EMPOWERED TO CHALLENGE EVERY CHALLENGE. I AM A SRISHAKTHIAN.

OUR METICULOUSLY DESIGNED TRAINING PROGRAM EMPOWERS EVERY SRISHAKTHIAN TO BECOME A REAL TIME SOLUTION PROVIDER, A CREATOR AND AN ENTREPRENEUR.

SRI SHAKTHI

INSTITUTE OF ENGINEERING AND TECHNOLOGY

(AN AUTONOMOUS INSTITUTE)

(Approved by AICTE, New Delhi, Affiliated to Anna University, Chennai)
L & T Bypass Road, Coimbatore - 641 062, Tamil Nadu, India.

BIOTECHRONZZ

THE TECHNICAL MAGAZINE

2021 - 2022

DEPARTMENT OF BIOTECHNOLOGY

BIOTECHRONZZ

THE TECHNICAL MAGAZINE

2021 - 2022

DEPARTMENT OF BIOTECHNOLOGY

SRI SHAKTHI

INSTITUTE OF ENGINEERING AND TECHNOLOGY

(AN AUTONOMOUS INSTITUTE)

(Approved by AICTE, New Delhi, Affiliated to Anna University, Chennai)

L & T Bypass Road, Coimbatore - 641 062, Tamil Nadu, India.

SRI SHAKTHI

INSTITUTE OF ENGINEERING AND TECHNOLOGY

(AN AUTONOMOUS INSTITUTE)

(Approved by AICTE, New Delhi, Affiliated to Anna University, Chennai)
L & T Bypass Road, Coimbatore - 641 062, Tamil Nadu, India.

National Assessment & Accreditation Council

Sri Shakthi Institute of Engineering and Technology (SIET) was established in the year 2006 by our honorable Chairman Dr.S. Thangavelu, with the zeal to provide quality Engineering Education to the young minds and to make them innovative employable Engineers.

Sri Shakthi is accredited by NAAC with A grade and also SIET is the youngest institution in India, accredited by National Board of Accreditation (NBA) for four courses namely Mech, ECE, CSE and IT. We have been consecutively recognized as the best industry connect institute with platinum ranking by the AICTE-CII survey of Industry- linked technical Institutions for the years from 2014 to 2017 and received awards under Established Engineering Institution for Electronics & allied courses in 2017 and in 2014 as Emerging Engineering Institution category as close competitor. Sri Shakthi symbolizes 'creative & progressive power' of dynamic youth and is ranked among top 10 percent of 3000 colleges across India to receive National Employability Award and The Times Group Award for Excellence in Education. We are the pioneer Institute in India, chosen by Indian Electronics & Semiconductor Industries Association to launch their premier courses on VLSI design and embedded product design

The inspirational leaders such as Padmashri A. Sivathanu Pillai, Padmashri R.M. Vasagam, Mylswamy Annadurai, Dr. Sandeep Garg, P. Venkat Rangan, Mr. Sanjeev Keskar, Mr. Srikantan Moorthy, A.K.Pattabiraman, Mr. Varadharajan, Ms. Hema Gopal, Mr. K. Ganesan, Madhusudan Atre, Mr. Vivek Pawar, Kamesh Namuduri, Mr. Jayaram Pillai, Mr. Veerappan, Mr. Parthasarathy, Mr. VA Shiva Ayyadurai, Kiran Bedi, Prof. John A Davis, KaviPerarasu Vairamuthu, Mr. Chetan Bhagat, Mr. Rajesh Nair, Mr. Kannan Ramamani and Mrs. Anuradha Srinivasan have visited our campus to inspire our students.

The institute is also collaborated with worldwide universities and industries to support our mission. Oracle, CISCO, National Instruments, Cadence, Xilinx, Infosys, Wipro, MindTree, AMI, Siemens, Dassault Systems, TTK prestige, HP Enterprise, Virtusa Polaris, Gyan Matrix, IESA, NASSCOM, IEI, ISTE, IEEE and ITB are few among them.

The institute currently offers ten bachelor's degree programs in the field of Agricultural, Bio Medical, Bio Technology, Electrical and Electronics, Electronics and Communication, Computer Science, Food Technology, Information Technology, Mechanical and Civil, and master degree programs in the fields of VLSI Design, Engineering Design, Structural Engineering, Computer Science and Engineering, Embedded System Technology

Message from Chairman

Dr. S. THANGAVELU
Chairman
Sri Shakthi Institute of Engineering and Technology
Coimbatore.

I am very happy that the Department of Biotechnology is again back into full energy on publishing their consecutive fourth edition of its Technical Magazine for the year 2021-2022. My heartiest congratulations to all the students of Department of Biotechnology for their efforts, who are supported by the enthusiastic faculty team. I am very much confident that this year's edition will be bringing out yet another tremendous issue.

My best wishes for the Editorial Board

Dr. S. Thangavelu
Chairman

Message from Principal

I am delighted to meet you through this page. Education is not only an act of acquiring knowledge but learning a skill to lead life and grooming ones' personality. Education of the highest order aims at guiding, inspiring, motivating and leading young men and women to become successful leaders to serve the country better.

Research is the key parameter to promote the individuality to horizon. In recent times, there is a rapid stride in all gamuts of modern branches of Biology. The students, faculties as well as the scholars ought to keep themselves abreast with the latest development to compete and emerge out successfully in the most challenging world.

Arranging International Conference as often as possible augurs well for the Sri Shakthi Institute of Engineering and Technology of higher learning especially in the Bioengineering and Technology for a wide range of exposure of new research finding and enrichment of knowledge and the most important is that their sequencial Technical Magazine release. Best wishes for the Team.

Dr. A. R. Ravikumar
Principal
Sri Shakthi Institute of Engineering and Technology
Coimbatore

PREFACE

Biotechronzz is the official technical magazine of the Department of Biotechnology, Sri Shakthi Institute of Engineering & Technology, a souvenir that showcases the myriad of talents possessed by the students. This year is the 4th Edition and we are proud to introduce the 4th Volume of Biotechronzz, a tradition that had taken roots since the first volume.

Right from the outset, we have been very meticulous with our planning, from the content we have received, to the layout and other particulars, to the final copy, we have all put in our hardest efforts to express the flair for science and language, shown by our students. Despite all the issues that arose throughout this roller coaster ride, we have made sure that the magazine fittingly reflects the magnificence that it deserves. This physical copy is the culmination of countless discussions, diligent efforts and the timely dedication of everyone involved. We hoped to achieve and maintain the highest calibre of the contents, and hope we did justice.

We hope this serves as yet another interesting edition. Our sincerest thanks to the Design Team for their committed efforts to breathe life to the vision we had in mind. Our heartfelt gratitude to our faculty advisors, staff, and teachers for supporting us in bringing together this edition, successfully.

We wish our readers a joyful reading experience. We hope you enjoy reading through it and draw as much inspiration from it as we did.

Editorial Board

EDITORIAL BOARD

ASSOCIATE EDITORS

VISION AND MISSION OF THE INSTITUTION

Vision

To make the institution one of our nation's great engineering schools, recognized nationally and internationally for excellence in teaching, research and public service. We seek to be the preferred destination for students, practitioners seeking an engineering education, employers hiring engineering graduates and organizations seeking engineering knowledge.

Mission

To Provide an encouraging environment to develop the intellectual capacity, critical thinking, creativity and problem solving ability of the students.

VISION AND MISSION OF THE DEPARTMENT

Vision

To cultivate scientific and technical manpower in Biotechnology to solve various problems and challenges faced by industry and academia for the betterment of society.

Mission

- To provide an academic environment that emphasizes critical thinking
- To equip students with knowledge and practical skills required for the industry and academia.
- To constitute Institute-Industry relationship via in plant training programs and projects.
- To establish Centre for excellence (COE) in the frontier areas of biotechnology.

PROGRAMME EDUCATIONAL OBJECTIVES (PEOs)

PEO 1	Identify, analyze and solve the biotechnological problems in product and process development.
PEO 2	Identify and control hazards in bioprocess industries
PEO 3	Apply modern computational, analytical tools and techniques to address biotechnological challenges.
PEO 4	Pursue life-long learning as a means of enhancing the knowledge base and skills for professional advancements.
PEO 5	Communicate effectively and demonstrate entrepreneurial and leadership skills.

PROGRAMME OUTCOMES (POs)

Engineering Graduates will be able to:

PO 1	Engineering knowledge: Apply the knowledge of mathematics, science, engineering, fundamentals, and an engineering specialization to the solution of complex engineering problems.
PO 2	Problem analysis: Identify, formulate, review research literature, and analyze complex engineering problems reaching substantiated conclusions using first principles of mathematics, natural sciences, and engineering sciences.
PO 3	Design/development of solutions: Design solutions for complex engineering problems and design system components or processes that meet the specified needs with appropriate consideration for the public health and safety, and the cultural, societal, and environmental considerations.
PO 4	Conduct investigations of complex problems: Use research-based knowledge and research methods including design of experiments, analysis and interpretation of data, and synthesis of the information to provide valid conclusions.

PO 5	Modern tool usage: Create, select, and apply appropriate techniques, resources, and modern engineering and IT tools including prediction and modeling to complex engineering activities with an Understanding of the limitations.
PO 6	The engineer and society: Apply reasoning informed by the contextual knowledge to assess societal, health, safety, legal and cultural issues and the consequent responsibilities relevant to the professional engineering practice.
PO 7	Environment and sustainability: Understand the impact of the professional engineering solutions in societal and environmental contexts, and demonstrate the knowledge of, and need for sustainable development.
PO 8	Ethics: Apply ethical principles and commit to professional ethics and responsibilities and norms of the engineering practice.
PO 9	Individual and team work: Function effectively as an individual, and as a member or leader in diverse teams, and in multidisciplinary settings.
PO 10	Communication: Communicate effectively on complex engineering activities with the engineering Community and with society at large, such as, being able to comprehend and write effective reports and design documentation, make effective presentations, and give and receive clear instructions.
PO 11	Project management and finance: Demonstrate knowledge and understanding of the engineering and management principles and apply these to one's own work, as a member and leader in a team, to manage projects and in multidisciplinary environments.
PO 12	Life-long learning: Recognize the need for, and have the preparation and ability to engage in independent and life-long learning in the broadest context of technological change.

PROGRAMME SPECIFIC OUTCOME (PSOs)

PSO 1 Knowledge and hands on training to solve engineering and scientific problems.

PSO 2 Ability to work in interdisciplinary areas of science and technology towards industrial and academic research applications.

PSO 3 Infer the potentials and impact of biotechnological innovations for finding sustainable ethical solutions to issues pertaining to health, environment and agriculture

BIOTECHRONZZ
2021-2022

MACHINE LEARNING APPROACH IN BIOINFORMATICS

Gautham Siddharth S, IV - BT

The origin of Bioinformatics can be from the Mendel's discovery of genetic inheritance in 1865. Since 1953 big revolution achievements took place by James Watson and FrancisCrick as they determined the structure of DNA. Bioinformatics is an interdisciplinary field that develops methods and software tools for understanding biological data. Machine learning is the adaptive process that makes computers improve from experience, by example, and by analogy. Machine learning includes the learning speed, the guarantee of convergence, and how the datacan be learned incrementally. We usuallyrefer to methods like Artificial Neural Networks (ANNs), Genetic algorithms (GAs), and Fuzzy systems along with hybrid methods including a combination of some of these methods.

While the first wave of computational analysis did focus on sequence analysis, where many highly important unsolved problems still remain, the current and futureneeds will in particular concern sophisticated integration of extremely diverse sets of data. These novel types of data originate from a variety of experimental techniques of which many are capable of data production at the levels of entire cells, organs, organisms, or even populations. The main driving forcebehind the changes has been the advent of new, efficient experimental techniques, primarily DNA sequencing, that have led to an exponential growth of linear descriptions of protein, DNA and RNA molecules. Other newdata producing work as massively parallel versions of traditional

experimental methodologies. Genome-wide gene expression measurements using DNA microrarrays is, in essence, a realization of tens of thousands of Northern blots. The large amounts of data create a critical need for theoretical, algorithmic, and software advances in storing, retrieving, networking, processing, analyzing, navigating, and visualizing biological information. In turn, biological systems have inspired computer science advances with new concepts, including genetic algorithms, artificial neural networks, computer viruses and synthetic immune systems, DNA computing, artificial life, andhybrid VLSI-DNA gene chips .

Computational tools for classifying sequences, detecting weak similarities, separating protein coding regions from non-coding regions in DNA sequences, predicting molecular structure, post-translational modification and function, and reconstructing the underlying evolutionary history have become an essential component of the research process. This is essential to our understanding of life and evolution, as well as to the discovery of new drugs and therapies.

Bioinformatics has emerged as a strategic discipline at the frontier between biology and computer science, impacting medicine, biotechnology, and society in many ways.

Large databases of biological information create both challenging datamining problems and opportunities, each requiring new ideas. In this regard, conventional computer science algorithms have been useful, but are increasingly unable to address many of the most interesting sequence analysis problems.

Machine-learning approaches (e.g. neural networks, hidden Markov models, vector support machines, belief networks),on the other hand, are ideally suited for domains characterized by the presence of large amounts of data, “noisy” patterns, and the absence of general theories. The fundamental idea behind these approaches is to learn the theory automatically from the data, through a process of inference, model fitting, or learning from examples. Thus they form a viable complementary approach to conventional methods. The aim of this book is to present a a

broad overview of bioinformatics from machine learing perspective.

Machine-learning methods are computationally intensive and benefit greatly from progress in computer speed. It is remarkable that both computer speed and sequence volume have been growing at roughly the same rate since the late 1980s, doubling every 16 months or so. More recently, with the completion of the first draft of the Human Genome Project and the advent of high-throughput technologies such as DNA microarrays, biological data has been growing even faster, doubling about every 6 to 8 months, and further increasing the pressure towards bioinformatics. In our minds, in fact, there is little difference between machine learning and Bayesian modeling and inference, except for the emphasis on computers and number crunching implicit in the first term. It is the confluence of all three factors—data, computers, and theoretical probabilistic framework—that is fueling the machine-learning expansion, in bioinformatics and elsewhere.

and it is fair to say that bioinformatics and machine learning methods have started to have a significant impact in biology & medicine.

REFERENCES:-

[1] C. YR and K. M, "Interpretable machine learning in bioinformatics," *Methods*, vol. 179, pp. 1–2, Jul. 2020, doi:10.1016/J.YMETH.2020.05.024.

[2] D. Hanauer, D. Rhodes, C. Sinha-Kumar, and A. Chinnaiyan, "Bioinformatics Approaches in the Study of Cancer," *Curr. Mol. Med.*, vol. 7, no. 1, pp. 133–141, Feb. 2007, doi: 10.2174/156652407779940431.

[3] R. Miotto, F. Wang, S. Wang, X. Jiang, and J. T. Dudley, "Deep learning for healthcare: review, opportunities and challenges," doi: 10.1093/bib/bbx044.

NEXT GENERATION SEQUENCING

Elakiya R V, IV - BT

Nucleic acid Sequencing can also be a way for determining the precise order of nucleotides present in a given DNA or RNA molecule. The chain termination method (Sanger or di-deoxy sequencing method), published in 1977, has remained the foremost commonly used DNA Sequencing technique. The Human Genome Project, led by the International Human Genome sequencing Consortium and Celera Genomics, was accomplished with first-generation Sanger Sequencing. After the completion of the Human Genome project, demand for inexpensive and faster sequencing methods has increased greatly. The demand has been driven by the development of second-generation sequencing methods (next-generation Sequencing).

Next-generation sequencing platforms perform massively parallel sequencing during which many fragments of DNA from one sample are sequenced in unison. Massively parallel sequencing, technology facilitates high throughput screening, which allows an entire genome to be sequenced instantly.

4

WORKING:-

The process of next-generation sequencing is as follows, consider a single genomic DNA sample.

1) Library Preparation

Libraries are created by fragmenting sample DNA and adding specific adapters to both ends. Fragments can then be amplified and purified. During the method of adapter ligation, distinctive index sequences, or “barcodes,” are

added to each library. The barcodes are used to distinguish between the libraries.

2) Cluster Amplification

Clusters are generated through bridge amplification. DNA polymerase moves throughout the length of the DNA strand, generating its complementary strand. The initial strand is washed away, leaving only the reverse strand.

3) Sequencing

During the sequencing step, libraries are loaded onto a flow cell and put down on the sequencer. The newly identified strings of bases, called reads, are then reassembled employing a known reference genome as a scaffold (resequencing), or in the absence of a reference genome (De novo sequencing).

4) Data Analysis

The data analysis software determines nucleotides (a process called base calling) and provided the accuracy of the base calls. Today, you may use intuitive data analysis apps to study NGS data to produce sequence alignment, variant calling, data visualization, or interpretation.

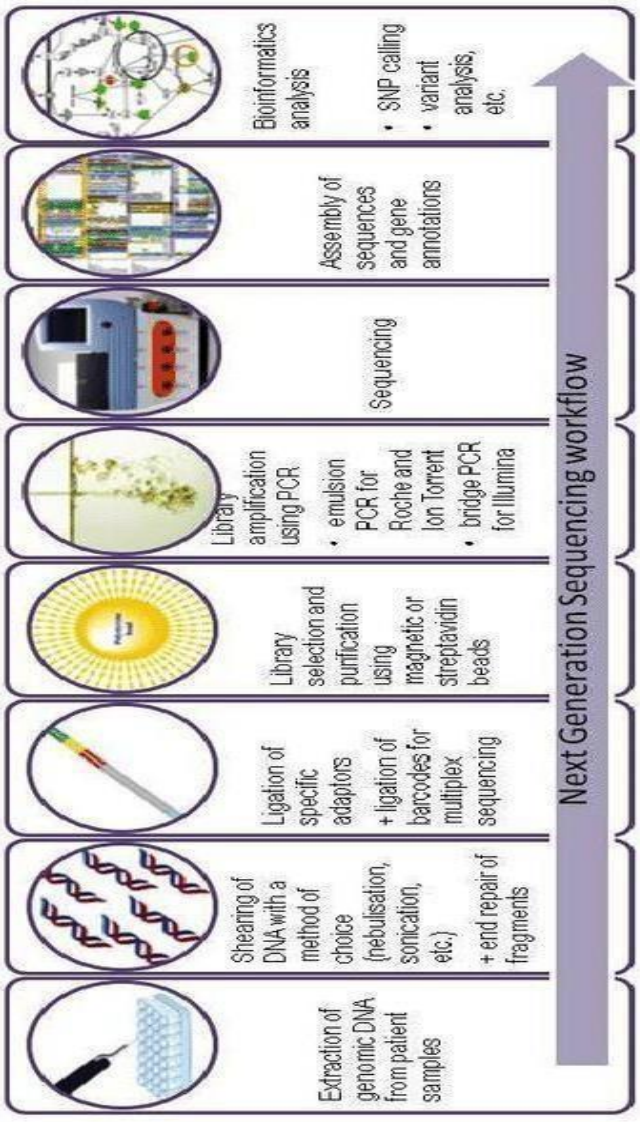


Figure 1: Flow Chart of the workflow of NGS.

TYPES:-

1) Illumina (Solexa) Technology

This technique is also called "bridge amplification" and works on sequencing by synthesis(SBS) technology where fragments of the genome to be sequenced are immobilized in a flow cell then, amplification synthesis reaction on a solid support (glass slide) that contains oligonucleotide sequences complementary to a ligated adapter, resulting clonal "clusters" consisting of about 1000 copies of each oligonucleotide fragment. Each glass slide can support many parallel cluster reactions. During the synthesis reactions, modified nucleotides, matching to each of the four fluorescently labeled bases, are incorporated and detected. These nucleotides also act as terminators of synthesis for every reaction, which is unblocked after detection for the successive round of synthesis. These reactions are iterated for 300 or more cycles.

2) Ion Torrent sequencing

Ion Torrent technology directly converts the data of nucleotide sequence into digital information on a semiconductor chip. This process exploits the fact that the incorporation of a dNTP into a growing DNA strand and involves the formation of a bond and thus the discharge of pyrophosphate and a positively charged hydrogen ion. The release of hydrogen ions results in changes within the pH of the solution, which is detected by a detector. The primary step during this approach includes library construction which involves DNA fragmentation and adaptor ligation. The fragments are clonally amplified on the small beads by emulsion PCR. Beads are primed for sequencing of nucleotides by annealing a sequencing primer, then placed into the wells of a silicon Ion chip to observe pH changes within single wells of the sequencer because the reaction proceeds stepwise. The unattached dNTP molecules are washed out before consequent cycle when a particular dNTP is introduced in it. If the introduced dNTP isn't complementary there is no incorporation and no biochemical reaction.

3) 454 pyrosequencing

In this technique, pyrophosphate is detected, which is the byproduct of nucleotide

incorporation when a base was incorporated during a growing DNA chain. Individual DNA fragments are ligated to adapters, amplified by PCR in an emulsion "bead" (emPCR) reaction. After DNA synthesis the chemical detection of reactions occurs during a picoliter-sized chamber where pyrophosphate release is measured utilizing a light-generating reaction.

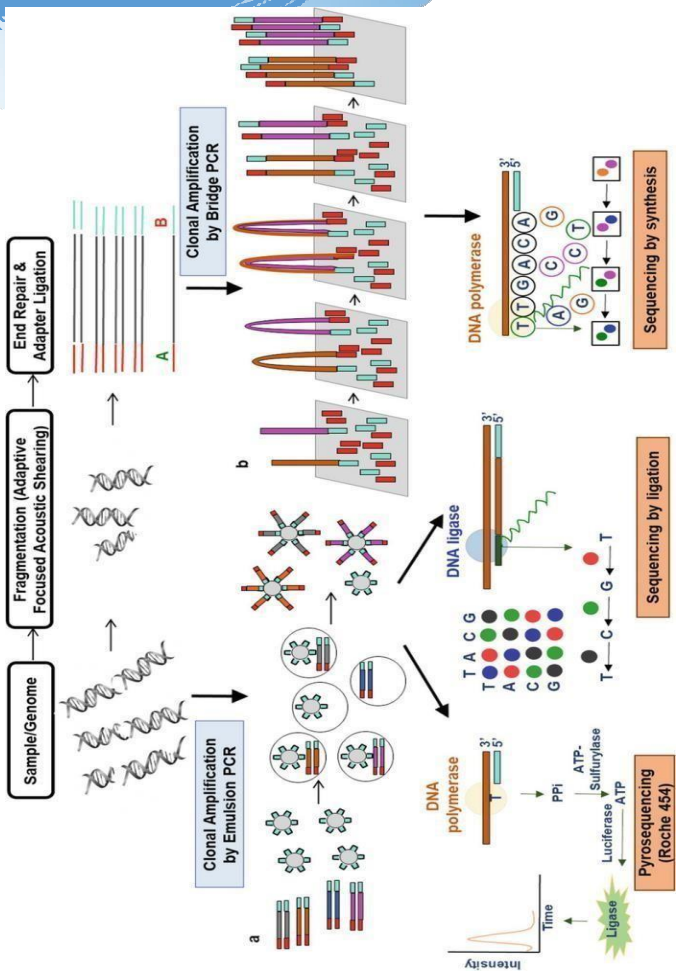


Figure 2: Flow Chart of the workflow of NGS.

APPLICATIONS:-

- Detection of unknown diseases caused by viral pathogens and discovery of Novel Viruses.
- Detection of Tumor Viruses.
- Characterization of the human virome.
- Study of Antiviral Drug Resistance.
- Quality Control and potency of Live-Attenuated Viral Vaccines.
- Epidemiology of viral Infections and evolution of virus

REFERENCES:-

[1] M. WR, M. JD, and M. ER, "Next-Generation Sequencing Technologies," *Cold Spring Harb. Perspect. Med.*, vol. 9, no. 11, Nov. 2019,doi:10.1101/CSHPERSPECT.A036798.

[2] L. Barzon, E. Lavezzo, V. Militello, S. Toppo, and G. Palù, "Applications of Next-Generation Sequencing Technologies to Diagnostic Virology," *Int. J. Mol. Sci.*, vol. 12, no. 11, p. 7861, Nov. 2011, doi: 10.3390/IJMS12117861.

BIOINFORMATICS AND SARS-COV-2 VIRUS

Srihasthini M, IV - BT

CoVid-19 infection caused by positive sense RNA virus is a severe acute respiratory syndrome (SARS-CoV-2) that becomes the cause for pandemic across the world in late 2019 till date. The acuteness of this pandemic and its spread all over the world produces an unprecedented effort of communities like medicine, biology, health, bioinformatics and computer science researchers leading to the rapid development of several vaccines. Group of researchers observed that SARS-COV-2 virus controls mitochondria indirectly when enters into the host (human body) results in Manipulating or regulating mitochondrial functions just by changing open reading frames like ORF-9B. Once virus controls mitochondria of cell, It stops the immune function of host cells and promote viral replication, causing COVID-19 disease.

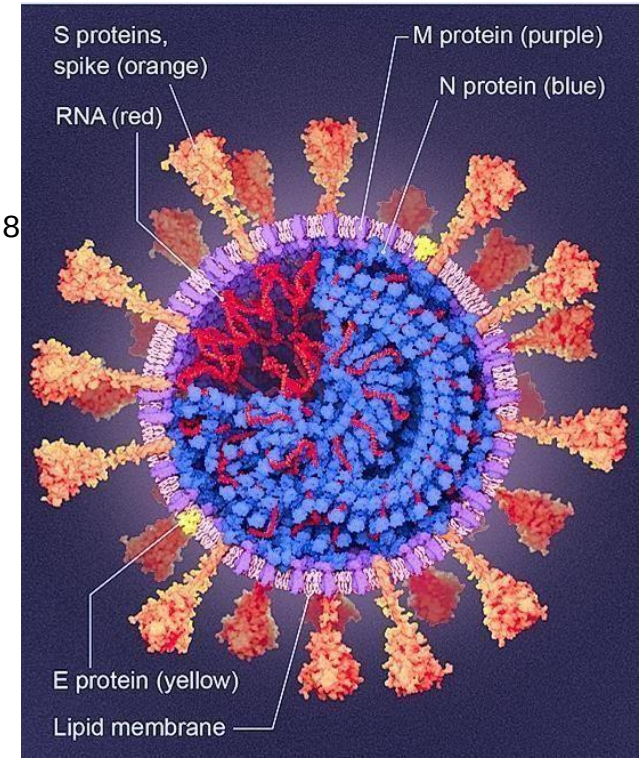


Figure 1: Describes the cross section presentation of SARS-CoV-2 virus particle

isolated from nose of infected person. It was noticed by the scientists that corona virus canbe visible in electron microscope due to its nanoscale size i.e. around 100 nm. S protein from spikes region of Corona virus represented by orange colour in the diagramis hundreds of times larger that extends fromthe surface and grab onto a human cell just by slipping inside. The structural proteins N,M and E represented by blue, purple and yellow colour in the diagram helps in formation of new virions form by movinginside the cell.

To control this virus, an urgent need is required to study and analyse the complete genome of SARS-COV-2 virus. It was suggested that Bioinformatics plays a major role in CoVid-19 drug discovery using different computational approaches with the help of various types of software's and tools. Bioinformatics software tools and databases for analysing and storing virus interactions helps in various ways. SARS-CoV-2 researches have several ideas and themes, including next-generation sequencing for genome detection, metagenomics and database storing various genome and variants.

NEXT-GENERATION SEQUENCING FOR SARS-COV-2 VIRUS:-

Next-generation sequencing [NGS] is the massive parallel sequencing tool majorly used in bioinformatics approaches that provides ultra-high throughput, speed and scalability to determine nucleotides order of targeted region of RNA/DNA or whole genome sequencing of any living organisms. Recently it was majorly used to characterize cancers at the transcriptomic, epigenetic and genomic levels. For detection of SARS-COV-2, Next-generation sequencing is the dominant technology that provides us the fundamental data about SARS-COV-2 virus like its origin and intermediate hosts. A group of scientists analyse Phylogenetic network of 160 complete SARS-CoV-2 genome sequences collected from around the world which revealed that there are three distinct but closely related variants of SARS-CoV-2. To perform Next generation sequencing, some steps are involved that are discussed below. (1) RNA extraction and fragmentation of input genomes. (2) Attaching adaptors for barcoding and preparation of a sequencing library. (3) Millions of fragments are simultaneously and

9

independently sequenced. (4) Human related DNA sequence reads are removed. (5) Coting's of long DNA stretches are assembled and aligned to a reference database for taxonomic classification.

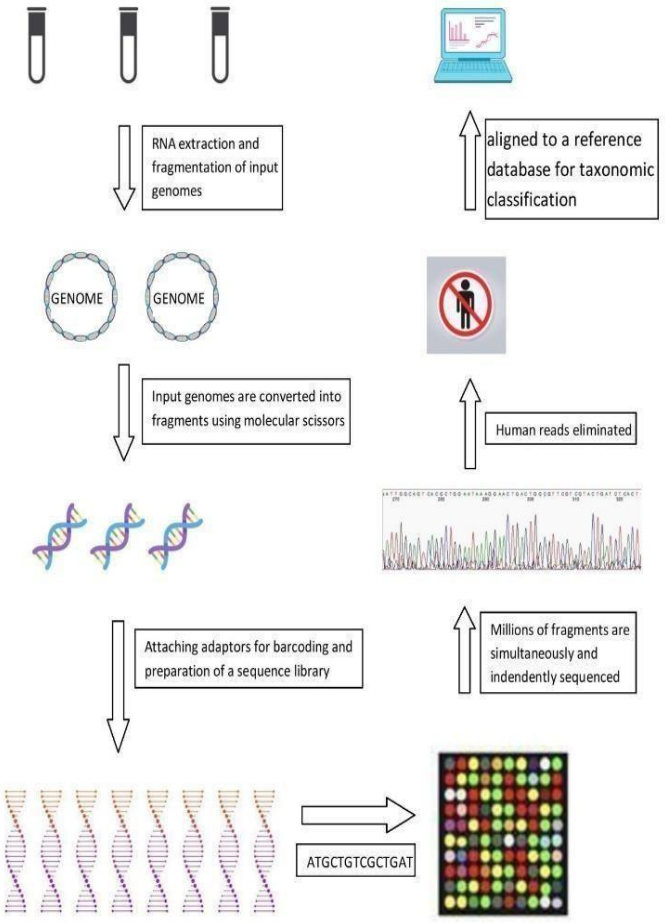


Figure 2: Flowchart for simple demonstration of Next generation sequencing steps

It was also observed that Shotgun metagenomics sequencing is an extremely powerful tool for the identification of previously uncharacterised pathogens like SARS-CoV-2 virus. It is a culture-independent technique that can interrogate all of the DNA in a sample, allowing the characterization of complex communities of microorganisms, without any prior knowledge of their genome sequences. Hence, shows its potency in SARS-CoV-2 virus detection and analysis.

Next-Generation sequencing are publicly available for researchers to study the origin of SARS-CoV-2. Also, hundreds of corona viruses and SARS-CoV-2 genomes were determined by using Next-Generation sequencing method.

CONCLUSION:-

In this COVID-19 pandemic, It was clear that ample amount of biotech researches are needed globally to prevent these kind of pandemics in near future. Present Bioinformatics tools are used widely for many vital functions like sequence data analysis, SARS-CoV-2 detection,

COVID-19 evolution, containment and tracking of COVID-19, discovery of potential drug targets and related therapeutic strategies. In this

article, It was pointed out that the next generation sequencing method is a potential tool that is widely used in SARS-CoV-2 virus genome analysis and could be helpful in future use for COVID-19 researches.

REFERENCES:-

[1] M. Cannataro and A. Harrison, "Bioinformatics helping to mitigate the impact of COVID-19-Editorial," *Brief. Bioinform.*, vol. 22, no. 2, pp. 613–615, Mar. 2021, doi: 10.1093/BIB/BBAB063.

[2] X. Chen *et al.*, "Next-Generation Sequencing Reveals the Progression of COVID-19," *Front. Cell. Infect. Microbiol.*, vol. 0, p. 142, Mar. 2021, doi: 10.3389/FCIMB.2021.632490.

[3] F. G and M. A, "COVID-19 vaccines: where we stand and challenges ahead," *Cell Death Differ.*, vol. 28, no. 2, pp. 626–639, Feb.2021, doi: 10.1038/S41418-020-00720-9.

[4] Q. C, W. AW, S. JT, L. NJ, and S. N, "Shotgun metagenomics, from sampling to analysis," *Nat. Biotechnol.*, vol. 35, no. 9, pp. 833–844, Sep. 2017, doi: 10.1038/NBT.3935.

[5] M. F *et al.*, "A complete protocol for whole-genome sequencing of virus from clinical samples: Application to coronavirus OC43," *Virology*, vol. 531, pp. 141–148, May 2019, doi: 10.1016/J.VIROL.2019.03.006.

[6] B. Hu, H. Guo, P. Zhou, and Z.-L. Shi, "Characteristics of SARS-CoV-2 and COVID-19," *Nat. Rev. Microbiol. 2020 193*, vol. 19, no. 3, pp. 141–154, Oct. 2020, doi: 10.1038/s41579-020-00459-7.

[7] R. Pereira, J. Oliveira, and M. Sousa, "Bioinformatics and Computational Tools for Next-Generation Sequencing Analysis in Clinical Genetics," *J. Clin. Med. 2020, Vol. 9, Page 132*, vol. 9, no. 1, p. 132, Jan. 2020, doi: 10.3390/JCM9010132.

[8] R. M, S. MN, S. S, and H. V, "Essential interpretations of bioinformatics in COVID-19 pandemic," *Meta gene*, vol. 27, Feb. 2021, doi: 10.1016/J.MGENE.2020.100844.

[9] K. K. Singh, G. Chaubey, J. Y. Chen, and P. Suravajhala, "Decoding SARS-CoV-2 hijacking of host mitochondria in COVID-19 pathogenesis," *https://doi.org/10.1152/ajpcell.00224.2020*, vol. 319, no. 2, pp. C258–C267, Aug. 2020, doi: 10.1152/AJPCELL.00224.2020.

[10] G. S. Watts and B. L. Hurwitz, "Metagenomic Next-Generation Sequencing in Clinical Microbiology," *Clin. Microbiol. Newsl.*, vol. 42, no. 7, pp. 53–59, Apr. 2020, doi: 10.1016/J.CLINMICNEWS.2020.03.004.

[11] P. C. Y. Woo, Y. Huang, S. K. P. Lau, and K.-Y. Yuen, "Coronavirus Genomics and Bioinformatics Analysis," *Viruses*, vol. 2, no. 8, p. 1804, 2010, doi: 10.3390/V2081803.

[12] J. S. Reis-Filho, "Next-generation sequencing," *Breast Cancer Res. 2009 113*, vol. 11, no. 3, pp. 1–7, Dec. 2009, doi: 10.1186/BCR2431.

[13] M. F. Konig *et al.*, "Preventing cytokine storm syndrome in COVID-19 using α-1 adrenergic receptor antagonists," *J. Clin. Invest.*, vol. 130, no. 7, pp. 3345–3347, Jul. 2020, doi: 10.1172/JCI139642.

PROTEIN STRUCTURE PREDICTION & VISUALIZATION

Harish.G.S, III - BT

Mid-20th century, a diverse research took place in bio-related (Bioinformatics) programs; protein structure, visualization, and sequencing of amino acids. Protein is ubiquitous and convoluted macromolecules within life organisms; differ from organism to organism. A different spatial shape and function toward molecules. A precocious pragmatic technique developed in the past several decades, leads to exponential growth. UniProt and Protein data Bank (PDB) helps to achieve much sequence directly. X-ray crystallography and NMR spectroscopy are currently empirical techniques for protein structure prediction. This information reveals a detail of protein structure prediction through virtual functioning to obtain a 3D dimensional protein model. Ultimate goal to obtain a desired structure based on sequence alignment. You may hear the name of Homology Modelling; it is a most accurate way to predict the protein structure. In case of no similarity found in PDB, can find out, and predictstructural similarity of target protein. Both homology modelling and threading methods are used to predict a sequence. On other hand, ab initio method has also been used. In this article a detailed prediction method is discussed, including conformation initialization, conformation search, structure selection and visualization of proteins.

STEPS IN PROTEIN STRUCTURE PREDICTION:-

1) Conformation initialization

The input of protein structure prediction is in 1D and output in 3D structure. The structural

template of homologues to target protein can be identified from the PDB database by sequence alignment. In contrast, the conformation copied from the template is close to the optimal one; in case of homology modelling. The two proteins without any sequential similarity fold into similar folds. Sometimes Conformational initialization is obtained from structural templates which are vastly better than any ones built from the scratch; it dramatically curtails the process of subsequent conformational search. The template free method is the best choice for hard target proteins of those non satisfactory templates to be identified.

2) Conformational Search

Next, run a simulation with a guide of a certain force field to know the near-native conformation one by one. Almost all protein structures assemble the simulation method and do conformational search. The protein conformational energy landscape is needed in the force field to depict the conformational search. Various machine learning methods like the hidden Markov model, artificial neural network have been used for deriving energy functions. Once the energy function is determined, look for the lowest energy conformation of the target protein. Other hand in searching, molecular dynamics simulation is commonly used.

3) Structure Selection

Following the conformational search, a bulk number of target structure protein is generated. The key point of structure selection is the assessment method for different native-like structures from non-native ones. CASP helps to assess the specific structural quality. The force field itself can filter structure, but what we need to be careful of is to design a force field between the accuracy and speed contradiction. The energy function can either be physics based or knowledge based. Another way is to select structure based on clustering in all structural similarity.

4) Reconstruction and Structure Refinement

Most prediction methods adopt a protein representation for conformational search, rather than what could be obtained from one reduced model. Through reduced models all-atom be reconstructed. The backbone and side chain are

reconstructed; methods used for side chains such as Scwrl, SCATD, RASP and so on. Structural refinement selection can be done through clustering methods. The structural issues in the reduced model can affect the quality of the final all-atom structure. In fact, they refine the reduced model and structure it according to the reconstruction schedule. Structure refinement also acquires a force field to conduct molecular dynamics and Monte Carlo, but the main purpose is to improve the quality of all-atoms.

5) Visualization

Plotting the coordinate of a protein structure in 2D plane (Secondary structure) or 3D plane (tertiary structure). Visualization of any protein molecule is necessary to study the interaction between ligand and the target, active site, body, angle rotation etc. Computational technology makes it very easy to visualize any structure and it saves the cost, manpower and time. In silico visualization provides you various online and offline tools to visualize, construct or edit any protein/chemical molecule.

The importance of in silico protein structure visualization is interactive, which gives us permission to manipulate the structure of protein molecules or any other molecule through graphical user interface according to your study or work purpose. Just at a click of a mouse you rotate, zoom in and out, and moves the structure in real time. You can study and analyse a segment of the molecule in great detail. It provides various shapes and colours for your structure; manipulation of protein structure may involve adding or removing charges, adding polar hydrogens, minimizing energy and identification of active sites for docking purposes.

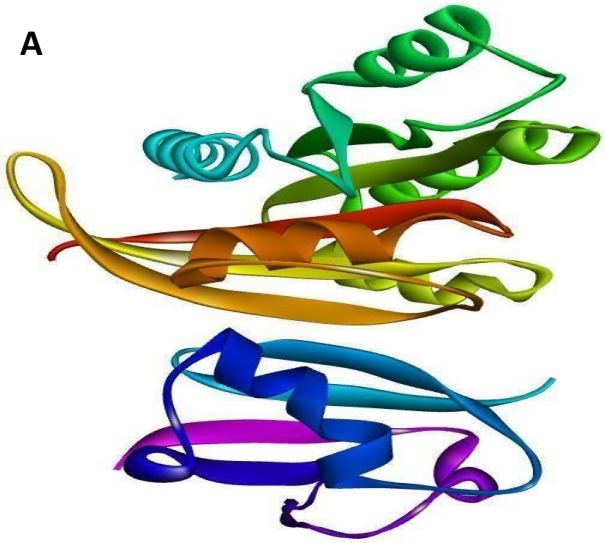
In-silico visualization provides various visualization styles as wire frame, ball and stick, space filling, solid spheres and ribbons. Wire frame is considered as the simplest form for structure visualization. Iti is just a line draw which represents the bond between atoms. It is a useful or skeletal view of the molecule where Cα of each residue are connected. Ball and stick model can be imagined as a sphere connected with a rod. The sphere represents the atom and the rod is the bond between atoms. In the space filling model, atoms are visualized as large solid

spheres according to the Vander waals radii of particular atoms. Ribbon diagrams are the most interactive form of visualization. Cylindrical or spiral ribbons indicate α-helices and β-sheets are represented by a flat arrow. This form allows easy identification and a clear view of topological areas of structure. Different visualization forms can be chosen as per convenience.

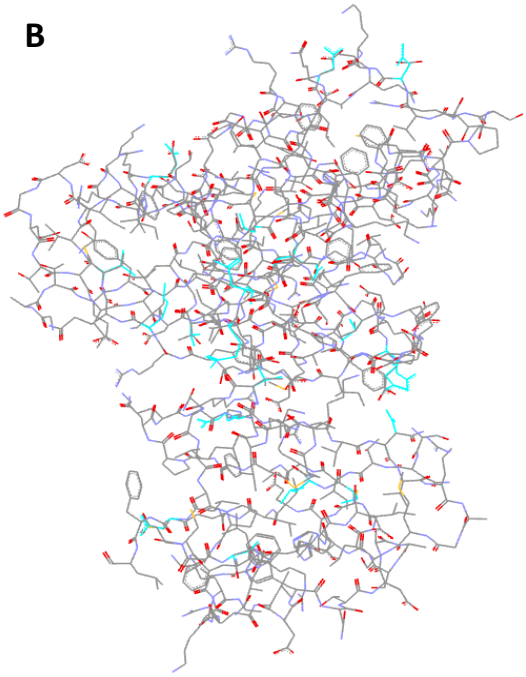
Here are list of some structure visualization tools: -

Rasmol	***http://www.openrasmol.org/***
Swiss-PDB Viewer	***https://spdbv.vital-it.ch/***
Mol-script	***www.avatar.se/molscript/***
Chime	***www.mdlchime.com/chime/***
Chimera	***https://www.cgl.ucsf.edu/chimera/***
Pymol	***https://pymol.org/2/***

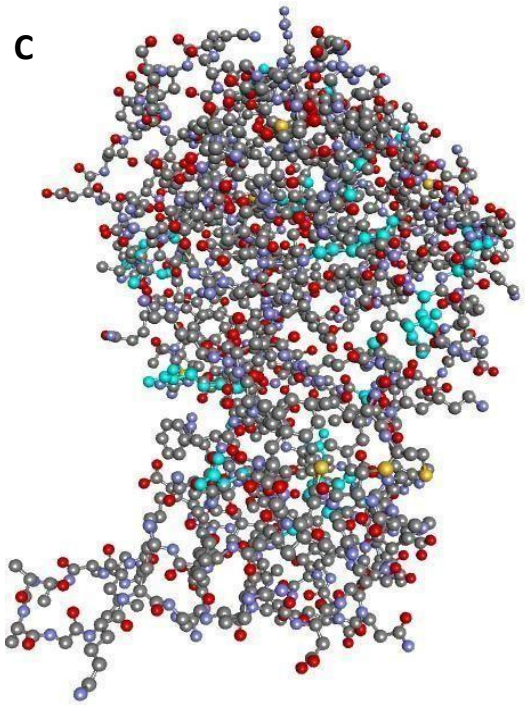
A



B



C



15

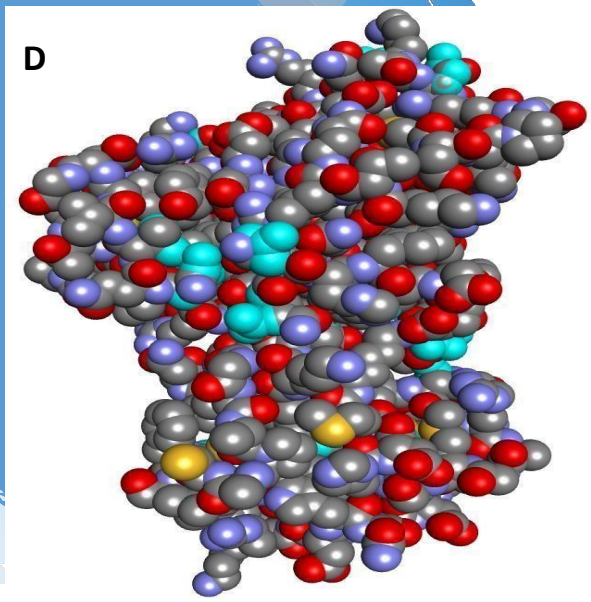


Figure 1: Examples of different visualization forms of protein molecules. (A) Ribbons (B) Wireframe (C) Ball and Stick (D) Space-filling Spheres

CONCLUSION:-

Protein structure prediction and visualization is an important step in study of gene expression and drug designing for a particular disease. Bioinformatics and computational biology really made it very easy to predict the structure of a particular protein molecule and its visualization. Various tools and applications are available to perform these steps as described above. Visualization gives a whole idea about the topology, molecular interactions, active sites and the geometry of the molecule. It helps for identifying the best position for drug interaction. Structure prediction and visualization makes your calculation for precise and accurate for docking which will result in time and money saving.

REFERENCES:-

[1] H. Deng, Y. Jia, and Y. Zhang, "Protein structure prediction," *Int. J. Mod. physics. B*, vol.32,no.18,Jul.2018,doi:10.1142/S021797921840009X.

[2] B. Y. Khor, G. J. Tye, T. S. Lim, and Y. S. Choong, "General overview on structure prediction of twilight-zone proteins," *Theor. Biol. Med. Model.*, vol. 12, no. 1, Dec. 2015, doi: 10.1186/S12976-015-0014-1.

[3] J. Moult, "Predicting protein three-dimensional structure," *Curr. Opin. Biotechnol.*, vol. 10, no. 6, pp. 583–588, Dec. 1999.

[4] T. Hameduh, Y. Haddad, V. Adam, and Z. Heger, "Homology modeling in the time of collective and artificial intelligence," *Comput. Struct. Biotechnol. J.*, vol. 18, pp. 3494–3506, Jan.2020, doi: 10.1016/J.CSBJ.2020.11.007.

[5] D. H, J. Y, and Z. Y, "Protein structure prediction," *Int. J. Mod. physics. B*, vol. 32, no. 18,Jul.2018,doi: 10.1142/S021797921840009X.

[6] X. Martinez, M. Chavent, and M. Baaden, "Visualizing protein structures — tools and trends," *Biochem. Soc. Trans.*, vol. 48, no. 2, pp. 499–506, Apr. 2020, doi: 10.1042/BST20190621.

16

COMPUTATIONAL BIOLOGY FOR AGING

Prithika.V.S & Gunasekaran.R, III - BT

Ageing in organisms is a process in which there is progressive decline in organism's health and can ultimately lead to death. The speed of ageing in different organisms is different, even when they are closely related. However, it is not clear yet, "What is the process of ageing?", but definitely genes play some role.

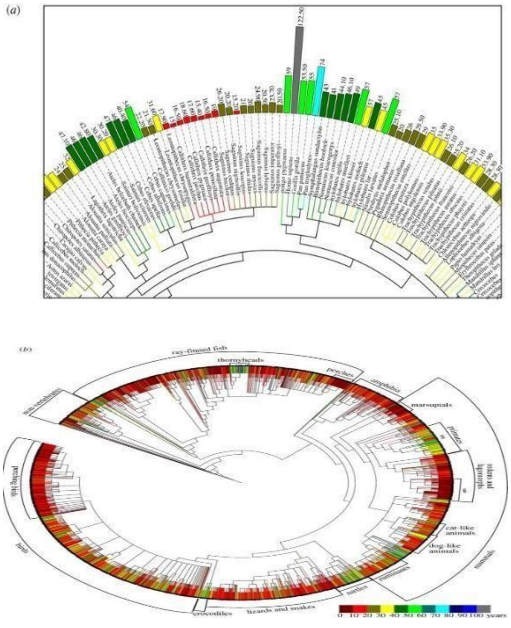


Figure 1(a, b): Bioinformatics analysis of phylogenetic clustering of longevity records

For finding the cause of ageing different computational biology comes into action. Computational biology comprises with computational tools which are available for researchers.

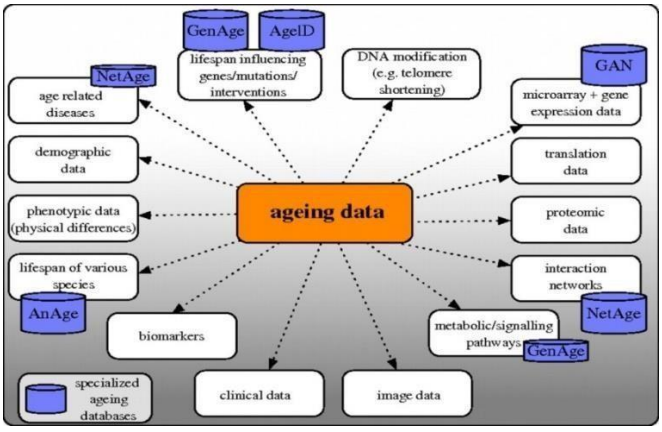


Figure 2: Bioinformatics analysis of phylogenetic clustering of longevity records

17

RESOURCES, DATABASES & TOOLS:-

Data collection in ageing researches are not easy to collect as there are different researches on different platforms around the world. A variety of data could be seen in the form of genomics, proteomics, metabolomic and transcriptomic. HUMAN AGEING GENOMIC RESOURCES (HAGR) database have following components: GenAge and AnAge .

1) GenAge

GenAge is a database related to ageing and genes. GenAge identifies gene pathways related to ageing & studies wrt to a database containing a list of human genes analysed for their connection with human lives.

2) AnAge

AnAge is an informative database related to ageing & life history of animals including previous records. AnAge was majorly developed for comparative biological studies for the ageing & life related aspect.

3) Gene Aging Nexus

Gene Aging Nexus is a web database and data search platform for microarray data on aging that is freely accessible to query, analyse & visualizing cross-species data on aging.

database	description	URL
GenAge (HAGR)	a database of genes related to longevity or ageing	http://genomics.senescene.info/genes
AnAge (HAGR)	a database of longevity and ageing in animal species	http://genomics.senescene.info/species
Gene Aging Nexus	a data mining platform for the biogerontological–geriatric research community	http://gan.usc.edu
AgeID	ageing genes and interventions database	http://uwaging.org/genesdb
NetAge	a database containing miRNA-regulated PPI networks for longevity, ARDs and ageing-associated processes	http://netage-project.org/

Figure 3: Databases currently available for searching and/or downloading data related to ageing

DATA PROCEDURAL WAYS:-

1) Gene-Expression Analysis

In this way of computational aging, most of the gene expression data originates from microarrays. For experiment at least 2 different conditional genes are taken & are hybridized in micro-arrays for the detailed bio-informatics

analysis. These -omic techniques such as (microarrays proteomics and metabolomics) requires specific computational methods. Combining the results of the different techniques is a general challenge in biological research which needs to be addressed in order to get a more complete understanding.

2) Proteomics & Metabolomics

As gene expression uses microarrays or Next Gen Sequencing, Proteomics works on protein profiling. Different proteomics techniques have different focuses like protein concentration, modification, complexions etc. The no of direct targeting proteomics studies is less. Protein changes are observed which could lead to cellular maintenance & several processes using transcriptional analysis.

Metabolomics is the examination of the metabolic processes in the cells or tissues throughout. Eg. Glucose or Oxygen species are important for ageing. The comparison of long lived mutant, if profiled by combining microarray, proteomics & metabolomics would be an interesting study.

3) Pathway Analysis

One of the main challenges in interpreting gene expression data is trying to understand the biological consequences of gene-expression changes. To tackle out the challenges in interpreting gene expression data, the pathway analysis is involved, be in signalling or regulatory pathway.

We have 3 approaches in pathway analysis to ageing:

i. Analysis of protein-protein interaction
ii. Gene-regulatory network analysis
iii. Modelling quantitative properties of reaction.

4) Image analysis

Various laboratories have developed tools for the expression & automated analysis of microarray images. As a second approach, image-textured analysis is done with two characteristics reflecting grey-level co-occurrence & directionaling.

This methods, fitted to estimate the age of normal living wormsfrom images, can be used to estimate how much younger a long-lived worm looks when compared with its chronological age.

COMPARATIVE ANALYSIS OF SPECIES & TISSUES:-

By comparison of different species can help for analysis of ageing and causes of ageing. For the comparison of data information on ageing in phenotypes, experiment details and other's knowledge about the organism's genomics.

Lifespan analysis of organism can also be done for the studies of comparative analysis. For the experimenting about ageing generally in yeast and invertebrates with worms, which are mostly used. These organisms have short lifespan and could be used as model organism for research purpose.

1) Within Species (Comparing genotypes)

By comparing genotype within species, certain information could be gained regarding ageing. Example: A study in human beings stated similarity and difference in expression changes in the medulla and cortex of kidney with age.

2) Within Species (Tissue Specificity)

Ageing could also be associated with changes in tissue specificity. Example: Decrease of genes which makes the mitochondrial electron transport chain with increasing age.

3) Within Species (Population Studies)

In all types of comparative studies the most powerful study is population based. Example: Datasets have been collected from different families which shows longitivity exceptionally. The long-lived have been established as 'model' populations in study of longitivit.

CONCLUSION:-

Computational systems modelling is a novel integrated approach that provides a powerful foundation for gaining an in-depth understanding of how human metabolism is perturbed by aging. It also highlighted the rationale for using computational systems models. The steps involved in the model

building process were also outlined, and a wide variety of models from cellular to whole body were discussed that emphasized the utility of modelling to aging research. It is highly probable that in future years computation systems modelling will be further embedded within systems biology.

Even the data is collected and organized from various ageing researches & studies for their examination, they have one thing which is common i.e. the techniques are dependent on Bioinformatics which is omnipresent in the way that it is used extensively in all the fields of ageing studies from genomics to proteomics.

The majority of the research in ageing involve proteomics, which results in making data sets with data from high-expression combining the resulting datasets could lead to more useful information results at the mechanism of ageing. As we are gaining the knowledge and information, there is a need for the betterment & development of the tools for more critical computational biology

REFERENCES:-

[1] M. T. M. Auley and K. M. Mooney, "Computational Systems Biology for Aging Research," *Interdiscip. Top. Gerontol.*, vol. 40, pp. 35–48, 2015, doi: 10.1159/000364928.

[2] R. A. Avelar *et al.*, "A multidimensional systems biology analysis of cellular senescence in aging and disease," *Genome Biol. 2020 211*, vol. 21, no. 1, pp. 1–22, Apr. 2020, doi: 10.1186/S13059-020-01990-9.

[3] D. Wieser, I. Papatheodorou, M. Ziehm, and J. M. Thornton, "Computational biology for ageing," *Philos. Trans. R. Soc. B Biol. Sci.*, vol. 366, no. 1561, p. 51, Jan. 2011, C

[4] R. Song, E. A. Sarnoski, and M. Acar, "The Systems Biology of Single-Cell Aging," *iScience*, vol. 7, pp. 154–169, 2018, doi: 10.1016/j.isci.2018.08.023.

21

BIOTECHRONZZ
2021-2022

BIOPROCESS MODELING

Bruce Joshua sinclair, III - BT

A procedure that delivers an organic material, for example, a hereditarily designed microbial strain, for commercial use. Production of an industrially valuable substance or fuel by natural interaction, like microbial fermentation or degradation. To get ready, produce, or treat (a substance) through a bioprocess. All in all, a bioprocess comprises of a cell culture in a bioreactor, which is a process ready to establish an ideal development climate. The focal object of a bioprocess is the cell. A living cell is a profoundly mind-boggling framework which is regularly characterized as the tiniest independent natural unit.

BIOPROCESS MODELING:-

To further develop process comprehension or execution, different programmed devices can be created: test systems ready to replicate framework practices, programming sensors which permit getting an estimation of an unmeasured sign or regulators to keep up with ideal circumstances.

22

This multitude of instruments depend on a portrayal of the thought about the considered system, a numerical model. Such a model might come in different shapes and be stated with changing levels of numerical formalism. When the model is laid out it can then be utilized, with sensible certainty, to predict execution under contrasting interaction conditions, and utilized for process plan, advancement, and control.

Input of plant or exploratory information is, obviously, expected to lay out or approve the model, yet the amount of information expected when contrasted with the experimental methodology is impressively diminished.

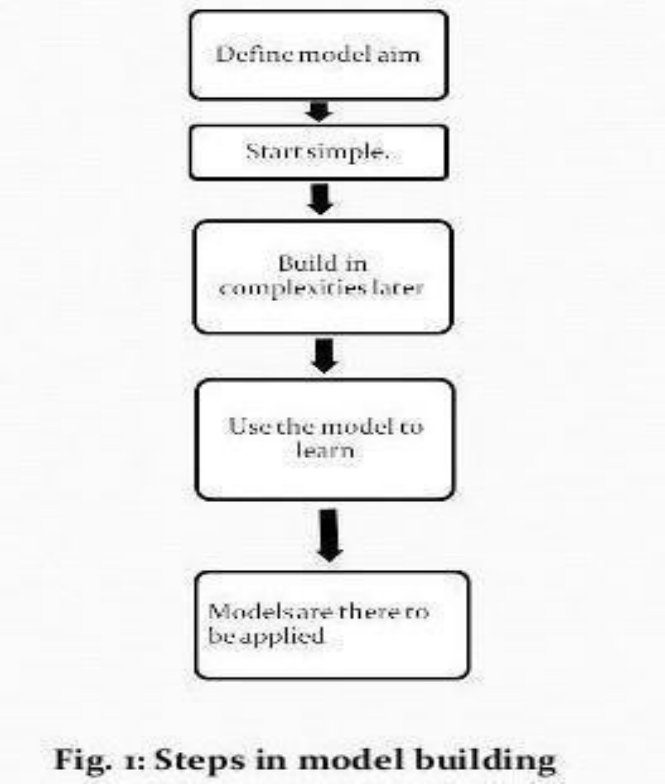


Fig. 1: Steps in model building

COMPARISON OF THE MODELING AND EMPIRICAL APPROACHES:-

Empirical Approach: Measure usefulness for all blends of plant working circumstances and make relationships.

Advantage: Little idea is important.

Disadvantage: Many examinations are required.

Modelling Approach: Establish a model and configure examinations to decide the model boundaries. Contrast the model conduct and the trial estimations. Utilize the model for rational design, control, and enhancement.

Advantage: Fewer examinations are required, and more prominent agreement is acquired.

Disadvantage: Time is expected for creating models.

GENERAL ASPECTS OF THE MODELING APPROACHES:-

A fundamental utilization of a cycle model is to dissect test information and to utilize this to describe the process, by appointingmathematical qualities to the significant processvariables. The use of a joined displaying and

recreation approach prompts the following benefits:

1. Modelling works on comprehension.
2. Models help in trial plan.
3. Models might be utilized predicatively for plan and control.
4. Models can be utilized in preparing and instruction.
5. Models might be utilized for process streamlining.

STAGES IN THE MODELING PROCEDURE:-

- Appropriate meaning of the issue.
- Planned in numerical terms.
- Mathematical techniques for arrangement with computerized recreation.
- The legitimacy of the arrangement relies upon the right decision of hypothesis (physical and numerical model), the capacity to distinguish model boundaries accurately and exactness in the mathematical arrangement strategy.
- Care and judgment should be taken with the end goal that the model doesn't become over complex.

CONCLUSION:-

In the roadmap of bioprocess development and manufacturing, process models play a crucial role at several stages. Enabled by advanced sensor technology, robotic HT experimental systems, enhanced computational power, versatile data management solutions, and a broad set of data analytics techniques, the biopharma industry faces a solid basis for the digital transformation

REFERENCES:-

[1] H. Narayanan *et al.*, “Bioprocessing in the Digital Age: The Role of Process Models,” *Biotechnol. J.*, vol. 15, no. 1, Jan. 2020, doi: 10.1002/BIOT.201900172.

[2] T. Scheper *et al.*, “Digitalization and Bioprocessing: Promises and Challenges,” *Adv. Biochem. Eng. Biotechnol.*, vol. 176, pp. 57–69, 2021, doi: 10.1007/10_2020_139.

FERMENTATION TECHNOLOGY IN INDUSTRIAL APPLICATION

Indhusree. V & Ilakiya. M, II - BT

Fermentation is one of the oldest techniques in food processing and is used for production of alcoholic beverages, breads, cheese, and other products. Louis Pasteur in the 19th century used the term fermentation in narrow sense todescribe the change brought about by yeast and other microorganisms growing in the absence ofair (anaerobically); he also recognized that ethyl alcohol and carbon dioxide are not the only products of fermentation.

This technique due to the mild condition of fermentation does not have deleterious effect on sensory features and nutritional value and also by-products of fermentation such as organic acids and ethanol are responsible for some flavour and aroma changes.

It can also be defined as the generation of energy involving an endogenous electron acceptor from the bacterial (enzymatic) oxidation of any organic material. The result of fermentation depends on the organic substrate, most frequently carbohydrate or protein, the applied catalyst in the form of either isolated enzyme or its microorganism producer, as well as the process conditions. Some important fermentation products:-

PRODUCT	ORGANISMS	USES
Ethanol	Saccharomyces cerevisiae	Industrial solvents, beverages
Glycerol	Saccharomyces cerevisiae	Production of explosives
Lactic acid	Lactobacillus bulgaricus	Food and pharmaceutical
Acetone and Butanol	Clostridium acetobutylicum	Solvents
α-amylase	Bacillus subtilis	Starch hydrolysis

A fermen tation process requires a fermenter or bioreactor for successful production because it provides the following facilities for the process such as contamination free environment,specific temperature maintenance, maintenance of agitation and aeration, pH control, monitoring Dissolved Oxygen (DO), ports for nutrient and reagent feeding, ports for inoculation and sampling, fitting and geometry for scale upm minimize liquid loss and growth facility for wide range of organism.

TYPES OF FERMENTER:-

(i) Simple fermenters (batch and continuous)

(ii) Fed batch fermenter

(iii) Air-lift or bubble fermenter

(iv) Cyclone column fermenter

(v) Tower fermenter

(vi) Other more advanced system

Figure 1. A Laboratory Fermenter

Depending on the fermenter different types of fermentation processes are involved. There are mainly three types of fermentation processes which are as follows:-

- Batch Fermentation
- Fed Batch Fermentation
- Continuous Fermentation

1) Batch Fermentation

Nutrients are added in the fermentation for the single time only and growth continues until the particular nutrients are exhausted. In the batch process when the microorganism is added into a medium which supports its growth, the culture passes through number of stages known as 'growth curve'.

A typical growth curve consists of following stages:-

a) **Lag Phase:** Immediately after inoculation, there is no increase in the number of the microbial cells for some time and this period is called lag phase.

b) **Acceleration Phase:** The period when th cell just start increasing in numbers is known as acceleration phase.

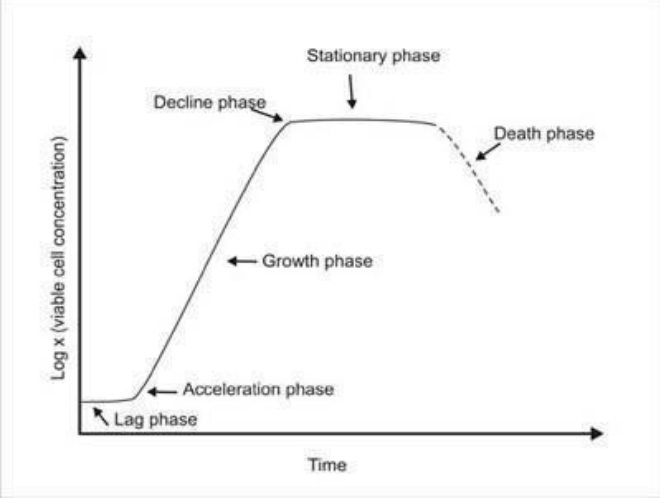
26

c) **Log or exponential Phase:** This the time period when the cell numbers steadily increase.

d) **Deceleration Phase:** The duration when the steady growth declines.

e) **Stationary Phase:** The period where there is no change in microbial cell number is the stationary phase. This phase is attained due to depletion of carbon source or accumulation of the end products.

f) **Death Phase:** The period in which the cell numbers decrease steadily is the death phase. This is due to death of the cells because of cessation of metabolic activity and depletion of energy resources.



Advantages and Disadvantages of Batch Fermentation:-

Advantages

a) It is easy to operate and low on maintenance.

b) It has a lower installation cost.

c) It has very low chances of contamination.

d) Easier to validate.

Disadvantages

a) It has considerable down time.

b) Higher labour costs.

c) Accumulation of toxic products.

2) Fed Batch Fermentation

In this type of fermentation, freshly prepared cultural media is added at regular intervals without removing the culture fluid. This increases the volume of the fermentation culture fluid. This increases the volume of the fermentation is used for production of proteins from the recombinant microorganism.

The total amount of the biomass in the vessel increases but biomass concentration is maintained constant.

Advantages and disadvantages of fed batch fermentation:-

Advantages

a) The operating cost, down time etc are less than batch but higher than continuous fermentation.
b) It has a high growth rate compared to batch fermentation.

Disadvantages

a) It has a higher installation costs than batch fermentation.
b) Large medium supply is required.
c) Requires sophisticated equipment to control feed rate and maximise productivity.

3) Continuous Fermentation

The growth rate and physiological conditions of microorganisms can be maintained by using a process of continuous culture (chemostat). In this the products are removed continuously along with the cell girth and addition of fresh culture media. This results in a steady or constant volume of the contents of the fermentor. This type of fermentor is used for the production of single cell protein (S.S.P), antibiotics and organic solvents.

Advantages and disadvantages of continuous fermentation

Advantages

a) Low down time.
b) Reduced labour time and operating costs.
c) Culture maintained at constant growth rate.
d) Smaller vessels are needed.
e) Higher productivity.

Disadvantages

a) Requires expensive, high quality and reliable equipment
b) Requires continuous product separation and purification.
c) It has increased risk of contamination due to extended operation.

The component parts of a fermentation process:-

(I) The formation of media to be used in culturing the process organismduring the development of the inoculum and in the productionfermenter.

28

(II) The sterilization of the medium, fermenters and the ancillary equipment.

(III) The production of an active, pure culture in sufficient quantity to inoculate the production vessel.7

(IV) The growth of organisms in the production fermenter under the optimum conditions for the product formation.

(V) The extraction of the product and its purification.

(VI) The disposal of effluents produced by the process.

The range of fermentation process. There are five major groups of commercially important fermentations: Those that produce microbial cells (or biomass) as the product, e.g. single cell protein, baker's yeast, lactobacillus, E. coli, etc. Those that produce microbial enzymes: catalase, amylase, protease, pectinase, glucose isomerase, cellulose, hemicellulose, lipase, lactase, streptokinase, etc. Those that produce microbial metabolites:

- Primary metabolites – ethanol, citric acid, glutamic acid, lysine, vitamins, polysaccharides, etc.
- Secondary metabolites – all antibiotics fermentation

Those that produce recombinant products: insulin, hepatitis B vaccine, interferon, granulocyte colony-stimulating factor, streptokinase. Those that modify a compound which is added to the fermentation that transformation process i.e. Biotransformation: phenylacetslcarbinol, steroids biotransformation etc.

REFERENCES:-

[1] M. Choudhary, S. Joshi, S. S. Bhagyawant,and N. Srivastava, "Advances in Fermentation Technology: Principle and Their Relevant Applications," *Princ. Appl. Ferment. Technol.*, pp. 53–63, Aug. 2018, doi: 10.1002/9781119460381.

[3] R. Joshi, V. Sharma, and A. Kuila, "Fermentation Technology: Current Status and Future Prospects," *Princ. Appl. Ferment. Technol.*, pp. 1–13, Aug. 2018, doi: 10.1002/9781119460381.CH1.

29

BOTOX: A BEAUTY OR BEAST?

Monish Kumar. R, II - BT

Today our society is too much obsessed with glamorous skin, lean figure and living in such a hyperesthetic society that results in demolition of our own lives. In between we all have heard a name, botox, used for facial and medical treatments and has become the primarily cause for deteriorating human health.

Botox is actually a pharmaceutically made drug which inhibits or slows down the muscle moment. It is made from Clostridium toxin, which the bacterium *Clostridium botulinum* produces. This toxin also leads to condition known as botulism. Botox derives from naturally occurring bacteria, C. botulinum, found in soil, lakes, forests, and the intestinal tracts of mammals and fish. This bacteria and its spores are usually harmless, but when its spores transforms and population increases it produces a deadliest neurotoxin known as botulinium toxin which causes botulism. From research it has been concluded that 1 gram of a crystalline form of the clostridium toxin could kill 1 million people and few kilograms of it could demolish entire race of human.

HOW DOES IT WORK?

Botox is basically a neurotoxin that disrupts the nerve signalling pathway, temporarily paralyzing the muscle moment. For muscle contraction, the nerves releases the chemical messenger known as acetylcholine which binds at the ending of nerve and muscle junction and

helps the muscle cells to contract. Botox injections inhibits the release of acetylcholine thus preventing the muscle to contract and helps the muscle to become less stiff.

WHY BEAUTY OR BEAST?

Botox is primarily used in cosmetic products and in facial surgeries worldwide for enhancing the beauty of face. According to the American Board of Cosmetic Surgery, Botox injections are the most widely used worldwide. In 2016, over 7 million people had Botox treatments. Its effects are temporary that lasts from 3 to 12 months depending upon the type of treatment.

TREATMENT MAINLY INCLUDES

- Removal of wrinkles around the eyes, known as crow's feet.
- Wrinkles between the eyebrows, known as frown lines or elevens.
- Lines at the mouth corner.
- Reducing symptoms of overactive bladder.
- Prevention of migraine.
- Crossed eyes, crown adjustment.
- Upliftment of lips.

Moreover, botox is widely used for camel's beauty contest in Saudi Arabia, where camels are beautified by lifting their lips, high hump, bushy eyelashes, etc.

So the questions arises is really botox is of such great importance for beautifying, the answer is no. As it can turn anyone into beauty but can also turn anyone into beast if not taken properly or

administered by non-professionals and also comprises of many risks and side effects.

RISKS & SIDE EFFECTS:-

- Eye dryness after eye wrinkle treatment.
- Upset stomach.
- Mild or sometimes severe pain, redness, stiffness at the site of injection.
- Temporary eyelid drooping.
- Temporary weakness or paralyzing conditions in nearby muscles.
- Different neuromuscular disorders, cardiovascular conditions.

From recent studies it has been seen that average cost for botox treatment ranges from 300-500 USD depending on the type of treatment, number of botox units involved and the person who gives the treatment.

CONCLUSION:-

Though botox is very useful in cosmetics and different facial treatments worldwide and can really turn anyone into beauty but it also comes with its own disadvantages which can also turn anyone to beast. Thus proper, limited and safe use of botox is very essential and the treatment must be taken by the professionals only otherwise it leads to asymmetrical conditions.

REFERENCES:-

[1] N. Althawadi, A. Ujam, and B. Visavadia, "Botox hiddendangers," *Br. Dent. J.*, vol. 232, no.4, pp. 192–193, Feb. 2022, doi: 10.1038/S41415-022-4006-3.

[2] J. Carruthers and A. Carruthers, "Botox: beyond wrinkles," *Clin. Dermatol.*, vol. 22, no. 1, pp. 89–93, 2004, doi: 10.1016/J.CLINDERMATOL.2003.11.013.

[3] S. K. Mendez-Eastman, "BOTOX: a review," *Plast. Surg. Nurs.*, vol. 20, no. 2, 2000, doi: 10.1097/00006527-200006000-00003.

32

BIOFUELS & BIODIESELS

Rupa. R & Madhumithraa.P, I - BT

Biofuels are the types of fuels which are derived from biomass (could be any plant or animal material which is used as fuels). From Sun we get electricity through photovoltaic conversion. Other way of getting energy is winds as due to uneven heating there is different pressure due to different temperature, due wind is flown from which with the help of windmills we get energy. These are renewable resources in which there is no production of greenhouse gasses and a fuel supply never runs out. Fossil fuel like coal, petroleum etc. needs millions of years so these are non-renewable. So, there is the need of that fuel arises which is renewable and less flammable that is biofuels. Genomic of cellulosic biofuels which could be alternative of fossils fuels have potential to meet demands as fossils fuels need millions of years for their generation.

INDIAN & GLOBAL SCENARIO OF BIOFUELS:-

According to report on March 24, 2009 the renewable energy can meet 35% of power requirement in India by 2030. MNRE (Minister of new and Renewable energy) haveprepared national policy on biofuels in which 20% blending of Biofuels to traditional petrol by 2017 so as to conserve non-renewable resources.

According to British Petroleum's statistical review of world energy 2016, India's oil consumption has increased from 180.8 million tons to195.5 million tonnes which are 8.1% increase in 2015 when compared to 2014 which is 4.5% of world's total oil consumption.

Global biofuels increased gradually by 7.4%, in 8.5% Brazilian agricultural territory 0.9% is devoted to sugarcane in which there is ethanol production, in Sao Paulo State of Brazil the bioethanol production contributes 57% offuels. Soybean and palm oil are major source of biodiesel

TYPES OF BIOFUELS:-

1) Hydrogen

Doesn't exist on earth as gas, we need to separate from other elements. There are many methods for producing hydrogen like Steam refining, electrolysis, or biological method. First two are common method in which hydrogen is not created biologically. For Biological production of Hydrogen there are many methods like in algae and cyanobacteria their bio photolysis of water and hydrogen is produced. In "dark" fermentation with the help of anaerobic organisms such as acidogenic bacteria used to produce hydrogen. For high yields of hydrogen, we use thermophilic microorganism is used. Microbiological hydrogen production is yet not developed or come into economical viable technology so it is lagging behind the expectation.

2) Methane/Biogas

In this Methane and carbon dioxide are produced by biogas plant. The raw material taken is organic house hold or industrial waste. Advantages of biogas is that we have option to use the polysaccharides constituent of plant material to produce energy. Cow manure, manure from other animals like pigs, chicken and horses, fat from slaughter waste or frying oil, organic house or garden waste, municipal solid waste and rotten stuff, organic rich industrial waste water is used as combustible substrate for biogas. Maize, clover, grass, willow etc. are grown for biogas production. Biogas formation from plant fibers works in three stages:-

1) Hydrolysis of polysaccharides, protein and fats into oligosaccharides and sugar
2) Acetogenesis that is synthesis if acetate, which includes the formation of acetate by the reduction of CO_2

34

and the formation of acetate from organic acids.

3) Methanogenesis with up to 70% (v/v) CH4 and 30% CO2 and products NH3 and H2s by slow growing archaea.

There are 2 types of biogas plants used in India one is Floating gas holder type of plant in which dome id floating and gas is taken out through outlet pipe, other is fixed type in this dome is fixed and the function is similar to floating holder type biogas plant.

3) Ethanol

Industrial ethanol production is done mainly from sugarcane molasses or enzymatically hydrolyzed starch that is from corn or other grains and batch fermentation with Yeast saccharomyces cerevisiae to create ethanol. The Byproducts in batch fermentation are CO2, methanol, glycerol etc. If ethanol is used as fuel there is no need rectified. Azeotrope of 95.57wt% ethanol with 4.43wt% water is used in ignition cars known as AEHC (alcohol etilico hidratado combustion) in Brazil. Higher water content causes problem when ethanol and gasoline mixtures partly as it leads to phase separation between water and gasoline. The glucose syrups with the help of yeast fermentation could lead to formation of ethanol. Which is processed 20% (v/v) of ethanol are produced in present day industrial yeast fermentation vessels from starch-derived glucose.

BIODIESEL:-

IMPORTANCE OF BIODIESEL

As we know that there will be future scarcity of fossil fuel worldwide so, there we have to come with an alternative of them and biodiesel seems to be that therefore there are some importance of them listed below-

1) Energy Independence

High cost of diesel leads to disproportionate impact on the poorest countries, 38 of which are net importers and 25 of Which import all of their oil; the question of trying to achieve greater energy independence one day through the development of bio-fuels has become one of an,

alternative as bio-fuels programme is being launched somewhere in the developing world.

2) Smaller Trade Deficit

Rather than importing other countries' ancient natural resources, we could be using our own living resources to power our development and enhance our economies. Instead of looking to the Mid-east for oil, the world could look to the tropics for bio-fuels. producing more bio-fuels will save foreign exchange and reduce energy expenditures and allow developing countries to put more of their resources into health, education and other services for their neediest citizens.

3) Growth

Bio-fuels create new markets for agricultural products and stimulate rural development because bio-fuels are generated from crops At the community level, farmers that produce dedicated energy crops can grow their incomes and grow their own supply of affordable and reliable energy. At the national level, producing more bio-fuels will generate new industries, new Technocrats, new jobs and new markets.

4) Cleaner Air

Bio-fuels burn more cleanly than gasoline and diesel. Using biofuels means producing fewer emissions of carbon monoxide, particulates, and toxic chemicals that cause smog, aggravate respiratory and heart disease, and contribute to thousands of premature deaths each year.

5) Less Global Warming

Bio-fuels contain carbon that was taken out of the atmosphere by plants and trees as they grew. The Fossil fuels are adding huge amounts of stored carbon dioxide (CO2) to the atmosphere, where it traps the Earth's heat like a heavy blanket and causes the world to warm. Studies show that bio-diesel reduces CO2 emissions to a considerable extent and in some cases all most nearly to zero.

INDIAN SCENARIO OF BIODIESEL:-

India, currently ranked fifth in the energy consumption, is expected to be ranked third by 2030. Therefore, there is an indication by the Indian government to use 20% biofuel. Hence,

there is a need to develop and modify the design of the fuel handling and fuel injection equipment (FIE) to deal with the proper blending of fuels. According to a study in 2015, under a BAU scenario, demand for diesel for transport is expected to grow from 46.9 billion liters in 2010 to 155.7 billion liters in 2030. Biodiesel demand for 20 percent blending targets is expected to grow 19.8 and 31.1 billion liters in 2020-21 and 2030-31, respectively. The increased move towards biofuels is spurred by global political, economic and environmental events, especially rising crude oil prices. Current sky touching hike in oil prices from US$60 and US$70/barrel in 2006 to price of US$ 140 a barrel in 2008 has threatened the economic stability of oil-dependent countries and of the world at large. The International Energy Agency projected that biofuels would be competitive with petroleum at petroleum prices of between US$60 and US$100 a barrel. That point has been crossed, and markets seem to be internalizing expectations of unstable and perhaps rising future oil prices. The competitiveness of biodiesel, however, depends heavily on the relative prices of oil and of agricultural feedstock for biodiesel.

NEED OF BIODIESEL:-

1) Biodiesel use helps improve air quality. While the actual numbers depend on the blend used, pure biodiesel is known to produce up to 76% fewer greenhouse gas emissions than petroleum diesel, as well as significantly less particulate matter, a known contributor to asthma and lung disease.

2) It's a sustainable product. No one knows exactly how long the world's oil reserves will last, but there's no doubt that they're limited. Unlike standard diesel, which is drawn from this finite petroleum supply, biodiesel is made from simple, plant-based and totally renewable ingredients, like vegetable oil. Sequential biodiesel is even more sustainable because it's made from used cooking oil recycled from local restaurants. This gives Sequential fuel a carbon footprint 85% smaller than petroleum diesel.

3) Biodiesel is compatible with diesel vehicles by default. Nearly all diesel engines dating back to 1993 can use biodiesel in place of petroleum diesel without a single modification. Plus, it can

37

be used on its own for optimum emission reduction or blended with petroleum diesel when you're seeking to maintain the power delivered by petroleum products.

4) Biodiesel use spurs economic development biodiesel offers a viable petroleum diesel alternative, it has a very bright future. Demand for the fuel continues to rise across the board, forecasting a booming industry packed with job opportunities. According to the National Biodiesel Board, 2.8 billion gallons of biodiesel were produced in the United States in 2016 and the industry supported 64,000 jobs nationwide.

5) Biodiesel is safer to store, handle and transport. We've likely heard horror stories about major petroleum spills, which can be environmentally devastating and even lead to massive explosions. Fortunately, using biodiesel significantly reduces the risk of these incidents. Pure biodiesel is completely non-toxic and has a much higher flash point than petroleum diesel, making it less likely to catch fire.

CONCLUSION:-

To reduce CO_2 emissions and fulfill the increasing energy demands, a horde of research endeavors have been commenced to develop renewable and sustainable energy resources, which must be environmentally friendly, and cost-effective. Though the researchers could obtain more than 95% yield from various feedstock and catalyst yet, thecommercialization of biodiesel and biofuel has not been accomplished. The feasibility ofproduction and utilization of biodiesel from various sources has been affected by severalparameters.

REFERENCES:-

[1] J. T. McEwen and S. Atsumi, "Alternative biofuel production in non-natural hosts," *Curr. Opin. Biotechnol.*, vol. 23, no. 5, pp. 744–750, Oct. 2012, doi: 10.1016/J.COPBIO.2011.12.019.

[2] R. Karpagam, K. Jawaharraj, and R. Gnanam, "Review on integrated biofuel production from microalgal biomass through the outset of transesterification route: a cascade approach for sustainable bioenergy," *Sci. Total Environ.*, vol. 766, Apr. 2021, doi: 10.1016/J.SCITOTENV.2020.144236.

38

PRODUCTION OF SCP'S FROM ANIMAL WASTES

Necthra. K, IV - BT

In recent times economical production of high-quality SCP with low nucleic acid can be achieved by using animal manure. To reduce the cost of protein feedstock for animal feed, the use of single cell protein (SCP) can be produced from waste of animal agriculture. Study reveals that chicken manure is the best substrate for SCP production by submerged fermentation using photosynthetic bacteria, regression analysis shows that the product was significantly influenced by chicken manure content, inoculum size, and cultivation time.

The animal feed cost accounts for 60%–70% of total livestock production costs it has increased significantly in recent times, and there is an increasing reliance on soybean meal and fish meal for protein supply in feeds. (SCP) proves to be one of the appropriate protein source and feed formulation as it can be used as protein supplement or replacement to replace the costly protein materials and also massive quantities of SCP can be produced in a short time. Henceforth, SCP is considered as a promising product to solve the problem of the high price of protein feed. Also it has been proved in 2018 ,that SCP can be produced on industrial wastewater to produce the protein feed and simultaneously can be used to treat wastewater in environmental management. These are basically a dietary single-cell microorganisms whose biomass or protein extracts are derived from pure or mixed microscopic algae, yeasts, mushrooms or bacterial cultures etc, hence these microorganisms can be used as protein-rich foods or dietary supplements but, they are mainly used as food for human and animal

consumptions.

SCPs are a good alternative to replacing protein of agricultural origin, since SCP production doesn't requires high water consumption besides it does not cover large areas of land, does not endanger environmental diversity and does not contribute to climate change also does not produce high greenhouse gas emissions, Furthermore to reduce the cost production of SCP, it is essential to use biodegradable agro - industrial by-products and waste as a source of nutrients for the cultivation of microorganisms., like chicken manure as mentioned above.

Animal wastes mostly includes manure from cow, buffalo, and poultry etc. There exists a serious disposal problem regarding animal manure as they can contaminate both surface and groundwater. Therefore, manure management is the important issues in order to minimize the waste and to reduce the pollution. SCP as being inexpensive has gained quite a popularity in this field.

MATERIAL REQUIRED:-

Basically, carotenoid-producing photosynthetic bacteria R. faecalis PA2 was used

Rhodopseudomonas faecalis it a gram-negative, anaerobic, phototrophic bacteria with polar flagella which was isolated from chicken faeces. It was cultivated in glutamate–malate medium with pH 6.8 and temperature 30 ± 2°C was maintained. Incubation was carried out under anaerobic condition. The next method was the production of animal manure media, using swine, chicken or cow manure, it was incubated for around 7 days at temperature of 45°Co dissolve the organic compounds and minerals in the manure.

Furthermore, more steps were included such as

1) Optimization of manure
2) Carotenoid productions
3) Amino acid content determination by in-house method and gas chromatography
4) Protein content in SCP by Kjeldahl method.

By the abovementioned methods and steps following results were observed:

As mentioned animal manure being rich in carbon and nitrogen sources was used, as it can be assimilated by bacteria for growth and metabolism purposes. From the logarithmic phase growth of the strain, grown in different

40

types of animal manure medium maximum specific growth rate of R. faecalis PA2 wasfound in chicken manure medium. As chicken manure contains high nitrogen content and the concentrations of free ammonia presenting in the medium was up to 300 mg/L as ammonia being an important nitrogen source for amino acid synthesis in bacteria, chicken manure proved quite best choice for SCP synthesis.

The following diagram represents conceptual pathway of protein biosynthesis using ammonia from chicken manure as the nitrogen source and stoichiometry of the pathway. There were also some analytical approaches for determining biomass content as well protein content in the SCP:

SCP production was also affected by several factors such as:-

1: effect of chicken manure content

2: inoculum size

3: pH and temperature

4: moisture content in manure medium

5: cultivation time and external factors for in vitro cultivation.

Furthermore, more methods like statistical methods were used for the prediction of SCP produced, for example, for optimization of culture condition etc. The statistical approach showed significant results for improving biomass, protein, and carotenoids in SCP produced from chicken manure by using R. faecalis PA2.

CONCLUSION:-

The result represents, the use of animal manure as sole substrate for SCP production, thus contributing to the reduction in cost production of medium considering the easy availability of animal manure as well as minimizing the pollution and contamination of animal waste in the environment.

REFERENCES:-

[1] S. Patthawaro and C. Saejung, “Production of single cell protein from manure as animal feed by using photosynthetic bacteria,” *Microbiologyopen*, vol. 8, no. 12, Dec.2019, doi: 10.1002/MBO3.913.

MALTOTRIOSE FERMENTATION

Raja. T & Palanikumar. M, II - BT

Maltotriose is basically a trisaccharide containing three glucose molecules joined by α-1,4 glycosydic bond. It is the second most widely used fermenting sugar found in Brewer'sbasket (15-20%) after Maltose (50-60%) & Glucose is the third largest (10-15%). Though Maltotriose is the second most widely sugar used by the Brewers, but in the priority for utilization and consumption by yeasts it is on the lowest. During fermentation when the glucose uptake reaches 50%, the yeast then starts utilizing maltose & maltotriose that too on a slower rate. The slower utilization rate of maltose & maltotriose could sometimes results in the generation of one of the common problems faced by the breweries that is the presence of high content of fermenting sugar in the finished beer and abnormal beer flavour. Utilization & metabolism of maltotriose during the seed fermentation is one of the major factors which determine the fermentation efficiency and product quality.

Maltotriose fermentation needs the presence of atleast one of the 5 homologous and unlinked MAL loci- MA1 though MAL4 and/or MAL6. Each loci has the presence of at least one emulate of three encoding separated gene for Maltase, Permease & positive regulatory protein which instigates the transcription of two previous genes in the presence of maltose.

Most of the studies and researches done on the maltotriose utilization have undergone with the analysis of environmental factors which can affect the utilization of this substrate source during the brewing process or fermentation process.

The primary researches shows that during the utilization, the maltose and maltotriose are transported across the plasma membrane with the help of district transport systems. Maltotriose transport activity in the yeast cells have been examined in a variety of industrial strains of yeasts, but the molecular identity of this permease was unknown till the years until when a new permease gene (AGT1) which shows wider substrate specificity was not found.

MATERIALS & METHODS:-

1) Materials

The materials needed are sugars- Glucose, Maltose, Maltotriose (at least 95% pure), p-nitrophenyl-α-D-glycopyranoside, phenylmethylsofonyl fluoride, glass beds, antimycin A, Ampholine (5.0pH -7.0pH) & 5-bromo-4-chloro-3-indoyl-α-glycopyranoside.

2) Strains & Culture Conditions

2 Strains are used in the fermentation of Maltotriose, i.e Strain70 & StrainBO1. Both of the strains are to be grown in Batch Culture at following conditions-

- Bactopeptone-20g
- Yeast Extract-10g
- Carbon Source (any of the sugar)-20g
- Temp- 28°C at 160RPM
- pH- 5.0

Cells are harvested at 2500 rpm for 3 min, at the Exponential phase of growth & washed twice with ice-cold distilled water before use. Alternatively, culture samples are to be centrifuged at 5000 rpm for 3 minutes and for the determination of ethanol & glycerol, the supernatant is cleared off.

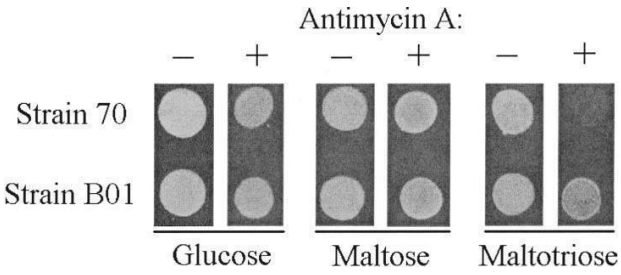


Figure 1: Growth on maltotriose is inhibited by antimycin A. Cells from strain 70 or B01 the indicated carbon sources in the absence (-) or

43

presence (+) of antimycin A, and incubated aerobically at 288C for 3 days.

3) Glucose, Ethanol & Glycerol Determination

- To check out the Glucose, Glucose oxidase & Peroxidase methods are used by using the commercial kits.
- Ethanol is determined in culture supernatants with the help of Gas Chromatography.
- For Glycerol determination, commercial enzymatic assay is used based on Glycerol kinase, Glucose-3-phosphate oxidase & peroxidase.

4) Cell Free Extraction

- To obtain cell free extracts, washed cells are to be suspended at 15mg/ml dry yeast in cold buffer (100mM MOPS-NaOH pH-6.8) having 1mM phenylmethyl-sulphonyl floride, 20%(by vol) glycerol & 1mM EDTA
- Cells are disrupted by vigorous shaking at vortex shaker for 5 minutes.
- The extracts are to be centrifuged at 10000 rpm for 5 minutes and the supernatants are used for total α-glycosidase determination.

5) α-glycosidase Assay

The total α-glycosidase activity is cells extract is determined by the hydrolysis of 1mM Buffer (1mM p-nitrophenyl, α-D-glycopyranoside in buffer A for 30°C). The α-glycosidase activity for maltose & maltotriose is checked in-situ with the help of permeabilized yeast cell.

6) Interpretations & Results

The respiratory inhibitor, antimycin A completely inhibits the growth of several wild types of Yeast strains on maltotriose but on the chosen sugars, Strain70 is able to produce ethanol from glucose & maltose whereas Strain B01 are able to produce equal amounts of ethanol from maltotriose as well.

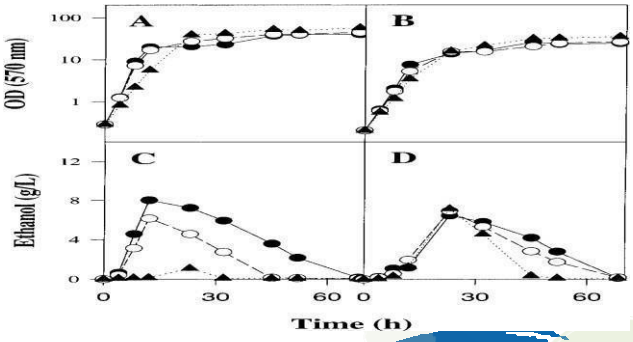


Fig: Batch growth and ethanol production by strain 70 (A and C) or strain B01 (B and D). ()

44

glucose, (+) maltose, or (~) maltotriose as carbon source. Almost similar results were there when glycerol is produced from the 2 strains.

7) Analysis of Maltose & Maltotriose Hydrolysis

Given yeast cells deliver several α-glycosidase isoforms, whereas some isoforms are able to hydrolyse both maltose & maltotriose, other isoforms are specific for α-methylglucosidase. Although these α-glycosidase activities are always purified and examined from the maltose grown cells. But there are different patterns for the α-glycosidase isoform from both strains but for maltose & maltotriose, the similar isoforms was expressed. So, our result states that there is no maltotriose specific α-glycosidase in these yeast strains.

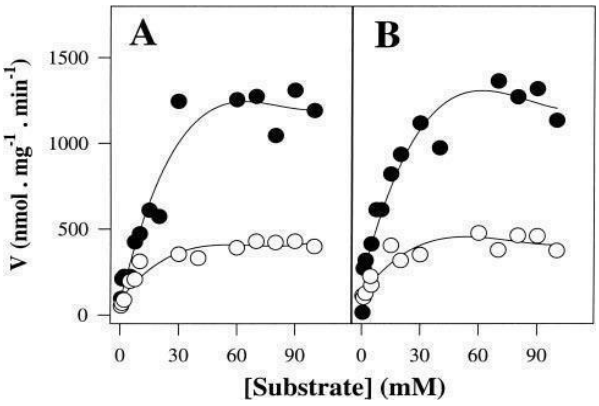


Fig: Kinetics of - glucoside hydrolysis by strain 70 (A) or strain B01(B). Maltose (•) or maltotriose (0)

CONCLUSION:-

The results obtained from the experiment clearly shows that maltotriose transport across the plasma membrane is a major limiting factor for the fermentation of it from the yeast cells. There are other attempts going on to improve maltotriose fermentation efficiency in the Industrial yeast for Baking & Brewery which also indicates the expression of maltose permeasae is also a limiting factor in the fermentation rate. But the Maltotriose permease which is encoded by AGT1 gene is believed to have greater efficiency for Industrial yeast, and for future, the genetic manipulation of the strains having permease can be a major interest.

REFERENCES:-

[1] C. R. Zastrow, C. Hollatz, P. S. De Araujo, and B. U. Stambuk, "Maltotriose fermentation by Saccharomyces cerevisiae," *J. Ind. Microbiol. Biotechnol.*, vol. 27, no. 1, pp. 34–38, 2001, doi: 10.1038/SJ.JIM.7000158.

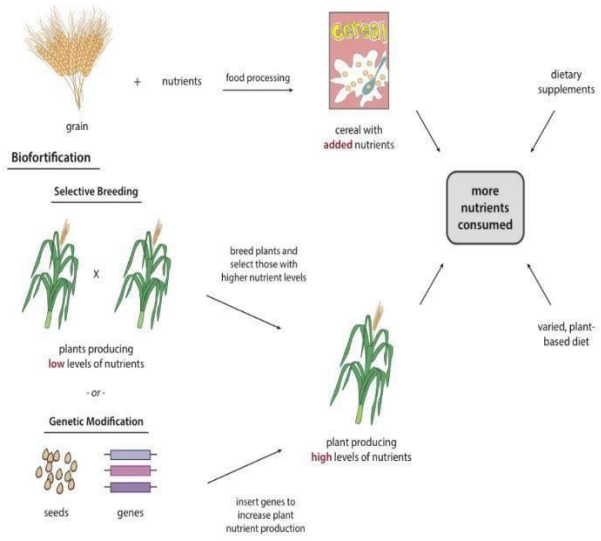
BIOFORTIFICATION

Sathish. K, II - BT

Biofortification of crops generally refers to their production with enhanced dietary value. This can be achieved either by using predictable discerning breeding or through genetic engineering. Biofortification differs from fortification as it aims to make plant foods naturally more nutritive rather than adding nutrient supplements to the foods during food processing.

This is an important enhancement on ordinary fortification when it comes to providing nutrients for the countryside poor people, who rarely have access to commercially fortified foods. Biofortification is seen as a forthcoming approach for dealing with deficiencies of micronutrients in low and middle-income countries. In the case of iron, the who expected that biofortification could help curing the 2.5 billion populace suffering from iron deficiency-induced Anaemia.

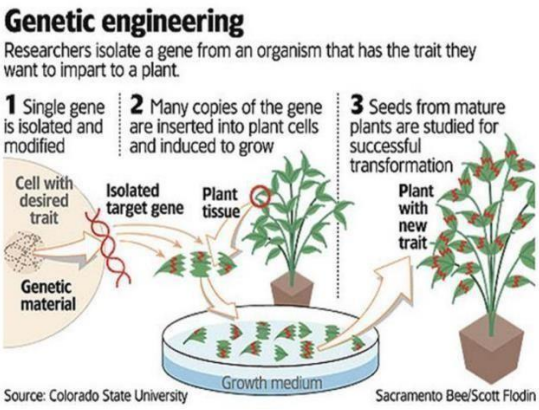
46



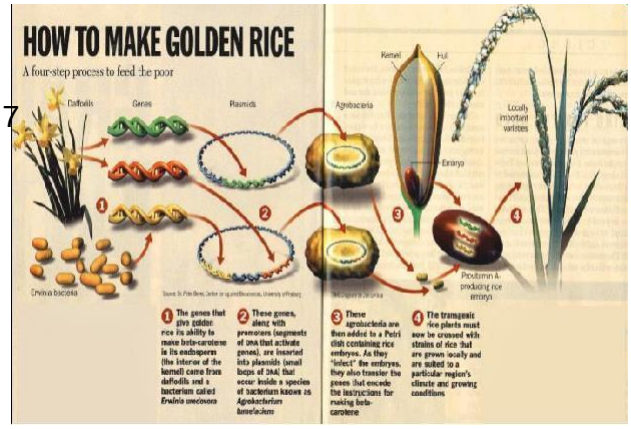
Here, we will only talk about biofortification through genetic engineering.

BIOFORTIFICATION THROUGH GENETIC ENGINEERING:-

Techniques of genetic engineering can be used to produce new crops with desirable characteristics. It utilizes a unambiguous gene sequence for the transfer of desirable distinctiveness from one organism to another. when a specific micronutrient is not naturally produced in crops, transgenic approaches are the only appropriate option to fortify such cropswith that specific transgenic crops have been produced by introducing novel genes, overexpressing the genes already present, downregulating the expression of certain genes, or interrupting the synthesis pathway genes of inhibitors.



Modern advancements in plant biotechnology enables us to better understand plant metabolisms, which has made it possible to increase micronutrients contents, such as zinc (Zn), iron (Fe), and vitamin A, in fastener foods to combat mineral malnutrition. There are more than 120 varieties of GM crops that have been regulated in the United States mostly version of herbicide tolerant or insect resistant. Most common example of transgenic crop is Golden rice, making process is as follows:-



ADVANTAGES:-

• Transgenic approaches allow us to achieve much higher micronutrients level in crop than predictable method.

47

• Superior amounts of several micronutrients can be combined in the same crop.

• Genetic engineering can also help to combine micronutrients with productivity augmentation agronomic traits, such as drought broadmindedness and pest resistance.

• It reduces the use of pesticide and insecticide during farming.

• It can feed a rapidly increasing population because it shows radically increased yields.

• More crops can be produced in small area.

• "Hidden hunger" can be eradicated through transgenic biofortification.

CONCLUSION:-

Micronutrients are essential for human growth and development, and their deficiency is a major concern that affects one in three people worldwide. It is clear that biofortification has a great capacity for improving the nutritive value of major crops. By the use of recombinant DNA technology, the availability of several essential micronutrients and vitamins could be increased. External fortification is not a very good idea because fortified food is generally available for urban population. In developing countries most of the inhabitants is rural and fortified food is either affordable or accessible to them, as long as a biofortified seed of major staple crops can be can be of great advantage to fulfill their nutritive necessities of poor populations at an affordable cost.. Among various strategies, biofortification through plant breeding is considered the most economical and sustainable approach to tackle micronutrient deficiencies.

REFERENCES:-

[1] A. Saltzman *et al.*, "Availability, production, and consumption of crops biofortified by plant breeding: current evidence and future potential," *Ann. N. Y. Acad. Sci.*, vol. 1390, no. 1, pp. 104–114, Feb. 2017, doi: 10.1111/nyas.13314.

[2] A. B. Jha and T. D. Warkentin, "Biofortification of Pulse Crops: Status and Future Perspectives," *Plants (Basel, Switzerland)*, vol. 9, no. 1, Jan. 2020, doi: 10.3390/PLANTS9010073.

48