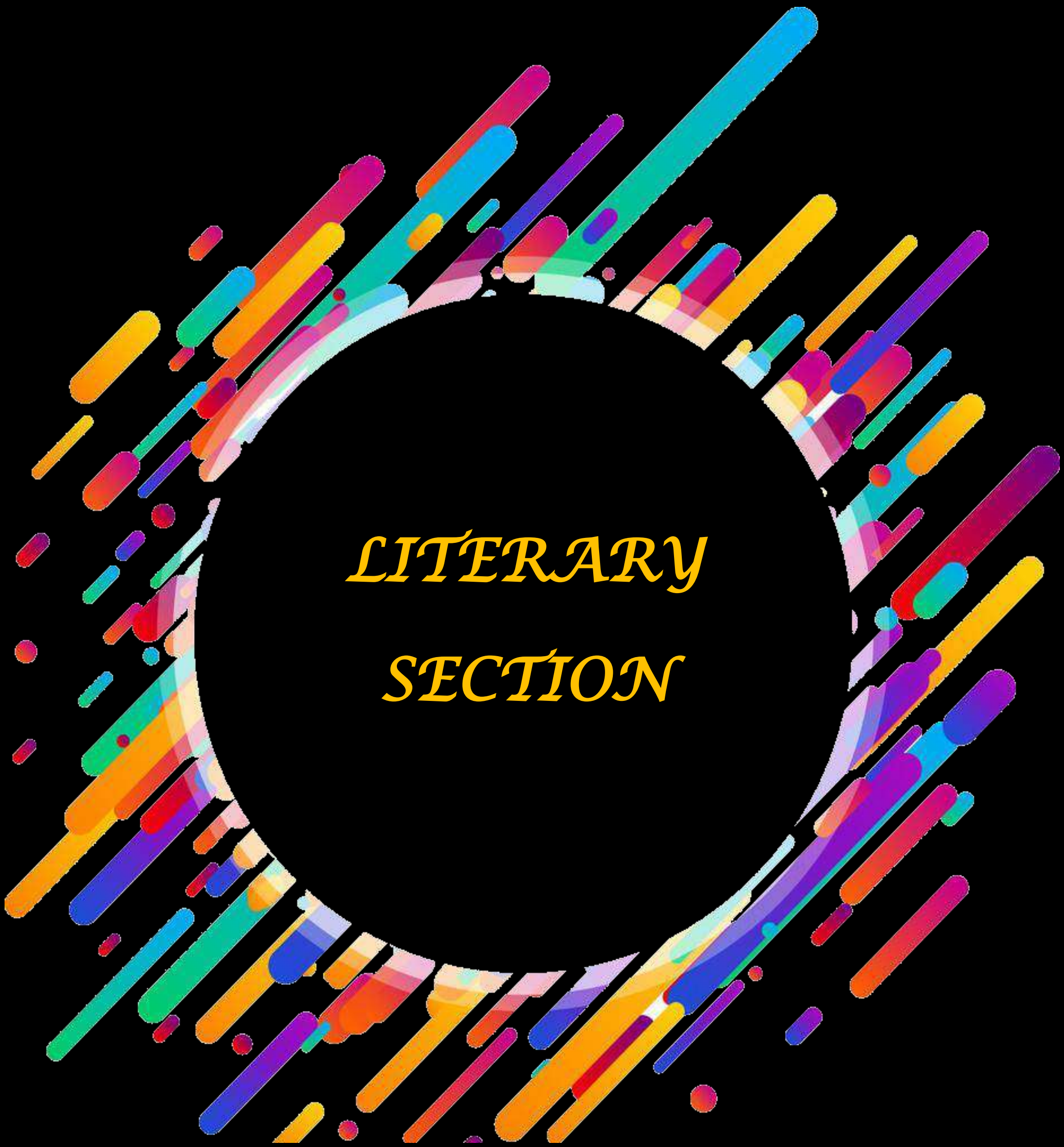


LITERARY SECTION

গল্পের মহামারী যে আজ ভীষণভাবে সত্যি

...........বর্ণা সাহা

বি. এস. সি ষষ্ঠ সেমেস্টার

ছোটবেলায় পাঠ্য ছিল শরৎচন্দ্র চট্টোপাধ্যায়ের লেখা ' মহামারির কবলে', জেনেছিলাম কলেরা কত ভয়াবহ রূপ ধারণ করতে পারে, জেনেছিলাম একটা অস্বাস্থ্যকর পুকুর কিভাবে বিপর্যস্ত করেছিল গ্রামের জনজীবন। মহাপুরুষদের জীবনী পড়ে জেনেছিলাম মহান নারী, মহান আত্মা ভগিনী নিবেদিতার কথা, যিনি নিজের জীবনের পরোয়া না করে দুর্দশাগ্রস্ত প্লেগ রোগীদের সেবা করে গেছেন নিঃস্বার্থ ভাবে।

তবুও বলব এতদিন অবধি মহামারির সাথে পরিচয় ছিল শুধুমাত্র বইয়ের পাতায়। তাই হয়তো আমাদের প্রজন্ম ঠিকঠাক অনুধাবন করতে পারেনি আদতে মহামারী কতটা আগ্রাসী। আর আজ সেই গল্পের মহামারীর থেকেও ভয়ঙ্কর রূপের অতিমারীকে “করোনা” রূপে সত্যি হতে দেখছি আমরা। করালগ্রাসী করোনার বিষদাঁত ভাঙার নিরলস চেষ্টা চালিয়ে যাচ্ছেন বিজ্ঞানীরা। দীর্ঘদিনের গবেষণায় ইতিমধ্যে মিলেছে বেশ কিছু সুফল। আবিষ্কৃত হয়ে চলেছে নানা ভ্যাকসিন, যা করোনার বিরুদ্ধে প্রতিরোধ ক্ষমতা গড়ে তুলতে সক্ষম হয়ে উঠছে।

যখন যখন করোনা তার বিষাক্ত হাত দুটো বাড়িয়ে দিয়েছে সাধারণ মানুষের শ্বাসরোধ করতে, তখন তখন ঢাল হয়ে দাঁড়িয়েছে ডাক্তার এবং নার্সের অক্লান্ত প্রচেষ্টা। যুদ্ধ চলছে। কখনো জিতছে ডাক্তার, নার্স... জিতিয়ে দিচ্ছে সাধারণ মানুষকে, শোনা যাচ্ছে সুস্থতার উচ্ছ্বাস। আবার কখনো জিতে যাচ্ছে নৃশংস করোনা, একের পর এক প্রাণকে করছে গ্রাস, অবশিষ্ট কেবলই স্বজন হারানোর বেদনা। নিজের জীবনের পরোয়া না করে লড়ে যাচ্ছে ডাক্তার ও নার্স। করোনা তাদেরও আক্রমণ করতে ছাড়ছেনা। মানে পরিস্থিতি টা ঠিক এরকম--- যমদূত ডাক্তারের পাশে দাঁড়িয়ে বলছে ," ডাক্তারবাবু, এবার যে আপনাকে আমার সাথে যেতে হবে।" প্রত্যুত্তরে ডাক্তার বলছে ," দাঁড়াও আসছি, এই আর কয়েকটা রোগী দেখে যাই!!" কেনই বা যাবেন ডাক্তারবাবু যমদূতের সাথে? তাহলে আমরা যারা সাধারণ মানুষ তারা বাঁচবো কেমন করে? কার ভরসায়? শুধু তো করোনা নয়, অগুনতি সব ব্যাধি পাল্লা দিয়ে বেড়ে চলেছে। ডাক্তার রা এভাবেই প্রতিনিয়ত নিজেদের জীবন বাজি রেখে যমদূতের সঙ্গে লড়ে যাচ্ছেন।

নাহ্, আমরা ভগিনী নিবেদিতা কে কেউ চোখে দেখিনি, শুধু গল্পে শুনেছি। কিন্তু এই ডাক্তার, নার্স দের মধ্যে আজ ভগিনী নিবেদিতার সেবাদর্শ মূর্ত হয়ে উঠতে দেখছি আমরা। পুলিশ, সাফাই কর্মীরা। ও স্বেচ্ছাসেবী সংগঠনগুলি ক্রমাগত চেষ্টা চালিয়ে যাচ্ছেন করোনাকে অবদমিত করার। তাদের যুদ্ধে অন্তরায় হচ্ছে বেশ কিছু স্বল্পবুদ্ধি বেপরোয়া মানুষজন,যারা প্রয়োজন না থাকলেও বাড়ির বাইরে বেরোচ্ছেন,করোনা বিধি কে বুড়ো আঙুল দেখিয়ে মাস্ক ছাড়া ঘুরে বেড়াচ্ছেন, খাবার খাচ্ছেন নোংরা হাতেই। স্যানিটাইজার ব্যবহার করে জীবাণুর ভিড় সরানোর কোনো প্রয়োজনই বোধ করছেন না। ফলস্বরূপ সংক্রমণ বাড়ছে। এরা বুঝতে পারছেন না যে, বাঁচতে হলে বাড়িতে থেকে জীবাণুমুক্ত থাকতে হবে ; আর এতেই ক্রমশ নিরস্ত্র হবে করোনা নামক অসুর।

যুদ্ধ একদিন ঠিক শেষ হবে। হয়তো খুব শিগগিরই, কিন্তু কবে.... জানিনা। শুধু এটুকুই জানি যে আমাদের জিততেই হবে। ইতিমধ্যে ভ্যাকসিন সম্পর্কে সচেতনতা গড়ে উঠেছে জনগণের মধ্যে। কিন্তু ভ্যাকসিন নিলেও সতর্কতা লঘু করলে চলবে না। মাস্ক পড়ে চলাচল করা এবং সবসময় নিজেকে স্যানিটাইজড্ রাখার চেষ্টা করতে হবে। আমাদের একটু অসাবধানতায় করোনার তৃতীয় ঢেউ এর কবলে পড়তে পারি আমরা। হ্যাঁ, জানি এ লড়াইয়ে করোনার প্রথম ও দ্বিতীয় ঢেউ আমাদের কাছ থেকে অনেক প্রিয়জনকে কেড়ে নিয়েছে, অনেক কিছুই হারিয়ে ফেলেছি আমরা। তবুও ভেঙে পড়লে চলবে না। আবার এই পরিস্থিতি কিন্তু আমাদের অনেক কিছুই শিক্ষা দিয়ে গিয়েছে। সবকিছু কে সাথে রেখেই একটা দৃঢ় মনোবল তৈরি করতে হবে, যে সবশেষে আমরাই জিতবো। দরকার শুধু আমাদের সঠিক সহযোগিতার। পাশে থাকবো, কিন্তু কাছাকাছি নয়। কারণ, গল্পের মহামারী যে আজ ভীষণভাবে সত্যি।।

বিভাগীয় ভ্রমণ - শৈল শহর দার্জিলিং

- তনুশ্রী সাহা -

বি. এস. সি ষষ্ঠ সেমেস্টার

Excursion....!! কথাটা শুনলে যেমন মনের মধ্যে প্রচন্ড উত্তেজনার সৃষ্টি হয়, খুশিতে মন ভরে ওঠে ঠিক তেমনই চোখের কোণায় একবিন্দু জলও উঁকি দেয়....মনে পড়ে যায় জীবনের প্রথম Excursion এ কাটানো সেই মূহুর্ত গুলো, যা কোনোদিনই ভোলার নয়। তখন আমরা প্রথম সেমিস্টারে উত্তীর্ণ হয়ে দ্বিতীয় সেমিস্টারে পা রেখেছি.... অপরিচিত ছেলেমেয়ে গুলির মধ্যে বন্ধুত্বটা বেশ গাঢ় হতে শুরু করেছে। তখনই হঠাৎ একদিন আমাদের এক নন্-টিচিং স্টাফ আমাদের অসিতদা এসে বললেন , “কীরে ? এবার তো তোদের Excursion আছে, জানিস তো!” কথাটা শোনামাত্র আমাদের বন্ধুমহলে তো বেশ ষোড়গোল পড়ে গেল। তারপর শিক্ষক-শিক্ষিকা ও বিভাগীয় প্রধানের সাথে কথা বলে Excursion Site ঠিক হল দার্জিলিং, 3 Night Stay। আর আমাদের নিয়ে যাবেন দিব্যেন্দু স্যার, নির্মলেন্দু স্যার, অনুরাধা ম্যাম আর অসিতদা। সেইমতো টিকিট বুকিং করা হল। যাবার আগে আমাদের HOD স্যার ওখানে কি সমস্যা হতে পারে, সমস্যায় পড়লে কি করতে হবে, কি কি জরুরি ওষুধ সাথে রাখতে হবে, শীতের পোশাক কতটা নিতে হবে এসব বলে দিয়েছিলেন। ওখানে গিয়ে mineral water ছাড়া অন্য কোনো জল খেতেও বারন করেছিলেন তিনি।

4th April, 2019 ছিল আমাদের যাওয়ার দিন। যথারীতি শিয়ালদহ স্টেশন থেকে সন্ধ্যে ৭:৩০ মিনিটের উত্তরবঙ্গ এক্সপ্রেস ট্রেনে উঠে পড়লাম আমরা সবাই। সেই রাতটা বেশ মজা করেই কেটে গেল, উত্তেজনায় কারোর চোখে তো ঘুমের লেশমাত্র নেই। পরদিন সকাল সকাল ট্রেন

পৌঁছে গেল NJP স্টেশন এ, নেমে পড়লাম আমরা। সেখান থেকে প্রাতরাশ সেরে গাড়িতে উঠে আমরা রওনা দিলাম হোটেলের উদ্দেশ্যে, Hotel Central View। যাওয়ার পথে অনেক জায়গায় গাড়ি থামিয়ে বেশ কিছু গাছপালার সাথে আমাদের পরিচিত করে দিয়েছিলেন স্যার ম্যামরা। বেশ কিছু plant collect ও করেছিলাম আমরা।

হোটেলে পৌঁছে ফ্রেশ হয়ে মধ্যাহ্নভোজ করার পর আমাদের একটু বিশ্রাম নিতে বললেন তারা। সেদিনই সন্ধ্যায় স্যার ম্যামরা আমাদের Darjeeling Mall-এ নিয়ে গিয়েছিলেন। এমনকি অপরিচিত জায়গায় কিছু কিনতে গিয়ে আমরা যাতে ঠকে না যাই সেজন্য আমাদের সাথে সাথে ছিলেন তারা। দিব্যেন্দু স্যার আমাদের মোমোও খাইয়েছিলেন। হোটেলে ফিরে রাতের খাবার খাওয়ার পর আমাদের থাকতে কোনো অসুবিধা হচ্ছে কিনা সেটা নিজেরা এসে দেখে গেছেন তারা।

পরদিন মানে 6th April সকাল থেকেই আকাশটা কেমন গম্ভীর হয়ে আছে। চারিদিক মেঘে ঢাকা, সাথে বৃষ্টিও হচ্ছে। কোথাও বেরোতে পারবোনা ভেবে আমাদের মন খারাপ হয়ে আছে আর সমানে স্যার ম্যামদের আমরা জিজ্ঞাসা করে যাচ্ছিলাম আজ আমরা কোথাও যাবো না? Zoo তে যাওয়ার কথা তো আজ, আমাদের কি যাওয়া হবেনা? কিছুক্ষণ পর বৃষ্টি প্রায় থেমে এল। তখনই আমরা সবাই ছাতা নিয়ে হাসিমুখে বেড়িয়ে পড়লাম Padmaja Naidu Himalayan Zoological Park & Himalayan Mountaineering Institute এর উদ্দেশ্যে।

হোটেল থেকে বেরিয়ে কিছুটা গিয়েই আমরা লাল *Rhododendron* গাছ দেখতে পাই। বেশ কয়েকটি ছবিও তুলে নিলাম আমরা। পুরো রাস্তাটা আমরা হেঁটেই গিয়েছিলাম। আর রাস্তার দুপাশের plant গুলি আমাদের চিনিয়ে দিচ্ছিলেন স্যার ম্যামরা ।

মাঝেমধ্যে আমাদের খুশি করার জন্য কখনও দিব্যেন্দু স্যার আবার কখনও নির্মলেন্দু স্যার গান ধরছেন। বেশ মজা করতে করতেই আমরা পৌঁছে গেলাম Zoo তে। ওখানে কত্তো পশুপাখি দেখেছিলাম আমরা, কিছু সাপ ও দেখেছিলাম।

তবে Red Panda -র দর্শন পাওয়াই সেদিনকার বিশেষ আকর্ষণ ছিল আমাদের কাছে। যদিও সে আমাদের বিশেষ পাত্তা দেয়নি, ঘুমাতেই ব্যস্ত ছিল। ওখানে আমরা Bengal Natural History Museum ও পরিদর্শন করেছি। সব দেখেশুনে ফিরে এলাম আমরা হোটেলে।

এই বৃষ্টিতে বেরিয়ে সবার জুতো আর সোয়েটার বৃষ্টির জলে পুরো ভিজে গিয়েছিল। তারপর হেয়ার ড্রায়ার দিয়ে সোয়েটার শোকানোর অভিজ্ঞতাটা বেশ মজার ছিল। ওইদিন বিকেলে বৃষ্টি থামার পর কেউ কেউ বেরিয়েছিল নিজেদের মতো, আবার কেউ কেউ হোটেলেই জমিয়ে চানাচুর মুড়ি খেতে খেতে আড্ডা মারছিল।

পরেরদিন মানে 7th April হঠাৎ খুব সকালে ঘুম ভেঙে যাওয়ায় বাইরে বেরিয়ে এক অভূতপূর্ব দৃশ্য চোখে পড়ে। দেখি যে পেঁজা তুলোর মতো মেঘগুলিকে সরিয়ে ওই দূর থেকে কাঞ্চনজঙ্ঘা পর্বতশৃঙ্গ উঁকি দিয়ে যেন সুপ্রভাত জানাচ্ছে আমাদের। তড়িঘড়ি সবাইকে ডেকে তোলা হলো। প্রায় ঘন্টাখানেক এই মনোরম দৃশ্য উপভোগ করলাম আমরা। তারপর মেঘের বুকে হারিয়ে গেল কাঞ্চনজঙ্ঘা পর্বতশৃঙ্গ। এই মেঘলা আকাশে সূর্যের দেখা পাওয়া যাবেনা বলে ভোরবেলা টাইগার হিল এ যাইনি আমরা। কাঞ্চনজঙ্ঘা দেখা দিয়ে আমাদের সেই খারাপ লাগাটা কোথাও যেন মুছে দিলো।

যাইহোক টাইগার হিল তো আমাদের যেতেই হবে plant collection এর জন্য। প্রাতরাশ সেরে আমরা গাড়ি নিয়ে বেরিয়ে পড়লাম টাইগার হিলের উদ্দেশ্যে। ওখানে গিয়ে আমরা বেশ কয়েকটি গ্রুপ ফটো তুললাম স্যার ম্যামদের সাথে আর সেলফি! সেতো গুনে শেষ করা যাবেনা। ওখানে দেখলাম একটা sunrise view tower তৈরি হচ্ছে, under construction। আমরা কয়েকজন লুকিয়ে sunrise view tower এর ছাদ থেকে ঘুরে এলাম। যদিও নিচে নেমে শুনলাম আমরা স্যার ম্যামদের চোখে ফাঁকি দিতে পারিনি। তবে এরজন্য আমরা বকা খাইনি, বরাবরের মতো আমাদের এই দুষ্টুমিকেও মাফ করে দিয়েছেন তারা।

এরপর শুরু হলো আমাদের plant collection। গাছ চেনানো তো আছেই, তার সাথে কিভাবে ওই ছোটো ছোটো গাছগুলো তুললে ওগুলো ছিঁড়ে যাবে না বা পাশের গাছগুলির কোনো অসুবিধা হবে না এবং ঠিক কতোটা পরিমাণে তুলতে হবে যাতে ওই প্রজাতিটির ভবিষ্যতে বংশবিস্তারে কোনো অসুবিধা না হয়, Biodiversity loss না হয় সব আমাদের ভালোভাবে বুঝিয়ে দিচ্ছিলেন স্যার ম্যামরা। তাই কিছু কিছু গাছ আমরা না তুলে সেগুলোর ছবি তুলে নিয়েছিলাম।

তারপর টাইগার হিল ও তার আশেপাশের এলাকা থেকে বেশ কিছু plant collect করে আমরা সিঞ্চুলে বজরংবলি দেবের মন্দিরে গেলাম। ওখানে কয়েকজন পূজোও দিলো। তারপর ভোগ প্রসাদ খেয়ে হোটেলে ফিরলাম আমরা।

সেদিন বিকেলে স্যার ম্যামদের অনুমতি নিয়ে আশেপাশের বিভিন্ন জায়গায় আমরা নিজেদের মতো করে ঘুরেছিলাম আমরা। রাতে স্যার ম্যামরা আমাদের Herbarium Preparation এর সময় plant গুলোকে কিভাবে pressing করতে হয়, তারপর কিভাবে বেঁধে রাখতে হয় এসব হাতে ধরে শিখিয়ে দিচ্ছিলেন।

পরদিন 8th April, সকাল সকাল প্রাতরাশ সেরে আমরা বেরিয়ে পড়লাম Lloyd Botanical Garden এর উদ্দেশ্যে। সেখানে আমরা *Ginkgo biloba*, herbal medicine উৎপাদনকারী *Thuja* tree, Greenhouse Conservation এ 'Bird of Paradise" plant, succulents, cactus, ferns এর sorus arrangement, circinate vernation, বিভিন্ন orchids দেখতে পেয়েছিলাম। এগুলো আমরা সবাই ক্যামেরাবন্দি করেছিলাম। Living Fossil *Ginkgo biloba* এর সম্পর্কে জানতে পেরেছিলাম আমরা। স্যার ম্যামরা আমাদের বিভিন্ন গাছ দেখাতে দেখাতে সেগুলোর ব্যাপারে অনেক information দিচ্ছিলেন । Greenhouse Conservation সম্পর্কে কিছুটা জানলেও এই ব্যাপারে কোনো Practical knowledge ছিল না। এখানে আমরা দেখলাম কিভাবে Greenhouse এ Conserve করা হয়। এছাড়াও আরো অনেক বিষয়ে সম্যক ধারণা তৈরি হয়েছিল আমাদের।

সেদিনই আমাদের ফেরার ট্রেন ছিল। মনমরা উদাসীন মুখগুলো নিয়ে গাড়িতে উঠলাম আমরা। মাঝে আমাদের একটি গাড়ির টায়ার পাংচার হওয়ায় রোহিনী তে কিছুক্ষণ অপেক্ষা করতে হয়েছিল আমাদের। ওখানে নির্মলেন্দু স্যার আমাদের সবাইকে কোল্ড ড্রিংকস খাইয়েছিলেন। তারপর আবার গাড়িতে উঠে NJP এর উদ্দেশ্যে রওনা দিলাম আমরা। স্টেশনে পৌঁছে আমরা স্যার ম্যামদের সাথে কয়েকটি গ্রুপ ফটো ও সেলফি তুলেছিলাম। বেশিরভাগ ফটো দিব্যেন্দু স্যারই তুলে দিয়েছিলেন।

কিছুক্ষণ পর আমরা ট্রেনে উঠলাম। আমাদের মন ভালো করার জন্য স্যার ম্যামরা আমাদের সাথে অনেক গল্প করছিলেন। দিব্যেন্দু স্যার আমাদের শোনপাপড়ি আর কফি খাইয়েছিলেন। এইভাবেই মজা করে রাতটা কেটে যায়। ৯ তারিখ সকালেই ট্রেন পৌঁছে যায় শিয়ালদহ স্টেশনে। ট্রেন থেকে নামার পর আমাদের প্রত্যেকেই বাড়ি ফেরার ট্রেনে তুলে দিয়ে তবেই স্যার ম্যামরা বাড়ির দিকে রওনা দিয়েছিলেন। আমরা সবাই ঠিকঠাক বাড়ি পৌঁছালাম কিনা, সবাই সুস্থ আছি কিনা সব খোঁজ নিয়েছিলেন তারা।

এভাবেই আমাদের প্রথম Excursion সম্পন্ন হয়েছিল। প্রথমবার বন্ধুদের সাথে দূরে ঘুরতে গিয়ে যেমন মজা হয়েছিল তেমনই অনেক জ্ঞান অর্জন করেছিলাম আমরা স্যার ম্যামদের থেকে। আর তার সাথে সাথেই আমাদের সঙ্গে শিক্ষক শিক্ষিকাদের সম্পর্কটাও আরও গভীর হয়েছিল। আমরা হয়তো তাদের মনে জায়গা করে নিতে পেরেছিলাম।

চতুর্থ সেমিস্টারেও আমাদের একটি Excursion হবার কথা ছিল ডুয়ার্সে। কিন্তু এই করোনা অতিমারির জন্য সেটা আর সম্ভব হয়ে ওঠেনি। টিকিট ক্যানসেল করতে হয়েছিল আমাদের। তবে এই প্রথম Excursion এর স্মৃতি আমাদের মনে আজীবন রয়ে যাবে। জীবনে হয়তো আরও Excursion হবে তবে প্রথমবারের মতো উত্তেজনা, আনন্দ হয়তো হবেনা। প্রথম অভিজ্ঞতা তো একটু অন্যরকম হয়, আর আমাদের স্যার ম্যামরা তাদের বন্ধুসুলভ ব্যবহার, স্নেহ, ভালোবাসা, জ্ঞান বিতরণের মাধ্যমে সেই অভিজ্ঞতাকে অনন্য ও অতুলনীয় করে তুলেছেন, যা আমাদের মনের মণিকোঠায় চিরকাল রয়ে যাবে।

বসন্তের কোলাখাম

-তৃষ্ণা হাজরা

দু একদিনের জন্য কোথাও বেড়াতে যেতে চান? বেশ বাড়ি থেকে সুটকেস আর গরম জামাকাপড় নিয়ে চলে যান শিয়ালদহ স্টেশন। সেখান থেকে কিছুক্ষন এর যাত্রা, নেমে পড়ুন ম্যাল জংশন। সেখান থেকে গাড়ি ধরে চলে যান কোলাখাম। কোলাখাম এমন একটি পাহাড়ি গ্রাম যেখানে কোনো মালিন্যই বুঝি নেই। 'কোলাখাম' দার্জিলিং-এ অবস্থিত একটি ছোট্ট সুন্দর পাহাড়ী গ্রাম। সেখানে চারিদিকে সবুজ আর সবুজ। দূরে অস্পষ্ট মেঘে ঢাকা পাহাড়।

সময়টা ছিল মার্চ। এই সময়টা কলকাতায় গরম ভালো না পড়লেও মোটামুটি গরমের শুরু বলা চলে। আমরা পাহাড়ে বৃষ্টির মজা নিতে বেড়িয়ে পড়লাম কোলাখামের উদ্দেশ্যে। এই সময়টা কোলাখামে বেশ বৃষ্টি হয়। সত্যিই কী অপূর্ব শোভা পাহাড়ের। রাস্তার দুধারে পাইন গাছের সারি যেন সকলের দৃষ্টি আকর্ষণ করছে। রাস্তার প্রতিটি বাঁকে যেন নতুন দৃশ্য অপেক্ষা করছে। আমরা পৌঁছানোর পরেই দেখলাম আকাশ মেঘলা। তারপরই ঝমঝম করে বৃষ্টি নামল। ঠান্ডাটাও বেশ জাকিয়েই পড়েছে। আমরা কোলাখাম কনিফারস নামক একটি হোমস্টেতে উঠলাম। তড়িঘড়ি মালপত্র নামিয়ে ব্যালকনিতে দাড়িয়ে প্রাকৃতিক সৌন্দর্য্যে মনোনিবেশ করলাম। দেখলাম দূরের পাহাড় কালো মেঘে একেবারে ঢেকে গেছে। পাহাড়ে বেড়াতে এলে যতক্ষন সূর্যের আলো থাকে ততক্ষণ পাহাড়ের সৌন্দর্য্য উপলব্ধি করা যায়, অন্ধকার নেমে এলেই ঘরবন্দী।

পরদিন ঘুম থেকে উঠে বেড়িয়ে পড়লাম। দূরের অস্পষ্ট পাহাড় বেশ ভালো দেখা যাচ্ছে, আকাশও বেশ রোদ ঝলমলে। চারপাশ যেন সূর্যের আলোয় নতুনভাবে সেজে উঠেছিল। পাখির কলরবে চারপাশ মুখরিত হচ্ছে। উড়ে বেড়াচ্ছে কতো রঙবেরঙের পাখি, সুন্দর সুন্দর সব প্রজাপতি। কতো পাখির ছবি তুলেছিলাম যেমন - সানবার্ড, রুফাসসিবিয়া, ভার্ডীটার, ফ্লাইক্ল্যাচার আরও কতো।আমাদের সেদিনকার গন্তব্য ছাংগে ফলস্ । কিছুটা যেতেই ঝর্নার জলের আওয়াজ কানে এলো। সেখানে কিছু সুন্দর মুহূর্ত কাটিয়ে ফিরে এলাম।

পরদিন লাভা-র উদ্দেশে রওনা হলাম। লাভার রাস্তাটি বেশ সুন্দর। রাস্তার দুধারে গাছপালা আর গাছপালা, বেশ ঘন জঙ্গল বলা চলে। চারপাশের দৃশ্য সুন্দর হলেও দুর্গম। সেখানকার মানুষরা বেশ পরিশ্রমী। লাভা পরিভ্রমন করে চলে গেলাম লাভা মনেস্ট্রিতে। মনেস্ট্রি অর্থাৎ যেখানে বৌদ্ধ ধর্মাবলম্বী বা লামারা থাকেন। বুদ্ধদেবকে দর্শন করলাম। তারপর আবার ফিরে এলাম হোম স্টে তে।

তারপর এলো আমাদের বাড়ি ফেরার দিন। সকালে আকাশ বেশ পরিষ্কার থাকায় হোম স্টে থেকেই কাঞ্চনজঙ্ঘা দেখা গেল। বরফে ঢাকা কাঞ্চনজঙ্ঘার উপর সূর্যের আলো পড়ায় বেশ চিকিমিকি

করছে পাহাড়ের চূড়া। সে এক অপরূপ দৃশ্য। বেড়ানোর শেষদিন প্রকৃতি এক দারুণ উপহার দিল আমাকে। প্রকৃতির মায়াজালে ঘেরা সুন্দর মায়াবী কোলাখাম ছেড়ে ফিরতে কষ্ট হচ্ছিল। গুডবাই জানিয়ে বিদায় নিলাম কোলাখাম থেকে।

বোটানির সাতকাহন

--- পূর্ণিমা ঘোষ

সালোক সংশ্লেষে হাতেখড়ি দশাচক্রের বাহাদুরি
স্লাইড সেটে নাজেহাল ক্রোমোজোম গুণতিতে ঝক্কিভারী।
টিমওয়ার্কে হার্বেরিয়াম, অনুভূতিটা আলাদাই
গাছ কালেকশন এর চক্করে অলিখিত জঙ্গল সাফাই।
বায়োকেমিস্ট্রির সমীকরণ ; ম্যাপিং সূত্র; জিনসমন্বয়
বুঝিয়ে দিয়েছে আচ্ছা মতো বোটানি মানে শুধু গাছ নয়।
দাঁত ভেঙে যাক তবুও নামকরণ চাই যথার্থ
অ্যানাটমি টের পাইয়েছে সূক্ষ্ম পার্থক্যের মাহাত্ম্য।
ব্যাকটেরিয়ার বংশবৃদ্ধি গোনা যেন আমাদের দায়
জীবাশ্মের জীবনকাহিনী ইতিহাসকেও হার মানায়।
শৈবাল ছত্রাক ছড়িয়ে ছিটিয়ে বজায় রেখেছে নিজস্বতা
বিশাল আকার শ্রেণিবিভাগে ভরিয়ে ফেলেছে বইয়ের পাতা।
ব্রায়োটেরিডোও করে চলেছে স্বমহিমায় বিচরণ
প্রযুক্তিবিদ্যাও থাবা বসিয়েছে, শোনেনি প্রকৃতির বারণ।
এক্সকার্শন এর জার্নি, সেতো স্মৃতি বোঝাই একচ্যাপ্টার
মনের ঘরে পুষে রেখে ফিরে যাওয়া যায় বারবার।
বছর ঘোরে; ব্যাচ পাল্টায় ; বদলে যায় কোলাহলের স্বর
শুধু সাক্ষী থাকে ক্লাসরুম পুনরাবৃত্ত হওয়া ঘটনার।
বিভিন্নতা স্বতন্ত্রতা সবই মিলেমিশে একাকার
বোটানি শুধু সাবজেক্ট নয়, বৈচিত্র্যের মধ্যে ঐক্যের সমাহার।।

ধর্ম

অদ্রিজা মুখার্জী

ধর্ম নিয়ে ছুটছে মানুষ,
ছুটছে সারা দেশ।
ধর্মের নামে মরছে মানুষ,
জ্বলছে সারা দেশ।।
ধর্ম কী? ধর্ম কেন?
কোথায়ে এটা বদ্ধ?
ধর্ম যত করছে মানুষ,
হচ্ছে বাগযুদ্ধ।।
জন্মাতে তুমি হিন্দু ঘরে,
পালিত হতে মুসলিম ঘরে,
এবার বোঝাও ধর্ম কী?
ধর্ম কয়ে কারে?
ধর্মের নামে দাঙ্গা হয়,
ধর্মেই আছে শান্তি ।
ধর্ম ভালবাসতে শেখাএ,
জেনেছ কি সত্যি?
ধর্ম নিয়ে হানাহানি,
ধর্ম করে কর্মহীন।
ধর্মের সব অতিচারী,
হয়ে ওঠো পরোপকারী।।
ধরমধ্বজা উঠবে যেদিন,
দেখবে এই দেশে,
মানুষ মেতেছে আনন্দেতে,
একসাথে মিলেমিশে।।
বিজ্ঞান যদি বলো তাকে,
আধুনিকতার দারুণ বাঁকে,
ধর্মে মেশাও বিজ্ঞানকে
কুসংস্কারী না থেকে।।

বর্ষণ ও অকৃতি

শ্রাবন্তী দে (প্রাক্তনী)

ঘড়িতে তখন ২.৩০; না, দুপুর নয়, রাত ২.৩০। বই পড়া, একটু লেখালিখি শেষ করে ঘুমোতে যাব। হঠাৎ ফোনের আলো জ্বলে উঠলো। তাকিয়ে দেখি সোশ্যাল মিডিয়ার নোটিফিকেশন, একখানি মেসেজ এসেছে, "Hi". অতো রাতে অচেনা অজানা ব্যক্তির মেসেজ দেখে বিরক্তই হয়েছিলাম; ভেবেছিলাম কোনো উত্তর দেবোনা, ওরকম তো কত মেসেজই আসে, সব গুলোর রিপ্লাই দিই নাকি! কিন্তু ওই যে,আমার ভাগ্যে তুই! সঙ্গে সঙ্গে আমার প্রতিবাদী মন নাড়া দিল "নাহ্, একে উত্তর দিতেই হবে। মাঝরাতে জ্বালাতন করার জন্য দু' চার কথা শোনাতেই হবে।" আমার এতো ভাবনা চিন্তার মাঝখানে আরও একটি মেসেজ এলো "Are you there?". আমার রাগ আরও খানিকটা বাড়লো। "আচ্ছা জ্বালাতন তো! দেখছে রিপ্লাই দিলাম না; তাও মেসেজ করছে! এর আজ নিস্তার নেই।"

অকৃতি :- Hello

বর্ষণ :- How are you?

অকৃতি :- I'm fine. What about you?

বর্ষণ :- ভালোই আছি।

তুমি কি করো? কোথায় থাকো?

অকৃতি:- কলেজে পড়ি। বাড়িতে থাকি।

আলাপচারিতা কালবৈশাখীর আকাশের থেকেও বেশি কালো ও থমথমে। এরই মধ্যে -

অকৃতি :- দেখুন; যদি আপনার flirting এর শখ থাকে, আপনি আসতে পারেন। আমার এত সময় নেই।

বর্ষণ :- না না,ভুল ভাবছেন। আমার সে ইচ্ছে একেবারেই নেই। তবুও বলে দেওয়ার জন্য ধন্যবাদ।

অকৃতি :- দেখুন আমি সোজা কথা সোজা ভাবে বলতে এবং শুনতে পছন্দ করি; তাই আগেই বলেদিলাম। এতে আপনি আমায় "ঠোঁটকাটা" বলতেই পারেন, কিন্তু এটাই আমি।

বর্ষণ :- বলে ভালোই করেছেন; তবে আবারও বলছি, সে ইচ্ছে আমার নেই।

অকৃতি :- থাকলেও রাখবেন না।

বর্ষণ :- হা হা।

অকৃতি :- হাসির মতো কিছু বললাম কি? দেখুন, এত রাতে একটি মেয়ে রিপ্লাই দিয়েছে বলে আপনি ভাবতেই পারেন এর সঙ্গে flirting করা যায়, তাই আগে ভাগেই বলে রাখলাম।

বর্ষণ :- আমি আবারও বলছি আমি ওরকম নই।

শুরু হলো কথোপকথন কিংবা বলা যায় প্রেমের সূত্রপাত! প্রতিবারের মতো সেদিনও আমায় ঝগড়া করতে দিসনি। বয়স তিন দশকের কোঠায় পৌঁছলেও দু'জনেরই মনটা ছিল শিশুর মতো। দু'জনেই খুব pampered হতে চাইতাম একে অপরের কাছে। যদিও তুই আমায় একটুও pamper করতিস না বলে আমার অনেক অভিযোগ ছিল।

এরপর একে অপরের ফোন নম্বর বিনিময়। শুরু হলো ফোনে কথা। দু'জনের কারো চোখে ঘুম নেই, নামমাত্র স্নান-খাওয়া। দুপুর গড়িয়ে বিকেল, বিকেল গড়িয়ে সন্ধ্যে, রাত, ভোর .....

এমনি এক ভোরবেলা, ঘড়িতে তখন ৫.২০; কথার মাঝখানে তুই হঠাৎ বললি "শক্ত করে জড়িয়ে ধর।"

অকৃতি :- আজ বলছিস "শক্ত করে জড়িয়ে ধর", শক্ত করে আঁকড়ে ধরার পর ছেড়ে পালাবি না তো?

বর্ষণ :- নাহ্! কখনও না!

অকৃতি :- বেশ, এই তবে ধরলাম; শক্ত করে জড়িয়ে!

শুরু হলো দু'জনের পথ চলা। চড়াই উতরাই পেরিয়ে একসঙ্গে পথ হাঁটা। হঠাৎ তোর ইচ্ছে হলো পাহাড়ে যাওয়ার। কিন্তু আমার পছন্দ সমুদ্র। কিন্তু, ওই যে; শেষ কথা তোকে বলতে হবে এবং সিদ্ধান্ত ও ঝগড়া, দু'টোতেই জয় তোকেই লাভ করতে হবে।

কিন্তু সেদিন এক অদ্ভুত তুই কে দেখেছিলাম! তুই আমার পছন্দে রাজি হলি। আহ্লাদিত আমি বললাম "বেশ, তবে আসছে পূর্ণিমায় আমরা সমুদ্র সৈকতে চাঁদের আলো গায়ে মাখবো।"

ভোরবেলা আমরা বেরোলাম। তখন সবে সূয্যি মামা পুব আকাশে উঁকি দিচ্ছেন। এর আগে এত ভোরে আমরা কখনও বেরোইনি। এর আগে এত ভোরে তোকেও কোনোদিন দেখিনি। সেদিন প্রথম তোর salt n pepper লুকের চুলগুলোকে সকাল বেলার সোনালী রোদ মাখতে দেখেছিলাম। খুব স্নিগ্ধ লাগছিল তোকে।

যাই হোক, আমরা আমাদের যাত্রা পথ ধরে সমুদ্রের কাছে ছুটে চলেছি আর music player এ খুব আস্তে

Beatles এবং Backstreet Boys বাজছে।

অবশেষে আমরা গন্তব্যে পৌঁছলাম। হোটেলে Check in করে তুই Receptionist কে বললি Luggage টা কিছুক্ষণ পর পৌঁছতে। Room No 303-র চাবিটা Reception থেকে নিয়ে আমার হাতে দিয়ে বললি "নে, চল"। অবাকই হয়েছিলাম; Luggage পরে পৌঁছবে, দরজা নিজেরা খুলবো! লিফটে উঠে তোকে জিজ্ঞেস করাতে তুই বললি "খামোখা দরজা খোলার জন্য কাউকে এই থার্ড ফ্লোর অবধি টেনে এনে কি লাভ?"

অকৃতি :- না, মানে। কিন্তু, Luggage?

বর্ষণ :- সামনে দেখ। থার্ড ফ্লোর এসে গেছে।

অকৃতি :- কিন্তু..

বর্ষণ :- সব "কিন্তু" পরে হবে এখন চল।

হাত ধরে টেনে নিয়ে গেলি 303 এর সামনে। তখনও আমি ধোঁয়াশায়। বললি, "নে, দরজা টা খোল। খুব tired লাগছে"

দরজা খুলেই চমকে গেলাম। "একি! আচ্ছা, এবার বুঝলাম কেনো তুই আসতে দিসনি কাউকে।" শক্ত করে জড়িয়ে ধরেছিলাম তোকে চোখ বন্ধ করে। সে যেনো এক স্বর্গসুখ! সারা ঘরময় মোমবাতি জ্বলছে আর গোলাপের পাপড়ি ছড়ানো। আর সেই গোলাপের গন্ধ সেদিন কেমন যেন মহুয়ার নেশার মতো লেগেছিল। গন্ধে মাতলাম দু'জনে। আর পেছনে বাজছে -

"যদি জানতেম আমার কিসের ব্যথা তোমায় জানতাম।"

কিছুক্ষণ পর স্নান সেরে Lunch করে তুই বললি "একটু rest নেবো, ভোরবেলা থেকে drive করে খুব tired লাগছে। বিকেল সন্ধ্যের দিকে beach এ যাবো।"

সন্ধ্যেবেলা দু'জনে beach এ গেলাম। সন্ধ্যে থেকে বেশ অনেকটা রাত কাটল beach এ। ভরা পূর্ণিমার আলোয় দু'জন দু'জনের কাঁধে মাথা রেখে অন্তহীন গল্প করতে করতে সাক্ষী হলাম জোয়ারে উত্তাল সমুদ্রের ঢেউয়ের পাড়ে আছড়ে পড়া, আবার পিছিয়ে যাওয়া।

দু'জনে ঘরে এলাম। তুই আমার হাতে একখানা খাম দিয়ে বললি "এটা আমাদের সম্পর্কের বোঝাপড়া", আর তুই চাস যেন ব্যাপারটা mutual হয়। আস্তে আস্তে খামটা খুললাম, ভেতরে একটা শক্ত মতো কার্ড -

অকৃতি :- শুভ পরিণয়, মানে বিয়ের কার্ড! কিন্তু আমাদের তো এখনও বিয়ের দিনক্ষণ কিছু ঠিক হয়নি, তাহলে তুই বিয়ের কার্ড নিয়ে এসেছিস কেনো? কার এটা?

বর্ষণ :- খুলে দেখ।

অকৃতির মনে বিরক্তি আবার সঙ্গে কিছুটা ভয়! কিন্তু ভয়টা ঠিক কি?

বর্ষণ :- আর সাতদিন পর আমার বিয়ে, বাবার বন্ধুর মেয়ের সঙ্গে। সবটা হঠাৎই ঠিক হয়েছে। আর আমি যদি বিয়েটা না করি তাহলে আমাদের deal crack করবে না। আর এই deal টা না হলে company র huge loss হবে। তাই...

এতক্ষণ যেমন ঢেউ পাড়ে আছড়ে পড়ে খানিকটা করে বালি ধুয়ে নিয়ে চলে যাচ্ছিলো, ঠিক তেমনি যেন আমারও পায়ের তলার মাটিটাও হঠাৎ করে সরে গেলো। তখন ভোর হয়ে এসেছে। Luggage গুছিয়ে বাড়ির ফেরার উদ্দেশ্যে রওনা হলাম। নাহ্, তখন আর Beatles বা Backstreet Boys নয়, তখন -

"আমার এ পথ, তোমার পথের থেকে অনেক দূরে গেছে বেঁকে।"

সবুজ প্রাণের লাগি

..........বর্ণা সাহা

বি. এস. সি ষষ্ঠ সেমেস্টার

খুব সামান্যই দাবী এদের;শুধু একটু খানি যত্ন।
না না, সন্তানতুল্য যত্ন পাবার আশায় এরা থাকে না।
তাদের আবদার করা স্নেহের পরিমানটা নিতান্তই নগণ্য।
আমাদের কাছে এর নাম পরিচর্যা,
কিন্তু ওদের কাছে সেটাই আদর।
দেখুন তো, কত অল্পেতেই খুশি ওরা;
এইটুকু ভালোবাসা দিতে
আমাদের কৃপণতা করা উচিৎ নয়।
সন্তানের জল-খাবারের খেয়াল
রাখি যেমন, ঠিক তেমনি যত্নে
ওদের জল-সারে সিঞ্চিত
করলেই ওরা খুশি।

আজকের ছোট্ট কুড়িটা
কালকের একটা পরিপূর্ণ
প্রস্ফুটিত ফুল উপহার দিতে প্রস্তুত।
সে দৃশ্য আমাদের জুড়িয়ে দেয় আঁখি,
উড়িয়ে দিতে জানে সমস্ত গ্লানি।

ভ্রমণ কাহিনী

পেত্রা ও মৃত সাগরের দেশ জর্ডান

-ধ্রুবা দাস

আমাদের পৃথিবীর সপ্তম আশ্চর্যগুলি আমাদের সত্যি অবাক ও বিস্মিত করে। এগুলি যেন আমাদের কথায় বর্ণনা করার বা চিন্তা করার একদমই বাইরে। আজ আমি যে ভ্রমণ অভিজ্ঞতা তুলে ধরতে যাচ্ছি সেটা হল জর্ডান দেশকে নিয়ে এবং এই দেশেই অবস্থান করে আছে পৃথিবীর সপ্তাশ্চর্যের একটি ‘Petra’।

২০১৭ সাল, গরমের ছুটি কাটাতে আমি আমার মা ও ভাইয়ের সাথে ঘুরতে যায় জর্ডানে। সেখানে আমার বাবা এক হসপিটালে রেডিয়োলোজি ডিপার্টমেন্টের ম্যানেজার হিসেবে কর্মরত ছিলেন। এবং সেই সূত্রেই আমাদের যাওয়া। আমরা দমদম থেকে এমিরেতস ফ্লাইটে দুবাই এবং সেখানে ৪ ঘন্টা অপেক্ষা করে সেখান থেকে ফ্লাইটে আম্মান (জর্ডানের রাজধানী) পৌঁছলাম।

আম্মান ছবির মতো সুন্দর পরিষ্কার একটি শহর, রাস্তার দুধারে সুন্দর গাছ সারি দেওয়া। আগে নাকি দেশটা পুরো মরুভূমি ছিল। কিন্তু এদেশের রাজা বিগত কুড়ি বছর ধরে গাছ লাগিয়ে পুরো দেশে জঙ্গল সৃষ্টি করেছেন এবং সেটা তো নিজের চোখের সামনে দেখতে পাচ্ছি। এখানকার বাড়ি ঘরগুলো পাথরের তৈরী তাই বাইরে ঠান্ডা বা তাপ ভিতরে প্রবেশ করে না। এখানকার মানুষদের ত্বক খুব ভালো। সম্ভবত অলিভ তেল খায় বলে। এখানকার আবহাওয়া আমার সবথেকে ভালো লেগেছে খুবই স্বাস্হ্যকর, বাইরে সূর্যের রোদ প্রখর অথচ একটুও গায়ে লাগবে না। কি সুন্দর, একটা ঠান্ডা মিষ্টি বাতাস বইছে সবসময়ই। এখানে গরমকালে রাত হয় অনেক দেরিতে। সন্ধ্যা হল সাড়ে সাতটা বেজে গেছে অথচ চারিদিকে বেজায় সূর্যের আলো। এখানে বাজার হল আলবালাত -এটা ডাউনটাউন নামে পরিচিত। এই দেশে ভালো বড়বড় সবজি চাষ করা হয়। খাবারে মশলা খুব কম থাকে। সামুদ্রিক মাছ পাওয়া যায়। রুটির প্রচলন বেশি। অত্যন্ত পুরু রুটি। জর্ডানবাসী খুব সৎ। এখানে মূলত মোটরগাড়ি ও আধুনিক বাইক চলে। এই গোটা দেশেই ট্রেনেই ট্রেনের ব্যবস্থা নেই। এই জায়গায় টেলিভিশনে মূলত আমাদের দেশের সিনেমা সিরিয়াল সব এদের আরবি ভাষায় ডাবড করে দেখানো হয়।

পেত্রা (Petra)-

রাজধানী আম্মান থেকে ২৩৬ কিমি দক্ষিণে পেত্রা অবস্থিত। এখানকার এক একটা টিকিটের দাম ৫০ দিনার (আমাদের দেশে ৫০০০ টাকা) এই জায়গায় ঘোরা, উটের, গাধার এবং খচ্চরের টানার গাড়ি পাওয়া যাচ্ছে। ফটক থেকে মূল পেত্রা প্রায় এক কিলোমিটার দূরত্বে। শুরু হল পাথরের উঁচু গিরিপথ, দুপাশে পাথরের দেয়াল এতটাই উচ্চতা বিশিষ্ট যে কোন কোন জায়গায় আকাশ দেখা যায় না। হাঁটছি তো হাঁটছি এক সময় মনে হল এই পথ যেন শেষ হবার নয় তখন হঠাৎ নাটকীয়ভাবে পথ শেষ হয়ে গেল এবং চোখের সামনে রূপ নিল পেত্রা দ্য ট্রেজারি। দুর্গম পর্বতের আড়ালে এর অনিন্দ্য সৌন্দর্য যেন লুকিয়ে ছিল হঠাৎ করে বাইরে বেরিয়ে এসেছে। বড়ো পাথর কেটে বানানো মন্দিরটা নীচের বারান্দায় ছয়টি স্তম্ভ ও দুটি মূর্তি এবং উপরের দিকে পাঁচটি মূর্তি। নীচে একটা দরজা আছে কিন্তু প্রবেশ নিষেধ। লালচে পাথর দিয়ে তৈরি বলে একে red rose city বলে। এরপর একটি মনাস্ট্রি দেখতে পেলাম হুবহু ট্রেজারির মতোই কিন্তু আকারে ট্রজারির চেয়ে বিশাল। একটা ব্যাপক বড় থিয়েটার আছে দেখলাম। খ্রিস্টপূর্ব ৪০০-২০০ পর্যন্ত পেত্রা ছিল আরবের নাবাতাইন রাজ্যের রাজধানী। একসময় এটা ছিল জনবহুল নগরী। এরাই পাথর কেটে তৈরি করে এই নগর। মন্দিরটাকে বলা হয় খাজনেত ফেরাউন। এরা প্রধান সব বাণিজ্যপথ নিয়ন্ত্রণ করতে পারত। ৫৫৫ খ্রি ভূমিকম্পে এটা ধ্বংস হয়। এটি এমন একটি জায়গা সরাসরি না দেখে তার প্রকৃত সৌন্দর্য উপভোগ সম্ভব নয়।

মৃত সাগর (Dead sea)-

পৃথিবীর সবচেয়ে নিম্নতম স্থান নামে পরিচিত এটি। এটির পূর্ব উপকূল বরাবর জর্ডান দেশ এবং পশ্চিম উপকূলে ইসরায়েল। মেন গেট দিয়ে No পর দেখলাম এখানে দুটো সুইমিংপুল আছে একটা ছোট আর একটা বড়। এখানেই একটা বাচ্চা ছেলের সাথে আমার খুব ভালো বন্ধুত্ব হয়েছে এর বয়স এক বছর নাম অ্যালেক্স, খুব কিউট আর ভীষন ভীতু কিছুতেই জলে নামবে না। এবার সিঁড়ি দিয়ে বেশ খানিকটা নীচে নেমে তবে দেখা পেলাম মৃত সাগরের ছোটবেলা থেকে পড়ে এসেছি এখানে কোনো উদ্ভিদ ও প্রাণী জন্মায় না দেখলাম সত্যিই তাই কোনো রকমের প্রাণী বা উদ্ভিদ নেই এখনে। বহু মানুষ চান করছে ডেড সি'র জলে কেউবা সারা গায়ে মাটি মেখে রোদ পোহাচ্ছে আবার কেউ জলে ভাসছে কারণ এখান কার বিশেষত্ব হল জলে কিছুই ডোবে না সবই ভেসে থাকে। আমি ডেড সি'র জলে হাত পা মুখ ধুলাম কিন্তু কিছুক্ষন পর দেখি সব জায়গায়

নুনের মতো সাদা প্রলেপ পড়ে গেছে আর এই সাগরের জল চিটচিটে খুব তাই বাইরে এত সুইমিংপুলের ব্যবস্থা তবে এর জল খুবই উপকারী ত্বকের পক্ষে।

লোহিত সাগর-

এই দেশের একদম দক্ষিণে লোহিত সাগর অবস্থিত। মেতে অনেকক্ষণ লাগবে তাই আমাদের অনেক ভোরে বেরোতে হল। পথে ওয়াদিরাম পড়ল লাল পাথরের সূদূর মরুভূমি অঞ্চল বেদুইনরা উট, ঘোড়া এবং ভেড়ার পাল চরাচ্ছে। আবার অনেক সিমেন্টের পাহাড় চোখে পড়ল গাড়ি করে সব সিমেন্ট কেটে নিয়ে যাচ্ছে। বেশিরভাগই পাহাড়ের উপর সবুজ জঙ্গল চরাই উতরাই পথ এক জায়গায় দেখলাম একধরনের ফল বিক্রি হচ্ছে লাল টকটকে মাঝারি আকারের নাম মুচমুচ খেতে খুব মিষ্টি। একসময় আকাবাতে পৌঁছালাম এটাই জর্ডানের একমাত্র সমুদ্র বন্দর এখানেই রেড সির অবস্থান। সমুদ্রের রং নীলাভ সবুজ। কূল থেকে ৫০ হাত অবধি জল কেবল হাঁটু পর্যন্ত নীচে মসৃণ বড়ো বড়ো পাথর কোন বালি বা মাটি নেই। এটা মূল সাগর থেকে সরু হয়ে এখানে এসেছে তাই এর প্রশস্ত কম। অনেকে বোটে করে ঘুরতে যাচ্ছে আমরাও উঠলাম দেখলাম এই সাগরের ঢেউ নেই আর হিংস্র প্রানীও নেই। ভোটের মেঝের মাঝখানে চৌকো কাঁচ লাগানো তার সাহায্যে সমুদ্রের বিভিন্ন মাছ, রঙিন বিশাল আকৃতির প্রবাল সব ই দেখতে পাচ্ছি। ঝলমলে আকাশ ঘন নীল জল আর দূরের সুন্দর শহর সব মিলিয়ে এক স্বর্গীয় অনুভুতি হচ্ছিল।

জেরাস-

এটি জর্ডানের সবচেয়ে বড় রোমান শহর ছিল। এখানে আছে এক উঁচু ফটক, স্তম্ভ, মন্দির। এরপর দেখলাম এক ব্যাপক বড় উঁচু স্থপতি নাম হেড্রিয়ান আর্চ। ঠিক এর পেছনে যেতে আমার সামনে এল এক বিশাল প্রাঙ্গন এবং এর চারপাশ ঘিরে পাথরের গ্যালারি এটা একটা বিশাল হিপ্পোড্রোম অর্থাৎ মল্লভূমি। ভাবলেই গায়ে কাঁটা দেয় যে শত শত বছর আগে ঠিক এখানেই গ্লাডিয়েটরা লড়ে গেছেন মানুষ বা পশুর সঙ্গে। চারপাশের অগণিত দর্শকের করতালি ও উল্লাস যেন আমিও শুনতে পাচ্ছি।

আম্মান সিটাডেল-

এটা প্রধানত বাইজেন্টাইন, মুসলিম, রোমানিয়ানদের বিভিন্ন ভাস্কর্যের ধ্বংসাবশেষ। এখানে হারকিউলিসের মন্দির আছে।

জর্ডান-ইজরায়েল বর্ডার-

প্রথমে আমরা এলাম জর্ডান রিভারের একদম উৎসস্থলে এবং এই রিভার বরাবর দুটি দেশের বর্ডার। এখানে সাধারণত কাউকে আসতে দেওয়া হয় না কারণ কিছু সন্দেহ হলেই ইজরায়েল থেকে গুলি করবে তাই পার্সপোর্ট চেক করে তারপর আমাদের গাড়ি যাওয়ার অনুমতি দেওয়া হল। তবে দেখলাম এখানকার সবাই ভারতীয়দের খুব সম্মান করে। নদীর ওপারে পাহাড়ের ধারে দিয়েই কাঁটা তারের বর্ডার এবং তারপর খেজুর গাছের জঙ্গল। পাশেই ইজরায়েল ভগবান যীশুখ্রিস্টের জন্মভূমি জেরুজালেম এর দেশ ভাবতেই কেমন রোমাঞ্চ অনুভব হল। উঁকি মারলাম যদি ওদেশের কাউকে দেখা যায় কিন্তু না, কেউ নেই। গাড়ি থামানোর চলবে না, যথাযথ স্পিড নিয়েই চলতে হবে, অগত্যা তাই করতে হল।

অ্যাজলুন দূর্গ-

এটা উঁচু পাহাড়ের চূড়ায় অবস্থিত দূর্গ বিশেষ। পাথরের তৈরি এই দূর্গের ভেতর একটা মিউজিয়াম আছে তাতে প্রাচীন অস্ত্র, পাত্র, মুদ্রা, পুঁথি বিভিন্ন ধরনের বন্দুক ইত্যাদি দেখলাম। ঘুরতে ঘুরতে দূর্গের দোতলায় এলাম, বেশ কিছু জায়গায় যাওয়া নিষিদ্ধ কারণ দূর্গের পেছনেই খাদ। দেখি যে একটা সিঁড়ি আছে তা দিয়ে দূর্গের সবচেয়ে উঁচু ছাদে যাওয়া যায় আমারা উঠলাম তবে সাবধানে দূর্গের পাথরগুলোর খুব স্লিপ। গিয়ে দেখি এখানে থেকে দূর দূরান্তে সবকিছু দেখা যায়। এখানে থেকেই গেলাম এক প্রাচীন থিয়েটারে। এটা খুব উঁচু জায়গায় তৈরি কারণ এইখান থেকেই একসাথে তিনটি দেশকে দেখা যায় ইরাক, সিরিয়া সৌদিআরব।

জর্ডান দেশ থেকে চলে এসেছি কিন্তু সেই দেশের মনমুগ্ধকর প্রকৃতি, জলবায়ু, ঐন্দ্রজাল সৃষ্টিকারী ঐতিহাসিক ভাস্কর্য নিজের স্মৃতির মণিকোঠায় বন্দি করে নিয়ে এসেছি।

সংরক্ষণ

...... অরিজিৎ দাস

(১)

সৌর বিগলিত পিন্ড শীতল হতে চাহে,
কঠিন তরল বাস্পে এ ভূধরে সঞ্জীবনী জাগে।
পঞ্চভূতে বিলীন এ বিশ্ব মোর
সবুজ চাদর গায়,
তেপান্তর ছাড়িয়ে সুগন্ধি তাহার
প্রান ভ্রমরারে যায়।
পুষ্প পত্রে সুশোভিত সুধারস টানে,
প্রাণীকূল বেড়ে ওঠে তব মাতৃস্নেহে।
শত বাহু বাড়ায়ে করে আচ্ছাদন
জীবকূল রক্ষা তার যেন জীবন সাধন।

(২)

তবু, ধীরে ধীরে ক্ষয়ে যায় সবুজ বসন খানি
নগরের পথে জন্মিল সে তো মনুষ্য নামক প্রানী।
বড়শির মতো বিঁধে যারা করে উৎখাত
ফুসফুসে কার্বন জমে, ঘটে অক্সিজেনের অভাব।
নগরায়নের যান্ত্রিক ঘূর্ণিপাকে বিধ্বস্ত উদ্ভিদকূল
কবে বুঝিবে?
তাদের মৃত্যু ও মোদের মৃত্যু দুই সমতুল ।

সবুজ বীথি

সন্তোষ কুমার জানা (প্রাক্তনী)

সেদিন নিঃসঙ্গ রাতে,

এক আমি চলি সবুজ বীথির পথ ধরে।

শহরটা স্তব্ধ, যেন লেপ মুড়ি দিয়ে শীতের উষ্ণ আমেজে মোহিত ।

শীতের হিমেল অনুভব করি সবুজ বীথির মাঝে দাঁড়িয়ে।

সত্যি তো! ব্যস্ত শহর এখন লেপের তলায়

গাছেরা যেন আমাদের সেবা ব্রতে সর্বদা প্রস্তুত,

দেখতে সরল বৃক্ষ দেবদূত ওরা।

ওদের কি মা বলেনা? যেমন মা শিশুকে বলে "রাত্রি অনেক ঘুমিয়ে পড়ো"

নাকি ওরাই সেই মা যার স্নেহ টাই স্পর্শমণি?

ভালোবাসার স্পর্শে মাটি ও অঙ্গার হয় পুষ্প খনি।

কি গ্রীষ্ম, কি বর্ষা, কিবা শীতকাল, অতন্দ্র দাঁড়িয়ে আছে সব সবুজ প্রহরি।

চারিদিকে বৃক্ষ দল বৃক্ষেরই ভুবন,

পাতা, ফুল, ফল, রেনু যেন সবই সবুজ

আশ্রিত আমি এভাবেই সবুজ বীথির মাঝে থাকি যেন চিরকাল।

হে অসীম ক্ষমা করো মানুষের যত অপরাধ ।

তিন বন্ধুর গল্প

--- স্নেহা সেন

এম. এস. সি দ্বিতীয় সেমিস্টার

সেন্ট মেরি কনভেন্ট স্কুলের তিনটে মেয়ের মধ্যে ক্লাস ফাইভ থেকে একটা মিষ্টি বন্ধুত্বের সম্পর্ক গড়ে উঠেছিল। ক্লাস ফাইভ থেকেই তিনজন একসাথে বোসত, সব কিছু কাজ একসাথে করত। ওদের নাম নন্দা, দিয়া আর রিয়া। ক্লাস টুয়েলভ পাস করে তিনজনেই শিলিগুড়ির নর্থ বেঙ্গল মেডিকেল কলেজে চান্স পেয়েছে । ওরা একটা পিজি নেয় যেখানে তিনজনে একসাথে থেকে পড়াশুনা করবে । আগস্ট মাস থেকে ওরা তিনজন একসাথে পিজি তে থাকা শুরু করল । এইভাবে দিব্বি পড়াশুনা, কলেজে আসা যাওয়া করতে করতে কি করে যে ডিসেম্বর মাস এসে গেল তারা টেরই পেলনা ।

শীতকালীন ছুটি উপলক্ষে পিজির বেশিরভাগ সটুডেন্ট ও কর্মরতা মহিলারা ঘরে চলে গেছে । কিন্তু তিনজন ঠিক করল যে ওরা ২৪শে ডিসেম্বর বাড়ি যাবে কারণ ওদের তখন ক্লাস চলছিল । ওদের কলেজের ছুটি শুরু হবে ২৪শে ডিসেম্বর থেকে সেই একেবারে ৪ঠা জানুয়ারিতে খুলবে । ২১শে ডিসেম্বর ওরা সবাই মিলে নিজের ঘরে যখন পড়াশুনা করছিল তখন ঠিক রাত ৮ টার সময় হঠাৎ একটা দমকা হাওয়া ঘরের ভেতর প্রবেশ করে এবং তারপরেই সাথেসাথে লোডশেডিং হয়ে যায় । দিয়া তখন মোমবাতি আর দেশলাই কাঠি খুঁজছে । অন্ধকারে কিছুই দেখতে পাচ্ছিল না ওরা। ঠিক এমন সময় হঠাৎ ওদের ঘরের দরজাটা নিজের থেকেই খুলে গেল। আর একটা হাসির আওয়াজ ভেসে এলো। ওদের ঘরে ঢুকে যেন কে হাসছে ! সবাই সবাইকে শক্ত করে জড়িয়ে ধরলো। খুব ভয় পেয়ে গেল ওরা। এভাবেই হাসিটা ৫ থেকে ১০ মিনিট থাকার পর আর হাসির আওয়াজ শোনা গেল না। হাসি বন্ধ হল এবং ঠিক তখনই কারেন্ট ও চলে এলো। এই কথাটা ওরা কাউকে জানতে দিল না।

ঠিক তার পরের দিন সকালে রিয়া এক জনের সাথে কথা বলতে নীচে গেল। দিয়া বাথরুমে আর নন্দা তখনও ঘুম থেকে ওঠে নি। রিয়া নীচ থেকে ওপরে উঠে দেখে ওদের ঘরে টেবিলের ওপর চা বিস্কুট তিন জনের জন্য রাখা আছে। দিয়া বাথরুম থেকে বেরিয়ে চা দেখে বলল - রিয়া তুই কি এই চা-টা নিয়ে এলি? রিয়া বলল না। দিয়া জিজ্ঞেস করল, তাহলে কি মাসি দিয়ে গেছে? রিয়া বলল আমি জানি না, তবে হতে পারে। আমি তো দরজাটা ঠেসিয়ে দিয়ে গেছিলাম, হয়তো তার জন্যই ভেতরে ঢুকে দিতে পেরেছে। দিয়া বলল জিজ্ঞাসা করবি মাসিদের, তখন রিয়া বলল দূর ছাড়তো, এমনিতেই খুব চা খেতে ইচ্ছে করছে - খেয়েনে । চা খাওয়ার পর কলেজে বেরোনোর সময় ওরা মাসিদের জিজ্ঞাসা করল, তোমাদের মধ্যে কি কেউ আমাদের ঘরে চা রেখে এসেছিলে? সবাই বলল না, আমরা তোমাদের ঘরে কেউ যায়নি। সেদিনও ওরা কাউকে কিছু বলল না ।

তার পরের দিন সকালে ওরা তিনজনে মিলে ঠিক করল যে ওদের তো এবার কলেজের ছুটি পরে যাবে, আবার অনেকদিন পর দেখা হবে তাই ওরা রাত্রিবেলায় ফ্রাইড রাইস আর চিলি চিকেন খাবে। ওরা ঠিক করল কলেজ থেকে ফেরার পথে খাবার কিনে নিয়েই ঢুকবে। এই কথা ঠিক করে ওরা তিনজনে কলেজে চলে গেল। কলেজ থেকে ফিরে এসে ওরা ওদের ঘরের লাইট জ্বালাতেই অবাক হয়ে গেল ! কে যেন ফ্রাইডরাইস আর চিলি

চিকেন প্লেটে করে ওদের ঘরে টেবিলের ওপর সাজিয়ে রেখে গেছে। এটা দেখার পর ওরা তিনজনে মিলে ঠিক করল যে, এই এতদিন ধরে যা যা ঘটনা ঘটছে সব কিছু ওরা পিজির মালিক কে জানাবে আর এই পিজিটা ছেড়ে দেবে। পরের দিন সকালে ওরা তিনজনে এই ঘটনা গুলো মালিক কে বলতে যাবে, ঠিক এমন সময় একজন মাসি ওদের তিনজন কে ডেকে জিজ্ঞেস করল যে - তোমরা তিনজন এত সকাল সকাল কোথায় যাচ্ছো ? তখন রিয়া বলল আমাদের ঘরে ভূতের উপদ্রব শুরু হয়েছে ।

একদিন দেখি আমাদের ঘরে চা বিস্কুট রাখা - অথচ সেদিন আমাদের ঘরে কোন মাসি চা বিস্কুট রেখে আসেনি আর আমাদের তিন জনের মধ্যে ও কেউ ঘরে চা বিস্কুট নিয়ে যায়নি। কিন্তু সেদিন আমাদের ঘরে সকালে চা বিস্কুট রাখা ছিল। আর কালকে কলেজ থেকে ফিরে এসে নিজেদের ঘরে আলো জ্বালাতে অবাক হয়ে যায়! কে যেন আমাদের ঘরে ঢুকে আমাদের তিন জনের জন্য প্লেটে করে ফ্রাইড রাইস আর চিলি চিকেন সাজিয়ে রেখে গেছে । অথচ আমাদের কাছেই চাবি ছিল। তাই আমরা ঠিক করেছি যে এই পিজির মালিক কে আজ কে আমরা আমাদের সাথে ঘটে যাওয়া সমস্ত ঘটনা জানাবো এবং আমরা তিনজন এই পিজিটা ছেড়ে দেবার সিদ্ধান্ত ও নিয়েছি।

তিনজনের মুখ থেকে সব কথা শুনে মাসি ওদের বলল - পিজি ছাড়ার কোন দরকার নেই । ওটা আসলে একজন মাসির কান্ডকারখানা। তার নাম ঝর্না। আজ থেকে চার বছর আগে সে এখানে রান্না করত। এখানে যারা থাকত তাদের প্রত্যেক সপ্তাহে তিনদিন নতুন নতুন রান্না করে খাওয়াতো। তার রান্নার হাত ছিল খুব ভালো। তাই তাকে সবাই খুব ভালোবাসত। হঠাৎ একদিন রান্না করার সময় সিলিন্ডার বার্স্ট হয়ে তার মৃত্যু হয়। ঘটনাটা ঘটেছিল ২১শে ডিসেম্বর। প্রত্যেক বছর এইসময় সে এখানে আসে আর এই পিজি তে যারা থাকে তাদের সবার জন্য নতুন নতুন রান্না করে সবার ঘরে রেখে দিয়ে আসে। প্রত্যেক বছর এই সময়ে তিনটে দিন ও এরকমটাই করে থাকে। সবাই ব্যাপারটা জানে তাই আর কেউ ভয় না। ও কারোর কোন ক্ষতি করে না।

এসব কান্ডকারখানা দেখে এখানকার সবাই বুঝতে পারে যে এগুলো সব ঝর্না মাসিরই কার্যকলাপ। তোমরা তিনজন এখানকার নতুন, তাই এসব দেখে ভয় পেয়ে গেছিলে। মাসির কাছ থেকে সব কথা শুনে ওদের ভয় কেটে যায় এবং তখনই সিদ্ধান্ত নিয়ে নেয় যে আর পিজি ছাড়বে না। এরপর ওদের কলেজে ছুটি পরে যাওয়াই তিনজন যে যার ঘরে চলে যায়।

উদ্ভিজ্জ

ইন্দ্রানী মুখোপাধ্যায়

(প্রাক্তনী বি. এস. সি অনার্স)

1. আজকাল মাথার পাশে এক অতিলৌকিক জানলা জেগে থাকে। জানলার কলকা টানা গ্রীল গ্রীলের ওপারে আম কাঁঠাল নারকেল গাছ, আর তাদের প্রলম্বিত বিচ্ছুরনের সবুজ। কখনো কখনো এখানে শুধু মেঘ --- সেই ধূসর সুদূর শ্যামলীমা মাখা মেঘের কাজল ছুয়ে ছুয়ে যায় গন্ধরাজের পাতা, ক্যাকটাসের কন্‌টুর। জানলাটা ক্রমাগত লৌকিক থেকে অতিলৌকিক বা বোধগামী থেকে দেবতাগামী হয়ে চলেছে। আমরা এখন বন্দী,আমরা এখন পৃথিবীর গভীর অসুখের বন্ধু।
2. এখানে মাঝে মাঝে বৃষ্টি নামছে অঝোর বৃষ্টি। এরকম বৃষ্টিতে সাজিয়ে রাখা তথ্যাদি ভিজে যায়। জানলাটাকে মাঝেমধ্যে ল্যাবরেটরির জানলা মনে হয়। জানলার পাশে যজ্ঞশালা। ধাবমান জীবনের গতিকে স্তব্ধ করে দিয়ে কোন প্রকার পরীক্ষায় মগ্ন পৃথিবীর আত্মা। মৃত্যুর বেদনা ও স্থায়িত্বের আনন্দের সমান্তরাল দুটি স্পেকট্রামের মধ্যিখানে একটু একটু করে সুস্থ হয়ে উঠছে পৃথিবী। আরেকটু সবুজ হয়ে উঠছে রোজ।
3. গতি থেমে যাওয়ার পরে শুধুমাত্র ঘাস গজাচ্ছে চারপাশে। নিটোল সবুজ ঘাস। এরকম ঘাস দেখলে শুকিয়ে আসা অশ্বক্ষুরাকৃতি হ্রদ এর চর মনে পড়ে। এরকম ঘাস আরো ঘন হলে মনে হয় হিমাচলের কোল। জলা পাহাড়ের রাস্তা ধরে যে মেয়েগুলো ঘুরে বেড়াতো তারা দেখেছিল এরকম ঘাস। ঘাসেদের কি ভালোবাসা যায়? সবুজের কতগুলো শেড তুমি আমায় খুঁজে এনে দিতে পারো? আদিগন্ত বিস্‌তৃত ঘাসেদের চরাচরে দু-একটা কাশফুলের দোলা দেখে কেউ কি হঠাৎ সবুজ ভালোবেসে ফেলতে পারে? ঘাস ভালোবেসে কেউ কি ভালবাসতে পারে উদ্ভিদবিদ্যাকে? আমার চেতনা জুড়ে হাজার হাজার সবুজের সমারোহ। কেউ কি সত্যিই পারে ভালোবাসার বোধ তার রঙ তার গতি তার চাওয়া ঠিক করে দিতে? উদ্ভিদবিদ্যার জটিল গবেষণা তার অধ্যাবসায় প্রগাঢ় তথ্যের আশেপাশে কাজলের মতো নীল মেঘ মেখে কোথাও কি ঘুরে বেড়ায় না ঘাসেদের ভালোবাসা? কে বলতে পারে কোন মাতাল জঙ্গলকে ভালোবেসে, কবেকার মখমলি ধানক্ষেত ভালোবেসে,কেউ উদ্ভিদবিদ্যা ভালোবেসেছিল? গ্রিলের কলকাপাড়ে আজকাল এরকম ঘাসের মতো নমনীয় কিছু

প্রশ্ন ঘোরাফেরা করে। কিছু আবছা স্মৃতি তাদের ভালোবাসা নিয়ে ঘোরাফেরা করে। জানলার এপারে ক্রমশই ভালোবাসার ল্যাবরেটরি গজিয়ে উঠছে।

4. ক্রমশ প্রসারিত হচ্ছে মহাজগৎ। কসমিক ফ্যাব্রিকে নকশী কাথার মত গল্পবুনছে চেতনা। আলোর আদি থেকে অন্ত পর্যন্ত খেলে যাচ্ছে সময়েয়ের ঢেউ। বোকা প্রেমিকার মত চেতনা হেরে যাচ্ছে চতুর্থ ডায়মেন্সনের খেলায়। তরঙ্গধর্মী মহাবিশ্বের নিখুঁত ছন্দ মায়াজাল এঁকে যায় শুধু দৃষ্টিপথে। হে মহাপ্রাণ ওঠো জাগো, প্রস্ফুটিত কর কুলকুণ্ডলিনী সহস্রধারা। কিছু নেই কিছু নেই এ মহাশূন্যে। জীবনের স্থূলতা শুধু অকারণ টেনে নিয়ে যায় মায়া গোধূলির দিকে। কমলা গোলাপি আলোয় ভরা গোধূলি। তার নিচে বিভ্রান্ত সবুজ। নেশাগ্রস্ত আবেশে পলক ফেলতে ফেলতে অবচেতনে নামে সন্ধ্যা। এবারে আঁধার ঘন হচ্ছে। গুল্ম যুগ জেগে উঠছে মাথার ভিতরে, শ্যাওলা গজাচ্ছে চারপাশে। ঘনীভূত রহস্যের মতো ঘন সবুজ শ্যাওলা। কিছু কাষ্ঠল লতা বেয়ে আসছে জানলায়। তীব্র থেকে তীব্রতর হয়ে উঠছে মহা বটবৃক্ষের মৃত্যুর হাহাকার। বড় গাছের যে কোনো বিকল্প হয় না... তবে কেন এই মৃত্যুবোধ... কেন এই বিমোহিত ভালোবাসা? ক্রমাগত অস্থির হয়ে হাতড়ে বেড়াচ্ছি চারপাশ। রোজ একটু একটু করে আমার কাছ থেকে যতই দূরে সরে যাচ্ছে উদ্ভিদবিদ্যা ততই আমার দেওয়াল জুড়ে গজিয়ে উঠছে আরও দু একটা শ্যাওলা। টবের মাটিতে গজাচ্ছে আরো কয়েকটা ক্যাকটাস। বাগানে শিউলি শরৎ। লতা,গুল্ম,বৃক্ষের শিকড় বাড়তে বাড়তে উঠে আসছে গলা পর্যন্ত। আরো দু-একটা ভালোবাসা জন্মাচ্ছে কাশফুলে,পদ্মের মৃণালে--- মৃনাল জড়িয়ে উঠছে পদ্ম গোখরো... প্রিয় সর্পিনী। কচুরিপানার ফুলের বেগুনি আভার ভিতরে ঘন নীল থেকে দু এক ছিটে হলুদ ক্রমাগত অস্থির করে তুলছে আমার চেতনাকে। ভাঙ্গা দেওয়ালে গজিয়ে ওঠা নিশিপদ্ম একটু একটু করে গিলে নিচ্ছে অপ্রয়োজনীয় অস্তিত্ব । সময়ের নাভিপদ্ম এক অনাদি বিস্তৃত কারাগার।পার্থিব শরীরকে জড়িয়ে ফেলছে লক্ষ-লক্ষ সবুজ লতা। মহীরুহরা ডাক দিচ্ছে অনাবিল সহজ সত্য কে খুঁজে পেতে। আমি কে কোথা থেকে এসেছি কোথায় যাচ্ছি? এই মহাবৃক্ষ জানে সবকিছু... চারপাশ থেকে নীলাভ সবুজ জঙ্গল একটু একটু করে এগিয়ে এসে ঢেকে ফেলে আমার বাড়ি, তারপর আমার ঘর, তারপর আমার বোধ। সমাহিত হয়ে বসি শূন্যতার কাছে। কালের কপোল থেকে যে আনন্দ সমুদ্র বয়ে গেছে মানব চেতনার দিকে তারই উৎস জুড়ে দেখি অঙ্কুরোদগম ঘটছে সত সহস্র বীজের। সেইখানে পথ চলা শুরু ভালোবাসার...।

5. খুব পুরোনো কোনো বাদলা রাতের পরে উদ্ভিজ্জ ভোর হয় এক ছোট্ট মেয়ের । নদীর কিনারে লাল ভেরেন্ডা, শীষ পালং আর আটশট্টির মেলা...সে বড় ভালোবেসে হাত বুলিয়ে দিচ্ছিল নরম কচি ঘাসেদের গায়। সহজ পাঠ হাতে নিয়ে সে নদীতীরে বসে পড়ে।

"কাল ছিল ডাল খালি,
আজ ফুলে যায় ভ'রে।
বল্ দেখি তুই মালী,
হয় সে কেমন ক'রে।

গাছের ভিতর থেকে
করে ওরা যাওয়া আসা।
কোথা থাকে মুখ ঢেকে,
কোথা যে ওদের বাসা।

থাকে ওরা কান পেতে
লুকানো ঘরের কোণে,
ডাক পড়ে বাতা সেতে
কী ক'রে সে ওরা শোনে।

দেরি আর সহে না যে
মুখ মেজে তাড়া তাড়ি
কত রঙে ওরা সাজে,
চ'লে আসে ছেড়ে বাড়ি।"

সাদা দাড়ি আলা দাদুটা কেন যে কিছু খুলে বলেনা! বড় হলে গাছেদের কথা পড়বে মেয়েটা। কেউ কি নেই যে তাকে শিখিয়ে দিতে পারে গাছেদের ভাষা? কেউ কি দেখিয়ে দিতে পারে না সেই পথ যেপথে ফুলেরা যাওয়া আসা করে?

Introducing The New "ME"

Barna Saha

(B.Sc. Sem VI)

I saw 'them' changing
With time...
I saw 'them' misbehaving
With me...
I saw 'them' showing
Selfishness to me...
I saw 'them' being happy
To criticize me...
I saw 'them' forgetting
Me when I need 'them'...
I saw 'them' planning
For a trap of danger for me.

I saw 'them' rewarding
Me with tears of pain...
I saw 'them' showing
The bitter truth, the bitter destiny
Of all caring, all affections...
I saw my entity achieving
A lot of lessons from
Their ignorance.

One day, I surprised 'them'
With my new version...
No old weak features
Were present there...
I stopped getting emotional,

I started handling every situation

Wisely and carefully.

I forgot what I was,

I became familiar with the ‘’New Me’’.

Unbelievably I noticed ‘them’

Hesitating before hurting me

In fear of happening boomerang.

How strange!! Isn’t it?

If you’re one of that so called ‘them’

You shouldn’t ask me , cause

You’re the creator of the “New Me”.

-

বিদায়বেলা

--- পূর্ণিমা ঘোষ

এম. এস. সি,২য় সেমিস্টার

এবার তোরা অন্য ঘাটে ভিড়িয়ে দিবি তোদের তরী,
সাফ্যলের পথে এগিয়ে যা এই কামনাই করি।
নতুন স্রোতে গা ভাসাবি নতুন কোনো সুখে,
জীবন যুদ্ধে জয়ী হয়ে ফিরিস যেন হাসিমুখে।
জীবনের সূচিপত্রে একটা অধ্যায় শেষ হল এবার তবে,
পাঠ যদি বা ভুলেও যাই সারাংশ তো মনেই রবে।
'টাচ্'-এ থাকবো প্রতিশ্রুতি টা সময় মিথ্যে করে দেবে,
সময়ের ছন্দেই বইবে জীবন অতীত টাই শুধু পড়ে রবে।
ভালো থাকিস ;সুস্থ থাকিস ;সময় এসেছে নেওয়ার বিদায়,
কখনো আবার সুযোগ পেলে আড্ডার ছলে,
স্মৃতিচারণ ই শুধু করবো নাহয়।

ART WORK
&
PHOTOGRAPHY

ART WORK-I

DOODLES
&
MANDALA

1st

ASHIMA BISWAS
(P. G. SEM-IV)

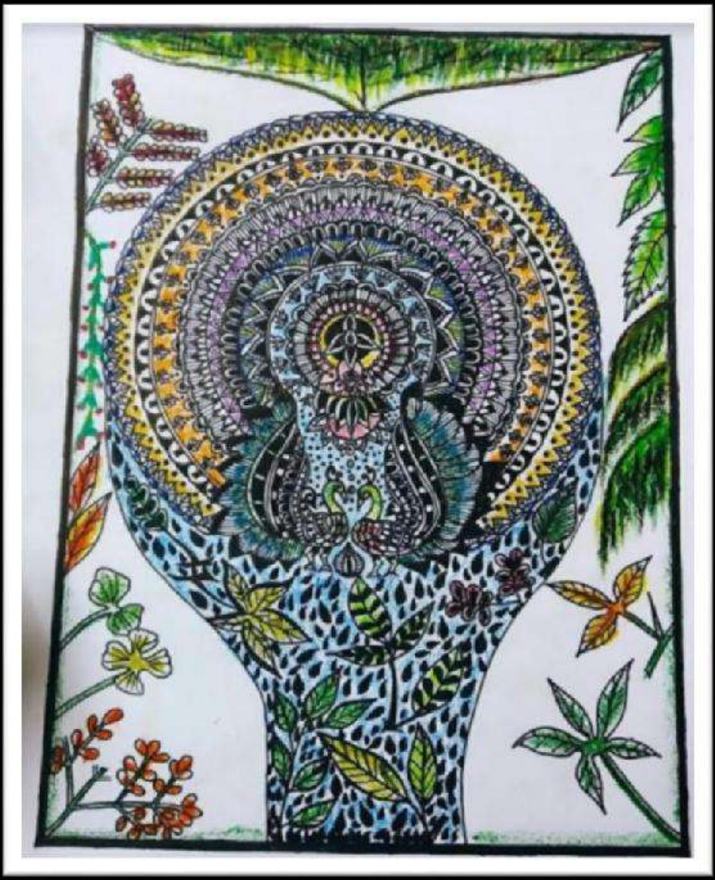
"Plants can create its own art"

Joint 2nd

SAMEMA AKHTER (P.G. SEM-II) ***"Bliss in Darkness"***

Joint 2nd

ARCHA BHATTACHARYA (P. G. SEM-II) ***"Undersea"***

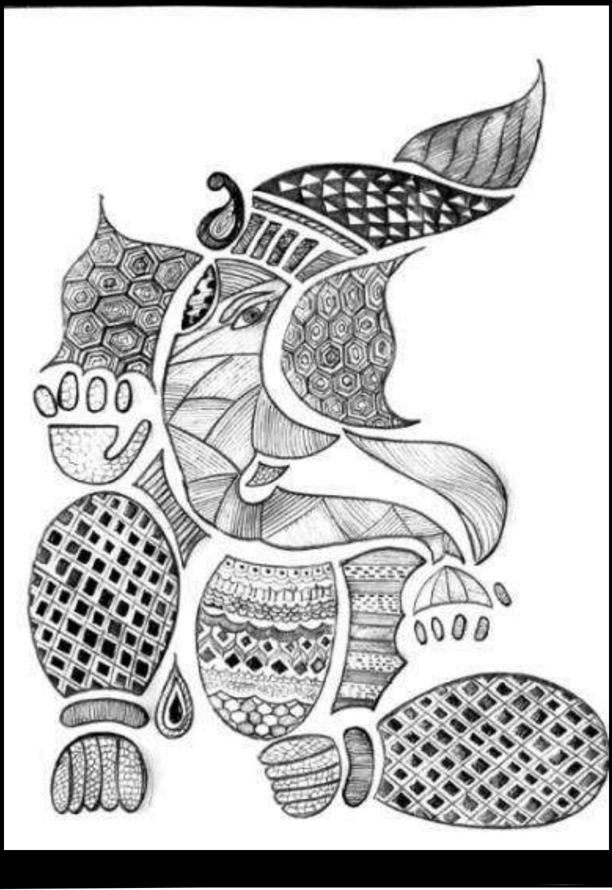


Joint 3rd

ADRIJA MUKHERJEE (P.G. SEM-II)
"Nature is present in its own creativity"

Joint 3rd

ANKITA PAUL (U. G. SEM-II)
“Plant atree and hope for future”



NAMRATA SARKAR (P. G. SEM-II)
“GANESHA”

“PHOTGRAPHY IS THE ART OF MAKING MEMORIES TANGIBLE” -DESTIN SPARKS

PHOTO GALLERY-I

JOINT 1st

"Let it fly in shine"
By ASHIMA BISWAS
(P .G. SEM-IV)

"Wasp"
By AKASH DEY (U. G. SEM-VI-BIO GENERAL)

“Natural signs of arrival of Maa Durga”

by DEBRAJ CHAKRABORTY (P. G. SEM-II)

Joint 2nd

“DRAGONFLY”

By AKASH DEY (U. G., SEM-VI-BIO GENERAL)

Joint
3rd

“Strings of Light”

By DEBRAJ CHAKRABORTY (P. G. SEM-II)

“Taste of Nectar”

**By ARCHA BHATTACHARYA
(P. G. SEM-II)**

Joint
3rd

“Gogonchumbi”

By ASHIMA BISWAS (P. G. SEM-IV)

SCIENTIFIC SNAP SHOTS

JOINT 1st

“Flower of *Andrographis paniculata*”

By RAJIB NARU (P. G. SEM-II)

“Nannandrium of *Oedogonium*”

By PRITIKANA SINHA (P. G. SEM-II)

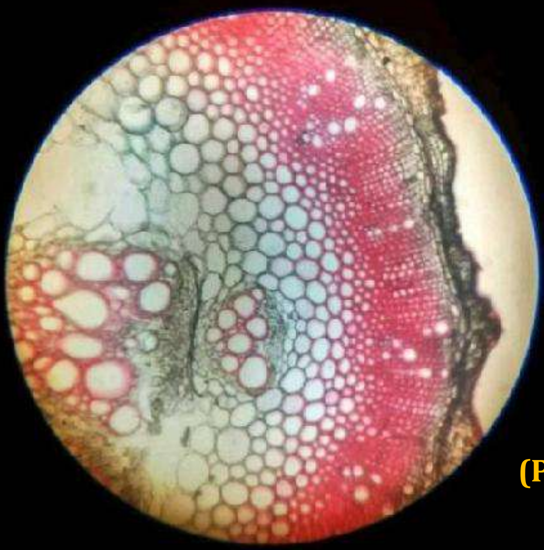
“Dacryopinax sp.”

By PRITIKANA SINHA
(P. G. SEM-II)

Joint
2nd

"Life in the Sunderbans"

By DEBRAJ CHAKRABORTY (P. G. SEM-I)



"T.S. of *Boerhaavia stem"*

By ASHIMA BISWAS

(P. G. SEM-IV)

"Bauhinia flower"

By RITIKANA SINHA
(P. G. SEM-II)

Joint
3rd

“Tremella sp.”

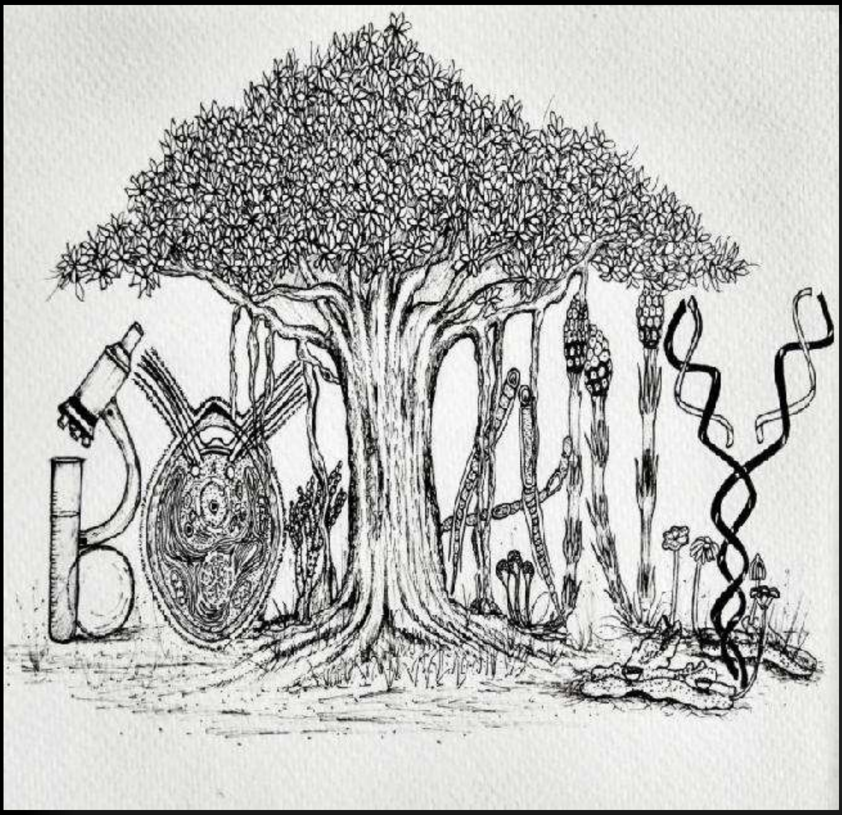
By DEBRAJ CHAKRABORTY (P. G. SEM-II)

“Daldinia sp.”

By DEBRAJ CHAKRABORTY (P. G. SEM-II)

ART WORK-II

SKETCHES & PEN ART



1st

"Botany"

By SAMEMA AKHTER
(P.G SEM-II)

Joint
2nd

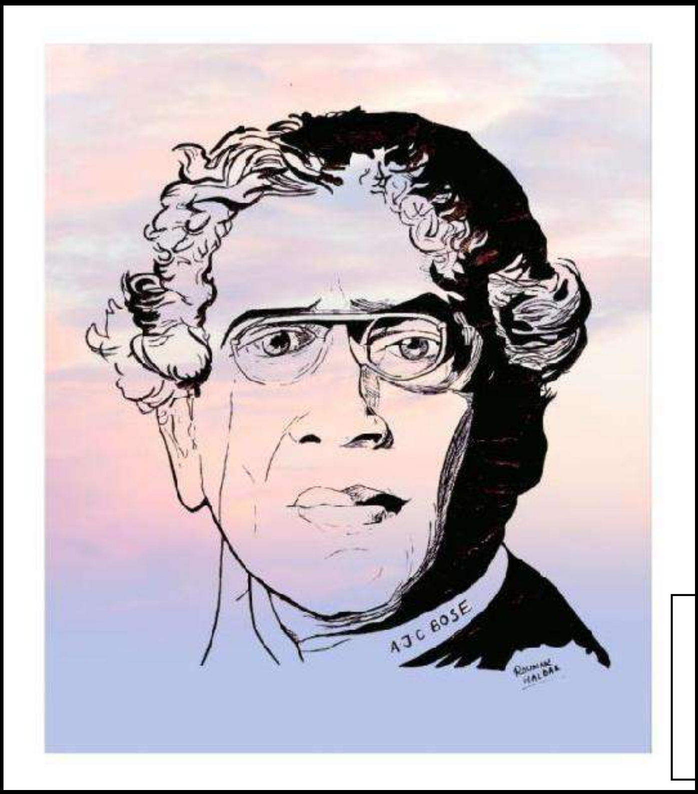
"Heart of Flowers"

By *SAMEMA AKHTER*
(P.G SEM-II)

Joint
2nd

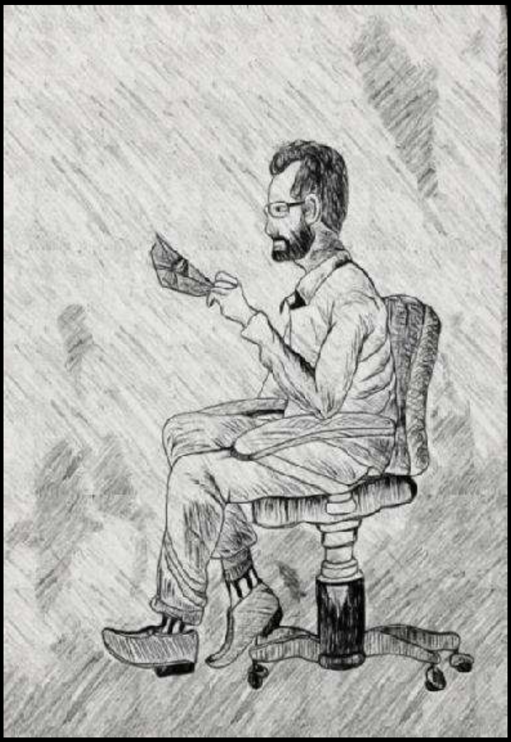
“Bonding with nature”

by ANKITA PAUL (U.G. SEM-II)



“Sir J.C. Bose”

By ROUNAK HALDAR
(U. G. SEM-IV)



“Loneliness”

By TAMAL DAS (U. G. SEM-VI)

Joint
3rd

“The unbreakable bond”

By BARNA SAHA (U.G. SEM-VI)

“Sunshine Woman”

By PRATYUSHA DEB (U.G. SEM-IV)

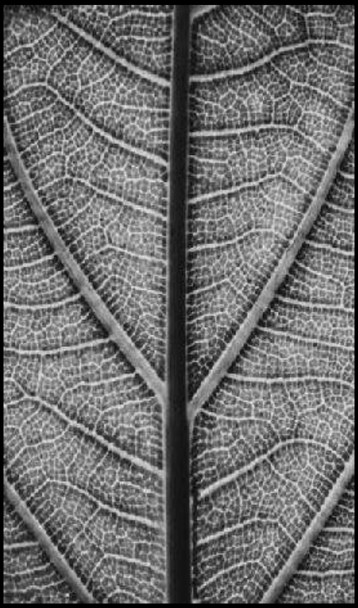
PHOTO GALLERY-II

PRITIKANA SINHA – P.G SEM-II

NAMRATA SARKAR – P.G.SEM-II

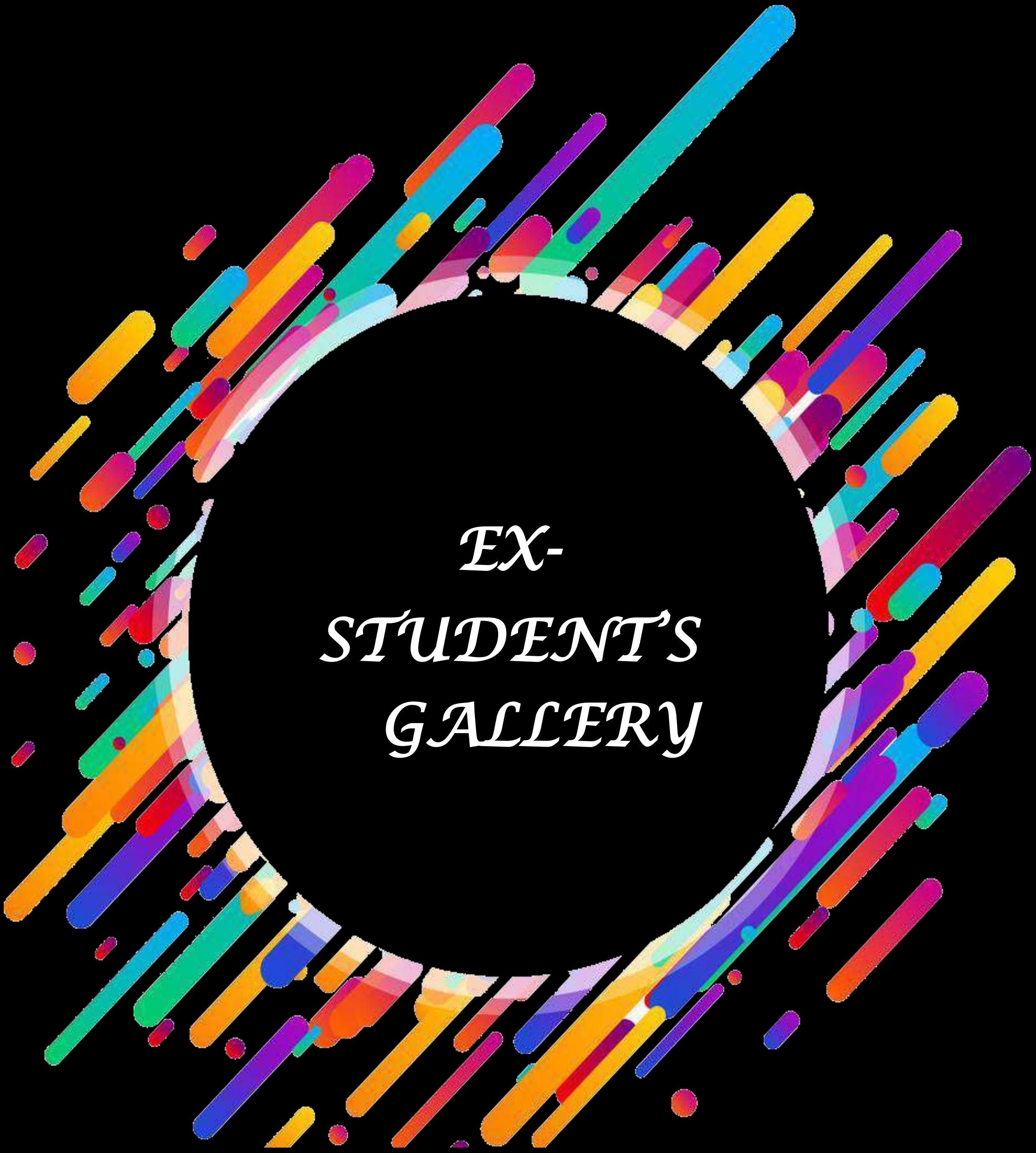
PRITIKANA SINHA – P.G SEM-II

SAMRIDHDHA BISWAS – U.G.SEM-IV



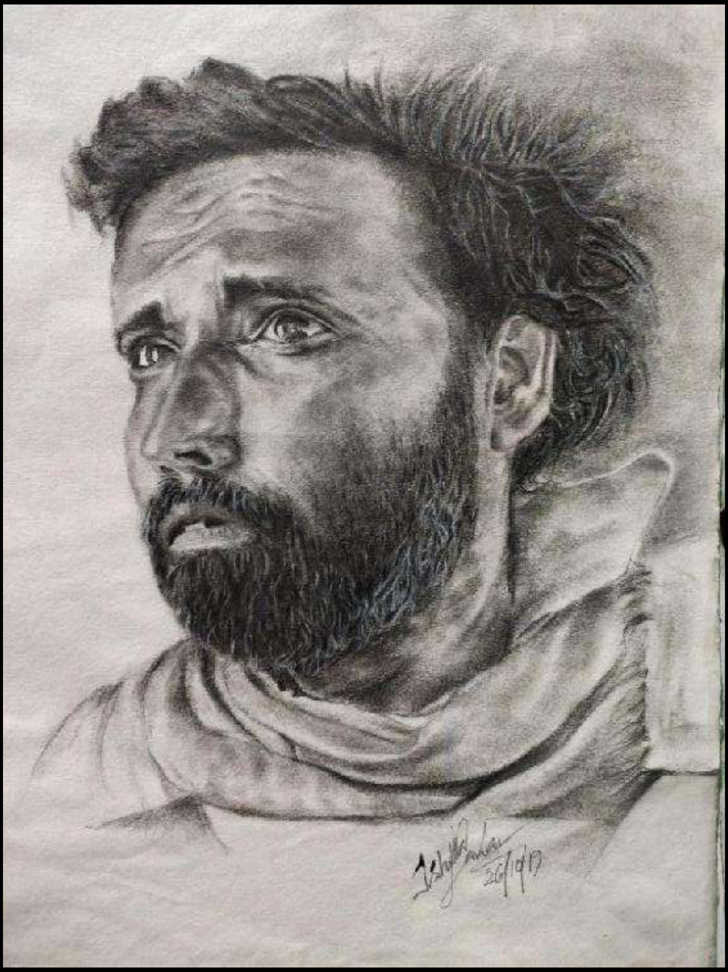
ASHIMA BISWAS – P.G.SEM-IV

AKASH DEY – U.G SEM-VI-BIO GENERAL



EX-STUDENT'S GALLERY

RONI JAVED – EX STUDENT (U.G)



ISHITA SARKAR – EX STUDENT (P.G)

MAYURIKA DAS – EX STUDENT (P.G)

SREETAMA RAY-EX-STUDENT (U.G)

INDRANI MUKHERJEE – EX STUDENT (U.G)

MAYURIKA DAS – EX STUDENT (P.G)

RONI JAVED – EX STUDENT (U.G)

SANDIP SINGH – EX STUDENT (U.G)

ISHITA SARKAR – EX STUDENT (P.G)

MOULI NAHAR – EX STUDENT (P.G)

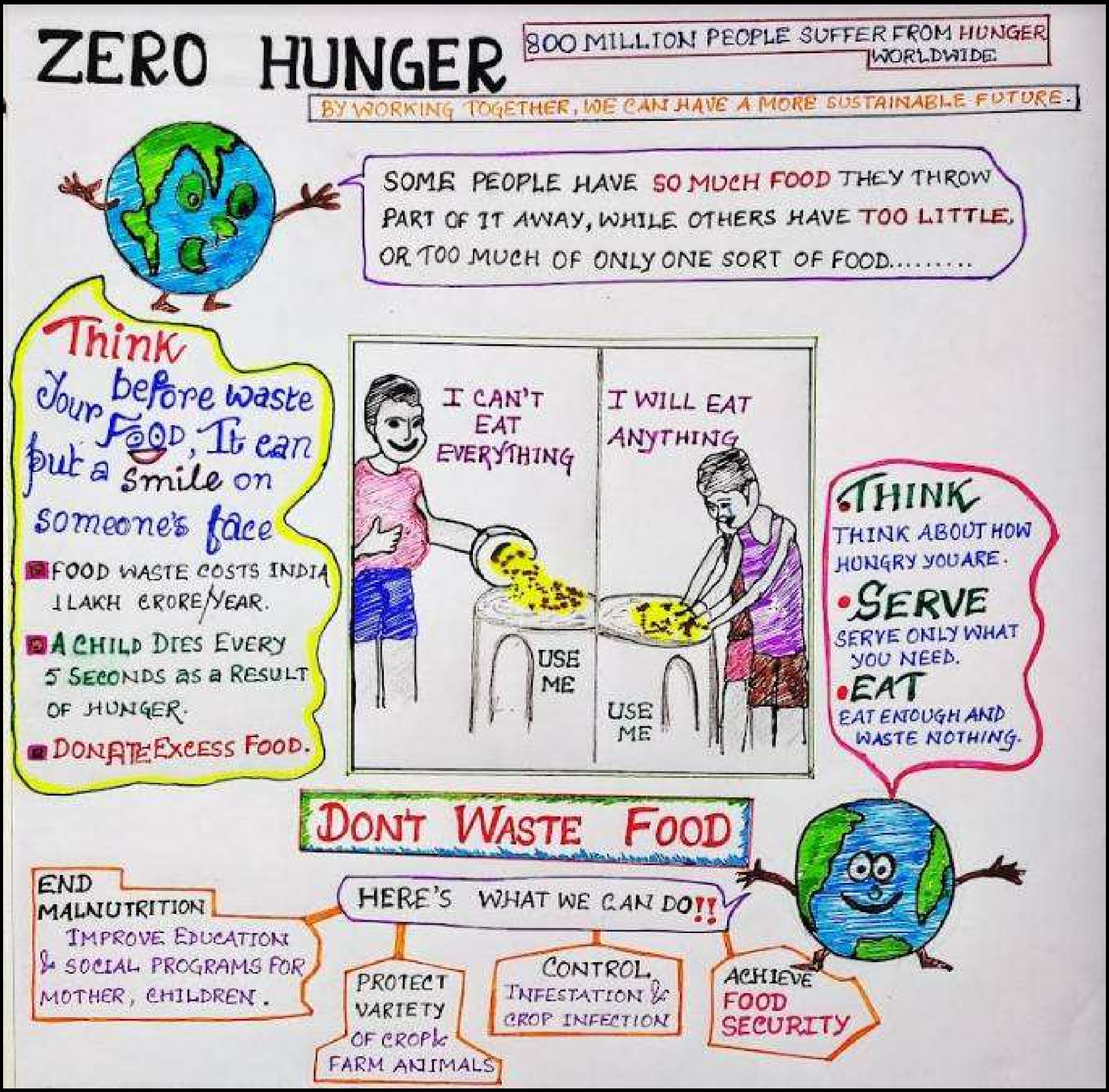
MOULI NAHAR – EX STUDENT (P.G)

MOULI NAHAR – EX STUDENT (P.G)

MOULI NAHAR – EX STUDENT (P.G)

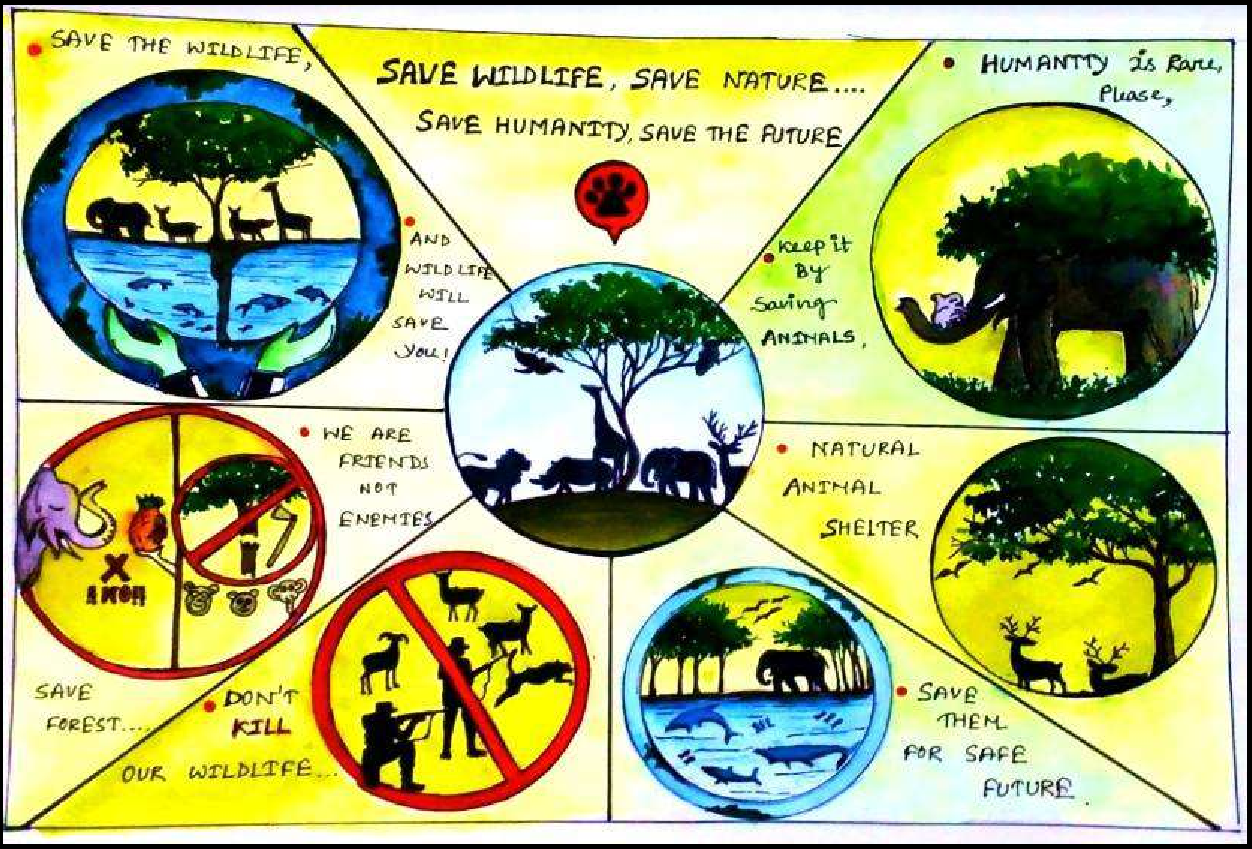
POSTER SECTION

1st PRIZE



PRITIKANA SINHA, M.SC. SEM 2

2ND PRIZE

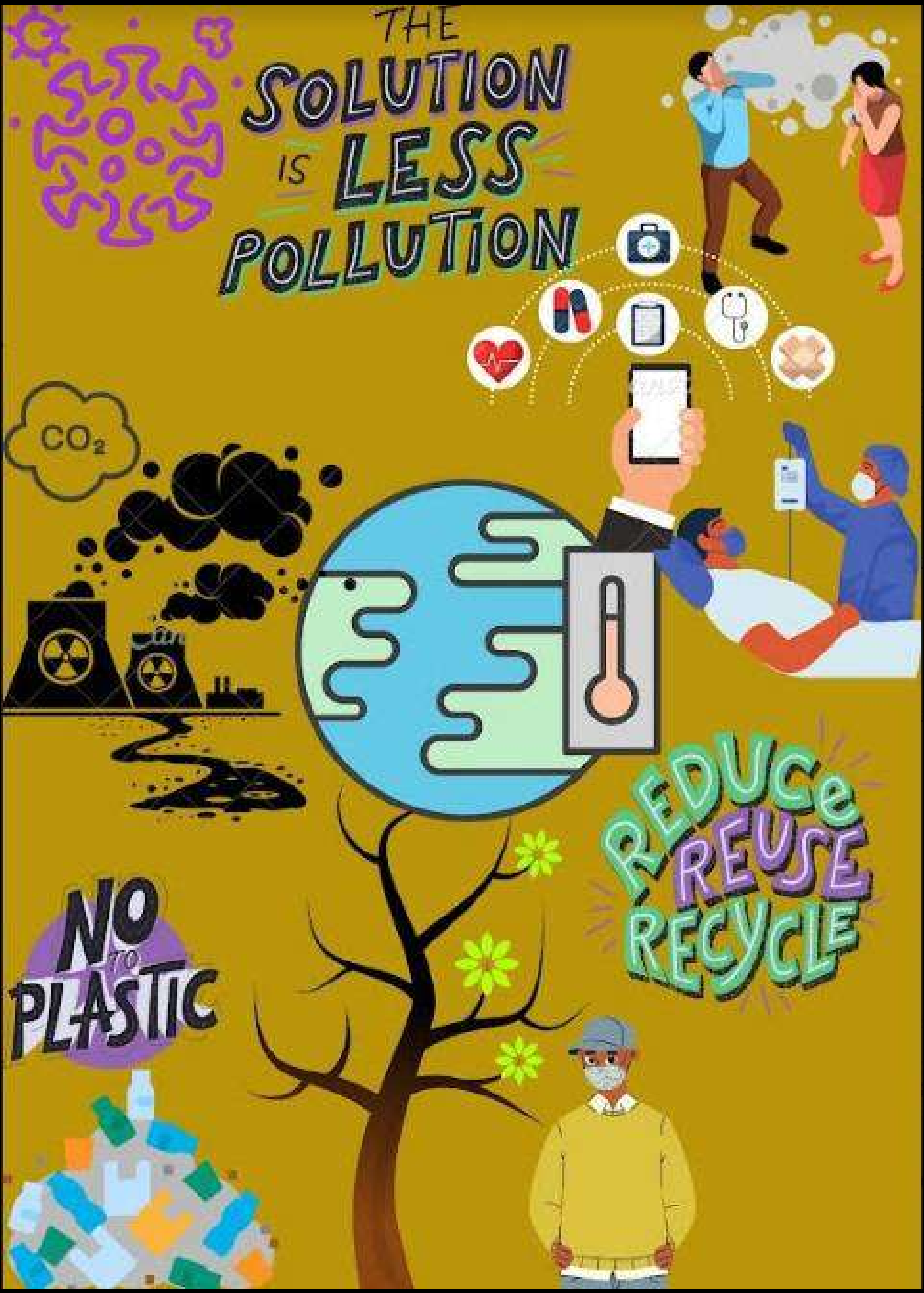


ANKITA PAUL, B.SC. SEM 2

3rd PRIZE (JOINT)

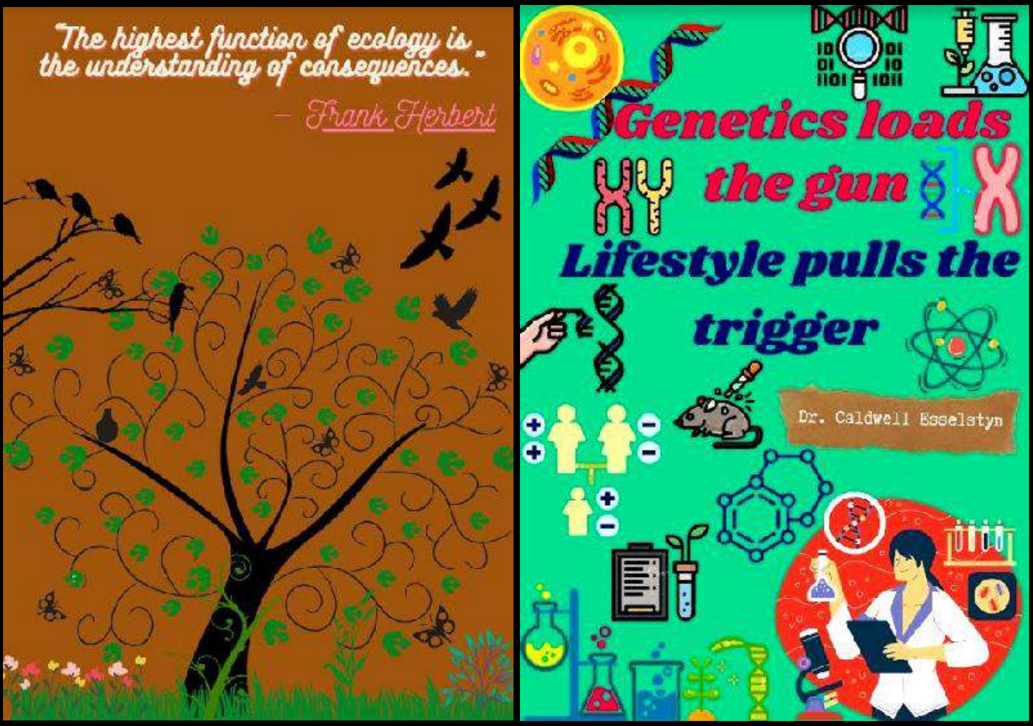
TANUSHRI SAHA, B.SC. SEM 6

3rd PRIZE (JOINT)

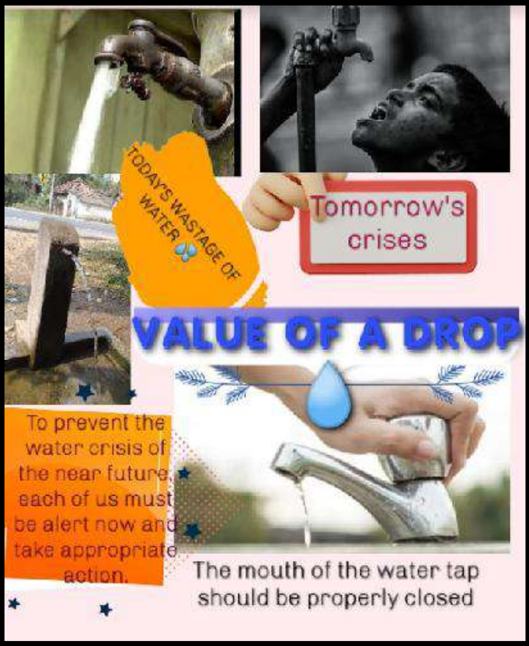


RAJIB NARU, M.SC. SEM 2

OTHER POSTER CONTRIBUTIONS

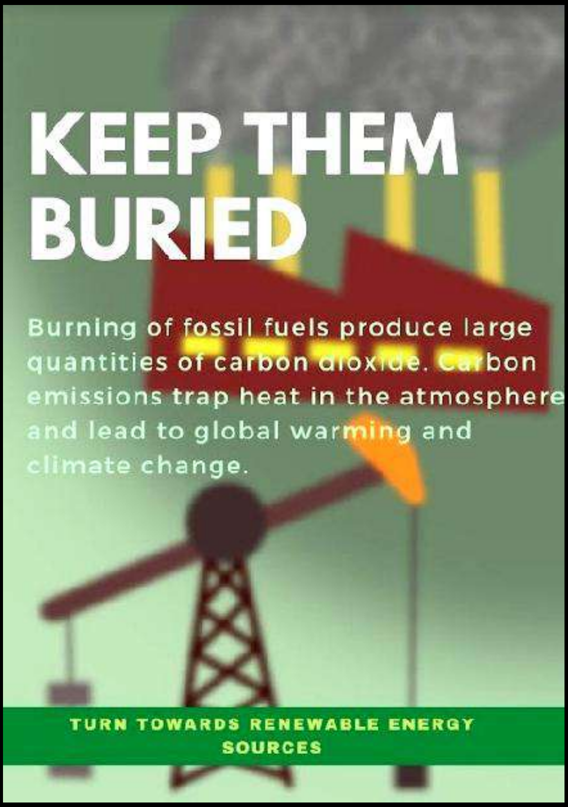


RAJIB NARU



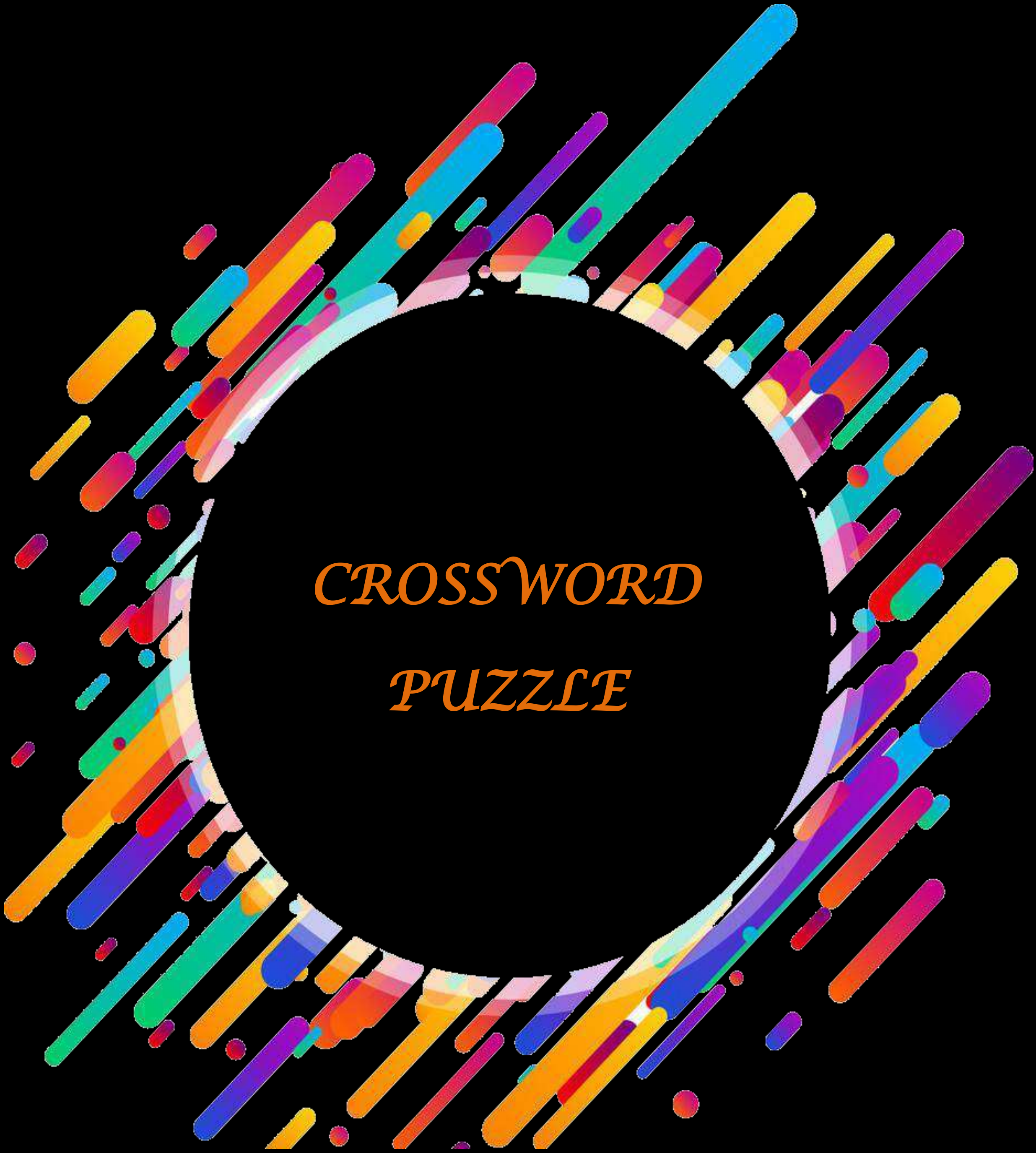
SWARNALY BISWAS **PURNIMA GHOSH**

EDINA BAG



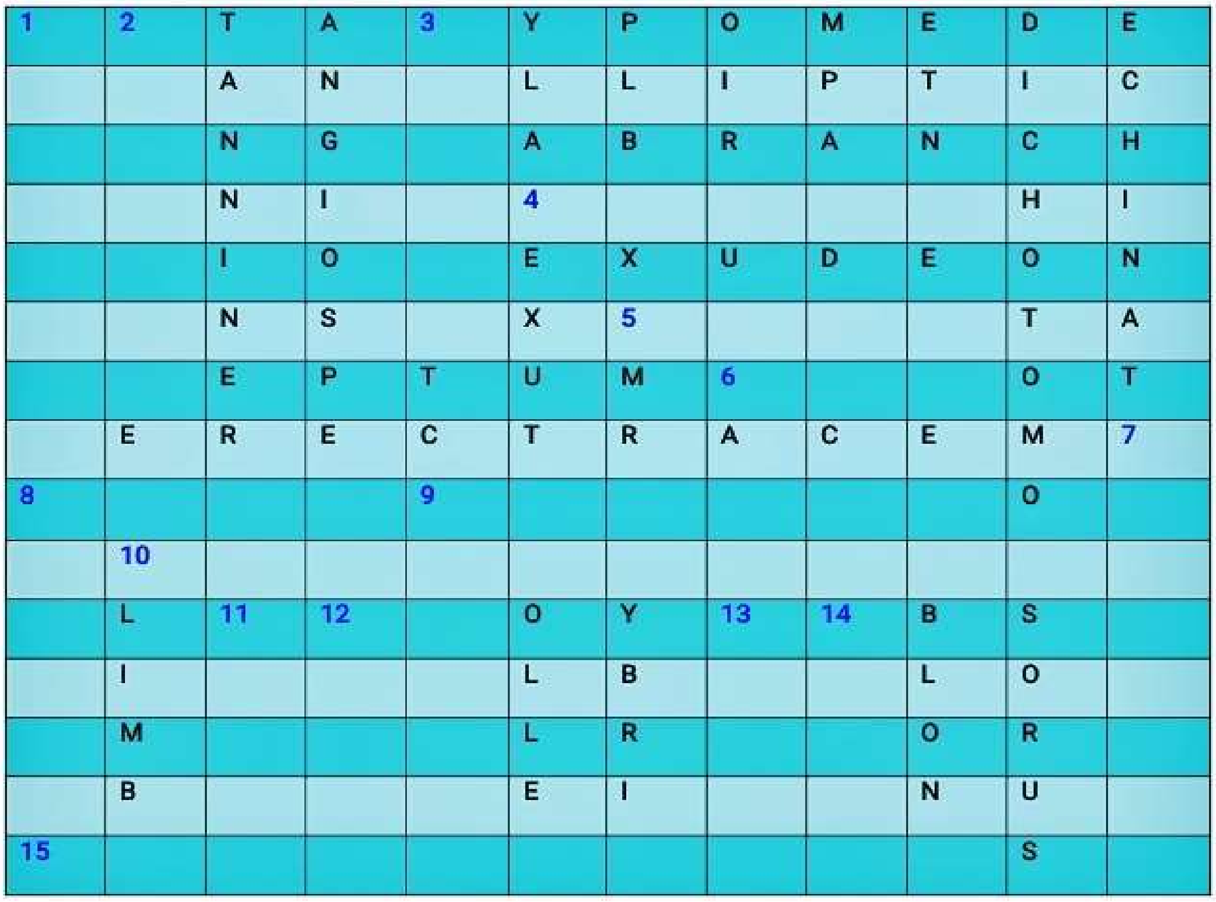
Burning of fossil fuels produce large quantities of carbon dioxide. Carbon emissions trap heat in the atmosphere and lead to global warming and climate change.

ARCHA BHATTACHARYA



CROSSWORD
PUZZLE

CROSSWORD PUZZLE-1



1	2	T	A	3	Y	P	O	M	E	D	E
		A	N		L	L	I	P	T	I	C
		N	G		A	B	R	A	N	C	H
		N	I		4					H	I
		I	O		E	X	U	D	E	O	N
		N	S		X	5				T	A
		E	P	T	U	M	6			O	T
	E	R	E	C	T	R	A	C	E	M	7
8				9						O	
	10										
	L	11	12		O	Y	13	14	B	S	
	I				L	B			L	O	
	M				L	R			O	R	
	B				E	I			N	U	
15										S	

Hints:

DOWN	
1. Endogenous phytohormone first discovered from Brassica napus in 1979	14. A hard, dry, indehiscent fruit of oaks with a single, large seed and cup like base
2. Movement of solvent through a semipermeable membrane towards high concentration of solute	**ACROSS**
3. A sugar riched, sticky liquid produced by the flowers and it attracts pollinating animals	4. Usually underground stem part modified for storage of food and bearing buds and scale leaves
7. Sword shaped leaf	5. Abnormal outgrowth of plant tissue caused by bacteria insects, fungi, nematodes etc.
9. A thick-walled zygote developed from a fertilized oosphere, especially in an oomycetes	6. A berry like fruit composed of an enlarged hypanthium surrounding numerous achenes
11. A type of inflorescence whose each floral axix terminates with a single flower, and the inflorescence develos basipetally or centrifugally	8. A modified leaf that bears sporangia
12. A tuft of hair on seeds, helps in wind dispersal	10. A plant that possesses only male flowers
13. A plant that spreads by creeping along the ground or climbs on other trees or walls	15. To downward

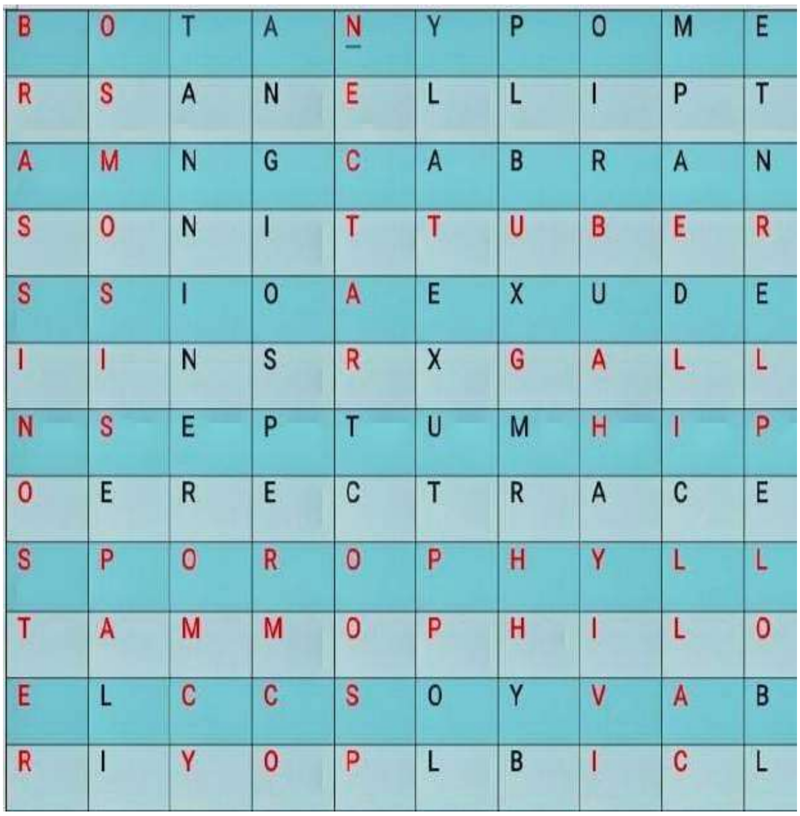
CROSSWORD PUZZLE-2

G	H	D	A	I	U	X	V	K	M	K	T	T	P
C	H	I	S	T	O	N	E	D	A	V	H	R	H
T	J	B	R	A	T	D	R	A	G	G	I	A	A
A	B	V	B	T	L	R	T	Z	N	J	O	N	R
S	T	R	Y	C	H	N	I	N	E	P	M	S	M
A	S	M	E	H	G	I	C	Q	S	O	A	F	A
F	G	I	N	K	G	O	I	Y	I	W	R	O	C
T	Y	S	N	X	W	F	L	E	U	A	G	R	O
Y	C	I	N	O	C	U	L	U	M	S	A	M	L
R	O	C	C	E	L	L	A	S	C	L	R	A	O
W	C	A	R	Y	O	P	S	I	S	T	I	T	G
E	Y	Q	S	E	M	N	T	T	S	W	T	I	Y
T	R	O	I	P	I	K	E	R	G	L	A	O	J
D	A	P	E	N	E	T	R	A	N	C	E	N	S

Answer the following questions to solve the below crossword:-

1. Inflorescence of family Lamiaceae
2. Largest bacterium ever discovered
3. Orcein is obtained from Lichen
4. Major alkaloid obtained from the plant *Strychnosnux-vomica*
5. An example of living fossil
6. The pathogen or any part of the pathogen that contacts with the plant at certain site to initiate the infection is termed as
7. One of the many processes by which the genetic material in the form of the naked DNA is transferred between the two microbial cells
8. Fruit of family Poaceae
9. Protein that provides structural support to a chromosome during the packaging of DNA
10. Branch of medicine concerned with drug and their use as medicine
11. Name the co-factor which is required by the kinase enzyme to function
12. Phenomenon to measure the proportion of individuals in a population who carry a specific gene and express the related trait

Crossword Puzzle-1 Answers (Red Ones)

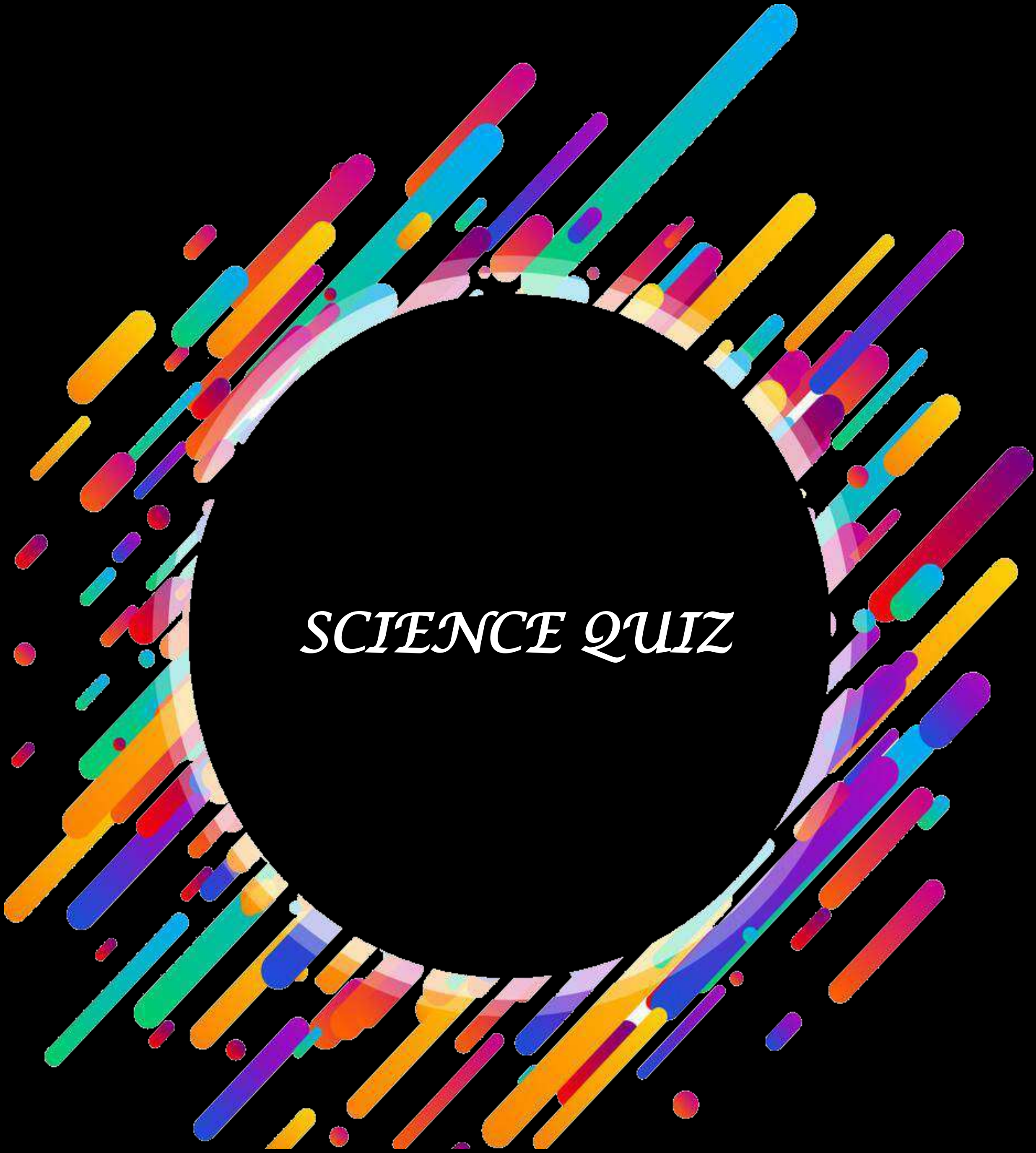


B	O	T	A	N	Y	P	O	M	E
R	S	A	N	E	L	L	I	P	T
A	M	N	G	C	A	B	R	A	N
S	O	N	I	T	T	U	B	E	R
S	S	I	O	A	E	X	U	D	E
I	I	N	S	R	X	G	A	L	L
N	S	E	P	T	U	M	H	I	P
O	E	R	E	C	T	R	A	C	E
S	P	O	R	O	P	H	Y	L	L
T	A	M	M	O	P	H	I	L	O
E	L	C	C	S	O	Y	V	A	B
R	I	Y	O	P	L	B	I	C	L

Crossword Puzzle-2 Answers

Answers:-

1. VERTICILLASTER
2. *Thiomargarita*
3. *Roccella*
4. STRYCHNINE
5. *Ginkgo*
6. INOCULUM
7. TRANSFORMATION
8. CARYOPSIS
9. HISTONE
10. PHARMACOLOGY
11. MAGNESIUM
12. PENETRANCE



SCIENCE QUIZ

1. **Fruits of this plant cure scurvy and are rich source of vitamin C?**

   A. Tomato
   B. Manihot
   C. Amla
   D. Periwinkle

2. **Known as sage herb and scientific name of this plant given due to its property to save people. Name the plant-**

   A. *Ocimum*
   B. *Salvia*
   C. *Rauwolfia*
   D. *Mimusops*

3. **Which of the following xerophytic plant has the property of curing asthma and cold?**

   A. *Prosopis julifera*
   B. *Acacia nilotica*
   C. *Ephedra gerardiana*
   D. *Welwitschia mirabilis*

4. **Wood of which tree is taken for carving idol of Lord Jagannath in Puri?**

   A. *Aegle marmelos*
   B. *Artocarpus integrifolia*
   C. *Azadiracta indica*
   D. *Mangifera indica*

5. **Lord Buddha attained divine knowledge under which of the following tree in Bodh Gaya?**

   A. *Ficus benghalensis*
   B. *Ficus benjamina*
   C. *Ficus religiosa*
   D. *Ficus racemosa*

6. **Which of the following crops has a variety with trade name Malayasian Orange?**

   A. Sugarcane
   B. Papaya
   C. Coconut
   D. Orange

7. **Holy basil or Tulsi (*Ocimum basilicum*) is regarded essential for the worshipping of which Hindu god?**

   A. Shiva
   B. Durga
   C. Vishnu
   D. Graharaj Shani Dev

8. **Highest number of chromosome (2n) is found in the plant specimen is a**

   A. Bryophyte
   B. Pteridophyte

C. Gymnosperms
D. Angiosperms

9. **Identify the plant specimen with one of the most slowly growing leaves**

A. *Sassurea lappa*
B. *Ranunculus sceleratus*
C. *Aconitum heterophyllum*
D. *Welwitschia mirabilis*

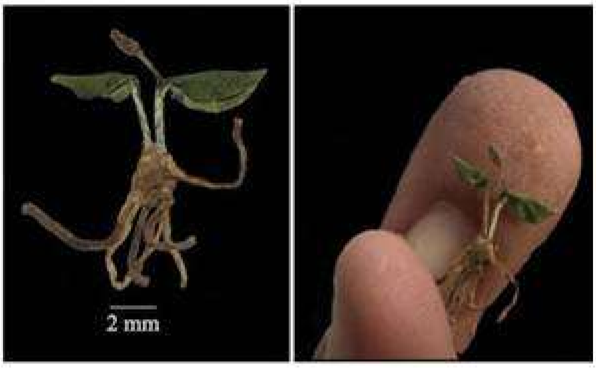
10. **Which of the following plants is NOT regarded necessary for worshipping Lord Shiva as per Hindu culture?**

A. *Aegle marmelos*
B. *Calotropis procera*
C. *Acanthus ilicifolius*
D. *Cannabis sativa*

11. **Which of the following countries is one of the leading producers of the painkiller and sedative opium obtained from poppy plants (*Papaver somniferum*)?**

A. Iran
B. Afghanistan
C. Thailand
D. Burma

12. **Identify below world's smallest terrestrial pterdiphyte discovered from the hills of Western Ghats, India?**



A. *Osmunda lancea*
B. *Marattia alata*
C. *Ophioglossum malivae*
D. *Vittaria dimporpha*

13. **The most abundant protein on earth is –**

A. Keratin
B. RUBISCO
C. Carbonic anhydrase
D. Catalase

14. **Rotenone, a respiratory poison has historically been used by indigenous peoples to catch fish is obtained from plant-**

A. *Vinca rosea*
B. *Lonchocarpus nicou*
C. *Nypa fruticans*
D. All of these

15. **Kalamkari is a type of hand-painted or block-printed cotton textile produced in Isfahan, Iran, and in the Indian state of Andhra Pradesh. Which of the following plant is used as a source of dye for the sarees under Kalamkari style?**

A. *Butea monosperma*
B. *Rubia tinctoria*
C. *Clitoria ternatea*
D. *Haematoxylon campechianum*

16. **Who among the following is the son of noted botanist Professor P.L. Swarnkar, is a plant physiologist and the founder of the "Save Guggul Movement", a community-based conservation effort to conserve threatened plant species, particularly guggul or *Commiphora wightii*?**

A. Chandi Prasad Bhatt
B. Anil Aggarwal
C. Rajendra Singh
D. Vineet Soni

17. Great Banyan tree in Acharya Jagadish Chandra Bose Indian Botanic Garden, Shibpur is about –

A. 100 years old
B. 150 years old
C. 200 years old
D. 250 years old

18. **Highly consumed tuber crop potato has its centre of origin in –**

A. Himachal Pradesh
B. Peru
C. Spain
D. Japan

19. **Famous Greek philosopher Socrates died when he was given with the poisonous extract of –**

A. Henbane
B. Charas
C. Hemlock
D. Aconite

20. **State plant of West Bengal is –**

A. *Ficus benghalensis*
B. *Mimusops elengi*
C. *Gmelina arborea*
D. *Alstonia scholaris*

21. **Saffron is a prized spice which is dried**

A. Bark
B. Seeds
C. Stigma and style
D. Petals

22. **Commonly called 'frog spawn' alga is**

A. *Callithamnion*
B. *Ceramium*
C. *Laminaria*
D. *Batrachospermum*

23. **Hans Krebs was awarded with Nobel prize in –**

A. 1923
B. 1953
C. 1972
D. 1975

24. **Barbara McClintock was awarded Nobel prize in medicine for her work in genetics on –**

A. Egg plant
B. Maize
C. Wheat
D. Cauliflower

25. **Which of the following trees has been mentioned in Indus Valley Civilization-**

A. Neem tree
B. Peepal tree
C. Coconut tree
D. Banana tree

Compiled by Dibyendu Sekhar Mahanty

Assistant Professor of Botany

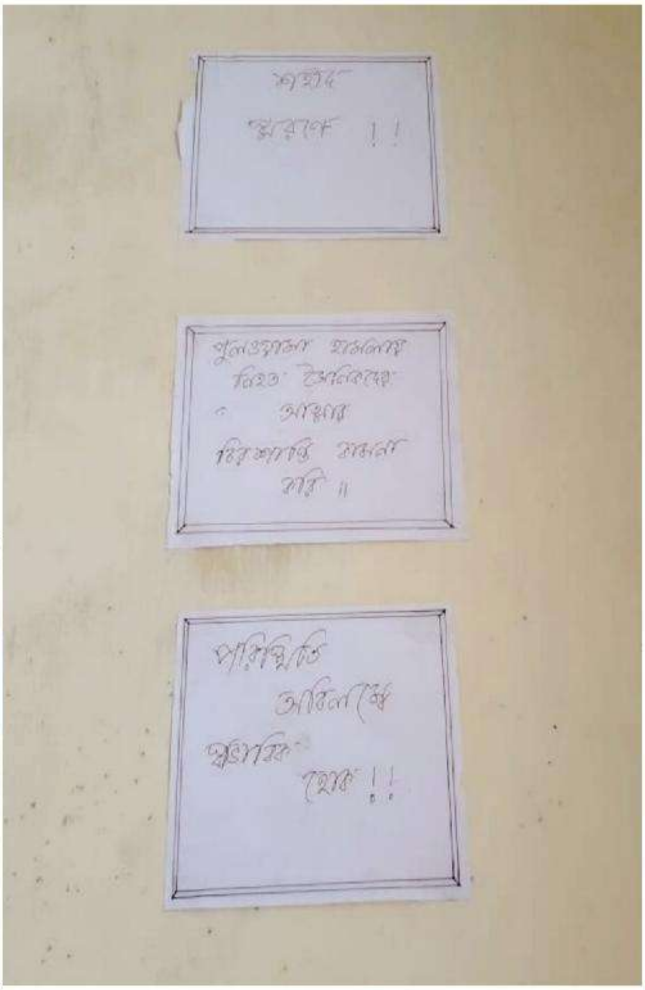
ANSWER KEY

1C, 2B,3C,4C,5C,6C,7C,8B,9D,10C,11C,12B,13B,14B,15B,16D,17D,18B,19C,20D,21C,22D,23B, 24B, 25B

DEPARTMENTAL ACTIVITIES

TEACHER’S DAY CELEBRATION, 2018

PAYING HOMAGE TO THE MARTYRS OF PULWAMA TERROR ATTACK 2019,15TH FEBRUARY

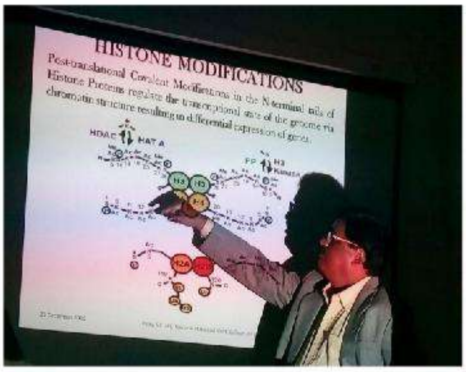


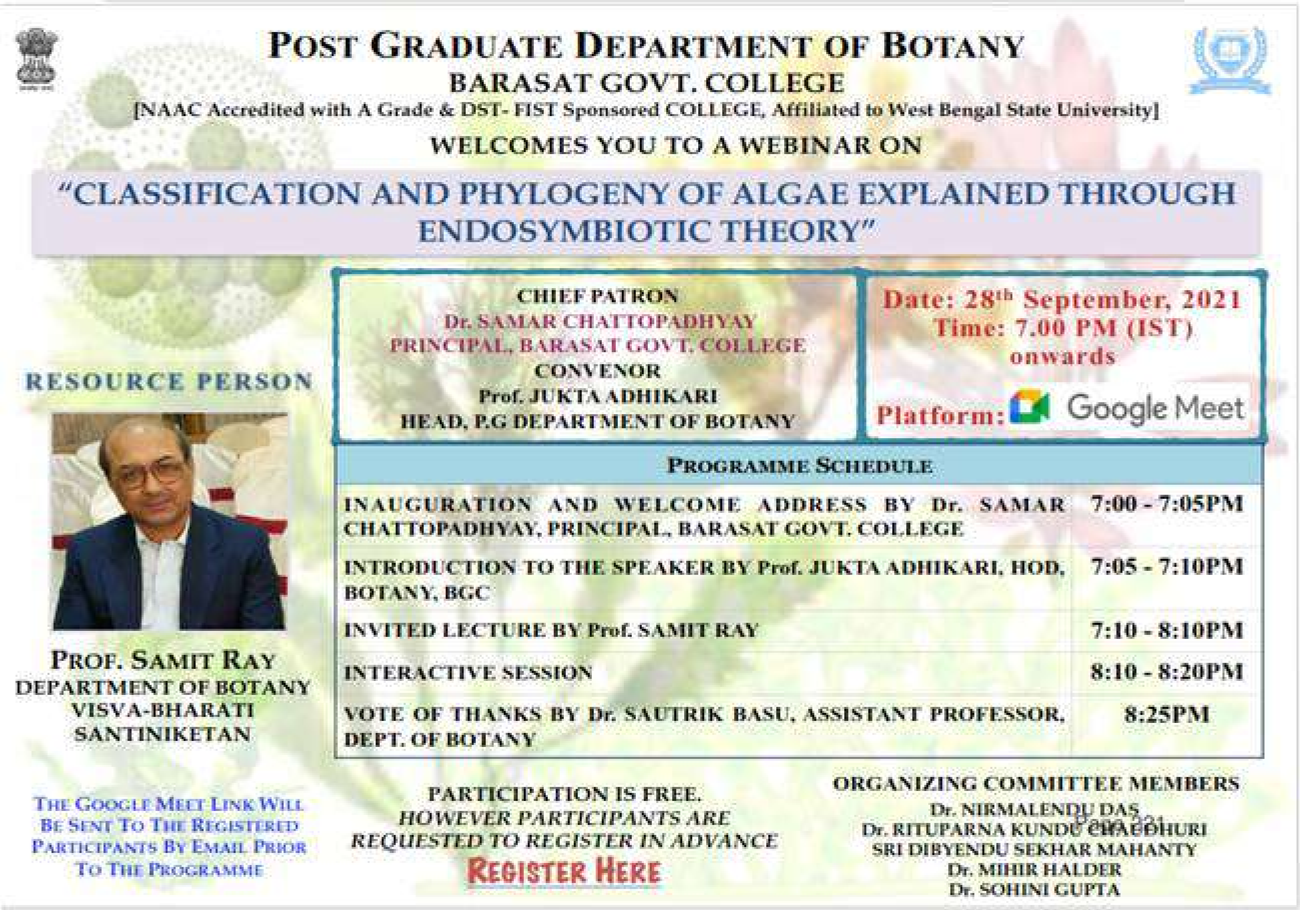
CELEBRATING MOTHER LANGUAGE DAY
21ST FEB, 2019

TEACHER'S DAY CELEBRATION, 2019

SEMINAR ON
STEM CELL AND REGENERATION THEORY

SEMINAR ON CHROMATIN STRUCTURE AND DYNAMICS RELATED TO CANCER





POST GRADUATE DEPARTMENT OF BOTANY

BARASAT GOVT. COLLEGE

[NAAC Accredited with A Grade & DST- FIST Sponsored COLLEGE, Affiliated to West Bengal State University]

WELCOMES YOU TO A WEBINAR ON

"CLASSIFICATION AND PHYLOGENY OF ALGAE EXPLAINED THROUGH ENDOSYMBIOTIC THEORY"

CHIEF PATRON
Dr. SAMAR CHATTOPADHYAY
PRINCIPAL, BARASAT GOVT. COLLEGE
CONVENOR
Prof. JUKTA ADHIKARI
HEAD, P.G DEPARTMENT OF BOTANY

Date: 28th September, 2021
Time: 7.00 PM (IST) onwards
Platform: Google Meet

RESOURCE PERSON

PROF. SAMIT RAY
DEPARTMENT OF BOTANY
VISVA-BHARATI
SANTINIKETAN

PROGRAMME SCHEDULE

INAUGURATION AND WELCOME ADDRESS BY Dr. SAMAR CHATTOPADHYAY, PRINCIPAL, BARASAT GOVT. COLLEGE	7:00 - 7:05PM
INTRODUCTION TO THE SPEAKER BY Prof. JUKTA ADHIKARI, HOD, BOTANY, BGC	7:05 - 7:10PM
INVITED LECTURE BY Prof. SAMIT RAY	7:10 - 8:10PM
INTERACTIVE SESSION	8:10 - 8:20PM
VOTE OF THANKS BY Dr. SAUTRIK BASU, ASSISTANT PROFESSOR, DEPT. OF BOTANY	8:25PM

THE GOOGLE MEET LINK WILL BE SENT TO THE REGISTERED PARTICIPANTS BY EMAIL PRIOR TO THE PROGRAMME

PARTICIPATION IS FREE.
HOWEVER PARTICIPANTS ARE REQUESTED TO REGISTER IN ADVANCE
REGISTER HERE

ORGANIZING COMMITTEE MEMBERS
Dr. NIRMALENDU DAS
Dr. RITUPARNA KUNDU CHAUDHURI
SRI DIBYENDU SEKHAR MAHANTY
Dr. MIHIR HALDER
Dr. SOHINI GUPTA

CAMARADERIE

U.G SEM-II

U.G SEM-IV

U.G SEM-VI

P.G SEM-II

LA FLOR

THE BLOOM OF HOPE

NO ONE CAN WHISTLE A SYMPHONY; IT TAKES A WHOLE ORCHESTRA TO PLAY IT.-H.E.LUCCOCK.

E-MAGAZINE

2021

POST GRADUATE DEPARTMENT OF BOTANY

BARASAT GOVERNMENT COLLEGE