

BIOPHYSICAL & BIOCHEMICAL TECHNIQUES

**Biswajit Mukherjee
Mohamed Jaffar A**



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e-mail: blackprintsindia@gmail.com

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CHAPTER 1

STUDY OF ANTIMICROBIAL PEPTIDES USING BIOPHYSICAL METHODS

Mohamed Jaffar A, Professor

Department of ISME, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id- mohamed.jaffar@atlasuniversity.edu.in

ABSTRACT:

Alternative medicines are now required since bacteria are becoming more and more resistant to traditional antibiotics. Antimicrobial peptides (AMPs) are a very promising alternative since they are a component of the human innate defense system and have a broad spectrum of activity against bacteria, viruses, protozoa, and cancer cells. The capacity of AMPs to target the bacterial cell membrane appears to be generally correlated with their mode of action. Uncovering their mode of action, and in particular comprehending the peptide-membrane interaction, is crucial to understanding and improving their impact. This can be done using a variety of biophysical methods, including atomic force microscopy, circular dichroism, fluorescence spectroscopy, and zeta potential measurement. The application of these biophysical approaches and the characteristics of AMPs-membranes interactions will be covered. Host defense peptides (HDPs), also known as antimicrobial peptides (AMPs), are a component of the innate immune response that is present in all kinds of life. Prokaryotic and eukaryotic cells differ fundamentally from one another, and these variances could serve as targets for antimicrobial peptides. These peptides are effective, broad-spectrum antibiotics that show promise as cutting-edge medicinal medicines. Gram negative and Gram-positive bacteria, enveloped viruses, fungi, and even altered or malignant cells have all been shown to be killed by antimicrobial peptides. Antimicrobial peptides, in contrast to the majority of traditional antibiotics, appear to regularly disrupt biological membranes, can generate transmembrane channels, and may even be able to boost immunity by acting as immunomodulators.

KEYWORDS:

Antimicrobial Peptides, Alternative Medicines, Bacteria, Medicines.

INTRODUCTION

The discovery of new antimicrobial agents that improve the efficiency and decrease the adverse effects, in contrast to conventional therapies, is of utmost importance because the effectiveness of antibiotics has been limited due to an increase in bacterial resistance. Broadly acting and less prone to bacterial resistance development, AMPs have been hailed as an interesting alternative to conventional antibiotic. They function against bacteria, viruses, protozoa, and cancer cells and are found in almost all species as a component of their innate immune system. AMPs cause bacterial cell lysis and death without being hazardous to the host cells because they prefer the bacterial cell membrane to the host cell. AMPs often have an amphipathic property, are short (less than 50 amino acid residues), and are cationic. However, because of their high sequence variability, these peptides can be categorized into four main groups according to their secondary structure.

Helical structure frequently exists as unstructured monomers in solution, but when it comes into contact with phospholipid bilayers, it adopts a helical conformation. It has been established that the connection with the bacterial cell membrane is essential for AMP activation. To increase effectiveness and lessen toxicity toward the host, it is crucial to

comprehend how AMPs interact with the bacterial membrane and identify the features or components that are responsible for the activity. Antimicrobial peptides are a distinct and varied class of molecules that are further broken down into subclasses based on the structure and arrangement of their amino acids. Antimicrobial peptides typically range in size from 12 to 50 amino acids. These peptides have a significant amount (often >50%) of hydrophobic residues as well as two or more positively charged residues given by arginine, lysine, or, in acidic environments, histidine.

These molecules' secondary structures fall into one of four categories: i) α -helical; ii) β -stranded because of the presence of two or more disulfide bonds; iii) β -hairpin or loop because of the presence of a single disulfide bond and/or cyclization of the peptide chain; and iv) extended. Many of these peptides lack structure when in free solution; however, when they are partitioned into biological membranes, they fold into their final form. The peptides have hydrophilic amino acid residues arranged along one side of a helical structure and hydrophobic amino acid residues arranged along the other side. The antimicrobial peptides' amphipathicity enables them to partition into the membrane's lipid bilayer. Antimicrobial peptides must have the ability to bind with membranes in order to function, while membrane permeabilization is not required. These peptides exhibit a range of antibacterial properties, including the ability to permeabilize membranes and act on a number of cytoplasmic targets. Antimicrobial peptides kill germs in a variety of ways, some of which may be exclusive to particular bacterial species. Some antimicrobial peptides, such as psoriasin, kill both bacteria and fungus, including numerous filamentous fungi. Peptides frequently target the cytoplasmic membrane, but they can also disrupt the creation of cell walls, proteins, and DNA.

Given that most bacterial surfaces are anionic or hydrophobic, as in the case of the antimicrobial peptide Piscidin, the initial interaction between the peptide and the target organism is electrostatic. By using "barrel-stave," "carpet," or "toroidal-pore" methods, their amino acid makeup, amphipathicity, cationic charge, and size enable them to bind to and insert into membrane bilayers to produce pores. As an alternative, they might enter the cell and bind chemicals that are essential for cell survival within. Intracellular binding models include inhibiting the formation of cell walls, changing the cytoplasmic membrane, activating autolysin, inhibiting the synthesis of DNA, RNA, and proteins, and inhibiting the activity of certain enzymes. The precise method of death is frequently unknown. Dual polarisation interferometry is a new method being used to examine these mechanisms. These peptides appear to be bactericidal rather than bacteriostatic, in contrast to many conventional antibiotics. In general, the minimum inhibitory concentration (MIC), which is the lowest concentration of medication that suppresses bacterial growth, is used to assess the antibacterial activity of these peptides.

Anti-gram-positive, anti-gram-negative, anti-fungal, anti-viral, anti-parasitic, and anti-cancer activities are just a few of the diverse properties that AMPs can have. According to a comprehensive examination of AMP functions, the two key characteristics of amphipathicity and charge best distinguish between AMPs with and without anti-gram-negative bacterial actions. This suggests that having strong amphipathicity and net positive charge may be preferred or possibly necessary for AMPs with anti-gram-negative bacterial activity. They can alter host gene expression, act as chemokines or induce chemokine production, inhibit the production of pro-inflammatory cytokines caused by lipopolysaccharide, promote wound healing, and modulate the responses of dendritic cells and cells of the adaptive immune response, in addition to directly killing bacteria. These immunomodulatory functions may be involved in the clearance of infection. Host defense peptides are essential for both infection prevention and clearance, according to animal models. Many peptides that were previously identified as "antimicrobial peptides" have apparently been demonstrated to have more important alternate roles. For instance, the

immunomodulator dusquetide works by binding to the protein p62, which is connected to the toll-like receptor-based signaling of infection. In a Phase III clinical trial, Soligenix (SGNX) is evaluating the peptide to see if it can help repair radiation-induced damage to the oral mucosa that results from head and neck cancer treatment.

Antimicrobial peptides typically have a net positive charge, allowing them to interact with negatively charged molecules including phospholipid phosphatidylserine, O-glycosylated mucins, sialylated gangliosides, and heparin sulfates that are exposed on the surfaces of cancer cells and bacteria. These peptides' diverse modes of action can be categorized into two groups: membranolytic and non-membranolytic antimicrobial peptides. There are four models that can be used to explain how membranolytic antimicrobial peptides break membranes: Barrel-stave model: The barrel-stave model proposes that AMPs interact with the lipid bilayer of the microbial cell membrane to form transmembrane channels or "barrel staves". These channels are believed to compromise the membrane's integrity, causing the microorganism to perish.

The carpet model proposes that AMPs adsorb onto the lipid bilayer of the microbial cell membrane, forming a dense layer that causes the membrane to become permeabilized. This model suggests that the AMP acts as a "carpet" that covers the surface of the cell, preventing the microbe from functioning properly. The toroidal model proposes that AMPs interact with the lipid bilayer of the microbial cell membrane to form toroidal structures, which are thought to pinch off sections of the membrane and lead to the formation of vesicles. This process is thought to disrupt the membrane's integrity and cause the death of the microbe. Disordered toroidal-pore model: According to this model, the disordered AMPs wrap around the lipid bilayer and create a pore, which disrupts the membrane's integrity and leads to the death of the microbe. Unlike the toroidal model, which suggests that the AMP creates a stable toroidal structure, the disordered toroidal-pore model suggests that the AMP is flexible and does not form a stable toroidal structure. The peptide-lipid pore complex becomes intrinsically disordered, with the orientation of the peptide not well defined.

DISCUSSION

The compartmentalization of the cell is accomplished by the plasma membrane, which also serves as a selective barrier to regulate the gradients necessary for life. Although phospholipids and proteins make up the majority of the membrane, each creature has a unique membrane makeup. For instance, whereas bacterial membranes contain a high proportion of anionic lipids like cardiolipin and phospholipids containing phosphatidylglycerol, eukaryotic membranes are primarily composed of neutral glycerophospholipids (such as phospholipids containing phosphatidylcholine or phosphatidylethanolamine head groups). Additionally, bacteria include negatively charged components on their surface, such as lipopolysaccharide and lipoteichoic acids in Gram-negative and Gram-positive bacteria, respectively, and have a greater electronegative transmembrane potential than eukaryotic cells[1]–[3]

AMPs have a preference for the negatively charged surface of bacterial membranes over neutral eukaryotic membranes due to their net positive charge. AMPs can be roughly split into two classes, however, depending on how they work: those that cause bacterial membrane rupture and those that traverse the membrane and attack an intracellular target without rupturing it. The first encounter between peptides and membranes appears to be mediated by electrostatic interactions between the hydrophilic amino acids of the peptide and the phosphate groups of the phospholipids. Following this first engagement, the peptide can insert itself into the membrane and either compromise the integrity of the plasma membrane or non-disruptively move into the cell's cytoplasm. The creation of membrane pores (the "barrel stave" and "toroidal pore" methods) or the buildup of peptide molecules on the

membrane surface the "carpet mechanism can both be used to explain how disruptive AMPs work. Nondisruptive peptides, on the other hand, can pass through the membrane and attack cytoplasmic targets such as nucleic acids and/or cellular proteins, or they may serve as an inhibitor of the creation of these substances. For instance, it has been demonstrated that the insect peptide pyrrhocoricin, which is proline-rich, binds to the heat shock protein DnaK and prevents chaperone-assisted protein folding. For disruptive and non-disruptive AMPs, a different amount of time is required to notice a loss of viability. While nondisruptive peptides work more slowly, disruptive peptides kill cells in a matter of minutes.

Molecular Models

Membrane interactions are crucial for the mechanism of action of AMPs, as mentioned above. Biological membranes are intricate, heterogeneous structures made up of hundreds of lipids and proteins, and they contain unique compositions in each of their domains. To separate the impact of the various cell components on the manner of action of AMPs, simple model membranes are frequently used. Some features that can be altered include the lipid charge, membrane viscosity, and the presence or absence of sterols. Model membranes can also be easily created using synthetic lipids or lipids that have been isolated from a certain kind of cell. Phospholipid vesicles, which are categorized according to their size and the number of lamellae that make them up, are the most often used membrane models. Large unilamellar vesicles (LUVs) are unilamellar vesicles with a diameter of 100 nm or greater. LUVs are selected as a model because of their large stability, similar lipid packing to that of biological membranes, and nonconstrained curvature at the molecular scale. In instance, the inherent fluorescence of peptides can be exploited to follow peptide-membrane interactions using fluorescence approaches. These vesicles can be used in the investigation of peptide-membrane interactions utilizing biophysical techniques[4]–[6].

Tiny unilamellar vesicles, or SUVs, are also widely employed, but because of their tiny size (20–50 nm) and high surface curvature, they have the potential to exhibit distorted lipid packing, which in turn could result in abnormal peptide packing and metastability. Although light scattering artifacts are less likely to occur in SUVs, the aforementioned drawbacks plus the ease with which LUVs' scattering artifacts may be remedied make LUVs the favored option. Giant unilamellar vesicles, or GUVs, with a diameter larger than 1 μ m can grow to the size of eukaryotic cells and are therefore particularly helpful for microscopy research. Additionally, human and bacterial cells (such as erythrocytes) can be utilized to explore peptide-membrane interactions. These cells are crucial for validating the outcomes of experiments using straightforward model membranes. However, there are limitations to how biophysical approaches may be applied to cells. For instance, it is impossible to separate the peptide's intrinsic fluorescence from the substantial cellular background fluorescence. This restriction necessitates the derivatization of AMPs using extrinsic fluorophores such as nitrobenzoxadiazole and rhodamine, which increases the experimental and financial costs and can change the characteristics of peptides. Additionally useful and generally a desirable addition to experimental data are theoretical models. However, the extrapolation that can be drawn from this research is constrained by the modest size of the virtual membrane patches, the small number of peptide molecules, and the short time periods that can be examined.

Permeabilization of Membranes

A membrane is a selective barrier; it lets some items pass but prevents others from doing so. These entities could be ions, molecules, or other tiny particles. Biological and manufactured membranes are the two broad categories into which membranes can be placed. Cell membranes, which are the exterior coverings of cells or organelles that permit the passage of specific components, nuclear membranes, which enclose the cell nucleus, and tissue membranes like mucosae and serosae are all examples of biological membranes. Humans

create synthetic membranes for use in labs and business (such as chemical factories)[7]–[9]. Although the idea of a membrane has been around since the eighteenth century, it wasn't widely applied outside of the lab until the end of World War II. Membrane filters were employed to evaluate the water for safety because the conflict had harmed Europe's drinking water supply. Membranes, however, were not extensively utilized because of their limited dependability, sluggish operation, inadequate selectivity, and high costs. With the development of microfiltration and ultrafiltration technologies, membranes were first widely used. These separation techniques, coupled with electrodialysis, have been used in large factories since the 1980s, and a number of seasoned businesses now supply the industry. The size of a membrane's pore determines how selective it is. They can be categorized as microfiltration (MF), ultrafiltration (UF), nanofiltration (NF), and reverse osmosis (RO) membranes, depending on the pore size. Additionally, membranes can have different thicknesses and either a homogeneous or heterogeneous structure. Particle transport can be active or passive, and membranes can be neutral or charged. Pressure, concentration, chemical, or electrical gradients in the membrane process can aid the latter.

Waste minimization

The membrane is discarded once its performance has significantly declined. Although they can also be energy recovered, discarded RO membrane modules are now categorized as inert solid waste and frequently dumped in landfills. However, numerous initiatives, including waste reduction, direct reapplication, and recycling techniques, have been created throughout the years to avoid this. Membranes also adhere to the hierarchy of waste management in this regard. This suggests that the least desirable course of action is disposal and landfilling, whereas the most preferred course is upgrading the design of the membrane, which results in a decrease in use at the same application. [10]–[12]

To adhere to the principles of the circular economy, RO membranes must overcome various environmental issues. They typically have a 5- to 10-year service life. The number of RO desalination plants has grown by 70% in the last two decades. These RO plants have grown dramatically in size, with some of them having a daily production capacity of more than 600,000 m³. This translates to 14,000 tonnes of membrane waste being generated each year and landfilled. A variety of preventative approaches are being developed to lengthen the lifespan of a membrane, including improving efficiency by merging the RO process with the pre-treatment process, creating anti-fouling technologies, and creating appropriate cleaning methods. Because there are fewer chemical additives in the saltwater feed and less operational maintenance is needed for the RO system, pre-treatment techniques save operating expenses. Inorganic (salt precipitation), Organic, Colloidal (particle deposition in suspension), and Microbiological (bacteria and fungi) fouling are the four types of fouling that can be observed on RO membranes. As a result, the development of an effective anti-fouling technique should be possible with the proper coordination of pre-treatment operations and chemical dosing, as well as an effective cleaning strategy that address different types of fouling. The majority of plants perform chemically enhanced backwash (CEB) on their membranes once a week. Additionally, to this maintenance cleaning, a thorough cleaning (CIP), recommended two to four times a year, is also advised.

Infrared spectroscopy

The force measurement, topography imaging, and manipulation are the three main capabilities of the AFM. The forces between the probe and the sample as a function of their mutual separation can be measured using AFMs in force measurement. This can be used to do force spectroscopy and evaluate the sample's mechanical characteristics, such as its Young's modulus, which is a measure of stiffness. For imaging, it is possible to create a high-resolution image of the three-dimensional shape (topography) of a sample surface using the

probe's response to the forces the sample places on it. This is accomplished by raster scanning the sample's position in relation to the tip and measuring the height of the probe, which corresponds to a continual interaction between the probe and the sample (see Topographic image for additional information). A pseudocolor plot is a common way to show the surface topography. Although Binnig, Quate, and Gerber's initial article on atomic force microscopy in 1986 speculated about the possibility of achieving atomic resolution, significant experimental obstacles had to be overcome before Ohnesorge and Binnig were able to demonstrate atomic resolution of defects and step edges in ambient (liquid) conditions in 1993. The scientific community had to wait a little while longer to see true atomic resolution of the silicon 7x7 surface after the STM's stunning spatial resolution was demonstrated by Giessibl using atomic photographs of this surface. In manipulation, the forces between the tip and the sample can also be employed to modify the sample's characteristics in a deliberate manner. Atomic manipulation, scanning probe lithography, and local cell stimulation are a few examples of this. Other characteristics of the sample can be assessed locally and displayed as an image, frequently with a similar high resolution, concurrently with the capture of topographical images. Mechanical traits like stiffness or adhesion strength and electrical properties like conductivity or surface potential are two examples of these properties. In fact, the bulk of SPM methods utilize this modality and are extensions of AFM.

CONCLUSION

AMPs have a broad spectrum of activity, are very effective, and have little toxicity, making them a viable substitute for traditional treatments. Understanding their mechanism of action is crucial for a broad application of such peptides, to enhance their activity, and to lower eventual toxicity. Their mode of action depends on peptide-membrane interaction. Understanding peptide-membrane interactions can be accomplished with the aid of biophysical approaches. When AMPs interact with model membranes, it is feasible to learn about peptide-membrane affinity, peptide in-depth placement, and membrane stability using lipid vesicles and fluorescence spectroscopic techniques. The secondary structure motifs of the peptides may be found using circular dichroism spectroscopy, and changes to the secondary structure brought on by contact with model membranes can be assessed. On the other hand, model membranes or living cells can be used with AFM and -potential. AMPs activities on model membranes and biological cells can be directly examined using AFM, and their potential can provide information on surface charge neutralization. Overall, it is reasonable to draw the conclusion that biophysical approaches are useful tools for researching the mechanism of action of AMPs and other membrane-active peptides since they provide information on the interactions between peptides and membranes.

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CHAPTER 2

CHARACTERIZATION OF *HELICOBACTER PYLORI* ENOLASE FROM A BIOCHEMICAL AND BIOPHYSICAL PERSPECTIVE

Rajesh Kumar Samala, Assistant Professor

Department of ISME, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id- rajesh.samala@atlasuniversity.edu.in

ABSTRACT:

Enolase is a crucial enzyme in the traditional glycolysis pathway in cells because it catalyzes the conversion of 2-phospho-D-glycerate to phosphoenolpyruvate. Enolase is highly conserved across a wide range of species, including humans and bacteria, demonstrating its significance in cells. Therefore, enolase is a good candidate for therapeutic development. The last ten years have seen the discovery of new uses for this enzyme. A typical human pathogen known as *Helicobacter pylori* is responsible for gastrointestinal illnesses, including gastric cancer. The analysis of the *H. pylori* enolase (HpEno) sequence in this study suggests that HpEno should be able to carry out the functions because the cofactor, plasminogen, host extracellular RNA, and catalytic site binding sites are all (at least partially) conserved. *E. coli* was used to overexpress and purify recombinant HpEno. HpEno shared similar secondary structural features with enolases from other species. In comparison to other homologs, the temperature-induced profiles show that HpEno is fairly stable to temperature. In terms of the unfolding reaction's kinetics, we discovered that the activation enthalpy connected to the thermal unfolding process is identical to the activation enthalpy for yeast enolase that has been previously reported, indicating a similar scaffold and kinetic stability. Despite testing a wide range of experimental circumstances, HpEno's enzymatic activity could not be found. Still, a considerably wider range of studies need be conducted to demonstrate the absence of activity.

KEYWORDS:

Biochemical, Biophysical Perspective, Enolase, Enzyme, Glycolysis.

INTRODUCTION

Enolase is an enzyme that catalyzes the often-vital process of gluconeogenesis, which converts 2-phospho-D-glycerate into phosphoenolpyruvate, and the dehydration of 2-phospho-D-glycerate into phosphoenolpyruvate during glycolysis. Other divalent cations can also activate this enzyme, which needs Mg^{2+} for catalysis. Enolase is a conserved protein that shares comparable catalytic characteristics across several organisms. The ubiquity of the enzyme and the sequence similarity between enolases from current organisms from various phyla suggest that the enolase gene was already present in those organisms' common ancestor and that it was diversified by organism speciation or by gene duplication within species. Enolase has also been referred to as a protein that has many roles in a number of biological and pathological processes inside a variety of subcellular compartments. Enolase from eukaryotic cells, for instance, controls the dynamics of the cytoskeletal filaments to influence cell shape. Bacterial enolase has been described as a significant virulence factor due to its binding to plasminogen and as a key component of the degradosome, where its roles are still poorly understood. Mammalian enolase participates in the transcriptional regulation of genes involved in cell proliferation.

Enolase has commonly been described as either an octamer in some thermophilic bacteria or a homodimer in the majority of species. The monomer's structure is made up of an N-terminal "+" domain that is followed by an eightfold "/" barrel domain. The inherent potential of a protein's folding pattern is revealed by the divergence of its sequences, structures, and

activities. Over 50% of people globally have the gram-negative bacteria *Helicobacter pylori* in their upper gastrointestinal tracts. Two or three antibiotics and one proton pump inhibitor are combined in the course of treatment to completely clear the illness. However, reports of resistant strains resulting in unsuccessful therapy are growing. This study suggests that novel approaches to the treatment of this infection are required. *H. pylori* has a small genome; many proteins have been lost during the course of its evolution, and the proteins that are still there can perform different tasks. Enolase from *H. pylori* (HpEno), an action-like protein, was brought down in our lab along with MreB, demonstrating that HpEno can coexist in a complex with MreB.

Therefore, the enolase protein in this bacterium may have different structural and functional properties. This is the first time that enolase has been produced and purified from a pathogen, and we have also examined some of its structural, biochemical, and biophysical properties in an effort to understand the structure-function relationship of this protein in *H. pylori*. The gram-negative, microaerophilic, spiral (helical), *Helicobacter pylori*, formerly known as *Campylobacter pylori*, is typically located in the stomach. Its helical structure is assumed to have evolved to allow it to pierce the mucoid lining of the stomach and spread infection. This shape gives rise to the genus name "helicobacter." The Australian doctors Barry Marshall and Robin Warren were the ones to discover the bacterium for the first; *pylori* has been linked to lymphoid tissue cancer in the stomach (diffuse large B-cell lymphoma) as well as cancer of the mucosa-associated lymphoid tissue in the esophagus, colon, rectum, or tissues around the eye. Extranodal marginal zone B-cell lymphoma of the cited organ.

Infection with *H. pylori* typically has no symptoms, although it can occasionally result in gastritis (stomach inflammation) or ulcers in the stomach or first section of the small intestine. Additionally, the infection has been linked to the emergence of several malignancies. Many researchers have hypothesized that *H. pylori* influences or protects against a variety of different disorders, but many of these connections are still debatable. According to certain research, *H. pylori* has a significant impact on the natural ecology of the stomach, such as the type of bacteria that populate the gastrointestinal system. According to other research, non-pathogenic *H. pylori* strains may correct stomach acid secretion and control hunger. Over 50% of the world's population was thought to have *H. pylori* in their upper gastrointestinal tracts in with colonization (or infection) occurring more frequently in underdeveloped nations.

However, the frequency of *H. pylori* colonization of the gastrointestinal tract has decreased in many nations over the past few decades. Up to 90% of individuals with *H. pylori* infections never develop symptoms or consequences. *H. pylori* infection, however, increases a person's lifetime risk of getting peptic. Acute infection can manifest as acute gastritis with nausea or stomach pain. When chronic gastritis results, the symptoms, if any, are frequently those of non-ulcer dyspepsia, including stomach aches, nausea, bloating, belching, and occasionally vomiting. Pain can happen at other times; however, it usually happens when the stomach is empty, in between meals, and in the early morning. The less frequent ulcer symptoms are nausea, vomiting, and appetite loss.

Black stools are a sign of gastrointestinal bleeding, which can also happen. Prolonged bleeding can cause anemia, which makes you feel weak and exhausted. Hematemesis, hematochezia, or melena may happen if there is significant bleeding. Duodenal ulcers are more likely to develop from inflammation of the pyloric antrum, which joins the stomach and duodenum, whereas gastric ulcers are more likely to develop from inflammation of the corpus, or stomach's body. *H. pylori* infection can cause gastric or colorectal polyps, which are benign growths of tissue that protrude from the mucous membranes of these organs. The majority of the time, these polyps are asymptomatic, but gastric polyps can occasionally lead to gastric outlet obstruction and dyspepsia as well as heartburn, bleeding from the upper

gastrointestinal tract, and constipation. In contrast, colorectal polyps can occasionally cause rectal bleeding, anemia, constipation, diarrhea, weight loss, and abdominal pain. People who have a persistent *H. pylori* infection are more likely to develop a malignancy that is directly linked to this infection. Stomach adenocarcinoma, diffuse large B-cell lymphoma of the stomach, extranodal marginal zone lymphomas of the stomach, rectum, esophagus, or ocular adnexa orbit, conjunctiva, and/or eyelid, which are less prevalent, are among these tumors.

DISCUSSION

Because *Helicobacter pylori* is microaerophilic, it needs oxygen, just not as much as the atmosphere does. It has a hydrogenase that can oxidize the molecule of hydrogen (H_2) produced by intestinal bacteria to produce energy. Oxidase, catalase, and urease are produced by it. There are five significant outer membrane protein families in *H. pylori*. The largest family include adhesins that are known and hypothetical. Porins, iron transporters, flagellum-associated proteins, and proteins with uncertain functions make up the remaining four groups. The outer membrane of *H. pylori* is made up of phospholipids and lipopolysaccharide (LPS), just like other common Gram-negative bacteria. The Lewis blood group antigens that are present on the stomach epithelium may be fucosylated and resemble the O antigen of LPS. Cholesterol glucosides, which are uncommon in other bacteria, are also present in the outer membrane[1]–[3].

Transcriptome

Sharma et al.'s differential RNA-seq analysis of transcription at single-nucleotide resolution was presented in 2010 and confirmed that important virulence locus like the urease (*ure*) operon or the *cag* pathogenicity island are known to be acid-induced (see below). More significantly, 1,907 transcriptional start sites, 337 major operons, 126 additional suboperons, and 66 monocistrons were all discovered in this study. Only about 55 transcriptional start sites (TSSs) for this species were discovered up to 2010. Notably, 27% of the major TSSs are also antisense TSSs, demonstrating that antisense transcription takes place throughout the whole *H. pylori* genome, just like it does in *E. coli*. About 46% of open reading frames, including many housekeeping genes, have at least one antisense TSS. The majority (about 50%) of the 5' UTRs support the AAGGag motif, which is situated roughly 6 nt (median distance) upstream of start codons as the consensus Shine-Dalgarno sequence in *H. pylori*. [4]–[6]

Virulence and pathogenesis-related genes

The goal of studying the *H. pylori* genome is to better understand pathogenesis the process by which this bacterium causes sickness. When mutated, about 29% of the loci exhibit a colonization problem. A common gene sequence thought to be responsible for disease, the *Cag* pathogenicity island, is about 40 kb long and contains more than 40 genes in two of the sequenced strains. When *H. pylori* strains are obtained from asymptomatic carriers of the infection, they frequently lack this pathogenicity island. One of the main virulence proteins produced by *H. pylori* is encoded by the *cagA* gene. Ulcer-causing potential is linked to bacterial strains that carry the *cagA* gene. A protein with a lengthy amino acid sequence (1186) is produced by the *cagA* gene. About 30 genes make up the *cag* pathogenicity island (PAI), some of which encode for the intricate type IV secretion system. The island was likely obtained by horizontal transfer from another bacterial species because of the low GC-content of the *cag* PAI in comparison to the rest of the *Helicobacter* genome. The pathogenesis of *H. pylori* is also significantly influenced by the serine protease HtrA. Both the translocation of CagA and the ability of the bacteria to traverse the epithelium of the host cells depend on the HtrA protein[7]–[10]. Another important virulence protein is related to the toxigenic *vacA*'s capacity to facilitate the development of intracellular reservoirs of *H. pylori* by disrupting the calcium channel TRPML.

Getting used to the stomach

Diagram demonstrating how *H. pylori* enters the stomach's epithelium. *pylori* uses its flagella to burrow into the mucus lining of the stomach to reach the epithelial cells beneath, where it is less acidic, in order to avoid the acidic environment of the core of the stomach (lumen). *H. pylori* can detect the pH gradient in the mucus and will chemotactically shift to the less acidic area. This also prevents the bacteria from being carried into the lumen by the mucus environment, which is continually flowing from the epithelium, where the bacteria are created, to the lumen interface, where they are broken down. Occasionally, *H. pylori* is located inside the epithelial cells themselves as well as in the mucus and on the inner surface of the epithelium. By generating adhesins, which bind to lipids and sugars in the membrane of the epithelial cell, it clings to the epithelial cells. The Lewis b antigen is present on the surface of stomach epithelial cells, and one such adhesin, BabA, binds to it. BabA is an acid-sensitive protein that can completely prevent *H. pylori* adhesion. According to one theory, BabA's ability to respond to acid promotes adhesion while also allowing for an efficient escape from environments with pH levels that are detrimental to the organism.[64] Increased amounts of the sialyl-Lewis X (sLeX) antigen expressed on stomach mucosa bind to another similar adhesin, called SabA.

H. pylori not only uses chemotaxis to avoid low pH regions, but it also produces a lot of urease, which converts the urea in the stomach to carbon dioxide and ammonia, neutralizing the acid in its surroundings. These interact with the potent environmental acids to create a neutralized environment around *H. pylori*. [66] Mutants lacking urease are unable to colonize. In actuality, urease expression is necessary for maintaining chronic infection as well as early colonization.

Purifying Proteins

The cost of producing proteins is still considerable, and there is a rising need for methods of protein purification that are both quick and inexpensive. It's essential to comprehend the various protein purification techniques and optimize the downstream processing to reduce production costs while maintaining appropriate levels of homogeneity. Protein purification can be either analytical or preparative. A significant amount of proteins are intended to be produced during preparatory purifications for later use. The creation of commercial items like enzymes (like lactase), nutritional proteins (like soy protein isolate), and specific biopharmaceuticals (like insulin) are a few examples. A number of preparative purification procedures are frequently used to get rid of bi-products, like host cell proteins, which could be dangerous for the patient's health.[3] For a range of research or analytical applications, such as identification, quantification, and examinations of the protein's structure, post-translational changes, and function, analytical purification generates a comparatively tiny amount of a protein. The yield and purification levels are taken into account at each stage of a protein purification procedure. Very little protein is left after a high level of purification and a low yield for experimentation. However, a high yield with poor degrees of purification results in the presence of several contaminants (proteins other than the one of interest), which obstruct research efforts[11]–[13].

Extraction

Each purification procedure begins with the disruption of the cells holding the protein in question if the protein of interest is not released by the organism into the surrounding fluid. One could, for example, utilize one of the following techniques, depending on how fragile the protein is and how stable the cells are: repeated freezing and thawing, sonication, high pressure homogenization (French press), homogenization by grinding (bead mill), and permeabilization using detergents (like Triton X-100) and/or enzymes (like lysozyme) are a few other methods of homogenization. Finally, differential centrifugation, which is the

process of centrifuging the homogenate at low speed, then again with a greater force to produce a pellet consisting of nuclei and supernatant, can be used to remove the cell debris. This results in a number of fractions with progressively lower densities, where one fraction is subjected to increasingly discriminating purification methods, during cell lysis, proteases are released, which begin breaking down the proteins in the solution. If the target protein is susceptible to proteolysis, it is advised to move forward swiftly and to keep the extract cold to impede digestion. As an alternative, one or more protease inhibitors might be added to the lysis solution just prior to cell lysis. In order to lessen the viscosity of the cell lysate brought on by a high DNA concentration, DNA must occasionally be added.

Ultracentrifugation

A procedure called centrifugation uses centrifugal force to separate mixtures of particles suspended in a liquid that have different weights or densities. The inertia of each particle produces a force proportionate to its mass when a vessel (usually a tube or bottle) containing a mixture of proteins or other particulate materials, such as bacterial cells, is rotated at high speeds. The resistance the liquid imposes on the particle balances the inclination of a given particle to go through the liquid as a result of this force. By "spinning" the sample in a centrifuge, big, tiny, and dense particles move outward more quickly than less massive particles or particles with more "drag" in the liquid. When particle suspensions are "spun" in a centrifuge, a "pellet" that is enriched for the most massive particles with little drag in the liquid may form at the bottom of the tank. Particles generally remain in the "supernatant" liquid, which can be extracted from the vessel to separate it from the pellet. The angular acceleration that is imparted to the sample, which is commonly quantified in reference to the g , determines the pace of centrifugation. If samples are centrifuged for a sufficient amount of time, the particles in the vessel will find equilibrium, accumulating specifically at a point where the buoyant density of the particles balances the centrifugal force. Such "equilibrium" centrifugation enables thorough particle cleaning.

Sucrose gradient centrifugation creates a linear gradient of sugar concentration in a tube, with the highest concentration at the bottom and the lowest at the top (usually sucrose, glycerol, or a silica-based density gradient media, like Percoll). A trademark owned by GE Healthcare enterprises is Percoll. The gradient is subsequently covered with a protein sample, which is then spun rapidly in an ultracentrifuge. As a result, heavier macromolecules migrate to the tube's bottom more quickly than lighter molecules. Particles receive increasing centrifugal force during centrifugation in the absence of sucrose as they move further from the center of rotation (the farther they move, the quicker they move). The issue with this is that there is only a narrow observable window for the useful separation range inside the vessel. The particle of interest will go considerably farther when a sample is spun twice as long, not twice as far. However, as the proteins move along a sucrose gradient, they come into contact with a liquid that is getting denser and more viscous. The centrifugal force will be balanced by a well-constructed sucrose gradient, causing the particles to move roughly in proportion to the amount of time they have spent in the field. "Rate zonal" centrifugations are used to separate samples using these gradients. The gradient is then fractionated and collected after the protein/particles have been separated. Ultra centrifugation is used in biochemistry for isolating biomolecules and examining their physical characteristics.

CONCLUSION

Temperature-induced denaturation scans were used to analyze the thermal stability of apo- and holo-HpEno. The denaturation patterns of HpEno in Tris-HCl (50 mM) buffer at pH 8 are displayed. Due to the melting temperatures being at or exceeding the highest possible temperature that our apparatus' Peltier accessory can withstand, the unfolding profiles of apo- and holo-HpEno could not be fully tracked. As a result, it is impossible to use the profiles

acquired under these experimental conditions to derive precise thermodynamic parameters from the thermal denaturation. For comparison, the same experimental conditions were used to produce the denaturation scans of yeast enolase. It is notable that the HpEno transitions appeared to occur at a temperature that was roughly 25–30 °C higher than that of yeast enolase. Furthermore, compared to yeast enolase, the denaturation profiles of HpEno are less cooperative. Cooperativity in thermal denaturation profiles is frequently taken as a sign of packing that is native-like. But cooperativity can also result from the development of dimers or higher order oligomers. At denaturation temperatures, none of the enolases were investigated in their oligomeric state, and CD signals occasionally failed to show dimer dissociation. In light of the unfolding temperatures, we therefore come to the conclusion that HpEno is a more stable protein than the enolases from other species, despite the fact that its denaturation transitions are less cooperative than those of yeast enolase.

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CHAPTER 3

BIOPHYSICAL PERSPECTIVES ON THE DEVELOPMENT AND TREATMENT OF CANCER

Suresh Kawitkar, Professor

Department of ISME, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id- suresh.kawitkar@atlasuniversity.edu.in

ABSTRACT:

The complex hierarchically self-organized structures that make up biological systems include nonlinear interactions. The work of physical forces required for many biological operations is converted from biochemical energy. We hypothesize that endogenous electrodynamic fields produced by microtubules are necessary for energy transmission. In cells, microtubules and mitochondria colocalize, with the microtubules acting as tracks for the movement of the mitochondria. In addition to converting energy, mitochondria create a spatially distributed proton charge layer and a strong static electric field as a result, which order the water in the surrounding cytosol. These effects set up the right circumstances for coherent electrodynamic field creation. Cancers have a significant impact on the routes that transmit metabolic energy. In cancer cells (Warburg effect) or fibroblasts linked to cancer cells (reverse Warburg effect), mitochondrial malfunction leads to altered or reconstructed frequency spectra as well as diminished or boosted electromagnetic field output. Interaction factors between cancer cells and healthy cells that are disrupted may encourage local invasion and metastasis. The normal apoptotic mechanism that cancer-transformed cells block can be activated using a therapeutic technique that targets defective mitochondria to restore their healthy functioning. The use of dichloroacetate in the treatment of cancer and the restoration of health may aid in the creation of new, highly effective medications that target mitochondrial activity.

KEYWORDS:

Biological, Biochemical, Biophysical Perspectives, Treatment of Cancer.

INTRODUCTION

Warburg et al. made the initial discovery that tumors exhibit partial inhibition of oxidative metabolism. He established that mitochondrial activity was down because of it. It took fifty years for the scientific community to completely comprehend this astounding insight. At a time when little was known about the internal organization of a live cell, it is important to note that Warburg saw biological systems as highly ordered structures. This led him to the logical conclusion that alterations in oxidative metabolism play a crucial role in the development and spread of cancer. Despite its true significance, this point of view was not recognized by the scientific community at the time of Warburg's discovery. Modern understanding of biological systems is linked to the concept of complexity (the reader is referred to Cohen and Havlin for a description of complex systems, and develops a simple model). Examples of complex systems made up of numerous elements that interact nonlinearly and are arranged into hierarchical structures include biological systems.

Emergent phenomena, in which the total exhibits properties not present in its component parts, are demonstrated by these networks of interconnected creatures. Therefore, the structured combination of components generates novel traits and forms of activity. Since they exchange mass, energy, and information with their surroundings, biological systems are open systems. These structures dissipate energy. Any biological system's entire complex develops by self-organization in thermodynamic conditions that are far from thermodynamic equilibrium. Another characteristic of biological systems based on interactions with their environment is adaptability. Interaction with the environment is not only passive but also

exhibits active action, leading to continual modifications of internal structure and patterns of activity. Reaction and activity routes can branch, which is a characteristic of all biological systems. Consequently, due to parallel interconnections, the utility of knowledge about the make-up and function of just one biological system component is restricted.

The central management and steering of biological systems is provided by mammalian brain activity. The brain gathers data from various levels of the hierarchical structure, analyzes it, and responds by issuing directive impulses. An essential component of the brain's control and command function are body communication networks with information conduits. However, up to this point, the analysis of information transfer in biological systems has been framed as a transfer of quality or an order of entities. It has not yet been feasible to reduce to a quantitative foundation, making it impossible to estimate the volume of information or channel capacity. It appears that the action potential's capacity to serve as a medium for information transfer along nerve fibers is insufficient to perform the necessary communication function. Mammalian species' internal cooperation and coordinated activity require high-capacity information flow between the brain, the central control unit, and the organs, the periphery. It was argued that photon information transfer is crucial to biology in general. Recent findings, which are significant, demonstrate that cancer cells can harm nearby healthy tissues through a physical information transfer process. Possible causes of the tissue alterations include biophotons released by cancer cells. Biophotons can travel through soft tissues, inside nerve fibers, and along other bodily structures that serve as conduits. Notably, experimental evidence of biophoton transfer along the nerves of rats has been produced. It has not yet been shown that the presence of pathological cancer affects how information travels to and from the brain.

Even after Warburg's passing, mitochondrial malfunction in cancer cells was seen as a minor consequence. Examining shape, composition, chemical processes, and information transfer by mass elements formed the foundation of most biological studies. It was not believed that physical processes in biological systems were a necessary component of living. Fröhlich subsequently postulated that coherent electrical polar oscillations, which produce electromagnetic fields, play crucial roles in the functioning of life and that cancer cells exhibit disruptions of these oscillations. Fröhlich was ahead of his time, like Warburg. At that time, neither the electromagnetic field's generating structures nor its measurement techniques had been identified. However, there was accumulating experimental evidence in favor of Fröhlich's theories. Electric and electromagnetic oscillations were discovered through measurements made on live cells. According to their permittivity, dielectric particles are drawn to the dielectrophoretic forces of the cellular oscillatory electric field. Hölzel and Lamprecht and Hölze carried out additional measurements that demonstrated the electric origin of the forces acting on dielectric particles. Despite the significant microtubule research at the time, Amos and Klug's discovery of cellular electromagnetic fields was not attributed to microtubules. Microtubules, however, have steadily emerged as important sources of electromagnetic interactions, according to both experimental and theoretical studies of cellular electromagnetic.

The water ordering that occurs in living cells is probably the most fascinating aspect related to the study of microtubules. Clear zones are layers of water that are free of solutes that are found around microtubules. The presence of a negative electrostatic charge at the microtubule surface was thought to be necessary for clear zone formation. Ling developed a hypothesis explaining how water molecules are ordered in the surface charges' electrostatic field at the interface. It was established that the clear (exclusion) zones were layers of organized water. Up to 0.1 mm away from the charged surface, interfacial water ordering can form. The ordered layer's strong electric field prevents ions from entering it, and tests taken in the 3.8–4.6 m range show that thermal fluctuations are reduced and UV absorbance at 270 nm is

increased. The water molecules are arranged in a layer that resembles a gel. According to the experimental findings reported by Tyner et al ordered water layers are produced around mitochondria.

Del Giudice et al, and Del Giudice and Tedeschi used the quantum electrodynamic theory to investigate the physical makeup of water. The liquid water is a blend of two different types of water: ordered water that forms coherent domains and bulk water, which has the consistency of gas. These two phases of water are macroscopically separated in the clear (exclusion) zones due to a strong electric field. Pelling et al. measured elastic oscillations of the yeast cell membrane in the acoustic range below 2 kHz, and they contrasted elastic and electric oscillations. External electromagnetic fields with frequencies between 0.1 and 0.3 MHz have the potential to impair the polymerization of microtubules in living cells. Measurements of electric oscillations at yeast and algal cell membranes in the frequency range of 1.5-52 MHz were made. The periods when the microtubules are arranged into a mitotic spindle, such as during metaphase and anaphase A and B, are also when the electrodynamic activity of synchronized yeast cells is at its highest. Vedruccio and Meessen conducted an experiment to measure the damping of the external electromagnetic field generated by cancer tissue at the frequency of 465 MHz and the first harmonic. Cancer cells' water may dampen microtubule oscillations with a lower level of organization. Cancer cells have a less structured appearance. Albrecht-Buehler detected cellular electromagnetic fields in the red and near-infrared region mediating interactions between cells.

Microtubules' electromagnetic resonance frequencies were determined by Sahu et al to be between 10 and 30 MHz and 100 and 200 MHz. The measurement of DC conductivity following the application of an oscillating signal at the appropriate frequency, as well as the transmittance and reflectance of microtubules without and with compensation for parasitic reactances of contacts in the frequency range of 1 kHz to 20 GHz, were used to identify the resonant frequencies. The length of the microtubule has no effect on how the oscillating signals are transmitted. DC conductivity was found to sharply increase at the resonant frequencies. The transmittance is high and the microtubule resistance is substantially lower than 0.04 for the specific frequencies. The quality factor of microtubule oscillators is very high. After the water has been released from the microtubule cavity, the resonance peaks are not visible. Microtubule is another type of multilayer memory that should be mentioned. 500 distinct bits may be stored and erased by electric current in a single microtubule. This essay provides an outline of the development of cancer as a pathological condition in a sophisticated biological system. The complex system's biochemical-genetic and biophysical connections are both present in the cancer transformation. The cooperation of mitochondria and microtubules in the creation of the cellular electromagnetic field and force effects is one of the most significant mechanisms engaged in these activities. We think that developing a biophysical knowledge of the intricate nature of cancer processes may considerably advance cancer detection and care.

DISCUSSION

The only activities of mitochondria are to produce ATP and GTP (adenosine and guanosine triphosphate) and to initiate apoptosis. In a cell, mitochondria play a variety of complicated roles. A special cooperative system in the cell is formed by mitochondria and microtubules. Proton transfer is the mechanism through which mitochondria change the environment. Pyruvate and fatty acid energy is converted into electrochemical proton gradient energy by being used to pump protons into the intermembrane gap. Through the outer membrane pores, which are freely permeable to molecules with a relative molecular mass of 5,000 daltons or less, protons seep into the cytosol from the intermembrane gap. Around each mitochondrion that is functioning properly, a layer of organized water and a powerful static electric field are

created. Solid fluorescent particles with a diameter of 30 nm were used to measure the strength of the static electric field[1]–[3].

The strongest electrical field (of around 3.5 MV/m) was detected at the outer mitochondrial membrane. The strength of the electric field weakens as distance increases in the vicinity of a single mitochondrion almost linearly. Significant levels of the electric field approximately 540 kV/m were detected even at a distance of 2 m from a mitochondrion. This reliance might match a mitochondrion's organized water layer. A phenomenon known as "water ordering" occurs when the water structure changes from a viscous liquid to a quasielliptical gel, having an impact on inner cellular functions, particularly by providing little damping for the cytoskeleton vibration system. The mitochondria occupy more than 20% of the cellular volume, with organized water making up the majority of the remaining space. Biological molecules, the cytoskeleton, and the cytosol are all exposed to a strong electric field. The electrochemical proton gradient across the inner membrane is used in the production of ATP. Over 40% of ATP is created with efficiency. Nearly 60% of the remaining untapped energy is released from mitochondria as heat, photons (UV photon emission was also seen), and chemical energy that is not used to produce ATP and GTP.

The locations of energy use determine where mitochondria are found. In the interphase, mitochondria are grouped around microtubules, the cytoskeleton's coordinating elements. It is widely known that the GTP molecules needed for the polymerization of assembly-competent tubulin dimers by microtubules are consumed by them. The precise location of mitochondria during the M phase is unknown. Tubulin heterodimers, which carry sizable electric dipoles, make up microtubules. An electromagnetic field is created by their oscillations (the electromagnetic character predominates at a greater distance from the source; the close field, with great energy and electric field characteristics, is called the electrodynamic field or the virtual photon field). A region of extremely nonlinear microtubule oscillations may be shifted by the strong static electric field surrounding mitochondria.

The cellular energy sources must be activated in order to create the electrodynamic field that microtubules in the cytoskeleton of the cell produce at various stages of the cell cycle. A fundamental requirement for oscillations and the creation of the electrodynamic field is an energy supply. Microtubules are dynamic polymers with a cylinder form that exhibit what is known as a dynamic instability process with phases of development interspersed with a catastrophe-like quick shortening. After a heterodimer is polymerized into a microtubule, GTP is hydrolyzed to GDP (guanosine diphosphate) in the β tubulin unit. This provides energy to the microtubules. ATP molecules serve as the energy source for the motor proteins' movement along microtubules while conveying "cargo". Microtubules get a portion of the motion's energy, while motor proteins may also interfere with coherence and damping. Unused energy released from mitochondria is most likely what gives microtubules the most energy during the interphase. Microtubule treadmilling in the mitotic spindle provides energy during the M phase by polymerizing from one end and depolymerizing from the other end. We contend that the generated electrodynamic field is a necessary component of biological cellular activity. Its function in the organization of biological matter interactions between systems, directional transport of mass particles and electrons and information transfer was carefully examined and characterized. These studies add something new to our knowledge of how live cells function biologically.

Disrupted Biophysical Processes in Cancer

Warburg believed that reducing the functional (and maybe structural) order in the cell was the result of partially suppressing the oxidative synthesis of ATP and replacing it with fermentative (glycolytic) activities. It was noted by him that "the adenosine triphosphate synthesized by respiration therefore involves more structure than adenosine triphosphate

synthesized by fermentation was his observation. All ensuing physical processes and biological activity that depend on mitochondria are disrupted by mitochondrial malfunction. For example, in kidney and liver cells, the generation of oxidative energy can be up to 100 times larger than that of fermentative energy in healthy cells. Only about half of the ATP produced by cancer cells is supplied by the mitochondria. Pyruvate dehydrogenase kinase (PDK) inhibits the pyruvate pathway, which results in one type of mitochondrial malfunction (known as the glycolytic phenotype). Numerous cancer forms have been linked to mitochondrial dysfunction. In this regard, we emphasize the following details: The majority of carcinomas have what is known as hyperpolarization of the mitochondrial inner membrane a diverse group of information channels and oncogenes leads to mitochondrial dysfunction with increased glycolysis and resistance to apoptosis and most solid tumors show an increased glucose uptake. These characteristics led Michelakis et al. to recommend DCA dichloroacetate as a key component of cancer therapies that may be successful in a wide range of different malignant tumors[4]–[6].

A crucial factor in determining how well the inner membrane is functioning is potential. The potential is determined by how well positively charged fluorescent dyes like Rhodamine 123 are absorbed and retained. Hyperpolarization is the phrase for significant absorption and retention. The absorption and retention, however, may also be influenced by the distribution of ions (such as K⁺) within the cell, the generation of lactate, and the degree of water ordering, and they need not perfectly match the actual potential of the mitochondrial inner membrane. Lack of mitochondrial hyperpolarization in some malignant tumor types, such as oat cells lung cancer, lymphomas, neuroblastomas, sarcomas, and other cancers may indicate a modified glycolytic phenotype or the presence of additional mitochondrial defects and apoptosis blocking. The pH gradient is lowered and the membrane potential is raised by an electrically neutral exchange of protons and potassium ions. The proton transfer may be reduced in cancer cells due to defects in the mitochondrial respiratory enzyme complexes and electron carriers in the mitochondrial inner membrane. However, in malignant tissue, another divergence appears. The reverse Warburg effect occurs, wherein fibroblasts connected to cancer cells with fully functioning mitochondria develop mitochondrial malfunction. Lactate, glutamine, and other energizing metabolites are transferred from the fibroblasts to the cancer cell. The absence of hyperpolarization may be correlated with the state of increased mitochondrial energy synthesis and activity. Therefore, two separate cancer pathways can be distinguished by the way a fluorescent dye is absorbed and retained.

Because living processes are dependent on the true mitochondrial membrane potential, it's feasible that this potential may promote both life and death Potential disruptions brought on by insufficient energy supply from pyruvate or fatty acids can have an impact on fundamental biological processes. Pyruvate dehydrogenase (PDH) kinases (PDK-1-PDK-4) control the activity of PDH enzymes. The PDH kinases impede the pyruvate pathway, which results in mitochondrial failure in the glycolytic phenotype cancer cell. poor levels of water ordering, a weakening of the static electric field surrounding a mitochondrion, a reduction in the outflow of unutilized energy, and poor K⁺ channel expression are all signs of hyperpolarization. It's significant to note that and does so by restoring normal mitochondrial activity, which results in normal cell function or activating apoptosis in the case of abnormal cells. Increased resistance to apoptosis is always correlated with hyperpolarization. Better PDK inhibitors than DCA should be developed, according to one study It should be noted that DCA targets PDK rather than the method of its synthesis, which might result in the creation of new pharmacological medicines in the future.

Cellular Filaments

A three-dimensional network made up of intermediate filaments, microtubules, and actin filaments ensures the mechanical integrity of a cell. The term "cytoskeleton" refers to this

network as a whole. To participate in various cellular processes, actin and tubulin proteins in their separate filaments bind a wide variety of other proteins, such as ARP and MAP proteins. Microtubules create electrodynamic fields all around them as they organize the cell into extremely dynamic structures. The organization of the cytoskeleton as well as the generated electrodynamic field, specifically its intensity, frequency spectrum, coherence, and spatial distribution pattern, can have a significant impact on a cell's mechanical properties, dynamic behavior throughout the cell cycle, including transport, and biological activity. Microtubules and other cytoskeleton elements are arranged geometrically to create the spatial pattern of the generated field. Before the malignant features of a cancer cell are fully developed, cytoskeleton disruptions are likely to be caused[7]–[9].

When examined under the influence of external forces, the mechanical properties of cancer and healthy cells from the same tissue are very different. Human-derived cells' deformability was assessed. Human nontumorigenic epithelial breast cells exhibit various deformability for the metastatic invasion of gastrointestinal malignancies, causes changes in the mechanical characteristics of human pancreatic cells. Around the nucleus, the keratin network contracts, the cell's elasticity declines, and the amount of energy lost through mechanical deformation rises. A produced electromagnetic field may mediate interactions at a distance greater than 0.1 millimeter, which could explain why long-range electrodynamic interactions are less strong than forces that form chemical bonds and biophysical touch interactions. Some morphological alterations used to assess the cytological and histological progression of cancer may be caused by cytoskeleton flaws. For instance, in the cytological images, the keratin network shrinking may be indicated by nuclear membrane wrinkles and irregularities in the distribution of the chromatin, such as coarse chromatin clumping.

In cancer cells with a glycolytic phenotype, as opposed to normal cells, mitochondrial failure may lead to a decreased intensity, a loss of coherence, and a spatially scattered pattern of the electrodynamic field created by microtubules.

The strength and coherence of the electrodynamic field that is generated as well as the pattern of spatial distribution of the microtubules affect the forces that interact between cells. There may be less force interaction between cancer cells than between normal cells or between a normal and a cancer cell. For instance, cancer cells may be drawn into healthy tissue by the normal cells around the tumor. This mechanical action might be a crucial component of malignant cancer cells' localized invasion of healthy tissue.

Metastatic processes are preceded by phosphorylated keratin filament shrinkage in response to SPC therapy. The resulting electrodynamic field's spatial pattern may sustain enough damage as a result of the cytoskeleton disarray to allow the cancer cell to break free from its contacts with neighboring cells, escape, and spread to other organs. The epithelial-to-mesenchymal transition is the name given to this process in the literature on cancer research. But we contend that it may be related to a further reduction in the electromagnetic field's strength, degree of coherence, and nonlinear characteristics of microtubules, as well as a disturbance of the frequency spectrum.

These pathways might have a close relationship to the extracellular matrix flaws that are known to be tied to the beginning of cancer. The resulting electrodynamic field is thought to play a role in the enslavement of cells inside a tissue.

The conditions for the formation of the electromagnetic field are the same for all of the cells and are identical. The cell cannot escape enslavement and begin independent functioning in the body without necessary adjustments. Additionally, the altered cell must get away from the immune system's watchful eye. To understand this effect, it is necessary to identify the electromagnetic field changes' zone of tolerance[10].

CONCLUSION

One of the crucial components of the biophysical processes occurring at the subcellular level is the excitation of electromagnetic fields in live cells. Its synthesis in live cells was said to be impossible because water viscosity dampening prevented it or because there weren't enough energy sources to excite cell oscillations.

However, the earlier authors failed to take into account water ordering, while the later authors failed to recognize the important nonlinear characteristics of the cellular system and the high-quality factor of biological oscillators. Microtubules produce cellular electromagnetic fields.

A functioning level of biophysical processes is established in live cells as a result of the interaction between microtubules and mitochondria.

The operation of the mitochondria is vital for the generation of electromagnetic fields by microtubules in live cells. Although chemical-genetic signaling controls mitochondria, other than inducing death, physical mechanisms are mostly responsible for their function. Energy conversion into ATP and GTP cannot be the only focus of mitochondrial function. Strong static electric fields are produced around mitochondria when protons are transferred from the matrix space into the cytosol.

These fields have an impact on the ordering of the water in the cytosol and have nonlinear effects on microtubules. Cell structure and overall cell activity depend heavily on mitochondria.

Biophysical processes are disturbed by their malfunction. In the vast majority of malignancies, this is the case. Mitochondrial dysfunction develops at a certain point in the development of cancer and has an impact on a variety of cell characteristics, including the spatial organization and functional order. Physical, genetic, and chemical processes are interconnected.

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CHAPTER 4

MERIDIAN AND ACUPOINT BIOPHYSICAL CHARACTERISTICS: A SYSTEMATIC REVIEW

Thiruchitrambalam, Professor
Department of ISME, ATLAS SkillTech University, Mumbai, Maharashtra, India
Email Id-thiru.chitrambalam@atlasuniversity.edu.in

ABSTRACT:

Acupuncture is a crucial component of traditional Chinese medicine (TCM) and is a simple, efficient treatment with little side effects. Meridian essence studies have recently taken the stage in contemporary TCM. Since the 1950s, numerous studies using a variety of technologies, including biophysics, biochemistry, and molecular biology, have shown that meridians indeed exist. The biophysical research on the electric, acoustic, thermal, optical, magnetic, isotopic, and myoelectric properties of meridians and acupoints is reviewed in this work. These results imply that meridians and acupoints differ from non-acupuncture points in their biophysical properties. Future research on the mechanisms of action and proof of efficacy of acupuncture should be conducted utilizing high-throughput technologies like omics and multicenter randomized controlled trials due to the shortcomings of earlier studies. Thin needles are put into the body during acupuncture a kind of alternative treatment and a part of traditional Chinese medicine (TCM). The theories and practices of TCM have been labeled as quackery since they are not founded on scientific understanding, and acupuncture is a pseudoscience.

KEYWORDS:

Acupuncture, Biophysical Characteristics, Meridians, Medicine.

INTRODUCTION

It is commonly acknowledged that meridians and acupoints have low resistance and high capacitance. Currently, scientists are examining acupoints' electrical characteristics as a potential way to investigate the workings of acupuncture. The temperature and resistance at the left and right pericardium, and sites 1 cm apart from all above acupoints were detected by Wang et al. using infrared thermal imaging and surface resistance measurement in 20 rabbits. The findings demonstrated that acupoints differed from non-acupuncture point controls in having high skin temperature and low electrical resistance, and that resistance values were inversely correlated with skin temperature. The existence of this phenomena has also been proven by other Chinese researchers. Additionally, Egot-Lemaire and Ziskin discovered that the acupoints' dielectric characteristics differed somewhat from those of the nearby non-acupuncture points, which varied from 50 GHz to roughly 61 GHz.

The results of other investigations do not, however, support the findings mentioned above. Ahn et al. measured the electrical impedance along pericardium and spleen meridians and corresponding parallel control segments in 23 human individuals using a four-electrode technique. The findings revealed that, in comparison to their respective controls, tissue impedance was often reduced along the pericardium meridian but not along the spleen meridian. Three acupoints and the areas around them were tested for electrical skin impedance using two devices by Pearson. The findings demonstrated that neither of the two nearby control locations nor any of the three acupoints tested had decreased skin impedance. Only 5 out of 9-point studies showed a positive association between acupoints and lower electrical resistance and impedance, while 7 out of 9 meridian studies showed a positive association between acupuncture meridians and lower electrical impedance and higher

capacitance, according to Ahn et al.'s systematic review of studies on the electrical characteristics of acupuncture structures. The claim that acupoints or meridians were electrically distinct was not clearly supported by the facts. Kramer et al. measured the skin resistance using an array of 64 electrodes. Electrical skin resistance measurements (ESRMs) were performed on the electrodes at the respective acupoints, and the results were contrasted with those of the electrodes nearby.

According to there was no discernible difference between the electrical skin resistance (ESR) at the majority of acupoints (62.8%) and the ESR in the vicinity. This was somewhat in line with other earlier, excellent research that had relatively unfavorable conclusions to make about this subject. The use of ESRMs for acupoint localization or diagnostic/therapeutic purposes could not, therefore, be inferred from the data. They also discovered in this research that the array used to measure ESR had exceptionally good repeatability after 1 minute but low reproducibility after 1 hour and 1 week. The phenomenon had a strong short-term reproducibility but a low long-term reproducibility. One straightforward reason might be a change in environmental parameters, such as artifacts, significant inter- and intra-individual variation in ESR, and ESR shift that could be brought on by trans epidermal water loss or skin hydration. The electrode size and variations in stratum corneum layer thickness (such as minor abrasions) may also have an impact on ESRMs. They also discovered that the 8 mm gap between the electrode centers may have prevented them from measuring the acupoint itself, which could have had an impact on the data' dependability.

Other researchers discovered that variations in skin condition (dry/moist, thickness, and integrity of the stratum corneum), electrode material, size, and shape, pressure exerted by the probe, duration of probe application, inclination of the probe tip on the skin, and variations in the device for measuring skin electrical current/resistance might be the potential confounders affecting the reproducibility and reliability of the device. Colbert et al. created a continuous recording system, a fully automatic multichannel device, to record skin impedance at several acupoints simultaneously over the course of 24 hours in order to overcome the restrictions. They used it to successfully identify that acupoints' skin impedance was lower than that of the surrounding non-acupuncture points. In addition, Colbert et al created an automated multichannel prototype system and measured electrical capacitance and resistance at eight skin sites in 33 healthy subjects for more than 2 hours. Only the acupoints on the liver and spleen meridians were found to have a lower resistance than their neighboring sites (4 mm distant), according to the data; all other comparisons revealed no appreciable differences.

Yang examined a number of potential causes of low resistance in order to investigate the mechanics behind electrical properties. He came to the conclusion that low resistance was caused by a relative higher interstitial fluid (tissue fluid) content, and the histological essence of meridians was bands with a relatively high interstitial fluid content in loose connective tissues. Others thought that the structural underpinning of the various skin resistances might be gap junctions. According to Tan, the concentration change of charged molecules in the relevant environment was one of the most significant variable elements determining the resistance in various body regions, in addition to the inherent organizational characteristics. Additionally, he came to the conclusion that the resistance of meridians would undoubtedly decrease when propagated sensation along channel (PSC) occurred in accordance with the bioelectric field with abundant ion along meridians. Other studies hypothesized that the electrical properties of meridians and acupoints were caused by mast cell release of histamine and serotonin (5-HT), local tissue release of noradrenalin (NA), nitric oxide (NO), tumor-related factors, and tumor-related factors. The initial reports of phonation and sound transmission in meridians date back to the 1980s, and scientists have since attempted to corroborate them in both animal and human studies. In 30 rabbits, Zhang et al. [36] identified 8 acupoints on the conception vessel, 11 acupoints on the governor vessel, and 2 mm-distance

control points on both sides of the acupoints. The findings demonstrated that acupoints had much larger sound wave amplitudes than non-acupuncture points. By measuring the sound wave's intensity, Wei et al. were able to confirm that the sound wave could travel through meridians and reach acupoints. Its conduction velocity was lower than bone conduction but greater than soft tissue conduction. A substantial connection between the tones and the meridians, which are described in the Yellow Emperor's Internal Medicine, was also discovered.

DISCUSSION

According to Wang, Bertarelli discovered in 1970 that the facial isotherm trace shown in infrared thermal photographs resembled human meridian patterns. Since that time, an increasing number of researchers have reported the thermal properties of meridian and acupoints from various angles. For instance, Hu et al used an infrared imaging device to observe the infrared radiant and discovered that the tracks were congruent with the 14 meridians the ancient Chinese had specified. Along the meridians, Zhang et al. measured the temperature at 5 and 10 mm subcutaneously, respectively. They discovered that acupuncture, which primarily originated in the epidermal layer, caused the high-temperature line to form along the meridians. Thermal factors may also contribute to the differentiation of the disorders. The constitutions of yang insufficiency, qi deficiency, and tranquility were reportedly distinguished using heat sensitivity measurements of meridians.[1]

The Optical Properties

Studies on optical properties are rather rare, and those that do exist tend to concentrate on high luminosity and the features of how light waves travel along meridian lines. 14 high luminous lines were observed on the surface of the body, according to Yan et al, and these lines differed noticeably from those on both sides of the body, which were 5 mm distant. Comparing the locations of the 14 regular meridians on the surface of the body specified by Huang Di Nei Jin with the high luminous lines where 1934 points are located, the rate of entirely overlapping region was 92.97%, and the percentage of basically consistent region was 6.72%. According to the findings, meridians and acupoints have highly luminescent biophysical characteristics. In order to examine the transmission properties of light waves along the meridians, Liu et al created an automatic measurement system. They discovered that meridians and non meridians varied significantly from one another. Additionally, they discovered that the pericardium meridian's average attenuation factor was lower than the spleen meridian.

Magnetic Properties

Meridians' and acupoints' magnetic properties are still not completely understood. In the national zero-magnetic laboratory in China, Li et al used functional magnetic resonance imaging (fMRI) and a superconducting quantum interference device (SQUID) to examine meridians, acupoints, the brain, and related organs. Along the low electric resistance channel, they discovered a reasonably steady circular stream of electromagnetic and chemical oscillation. In order to create an oscillatory network, competition between various frequency oscillations frequently resulted in resonance in certain body positions. Moreover, the position of unusual places in the body, which may have been meridians and acupoints with regulatory functions, was dominated by the electromagnetic and chemical oscillation circulation. The magnetic field of the human body. The study of meridians and resting-state brain networks using functional magnetic resonance imaging (fMRI) has grown in prominence recently. fMRI was utilized by Zhang et al. to examine the specificity of acupuncture. distinct brain regions were improved by acupuncture gallbladder (GB) 40 with kidney (KI) 3 as a control (belonging to the same nerve segment but distinct meridians). It proved that different

acupoints in acupuncture could have various modulatory effects on resting-state networks (RSNs)[2]–[4].

Cao conducted another intriguing experiment in which he investigated the effects of acupoint magnetic stimulation on the temperature field along meridians. The infrared imaging temperature measurement was utilized to directly detect the distribution of temperature along the governor vessel on rabbit and human bodies in order to explore the variation of temperature field before and after magnetic stimulation at acupoints. The temperature of acupuncture points on the governor vessel varied considerably from non-acupuncture points. This demonstrated how changing temperatures along meridians could result from magnetic stimulation of acupoints.

Migration of Isotope Along Meridians

The earliest evidence of isotope migration along channels was found in the 1950s. It is a fairly straightforward physical event that abides by physical principles. Meng and his team in China demonstrated in the 1980s that after injecting the isotope into an acupoint, sluggish movement along channels was seen. The channels shown were comparable to the meridians described in ancient Chinese literature. But they simply served to demonstrate that the lymphatic network had nothing to do with the channels. The neurological and vascular systems were unaffected. Minipigs were found to have low hydraulic resistance channels along meridians in 2008 by Zhang et al. In comparison to nonmedian environments, more fluid flows along meridian lines due to the low hydraulic resistance. Six minipigs had their stomach meridians found via isotope tracing. In two instances, it was demonstrated that an isotope migration down the meridian toward the other low hydraulic resistance point could be observed after injecting 0.1 mL into one low hydraulic resistance site. These results led them to the conclusion that the isotope migration in the human body represented the flow of interstitial fluid via low hydraulic resistance channels[5]–[7].

Myoelectric Activities

In China, PSC is frequently studied using myoelectricity. The strong ties between the PSC and the nerve-skeletal system were demonstrated by Zhu et al. In their research, myoelectricity and propagated feeling were observed throughout the large intestine meridian when large intestine (LI) 4 was stimulated. Anesthesia with a brachial plexus block, however, might stop this occurrence. The longissimus muscle's myoelectric activity was similarly discovered to be the basis of PSC in another rat study by Ma et al. These studies demonstrate that meridians exhibit overt myoelectric activity, and that myoelectricity and propagated feeling are tightly connected[8], [9].

Recap and Proposed Directions

Meridians and acupoints have various biophysical characteristics that set them apart from non-acupuncture points, according to recent studies. Among the characteristics are electric ones (high electrical potential, conductance, and capacitance, low impedance and resistance), thermal ones (infrared radiant tracking along the meridians), acoustic ones (high guide sound with 2–15 Hz frequency, 0.5–10 mV amplitude, 6.2–10 cm/s bidirectional conduction velocity, and being similar with sharp wave or sine wave), and optical ones (high luminous properties and low dispersion). As a result, science supports the existence of meridians[10]–[12].

These biophysical characteristics serve as the foundation for PSC and subsequent studies on the shape and functional routes of meridians. When all of the properties are taken into account rather than relying on just one, they may also help with diagnosing illnesses, investigating novel therapies, elucidating pathogenesis, and differentiating symptomatic types and constitutions in TCM. Future basic studies should employ systemic biology techniques

like proteomics, genomics, transcriptomics, and other omics in addition to traditional methods like electric, acoustic, optical, and magnetic methods to reveal the multitarget and multipath mechanisms of action. Clinical studies, particularly sizable randomized controlled trials, should be used to support the fundamental findings further. To demonstrate the therapeutic benefit, this type of research should stress the suitable disorders suggested for acupuncture intervention.

There are numerous acupuncture variations that have their roots in various philosophies and the methods used depend on the nation where the procedure is carried out. However, it can be divided into two main foundational philosophical applications and approaches: the first is the contemporary standardized form known as eight principles TCM, and the second is an older system that is based on the ancient Daoist wuxing, more popularly known as the five elements or phases in the West. Although acupuncturists claim that it can be utilized for a variety of other illnesses, acupuncture is most frequently used to try to relieve pain. In most cases, acupuncture is only used in conjunction with other types of therapy.

Trials and systematic reviews of acupuncture often come to the conclusion that there is insufficient evidence to support its therapeutic efficacy. When performed by qualified professionals utilizing a clean needle method and single-use needles, acupuncture is usually considered to be safe. It has a low rate of primarily mild negative effects when administered properly. When mishaps and infections do happen, they are usually the result of practitioner negligence, especially when sterile procedures are used. According to a 2013 assessment, there were a lot more reports of infection transmission throughout the previous ten years. Pneumothorax and infections were the most often reported adverse effects. Since major adverse effects are still being recorded, it is advised that acupuncturists have adequate training to lower the risk.

Traditional Chinese ideas like qi, meridians, and acupuncture points have not been supported by histology or physiological research. The life force energy (qi) and meridians, which were a significant component of early belief systems, are no longer supported by many modern. Although some scholars contend it may have been used earlier, acupuncture is thought to have its roots in China around 100 BC, around the time *The Inner Classic of Huang Di* (Huangdi Beijing) was published. Regarding the impact of lunar, cosmic, and earthly cycles, yin and yang energies, and a body's "rhythm" on the efficacy of treatment, various assertions and belief systems have developed over time. Due to shifts in the country's political leadership and a preference for rationality or scientific medicine, acupuncture's acceptance in China has fluctuated.[28] After being introduced to Japan by medical missionaries in the sixth century AD, acupuncture eventually made its way to Europe, starting in France.[28] As acupuncture gained popularity in the 20th century and extended to the United States and other Western nations, its metaphysical components that ran afoul of modern science were occasionally dropped in favor of just inserting needles into acupuncture points..

CONCLUSION

An example of alternative medicine is acupuncture. Although it can be used to treat a variety of illnesses, it is most frequently used to relieve pain. In most cases, acupuncture is only used in conjunction with other types of therapy. For instance, according to the American Society of Anesthesiologists, it should only be used in conjunction with traditional therapy when treating nonspecific, noninflammatory low back pain. Thin needles are inserted into the skin during acupuncture treatments. A normal session involves lying still while five to twenty needles are inserted; the majority of the time, the needles will be left in place for 10 to twenty minutes. This is according to the Mayo Foundation for Medical Education and Research. Mayo Clinic. Application of heat, pressure, or laser light may be involved. Acupuncture is traditionally customized and founded on philosophy and intuition rather than scientific

evidence. There is also a non-invasive therapy known as "sunshiny" or "shikhara" that was created in early 20th-century Japan and uses a complex collection of tools instead of needles to treat youngsters.

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CHAPTER 5

COMPUTATIONAL DRUG DISCOVERY FOR ATP-BINDING CASSETTE PROTEINS: BIOPHYSICAL APPROACHES

Shashikant Patil, Professor

Department of uGDX, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id-shashikant.patil@atlasuniversity.edu.in

ABSTRACT:

The majority of therapeutically important drug targets are membrane proteins, yet there aren't many atomic resolution structures of this type of proteins available. The biophysical properties of these polytopic transporters, receptors, and channels have hindered structural characterization, although current advancements in in vitro approaches attempt to address these issues. The ATP-binding cassette (ABC) superfamily is one such class of membrane proteins that is widely expressed in the human body, necessary for healthy physiology, and disease-causing when mutated, but does not have enough structural representation in the Protein Data Bank. However, recent advances in biophysical methods (such as cryo-electron microscopy) have made it possible to characterize previously "hard-to-study" ABC proteins at high resolution, offering insight into their molecular mechanisms-of-action as well as revealing novel druggable sites for the development of new treatments. The development of novel small molecule therapeutics that are easily transferable from the computer to the bench and ultimately to the patient's bedside is now greatly facilitated by these new developments. Computational methods (such as virtual screening, molecular dynamics simulations, and structure-based drug design) have a lot of room to do this. In this study, we examine the application of cutting-edge biophysical methodologies and tried-and-true in silico methods to the discovery of drugs to treat disorders brought on by malfunctioning ABC proteins.

KEYWORDS:

ABC Proteins, Channels, Drug Discovery, Drug Targets.

INTRODUCTION

The adenosine triphosphate- (ATP-) binding cassette (ABC) protein superfamily is made up of transmembrane proteins that use the energy produced by ATP binding and hydrolysis to move ions or solutes across lipid bilayers in certain cell types throughout the body. ABC transporters can be classed as importers (bringing solutes into the cell) or exporters (expelling solutes from the cell) depending on the direction of transport. In bacteria and archaea, both importer and exporter ABC proteins are present, whereas only exporters are discovered in eukaryotes. The fact that mutations in numerous ABC transporter superfamily members have been linked to illnesses in humans emphasizes the significance of ABC transporters. Importantly, several ABC proteins mediate the efflux of these biomolecules and their metabolites across specific tissues, and as a result, they play a role in the absorption, distribution, and excretion of drugs, a number of ABC proteins have shown significance in mediating multidrug resistance, such that overexpression of these proteins in malignant tissues prevents chemical buildup via active transport, resulting in relapse and cancer progression. Together, it is evident that ABC proteins play a significant role in a number of physiological processes and disorders that are linked to them in humans. In contrast, ABC importers and exporters are crucial for bacterial and archaeal cell membrane transport of nutrients and toxins, respectively. One of the biggest and arguably one of the oldest gene families is the transport system superfamily known as the ATP-binding cassette transporters (ABC transporters). All existing phyla, from prokaryotes to humans, have it as a member. Translocases include ABC transporters. Multiple subunit ABC transporters frequently include one to two transmembrane proteins and one to two membrane-associated AAA ATPases. The energy required for the transport of substrates

across membranes, whether for uptake or export of the substrate, is provided by the binding and hydrolysis of adenosine triphosphate (ATP).

A solute-binding protein called an extra cytoplasmic receptor is also present in the majority of uptake systems. Some homologous ATPases work in procedures unrelated to transport, like RNA translation and DNA repair. Despite the fact that the integral membrane proteins appear to have evolved independently several times, and as a result, comprise different protein families, ABC transporters are thought to be a subset of the ABC superfamily based on similarities in the sequence and organization of their ATP-binding cassette (ABC) domains. Based on their high-resolution three-dimensional structures, it is conceivable that the integral membrane proteins of ABC uptake systems also evolved at least three times independently, similar to the ABC export. While exporters move lipids, sterols, medicines, and a wide range of primary and secondary metabolites, ABC uptake porters take up a wide range of nutrients, biosynthetic precursors, trace metals, and vitamins. Cystic fibrosis, tumor resistance, and a number of other hereditary disorders affect humans because of some of these exporters. In both prokaryotic and eukaryotic organisms (including humans), high levels of expression of the genes encoding some of these exporters lead to the development of drug resistance to a variety of substances, including antibiotics and anti-cancer medicines.

prokaryotes and eukaryotes have produced a large number of ABC transporters that have been described. ABC genes are crucial for a variety of cellular functions, and mutations in human genes are the root cause or aggravating factor in a number of hereditary disorders. In humans, 48 ABC genes have been identified. Many of them, including cystic fibrosis, adrenoleukodystrophy, Stargardt disease, drug-resistant tumors, Dubin-Johnson syndrome, Byler's disease, progressive familial intrahepatic cholestasis, X-linked sideroblastic anemia, ataxia, and persistent and hyperinsulinemic hypoglycemia, have been characterized and shown to be causally related to diseases that affect humans. ABC transporters have also been linked to multiple drug resistance, and some of them were first discovered in this way. When cancer cells overexpress the ABC transport proteins, they can export cancer treatments and make tumors resistant to ABC transporters are crucial for pathogenicity, virulence, and cell survival. Iron ABC uptake systems, for instance, are significant virulence effectors. To scavenge iron that is complexed with erythrocytes or high-affinity iron-binding proteins, pathogens use siderophores like Enterobactin. Bacteria release these high-affinity iron-chelating molecules, which reabsorb iron into iron-siderophore complexes. *Agrobacterium tumefaciens*' gene produces glucose and galactose importers, which are also linked to unfavorable changes taking place inside the cell. For instance, osmosensing ABC transporters that regulate solute intake are activated to balance a potentially fatal increase in osmotic strength. Some bacterial ABC proteins are involved in the control of a number of physiological processes in addition to their role in transport.

In bacterial efflux systems, certain substances that need to be extruded from the cell include surface components of the bacterial cell (e.g., capsular polysaccharides, lipopolysaccharides, and teichoic acid), proteins involved in bacterial pathogenesis (e.g., hemolysis, heme-binding protein, and alkaline protease), heme, hydrolytic enzymes, S-layer proteins, competence factors, toxins, antibiotics, bacteriocins, peptide antibiotics, drugs and siderophores. Additionally, they are critical components of metabolic processes such as the creation of extracellular polysaccharides and cytochrome biogenesis. Human ABC transporters have a role in a number of disorders caused by polymorphisms in ABC genes and sporadically by the total dysfunction of a single ABC protein. Mendelian diseases and complex genetic disorders such as cystic fibrosis, familial intrahepatic cholestasis, adrenoleukodystrophy, Stargardt disease, Tangier disease, immune deficiencies, persistent hyperinsulinemic hypoglycemia of infancy caused by focal adenomatous hyperplasia, Pseudoxanthoma elasticum, X-linked sideroblastosis and anemia, age-related macular degeneration. Multiple

drug resistance (MDR) against a number of structurally unrelated medicines is caused by the human ABCB (MDR/TAP) family. In addition to lipid transport, ABCB1 or MDR1 P-glycoprotein is also involved in numerous biological activities. It has been discovered to mediate the release of the steroid aldosterone by the adrenals, and its suppression prevented dendritic immune cells from migrating, which may be connected to the movement of the lipid platelet activating factor (PAF) outside the body. Additionally, it has been observed that in ABCB1 transfected cells, ABCB1 promotes the transfer of cortisol and dexamethasone but not progesterone. Cholesterol, short- and long-chain analogues of phosphatidylethanolamine (PE), phosphatidylserine (PS), sphingomyelin (SM), and glucosylceramide (GlcCer) can also be transported by MDR1. It is possible that the MDR1 transporter's multispecific transport of a variety of endogenous lipids will have an impact on the transbilayer distribution of lipids, particularly PS and PE species, which are typically more abundant on the inner plasma membrane leaflet.

More recently, it has been discovered that the placenta contains ABC-transporters, suggesting that these molecules may protect the developing embryo against xenobiotics.[20] As opposed to term placentae, preterm placentae exhibit higher levels of placental expression of the ABC-transporters P-glycoprotein (P-gp) and breast cancer resistance protein (BCRP), with P-gp expression being even higher in preterm pregnancies with chorioamnionitis.[21] Increased placental ABC-transporter expression was, to a lesser extent, correlated with rising maternal BMI, but only in preterm infants.

DISCUSSION

Many of the conventional in silico structure-based technologies can be utilized to speed up drug development using solved structures of disease-associated ABC. The general approach to drug discovery and rational drug design for diseases brought on by missense mutations to specific ABC superfamily members involves modeling these side-chain variants onto the tertiary protein structure, followed by molecular dynamics (MD) simulations to "relax" the biomolecular system and allow it to reach its lowest energy conformation within the biological constraints of a phospholipid bilayer. With the help of these energy-efficient mutant ABC protein structures, disease-relevant conformations can be sampled, potentially leading to the discovery of druggable pockets and aberrant structural motifs, as well as therapeutically important target-specificity for the creation of small molecule modulators. However, as was already indicated, non-human species account for the majority of ABC proteins that have been structurally characterized and reported in the Protein Data Bank to far. As a result, homology modeling is frequently used at the start of attempts for developing ABC-centric[1]–[4] drugs. Many of the human models created and published over the past ten years were based on the X-ray crystal structures of homologous bacterial and they have proven to be sufficiently useful for drug development using in silico medicinal chemistry and virtual screening techniques, particularly for Cystic Fibrosis (using CFTR/ABCC7 models; To yet, no chemical found in these in silico research has been successfully translated to the clinic, despite having positive effects in vitro. For this reason, care must be taken when using modeled human structures to direct drug development efforts. Therefore, it is desirable to directly characterize the structure of human ABC proteins, as this would reduce the dangers of utilizing bacterial structure-based homology models (such as poor sequence identity and structural variety). Cryo-EM has recently, successfully, and frequently been used to resolve the complex, polytopic, and typically asymmetric nature of this protein superfamily (even human structures) at higher resolutions (and near full-length polypeptides) than previously possible, which is significant because it has overtaken the usefulness of X-ray crystallography and NMR spectroscopy in the ABC protein field over the past decade.

Best-in-class medicines can be created employing these superior, human disease-relevant biophysical structures. Homology modeling MD simulations virtual screening some examples

of appropriate medicinal chemistry approaches facilitated by well-established *in silico* techniques that can and have been used to drive therapeutic discovery for ABC proteins, primarily those that require functional inactivation (i.e., ABCC1, ABCB1, and ABCG2 as previously mentioned). For instance, ABCB1 inhibitors have been discovered utilizing a variety of *in silico* methods, and these small compounds are currently being tested for tumorigenicity inhibition both *in vitro* and *in vivo*. The use of MD simulations as a computational tool has also shed light on the conformational dynamics, ATP-dependent transport/gating cycles, and potential mechanisms of action of small molecule modulators of certain ABC proteins.

This approach takes into account the biophysics and biochemistry of ABC proteins ensconced in their natural phospholipid bilayer context, revealing physiologically-relevant details concerning conformational dynamics as well as possible druggability. Because of this, MD simulations can be used to sample conformational states that could be challenging to structurally define using current biophysical methods, giving useful insight into the probable druggability of particular functional transition states. Virtual screening is an additional *in silico* approach that has been used successfully to find and assess lead, drug-like small molecule candidates for a number of ABC proteins, primarily ABCB1. As a result, chemical libraries containing tens of thousands to millions of molecules can be effectively and quickly computationally screened against a desired ABC protein target. Usually, this strategy is applied to focus the chemical space of potential modulators on those with strong scaffolds. A representative chemical is then selected for *in vitro* validation experiments after lead candidates are graded in terms of the scaffold compatibility and complementarity to the target of interest. QSAR and SBDD are further strategies that have proven effective in addressing the drug design issue. While SBDD uses scaffolds of known modulators to precisely reposition/modify chemical moieties in order to improve predicted binding affinity and thus putative drug efficacy, QSAR aims to identify bioactive modulators by evaluating the predicted functional activity of a spectrum of drug derivatives. Importantly, these *in silico* methods have been successfully applied in numerous instances to generate small molecule modulators of ABC transporters[5]–[8].

The "Golden Triangle" and Lipinski's "Rule of 5" are two examples of recognized (and predictive) drug development algorithms that must be followed by any small molecules discovered utilizing the mentioned *in silico* methods. Both parameters are concerned with the physicochemical characteristics of tiny molecules, particularly their molecular weight, hydrophobicity (measured by their partition and distribution coefficients, or logP and logD, respectively), and computed hydrogen-bond acceptors and donors. While the Golden Triangle seeks to computationally optimize oral absorption/permeability as well as drug clearance, Lipinski's rules assess drug plausibility in terms of oral bioavailability in humans and take into account a drug's pharmacokinetics (i.e., absorption, distribution, metabolism, and excretion). Any *in silico*-based discovery of a putative ABC protein modulator must satisfy these requirements in order to have potential therapeutic value in the clinic. These algorithms classify compounds based on molecular weight and logD in order to evaluate drug-likeness, efficacy, potency, clearance, and permeability.

Development of Therapy for Multidrug Resistance

In all three domains of life—bacteria, archaea, and eukarya—ABC proteins are present and play a variety of crucial physiological activities essential to normal biology. No exemption applies to ABCB1, although in humans, excessive expression of this ABC transporter results in illness. Due to its prominent expression in cancer patients' tumors, ABCB1 was the first ABC protein to be discovered and cloned. The polyspecific drug efflux pump ABCB1 is necessary for the movement of xenobiotics and physiological substrates across several body tissues, but in cancer, this protein activates a survival response and overexpresses itself in order to efflux

chemotherapeutic. Since specific ABCB1 inhibitors may increase intracellular concentrations of cotreated chemotherapies, ABCB1 is a crucial target for adjuvant cancer therapy. Third generation ABCB1 inhibitors, developed in part using the biophysical structure of ABCB1 as a template for small molecule discovery, have demonstrated efficacy against tumorigenesis.

The ABC superfamily's most distinctive member is another ABC protein called CFTR (ABCC7). The creation of high-throughput, target-based initiatives for the discovery of Cystic Fibrosis drugs was made possible by the cloning of the CFTR gene and the finding of CFTR as a phospho-regulated chloride channel. Interestingly, these efforts resulted in the creation of two Cystic Fibrosis mutation-specific small molecule treatments, a milestone that would be warmly embraced for other disease-associated ABC proteins. A molecular understanding of drug synergy could not be achieved using *in silico* tools alone, despite the importance of the structure-based homology models of CFTR in classifying various experimental drugs based on their site of action on the tertiary structure of CFTR. Additionally, the structure of CFTR was recently solved thanks to recent advancements and improvements to cryo-EM-based techniques, opening the door for later structure-based drug development of the next generation of more potent Cystic Fibrosis.

An essential ABC family member necessary for adaptive immunity is the transporter associated with antigen processing (TAP1/ABCB2). A macromolecular compound that is transported to the plasma membrane enables foreign antigen to be recognized by CD8+ T lymphocytes. This is significant since the herpes simplex virus is a distinct pathogen that expresses a peptide-based inhibitor of TAP1 to dodge this immune response. Again, with the advent of new advancements and enhancements to cryo-EM-based techniques, the binding site of this inhibitor peptide was recently identified, and its mode of action was clarified, further enabling the possibility of SBDD of small molecule modulators of the herpes simplex virus. Last but not least, when more ABC proteins are physically described in various conformations utilizing cutting-edge biophysical techniques, our comprehension of the similarities (and differences) between each distinct family member will be further clarified. This may make it easier to identify druggable binding sites that are only found in each target's mutant form, enabling effective *in silico* virtual screening and SBDD activities for the creation of ABC- and mutation-specific therapies. The ABC superfamily's use of pharmaceuticals may benefit from this strategy as well. Ivacaftor (Kalydeco®), a potentiator specific to CFTR/ABCC7, has recently been used to treat individuals with mutations in ABCB4, a similar ABC protein. This study emphasizes the significance of accurate structure-based classification of proteins and homologous family members with respect to translational drug discovery. Both *in silico* and *in vitro* methodologies were utilized synergistically to support this notion[9]–[11].

CONCLUSION

ABC proteins are necessary for healthy physiology and, when mutated, can lead to illness. This family of membrane proteins is being structurally characterized by biophysical approaches, and recent advancements in some techniques, particularly cryo-EM, have revealed the tertiary structure of some disease-relevant ABC proteins. This structural data lays the groundwork for activities focused on *in silico* drug research and discovery (such as virtual screening and QSAR) that aim to fix misfolded and/or defective mutant ABC variants. In order to improve structural defects brought on by various mutations, potentially druggable sites can be found and investigated in terms of their compatibility with small molecule therapeutics. Additionally, specific modulators can be created using a variety of well-established *in silico* methods. Together, the development of high-resolution structures of these proteins related to human disease offered numerous opportunities to apply research from the lab to the clinic.

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CHAPTER 6

SKIN BIOPHYSICAL FEATURES IN KERATOCONUS PATIENTS: A CONTROLLED STUDY

Raj Kumar, Assistant Professor

Department of uGDX, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id-raj.kumar@atlasuniversity.edu.in

ABSTRACT:

Bacterial infections continue to be a leading cause of morbidity and mortality despite the existence of multiple effective antibiotics and other antimicrobial tools. Additionally, the demand for developing new bactericidal techniques has grown dramatically as a result of the rising worry regarding infections linked to biofilms and multidrug-resistant bacterial strains. As a result, the field of antimicrobial chemotherapy has given significant attention to novel and emerging nanoparticle-based materials. The activities of nanoparticles as an antimicrobial tool, their method of action, their impact on bacteria that have developed drug resistance, and the dangers associated with their usage as antibacterial agents are all covered in the current review. The effectiveness of nanoparticles in the clinical setting, as well as their special qualities and mode of operation as antibacterial agents, are all examined in detail. A substance that either eliminates bacteria or prevents their growth is an antimicrobial. Antimicrobial drugs can be categorized based on the microorganisms they are most effective against. Antibiotics are used to treat bacteria, whereas antifungals are used to treat fungi. They can also be categorized based on how they are used. Antimicrobial prophylaxis and antimicrobial chemotherapy are the terms used to describe the use of antimicrobial medications to treat and prevent infections, respectively.

KEYWORDS:

Antimicrobial, Bacterial, Materials, Medication.

INTRODUCTION

Still a leading cause of morbidity and mortality, bacterial infections. The need for new bactericidal techniques has grown in response to the multidrug-resistant bacterial strains and biofilm-associated illnesses. As a result, the field of antimicrobial chemotherapy has given significant attention to novel and emerging nanoparticle-based materials. In relation to surfaces, bacteria are naturally present in medical and industrial environments. It is now widely acknowledged that the majority of bacteria live in microbial communities, which are frequently made up of numerous species that interact with one another and their environment. Despite the fact that most modern microbiological research focuses mostly on pure culture planktonic bacteria, this fact is still true. It is becoming more well acknowledged that bacterial surface contamination, or the adherence, persistence, and colonization of surfaces by bacteria, is bad for society and public health. Over 80% of microbial infections in the body are caused by infectious diseases associated with biofilms, which increases patient morbidity and costs of care.

Agglomerates of microorganisms that attach to a substrate form biofilm. Prior to secreting binding molecules such as adhesion proteins that lead to irreversible attachment, the bacteria first bond reversibly to the surface. When the bacteria are in place, they multiply and form colonies inside peptidoglycan envelopes, which promotes the maturation of a biofilm. In addition to becoming inaccessible to antibacterial treatments and the body's immune system at this point, the bacteria also serve as a reservoir for persistent infections throughout the body. This is why biofilms pose a serious risk to human health. Additionally, biofilms are resistant to standard antibiotics and respond poorly to them. Therefore, bacterial infections

continue to be difficult to treat despite the availability of many powerful antibiotic medicines and other contemporary antibacterial tools.

Today's antimicrobial materials utilized in clinical settings suffer from serious flaws, such as poor antimicrobial activities, a danger of microbial resistance, difficulties monitoring and extending the antibacterial functions, and trouble operating in a dynamic environment. Therefore, there is an urgent demand for long-lasting antibacterial and biofilm-preventing materials in the fields of medicine and dentistry. Due to a lack of better options, antibiotics are currently used to treat the majority of biofilm-associated illnesses. It is well known that traditional antibiotics do not effectively treat mature biofilms; instead, substantially greater dosages of the drugs are necessary because all such medicines have trouble penetrating the extracellular polysaccharide sheath that surrounds the biofilm. Agents active against planktonic bacteria but not biofilms fail to treat patients because biofilm-associated bacteria are 100–1,000 times less sensitive to antibiotics than planktonic bacteria. Additionally, while smaller doses are typically employed, high amounts are frequently intolerable by the host organism and ineffective. Additionally, there is a significant chance that germs will develop resistance to traditional antibiotics. When mixed bacterial biofilms are created and several antibiotics are utilized to attack the complex microflora, this problem is made more challenging. As a result, various antimicrobial protection strategies are needed. Today, nanotechnology offers a reliable framework for modifying the physicochemical characteristics of a variety of materials to produce potent antimicrobials. As active antibacterial groups, nanomaterials may be strategically useful due to their extremely large surface area in comparison to their size. Even when utilized in modest doses, nanosized particles may still have considerable activity. As a result, NM might be used instead of antibiotics to treat bacterial infections.

The three primary bacterial targets that are now the focus of antibiotic treatment are cell wall formation, translational machinery, and DNA replication. Unfortunately, bacterial resistance to each of these ways of action is possible. In addition to efflux pumps, which provide multidrug resistance against different antibiotics, other mechanisms of resistance include enzymes that modify or degrade the antibiotic, such as β -lactamases and aminoglycosides, modifications of cell components, such as cell walls, as seen in vancomycin resistance and ribosomes in tetracycline resistance. The majority of the resistance mechanisms seen with antibiotics are irrelevant because nanoparticles' mode of action is mostly through direct contact with the bacterial cell wall, without the need to penetrate the cells. This gives rise to the possibility that nanoparticles may induce bacterial resistance less than antibiotics do.

This paper describes the potential of several NM as antibacterial agents. There is a full discussion of the toxic and biocompatibility features as well as the antibacterial mode of action of nanoparticles and how their interactions with microbial cells result in cell death. Antiseptics, which are applied to living tissue and help prevent infection during surgery, disinfectants and antibiotics are the three main categories of antimicrobial agents. Disinfectants kill a wide variety of microbes on non-living surfaces to stop the spread of disease. The term "antibiotic" used to refer exclusively to preparations made from living microbes, but it is now widely used to denote synthetic substances like sulfonamides or fluoroquinolones. Although the term was once only used to refer to antibacterials its usage has since expanded to refer to all antimicrobials. Bacteriostatic agents, which inhibit or stop bacterial growth, and bactericidal agents, which kill bacteria, are two other categories of antibacterial agents. Further developments in antimicrobial technologies have led to systems that can do more than only prevent bacteria growth in response. Instead, some forms of porous medium have been created that can kill microorganisms immediately upon contact. Antimicrobial resistance may arise as a result of excessive or improper usage of

antimicrobials. Use of antibiotics has been widespread for at least 2000 years. Specific molds and plant extracts were employed by the ancient Greeks and Egyptians to heal infections.

Microbiologists like Louis Pasteur and Jules Francois Joubert studied bacterial rivalry in the 19th century and debated the benefits of regulating these interactions in medicine. The distinction between anaerobic and aerobic bacteria was first made thanks to Louis Pasteur's research on spontaneous growth and fermentation. Joseph Lister introduced antiseptic techniques, such as sterilizing surgical instruments and debriding wounds, into surgical processes as a result of the knowledge gained by Pasteur. The number of infections and subsequent mortality linked to surgical procedures were significantly decreased by the application of these antiseptic treatments. The microbiology research of Louis Pasteur also contributed to the creation of numerous vaccinations against serious illnesses including rabies and anthrax. When Alexander Fleming returned from vacation on September 3, 1928, he found that the antibiotic fungus *Penicillium rubens* had caused a Petri dish of *Staphylococcus* to be divided into colonies. Despite their struggles to isolate the antibiotic, Fleming and his colleagues discussed its medicinal potential in the *British Journal of Experimental Pathology* in 1929. Using Fleming's discovery, Howard Florey, Ernst Chain, and Edward Abraham purified and extracted penicillin in 1942 for medical use, winning them the 1945 Nobel Prize in Medicine.

DISCUSSION

Since they may fill the gaps where antibiotics typically fall short, nanomaterials acting as supplementary antibacterials to antibiotics are extremely promising and attracting significant research. Combating biofilm and mutants with multiple drug resistance is part. Metal, metal oxide, and organic nanoparticles, which are now used as antimicrobial NM, exhibit a variety of intrinsic and modified chemical composition features. It follows that the fact that they have a variety of activity modes is not surprising. The target bacteria also differ substantially in terms of their genetic makeup, which has an impact on the construction of their cell walls, crucial metabolic processes, and numerous other aspects that, if interrupted, might be fatal to the microorganisms. Additionally, the physiological state of the bacteria, such as whether they are planktonic, biofilm-forming, growing rapidly, sedentary, or hungry, may have a significant impact on how sensitive they are to NM. The NM's toxicity in various circumstances depends on the bacteria-to-NM ratio. Aeration, pH, and temperature are just a few of the environmental parameters that determine how toxic NM is to bacteria. The size, shape, chemical modification, solvent utilized, mixing in different ratios with other nanoparticles, and other physicochemical characteristics of the particles all have a significant impact on their antibacterial activity. It is also understandable given this complexity that many aspects of the NM antibacterial method of action and level of risk they cause remain unknown, and one might find conflicting accounts about them in the literature. The research of antimicrobial nanotechnology involves employing biofilms to damage a bacterium's cell membrane, administer an electric charge to the germ, and cause instantaneous cellular death via a "mechanical kill" procedure, preventing the original bacteria from evolving into a superbug [1]–[3].

Long atomic chains that can break through the cell wall make up the biofilms. These spikes are much too small to harm mammalian big cells; they are around the size of a human hair. These atom chains have a strong positive charge that draws in negatively charged microorganisms. Nanotechnology has been used to tackle the problem of superbugs and multiple drug-resistant pathogens by developing a new class of antimicrobials.

Issue statement

A study that was released in the *Archives of Internal Medicine* on February 22, 2010, estimates that 1.7 million hospitalizations per year are impacted by healthcare-associated

infections The most common nosocomial diseases can survive or remain on surfaces for months, creating a risk of transmission that never goes away. Most gram-positive bacteria can survive for months on dry surfaces, including *Enterococcus* species *Staphylococcus aureus* and *Streptococcus pyogenes*. It has been discovered that VRE can persist on surfaces for longer than three days after being cultivated from regularly handled things. It has been demonstrated that vancomycin-resistant enterococci can survive for up to 18 hours and fungus can survive for more than five days on dried cotton fibers.

Antimicrobials developed using nanotechnology have the potential to prevent the transmission of bacteria by reducing the quantity of infectious agents at common contact points The Environmental Protection Agency has approved these new therapies, and they are being considered for use in hospitals and other places where communicable diseases can spread easily, like prisons and cruise ships. The first steps in preventing the emergence of superbugs are taking environmental precautions and using antibiotics appropriately. Studies show that even when a patient doesn't actually require an antibiotic, a doctor is much more likely to prescribe one if they think the patient does [4]–[7].

Nanoparticles inorganic

A particle of matter with a diameter of one to one hundred nanometres is commonly referred to as a nanoparticle or ultrafine particle. The word may also refer to fibers and tubes that are smaller than 100 nm in only two directions, or larger particles up to 500 nm. Smaller metal particles are typically referred to as atom clusters at the lowest limit, which is smaller than 1 nm. Since their smaller size influences very different physical or chemical properties, such as colloidal properties, ultrafast optical effects or electric properties, nanoparticles are typically distinguished from microparticles, "fine particles", and "coarse particles" In contrast to colloidal particles, which typically range in size from 1 to 1000 nm and are more sensitive to Brownian motion, they typically do not sediment.

Nanoparticles are significantly smaller than the visible light spectrum, making it impossible to observe them with standard optical microscopes. Instead, they must be viewed with electron microscopes or laser microscopes. For the same reason, nanoparticle suspensions in transparent media may be transparent, in contrast to suspensions of bigger particles, which often scatter some or all incident visible light. Nanoparticle separation from liquids necessitates unique nanofiltration techniques since nanoparticles readily pass through ordinary filters, such as everyday ceramic candles When compared to bigger particles of the same chemical, nanoparticles frequently exhibit significantly different properties. Since an atom's usual diameter ranges from 0.15 to 0.6 nm, the majority of a nanoparticle's substance can be found within a few atomic distances of its surface. Consequently, it's possible that the surface layer's characteristics will prevail over those of the bulk material. Since the interactions between the two materials at their interface also become relevant, this effect is particularly potent for nanoparticles distributed in a medium of dissimilar composition.

Idealized representation of a platinum nanoparticle with a diameter of roughly 2 nm that reveals individual atoms. Numerous fields, including chemistry, physics, geology, and biology, investigate nanoparticles because they are present in nature on a large scale. They frequently display phenomena that are not seen at either size because they are at the interface between bulk materials and atomic or molecular structures. They are a significant contributor to atmospheric pollution and essential components of a variety of industrial goods, including paints, plastics, metals, ceramics, and magnetic goods. One subfield of nanotechnology is the creation of nanoparticles with particular characteristics.

Although nanoparticles tend to sustain a variety of dislocations that may be seen with high-resolution electron microscopes, they often have fewer point defects than their bulk counterparts However, the dislocation mechanics of nanoparticles differ from those of the

bulk material, and this, along with their distinct surface structures, gives rise to mechanical properties that are distinct from the bulk material. Anisotropy is the property of non-spherical nanoparticles, such as prisms, cubes, rods, etc., that depends on both form and size for their properties. Due to their intriguing optical properties, non-spherical nanoparticles of gold, silver, and platinum are finding use in a variety of fields. Nanoprisms' non-spherical geometries result in colloidal solutions with high effective cross-sections and richer hues. Utilizing them for molecular labeling, biomolecular assays, trace metal detection, or nanotechnical applications is made possible by the ability to change the resonance frequencies by adjusting the particle geometry. Under unpolarized light, anisotropic nanoparticles exhibit a particular absorption behavior and stochastic particle orientation, revealing a unique resonance mode for each excitable axis.

Aluminum Oxide

The inorganic compound with the chemical formula TiO_2 is titanium dioxide, also referred to as titanium oxide or titania. It is known as titanium white, Pigment White 6, or CI 77891 when used as a pigment. Although mineral forms can seem black, it is a solid that is insoluble in water and is white in color. It can be used as a pigment in a variety of products, such as paint, sunscreen, and food coloring. Its E number for usage as food coloring is E171. In 2014, global production surpassed 9 million tonnes. Two-thirds of all pigments are thought to contain titanium dioxide, and the market for pigments based on the oxide has been evaluated at \$13.2 billion. Due to its brightness and extremely high refractive index, which is only surpassed by a select few other materials, titanium dioxide, which was first mass-produced in 1916, is the most often used white pigment. To maximize the amount of visible light reflected, titanium dioxide crystal size should be around 220 nm. However, titanium dioxide frequently exhibits aberrant grain development, particularly in its rutile phase. The occurrence of aberrant grain development alters the physical behavior of TiO_2 by causing a small number of crystallites to deviate from the mean crystal size. Purity has a significant impact on the finished pigment's optical characteristics. Some metals can perturb the crystal lattice to the point where the effect can be seen in quality control with as little as a few parts per million. The annual global consumption of pigmentary TiO_2 is estimated to be around 4.6 million tons, and this figure is projected to climb as demand rises [8]–[10].

In powder form, TiO_2 is a powerful opacifier that is used as a pigment in paints, coatings, plastics, papers, inks, foods, dietary supplements, medications, and the majority of toothpastes. In fact, two-thirds of toothpastes sold in France in 2018 contained TiO_2 . It can be found in a variety of dishes, including ice cream, chocolate, all kinds of sweets, creamers, desserts, marshmallows, chewing gum, pastries, spreads, dressings, cakes, and many more. It is frequently casually referred to in paint as "brilliant white," "the perfect white," "the whitest white," or other phrases of a similar nature. The titanium dioxide particles are optimally sized to increase transparency. Its refractive index and color make it an ideal reflecting optical coating for dielectric mirrors when it is deposited as a thin film. It is also used to create ornamental thin films like those seen in "mystic fire topaz."

Some grades of modified titanium-based pigments are man-made pigments that have two or more layers of different oxides, frequently titanium dioxide, iron oxide, or alumina, to produce glittering, iridescent, or pearlescent effects akin to crushed mica or guanine-based products. These pigments are used in sparkly paints, plastics, finishes, and cosmetics. A limited color change is also possible in some formulations in addition to these effects, depending on the way and angle the finished product is illuminated as well as the thickness of the oxide layer in the pigment particle; one or more colors appear by reflection while the other tones appear due to interference of the transparent titanium dioxide layers. By calcining titanium salts at temperatures of 800 °C, the layer of titanium dioxide is sometimes produced in conjunction with iron oxide in certain products. Iriodin, a pearlescent pigment made from

mica covered in titanium dioxide or iron oxide, is one illustration. These titanium oxide particles have an iridescent appearance, in contrast to the opaque appearance of typical ground titanium oxide pigment acquired from mining, where just a small portion of the particle's diameter is taken into account and the effect is solely the result of scattering.

CONCLUSION

By cationic ring-opening polymerization of 2-alkyl-1,3-oxazolines and terminating the macromolecule with a cationic surfactant, antimicrobial polymers with just one biocide end group on the polymeric backbone were created. Compounds with a heterocyclic ring including an atom of nitrogen are known as quaternary pyridiniums. The polymer chain's pyridinium group affects the antibacterial action. Imidazole derivatives are a different kind of antibacterial polymer having aromatic/heterocyclic groups. While its alkylated form has the ability to assemble electrostatically despite lacking the hydrogen bond-forming ability of free imidazole, free imidazole has the ability to make hydrogen bonds with medicines and proteins.

They exhibit increased biodegradability, are chemically stable, and are biocompatible. N-vinyl imidazole and phenacyl methacrylate were combined to create copolymers, which exhibit potent antibacterial properties against a range of bacteria, fungus, and yeas. Primary, secondary, and tertiary amino functionalities are present in the synthetic, nonbiodegradable cationic polymer known as polyethyleneimine. A variety of organic and inorganic, synthetic and natural, monolithic and porous surface materials, including commercial plastics, fabrics, and glass, were coated with PEI. These immobilized surfaces caused the inactivation of pathogenic and antibiotic-resistant strains of bacteria and fungi that are airborne and waterborne, without any evidence of the establishment of resistance. According to reports, the primary mechanism for antibacterial action is cell membrane disruption. The cells of mammals cannot be harmed by these surfaces. Strong bactericidal action is also shown by N-alkylated PEIs immobilized over various woven textiles against a variety of airborne Gram-positive and Gram-negative bacteria. Activity is significantly impacted by Mw of PEI.

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CHAPTER 7

NANO-BIOR PHOTOCATALYST PHYSICAL SYNTHESIS AND PHOTOCATALYTIC ACTIVITY

Shweta Loonkar, Assistant Professor

Department of ISME, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id- shweta.loonkar@atlasuniversity.edu.in

ABSTRACT:

By employing an ethylene glycol solution and hydrothermal synthesis photocatalysts were successfully created. By using X-ray diffractometry scanning electron microscopy (SEM), photoluminescence, and UV-vis diffuse reflectance spectroscopy the nano-Bior photocatalysts were characterized and investigated. The catalytic ability toward photodegradation of rhodamine was also investigated. The outcomes demonstrated that while the nano-Bior photocatalyst's crystallinity grew with the amount of deionized water applied, it decreased as the concentration was raised. The nano-Bior photocatalyst's shape evolved from microspheres to cubes to a mixture of microspheres and flakes when the concentration was increased, and from microspheres to flakes as deionized water was added. According to the findings, concentration and solvents had a significant impact on the bandgap energy values of the nano-Bieber photocatalyst, and the photocatalyst demonstrated good photocatalytic activity toward the photodegradation of Rheba. When the concentration was raised, the photocatalyst degradation yields decreased; when deionized water was added, they increased. When the concentration was raised, the photocatalyst's PL intensity increased; when deionized water was added, it decreased.

KEYWORDS:

Nano-Bior, Photocatalyst, Physical Synthesis, Photocatalytic Activity.

INTRODUCTION

Due to the strong connection between water resources and people's everyday work and lives, the subject of global water pollution has gained significant attention in recent years as a result of the economy's rapid growth. The textile industry and wastewater containing organic dyes, which are difficult to degrade due to their poor biodegradability, are one of the many factors that can lead to water pollution. Because of their distinctive structure and superior photocatalytic qualities, semiconductor bismuth halide based photocatalysts have received a lot of attention from researchers. Due to its modest bandgap, open layered structure, strong oxidation ability, indirect transition mode, high visible light response ability, and excellent stability, the ultrasound-assisted, and the electrospinning approach. The most often employed synthesis processes among them are hydro- and solvothermal techniques. Because of the slow rate of product formation, the ease with which reaction conditions can be controlled, and the stability of the reaction environment during the water- (solvent-) based thermal reaction, the structure, morphology, crystallinity, and phase formation of the photocatalysts can be effectively obtained through controllable synthesis. Ethylene glycol (EG) was used as the solvent in the solvothermal process to create nano-BiOBr microspheres, for instance. However, nano-BiOX microspheres were made with the same solvent EG and different solvothermal techniques. Deionized water (DI) was used as the solvent in the solvothermal process to create

As a result, the goal of the current study is to produce nano-BiOBr photocatalyst by employing CTAB and $\text{Bi}(\text{NO}_3)_3 \cdot 5\text{H}_2\text{O}$ as raw materials and EG and DI as the solvent under various concentrations. It was also thoroughly studied how varied solvents and precursor concentrations affected the structure, morphology, optical characteristics, and photocatalytic

activity. In chemistry, photocatalysis is the acceleration of a photoreaction when a photocatalyst is present. This catalyst's excited state "repeatedly interacts with the reaction partners, forming reaction intermediates, and regenerates itself after each cycle of such interactions." The catalyst is frequently a material that, when exposed to UV or visible light, produces electron-hole pairs that result in the production of free radicals. Heterogeneous, homogeneous, and plasmonic antenna-reactor photocatalysts are the three primary categories of photocatalysts. Each catalyst has a different use depending on the desired application and necessary catalysis reaction.

The idea was first introduced in 1911 by German scientist Dr. Alexander Eibner, who used it to illuminate how zinc oxide (ZnO) bleached the dark blue pigment Prussian blue. Around this time, a paper by Bruner and Kozak on the degradation of oxalic acid in the presence of uranyl salts under illumination was published. Landau published a piece in 1913 that described the concept of photocatalysis. They made contributions that resulted in the invention of actinometric measurements, which serve as the foundation for calculating the photon flux in photochemical processes. After a pause, Baly et al. employed colloidal uranium salts and ferric hydroxides as catalysts to produce formaldehyde in the presence of visible light in 1921.

TiO₂ was discovered by Doeve and Kitchener

As ultraviolet light is absorbed by TiO₂, a highly stable and non-toxic oxide, it could operate as a photosensitizer for bleaching dyes in the presence of oxygen. electrode, hydrogen gas was generated as electrons moved from the anode to the platinum cathode. Given that the bulk of hydrogen is produced through the reforming and gasification of natural gas, this was one of the earliest instances of hydrogen generation from a clean and affordable source. Findings by Fujishima and Honda sparked additional innovation that adding a noble metal, such as platinum or gold, to the electrochemical photolysis procedure might boost photoactivity without the need for an external potential. The synthesis of hydrogen on the surface of strontium titanate (SrTiO₃) via photogeneration and the production of hydrogen and methane from the lighting of TiO₂ were both described by Wagner and Somorjai in 1980 and Sakata and Kawai in 1981.

Commercial photocatalysis has not yet been developed. Its assessment of the electrochemical photolysis of water, one of the main challenges is to create a photoelectrochemical (PEC) tandem cell that is both affordable and energy-efficient and can "mimic natural photosynthesis". Semiconductors and transition metal oxides make up the majority of heterogeneous photocatalysts. Semiconductors, as opposed to metals, which have a continuum of electronic states, have a void energy zone where no energy levels are present to encourage the recombination of an electron and hole created by photoactivation in the solid. In the MO diagram of a semiconductor, the band gap is the energy difference between the filled valence band and the empty conduction band. An electron excites from the valence band to the conduction band, creating an electron hole in the valence band, when the semiconductor absorbs a photon with energy equal to or greater than the material's band gap. An exciton is this electron-hole pair. The excitation energy of the electron can be released as heat when the excited electron and hole join again. Such exciton recombination is undesired and more cost-effective at higher levels. Extending exciton lifetime and improving electron-hole separation are frequently the focus of efforts to create useful photocatalysts. These efforts may rely on structural elements like phase hetero-junctions (such as anatase-rutile interfaces), noble-metal nanoparticles, silicon nanowires, and substitutional cation doping. Designing photocatalysts with the ultimate purpose of facilitating reactions between excited electrons and oxidants to produce reduced products and/or between produced holes and reductants to produce oxidized products. At the surface of semiconductors exposed to light, oxidation-reduction reactions occur as a result of the production of positive holes (h⁺) and

excited electrons (e⁻) A hydroxyl radical is created in one mechanism of the oxidative reaction when holes interact with the moisture on the surface. Beginning with photon (h ν) absorption-induced exciton production on the metal oxide (MO) surface, the reaction.

DISCUSSION

The experimental science known as X-ray crystallography employs incident X-ray beams to diffract into numerous distinct directions in order to identify the atomic and molecular structure of crystals. An image of the density of electrons within the crystal can be created in three dimensions by measuring the angles and intensities of these diffracted beams. The mean locations of the atoms in the crystal, their chemical bonds, their crystallographic disorder, and several other details can all be inferred from this electron density. Since many substances, including salts, metals, minerals, semiconductors, as well as different inorganic, organic, and biological molecules, can crystallize, X-ray crystallography has played a crucial role in the advancement of numerous scientific disciplines. The size of atoms, the lengths and types of chemical bonds, and the atomic-scale variations between diverse materials, particularly minerals and alloys, were all determined using this technique during the method's early decades of use. Numerous biological compounds, including vitamins, medications, proteins, and nucleic acids like DNA, were also found to have structures and functions thanks to this technique.

The main technique for identifying the atomic structure of novel materials and differentiating them from ones that appear to be similar in previous studies is still X-ray crystallography. Additionally, unexpected electrical or elastic properties of a material can be explained by X-ray crystal structures, as can chemical interactions and processes, as well as the development of medications to treat ailments. X-ray crystallography is connected to a number of different atomic structure determination techniques. Both neutron and electron scattering can result in comparable diffraction patterns, and the Fourier transform can be used to analyze neutron scattering. If large enough single crystals cannot be found, other X-ray techniques can be used to get less precise data. These techniques include fiber diffraction, powder diffraction, and small-angle X-ray scattering (SAXS), if the sample is not crystalline. The atomic structure of the material under inquiry can be ascertained via electron diffraction, transmission electron microscopy, and electron crystallography if it is only available as nanocrystalline powders or has low crystallinity.

The early development of X-rays and crystals in science

Snowflakes' hexagonal symmetry is due to the tetrahedral configuration of hydrogen bonds around each water molecule. Although traditionally praised for their beauty and regularity, crystals were not properly studied until the 17th century. The hexagonal symmetry of snowflake crystals, according to Johannes Kepler's theory in *Sterna seu de Nive Sexangular* (A New Year's Gift is the result of regular packing of spherical water particles[1]. The experimental studies of crystal symmetry were invented by the Danish physicist Nicolas Steno in 1669. Steno demonstrated that every example of a specific kind of crystal had the same angles between the faces. Every crystal face may be described by straightforward stacking patterns of identically sized and shaped blocks, as was found by René Just Haüy in 1784. As a result, William Hallows Miller was able to create the Miller indices, which are still used to identify crystal faces today, in 1839, giving each face a distinctive label of three tiny integers. According to Hay's research, crystals are composed of an ordered three-dimensional arrangement of atoms and molecules known as a Bravais lattice; a single unit cell is repeated endlessly along the three main directions. A comprehensive list of a crystal's potential symmetries was developed in the 19th century by Johan Hessel, Auguste Bravais, Evgraf Fedorov, Arthur Schönflies, and (later) William Barlow (1894). Although Barlow made some crystal structure predictions in the 1880s that were later confirmed by X-ray

crystallography the data at the time was insufficient to consider his models as definitive [1]–[3]. Illustration of the water molecule arrangement in ice, highlighting the hydrogen bonds that keep the substance together. X-rays were discovered in 1895 by Wilhelm Rontgen. When X-rays were first discovered, physicists were unsure of their nature but eventually surmised that they were electromagnetic radiation waves. The electromagnetic radiation described by Maxwell's theory was widely accepted, and investigations by Charles Glover Barkla shown that X-rays displayed electromagnetic wave features such as transverse polarization and spectral lines similar to those seen in visible wavelengths. Barkla also invented the x-ray nomenclature. He first identified two distinct diffraction beam types in 1909 and gave them the letters "A" and "B" before assuming there would be lines before "A" and starting an alphabet numbering system with the letter Arnold Sommerfeld's lab conducted single-slit studies that revealed X-rays had a wavelength of around 1 angstrom. Because X-rays are both waves and photons with particle characteristics, Sommerfeld named this wavelike kind of diffraction Bremsstrahlung. Albert Einstein first proposed the idea of a photon in 1905, but it wasn't until Arthur Compton's X-ray experiment in 1922 that he was able to confirm it. Because X-rays have particle-like characteristics, such as the ability to ionize gases, William Henry Bragg argued that X-rays are not electromagnetic radiation in 1907. Since Max von Laue's finding of X-ray diffraction in 1912 disproved Bragg's theory, most scientists now agree that X-rays constitute an electromagnetic radiation.

X-rays can be thought of as waves of electromagnetic radiation, much like crystals are regular arrangements of atoms. X-ray rays are largely reflected off of atoms by their electrons. An X-ray impacting an electron causes secondary spherical waves to radiate from the electron, just as an ocean wave striking a lighthouse causes subsequent circular waves to emerge from the lighthouse. Elastic scattering is the term used to describe this phenomenon, and the electron (or lighthouse) is the scatterer. A regular array of spherical waves results from a regular array of scatterers. Even though these waves interfere destructively in most directions, Bragg's law states that they add constructively in the following few directions:

The distance d between the diffracting

The incident angle is given by theta, the beam's wavelength is given by λ , and n is any integer. Reflections are spots on the diffraction pattern that represent these particular directions. As a result, an electromagnetic wave (the X-ray) impinges on a regular array of scatterers (the repeating arrangement of atoms within the crystal), which causes X-ray diffraction to occur. Since the wavelength of X-rays is often in the same range (1-100 angstroms) as the distance d between crystal planes, X-rays are employed to create the diffraction pattern. Diffraction is theoretically produced by any wave striking a regular array of scatterers, as first proposed by Francesco Maria Grimaldi in 1665. The gap between the scatterers and the wavelength of the impinging wave should be comparable in size to cause considerable diffraction. As an example, James Gregory first noted the diffraction of sunlight through a bird's feather in the later 17th century. David Rittenhouse built the first man-made diffraction gratings for visible light in 1787, and Joseph von Fraunhofer did the same in 1821. However, the wavelength of visible light, which is typically 5500 angstroms, is too long to witness crystal diffraction. The separations between lattice planes in a crystal were not known for sure before the first X-ray diffraction tests [4]–[6].

Max von Laue and Paul Peter Ewald had a discussion in Munich's English Garden in 1912 that gave rise to the concept that crystals may be utilized as an X-ray diffraction grating. For his thesis, Ewald developed a resonator model of crystals; however, because the wavelength of visible light was far greater than the distance between the resonators, this model could not be verified. Von Laue hypothesized that X-rays might have a wavelength similar to the unit-cell spacing in crystals after realizing that electromagnetic radiation of a shorter wavelength was required to perceive such small spacings. With the help of two technicians, Walter

Friedrich and his assistant Paul Knipping, Von Laue was able to record the diffraction of an X-ray beam as it passed through a copper sulfate crystal on a photographic plate. After being developed, the plate revealed a significant number of distinct spots organized around the spot created by the core beam in a pattern of intersecting circles. Von Laue received the 1914 Nobel Prize in Physics for developing a rule that links scattering angles to the dimensions and orientation of unit-cell spacings in crystals.

Development

Although diamonds (top left) and graphite (top right) are both made entirely of carbon, X-ray crystallography has shown that their atom arrangements (bottom) are what give them their distinct qualities. Diamond is strong in all directions because of the tetrahedral arrangement of the carbon atoms and the single covalent bonds that hold them together. Graphite, on the other hand, is made up of layered sheets. Because there are no covalent links between the sheets, graphite is simple to separate into flakes. The bonding inside the sheet is covalent and has hexagonal symmetry.

Following Von Laue's groundbreaking discovery, the area quickly advanced, most notably under the leadership of physicists William Henry and Lawrence Bragg. The younger Bragg created Bragg's law, which links the observed scattering with reflections from uniformly spaced crystal planes. The father and son Bragg team's work in crystallography earned them a share of the 1915 Nobel Prize in Physics. Early structures were typically straightforward and characterized by one-dimensional symmetry. However, over the ensuing decades, advances in computational and experimental techniques made it possible to determine accurate atomic positions for more intricate two- and three-dimensional arrangements of atoms in the unit-cell. It was instantly recognized that X-ray crystallography had the ability to reveal the structure of molecules and minerals, which had hitherto only been inferred inferentially through chemical and hydrodynamic tests. Even though the earliest buildings were made of simple inorganic crystals and minerals, they nonetheless displayed basic physics and chemistry principles. Table salt's structure was the first atomic-resolution structure to be "solved" (i.e., established) in 1914. The table-salt structure's electron distribution demonstrated that crystals are not always made up of molecules that are covalently bound to one another and established the presence of ionic compounds [7]

The related technique of powder diffraction which was created independently by Albert Hull in 1917 and Peter Debye and Paul Scherrer in 1916, was used to solve the structure of graphite. Two groups independently determined the structure of graphite in 1924 using single-crystal diffraction. In order to ascertain the structures of other metals, including iron and magnesium, Hull also applied the powder approach [8]–[10].

CONCLUSION

The composition and low abundance observed in this cyclonic eddy were affected by surface tows made in this month in addition to the cyclonic eddy's effect on dispersion. Lower filtration effectiveness and collections of primarily surface fish larval assemblages were the results of the surface tow method as opposed to Bongo tows. There were also not many mesobathy and shallow-demersal pelagic species. However, the fish larvae's tropical-subtropical biogeographic affinity discovered during surface tows in September was typical of the summertime. Other zooplankton groups have been reported to have similar ZV collections and higher filter efficiency. These distinctions between surface and oblique tows may also be crucial in explaining mesoscale impacts. However, despite the variations in the methodology, the examination of the distribution patterns of fish larvae from surface and oblique tows shows that the correlations between abundance and environmental factors are the same in both cases. Additionally, the oceanographic and biological data may restrict some inferences connected to its evolution across time, giving just a cursory glimpse of the

activities taking place at that precise moment, when sampling is not done widely in time and space over eddy and/or front structures.

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CHAPTER 8

RATIONAL, BIOPHYSICAL ASPECTS, AND INTEGRATION IN MULTIMODAL IMAGING OF HUMAN BRAIN ACTIVITY

Shefalika Narain, Professor

Department of ISDI, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id- shefalika.narain@atlasuniversity.edu.in

ABSTRACT:

Most imaging and electrophysiological studies of human brain activity, up until quite recently, have focused on single-modality data, which are frequently linked with easily observable or experimentally altered behavioral or brain state patterns. Using data from many devices to combine observations or measurements is known as multi-modal imaging. We go over the objectives of multi-modal imaging and how they might be met with specific examples of applications. We also go over some fundamental physiology that is crucial to comprehending the link between hemodynamic and electrophysiological signals, given the significance of these signals in modern multi-modal imaging applications. Neuroimaging is the use of quantitative (computational) tools to investigate the composition and operation of the central nervous system. It was created as an impartial, non-invasive method of doing scientific research on a healthy human brain. It is increasingly being used for quantitative research investigations on mental illness and brain disorders. Neuroimaging is not a medical specialization but rather a highly interdisciplinary field involving neuroscience, computer science, psychology, and statistics. Neuroradiology and neuroimaging can occasionally be mistaken.

KEYWORDS:

Activity, Brain, Electrophysiology, Human.

INTRODUCTION

Since the middle of the 1990s, researchers interested in the study of spontaneous brain activity, particularly epilepsy, have taken a greater interest in synchronous multi-modal imaging, in which two or more modalities are used simultaneously. The simultaneous use of EEG-fMRI (and optical imaging techniques like NIRS) with temporal resolutions of the order of a second or less has led to a variety of applications in and outside the field of epilepsy, despite the fact that the electroencephalogram (EEG) was previously combined with PET. Gaining a more comprehensive understanding of the targeted brain activity is the main driver behind the integration of data from several modalities. The idea that all measures relate to the same activity in location and time is implicit in multi-modal integration or multi-modal imaging. Multi-modal integration can therefore, at its most fundamental level, refer to the spatial coregistration of the observations. Coregistration in time can refer to one of two things: either measurements are made simultaneously (at the same time of day), for example, simultaneous EEG-fMRI of incidental epileptic discharges, or monomodality measurements are made serially, or at the same time relative to an event but not simultaneously. Examples include separate ERP and fMRI investigations in response to the same stimulus that were later combined through response correlation (as a function of some externally controlled factor) or the spatial coregistration of independently determined source localization estimates. The retrospective integration of serially acquired datasets is actually limited to the reproducible aspects of the activity of interest, such as effects averaged across repeated events. Serial multi-modal integration implies a degree of predictability and, more importantly, reproducibility of the events.

In the context of this discussion, the integration of electrophysiological and hemodynamic signals (BOLD, CBF, CBV) is particularly crucial due to their inherent significance and complementarity as well as the availability of data. Given the clear connection between EEG/MEG and neural synchronization, electrophysiological markers are particularly significant. However, localization based on EEG/MEG has significant limitations. The more indirect relationship between hemodynamic signals and neuronal activity is partially offset by our ability to create 3D brain maps, especially for fMRI, that almost completely cover the entire brain and have high spatial resolution. Although several studies have proven that BOLD fluctuations can be linked to other types of brain activity, including the recent haemodynamic response to external stimuli, which makes fMRI possible and helpful, there is still more to learn. In recent years, studies have concentrated more intently on the connection between the BOLD effect and microscopic neuronal activity. The 'human circulation balance,' which could non-invasively assess the redistribution of blood during emotional and intellectual activity, was created by the Italian neuroscientist Angelo Mosso and is the first chapter in the history of neuroimaging.

The method of ventriculography was first used by American neurosurgeon Walter Dandy in 1918. Filtered air was directly injected into one or both of the brain's lateral ventricles to produce X-ray pictures of the ventricular system. Dandy noted that air injected into the subarachnoid space through a lumbar spinal puncture might infiltrate the cerebral ventricles and also show the cerebrospinal fluid compartments surrounding the base of the brain and over its surface. Pneumoencephalography was the name of this method. Cerebral angiography, which allowed for the precise visualization of both normal and diseased blood arteries in and around the brain, was developed by Egas Moniz in 1927. The invention of computed axial tomography (CAT or CT scanning) by Allan McLeod Cormack and Godfrey Newbold Hounsfield in the early 1970s made it possible for researchers and clinicians to obtain ever-more-detailed anatomical images of the brain. For this work, Cormack and Hounsfield were awarded the 1979 Nobel Prize in Physiology or Medicine. The creation of radioligands made it possible to do brain positron emission tomography (PET) and single-photon emission computed tomography (SPECT) shortly after the invention of CAT in the early 1980s.

Magnetic resonance imaging (MRI or MR scanning) was created roughly concurrently by scientists like Peter Mansfield and Paul Lauterbur, who won the 2003 Nobel Prize for Physiology or Medicine. Early in the 1980s, MRI was made clinically available, and the decade that followed saw a remarkable explosion of technical advancements and diagnostic MR applications. Scientists quickly discovered that the appropriate kind of MRI could also image the significant blood flow changes detected by PET. The development of functional magnetic resonance imaging (fMRI), which has since grown to dominate the field of brain mapping due to its low level of radiation exposure, low level of invasiveness, and relatively wide availability, took place. The field of neuroimaging advanced to the point in the early 2000s that just a few practical uses of functional brain imaging are now viable. Simple brain-computer interfaces are the major application area. A volume (picture) with a 100-micrometer resolution set a new world record for the spatial resolution of a whole-brain MRI in 2018. Getting the samples took around 100 hours. An x-ray tomography scan at the ESRF (European synchrotron radiation facility), which had a resolution of around 25 microns, set the spatial world record for a complete human brain. A scan typically takes 22 hours. This image was a component of the human organ atlas, which also includes similarly detailed x-ray tomography scans of other bodily organs.

The concept that the net magnetization vector can be changed by exposing the spin system to energy at a frequency equal to the energy difference between the spin states (e.g., by a radio frequency pulse) is fundamental to magnetic resonance imaging. It is feasible to make the net

magnetization vector orthogonal to that of the external magnetic field if enough energy is supplied to the system. Following a neurological examination in which a doctor has determined that a patient has or may have a neurological disease, neuroradiology is frequently used to further examine the patient. Head trauma, stroke-like symptoms, such as sudden paralysis or numbness in one side of the body or trouble speaking or walking, seizures, rapid onset of severe headaches, and abrupt changes in state of consciousness for unknown reasons are common clinical indications for neuroimaging.

Simple syncope is one of the more frequent neurological conditions that a person may suffer. Routine neurological imaging is not recommended because there is a very low chance of finding a cause in the central nervous system and the patient is unlikely to benefit from the procedure in cases of simple syncope where the patient's history does not suggest other neurological symptoms. For patients with migraine headaches that are stable, neuroradiology is not advised. According to studies, having migraine does not put a patient at higher risk for an intracranial condition.[10] A migraine diagnosis that specifies the lack of other issues, including papilledema, would not suggest the necessity for radiological tests. When making a thorough diagnosis, the doctor should take into account the possibility that the headache has a cause other than a migraine and may necessitate radiological testing.

DISCUSSION

Neuronal activity and BOLD signal change are linked by a long series of factors and events and the transitions between them are not smooth. The metabolic demand is influenced by neurovascular coupling caused by neural activity. The haemodynamic reaction to metabolic changes depends on physiological variables such as local cerebral blood flow, the ratio of deoxyhaemoglobin to oxyhaemoglobin, blood volume, and vascular geometry. Because of this, conclusions drawn from fMRI about brain activity depend on the correctness, viability, and effectiveness of previously established models and hypotheses. By building on the Balloon model of Buxton et al. which explained how evoked changes in blood flow were translated into oscillations in blood oxygenation level, Friston et al. developed a model that clarifies the fundamentals of the BOLD signal. The Balloon model was incorporated into a hemodynamic input-state-output model that also took into account the dynamic perfusion variations that depend on underlying synaptic activation. The relationship between blood flows and BOLD is not linear, contrary to the assumption made in the Friston et al. model that brain activity and metabolic demand are linearly related. The model offers some level of explanation for the biphasic shape of the haemodynamic response function, which exhibits a positive peak at approximately 6 seconds after the event or stimulus begins, followed by a negative undershoot at approximately 15 seconds (first to second peak amplitude ratio of 6), and then a gradual return to baseline[1], [2].

The idea that various measures of neuronal activity and BOLD signal have a linear relationship is generally accepted and is supported by some experimental research, including but not limited to. However, it was shown that BOLD responses might exhibit nonlinear refractoriness at incredibly brief interstimulus intervals. A nonlinear refractoriness of the BOLD response, possibly of haemodynamic origin, was demonstrated by the finding in another study that the BOLD signal increases linearly with positive stimulus amplitude, but for negative stimulus amplitude highly nonlinear behavior results. These investigations highlight the fact that the interstimulus interval selection has a significant impact on the outcomes of evoked activity fMRI studies. Models of the BOLD effect have a tough time taking into consideration a number of variables in the series of events from neuronal activity to vascular alterations. For instance, the specifics of the vascular design and the existence of sizable veins close to the stimulated neurons. The results could be influenced, and the spatial resolution of the BOLD signal could be constrained by the microvascular density, which is lower than that of neurons and is influenced by significant vessel contribution.

It is still unknown which element, or expression, of neuronal activity—potential firing vs synaptic activity—is best reflected in the BOLD signal. The conflicting viewpoints on this issue were examined in, which reviewed the issue. In particular, empirical evidence was cited to support the idea that cortical cells' spikes account for only a small portion of the brain's resting energy consumption, and that up to a small portion of regional cerebral blood flow increases may be dependent on postsynaptic activity. However, a link between spiking activity and the BOLD signal was revealed in another contribution. In actuality, there is a connection between spiking activity and synaptic potentials. The BOLD signal, however, was found to correlate (Local Field Potentials) LFPs better than multiunit spiking activity, according to comparative investigations. The results of the same study imply that rather than reflecting a specific area's spike output, the BOLD contrast mechanism reflects its input and intracortical processing.

There have been reports of BOLD declines in response to some stimuli and events, such as epileptic spikes, as opposed to the brief negative undershoot of "positive" haemodynamic response function. A negative BOLD response was seen outside of the stimulated regions of the visual cortex, as evidenced by local declines in neural activity as represented in terms of LFP power below the level of spontaneous (background) activity, according to concurrent fMRI measurements and electrophysiological recordings. There is currently disagreement regarding the connection between neural inhibition and BOLD. Since inhibitory activity costs energy, just like excitatory processes do, inhibition may be accompanied by higher metabolic demand, which may be expressed as a rise in BOLD. However, as the majority of brain connections are excitatory, a reduction in excitatory activity brought on by inhibition may result in a reduction in blood flow. According to experimental findings, both claims might be true. Similar increases in cerebral blood flow were seen by Mathiesen et al. during activation of the cerebellum's excitatory and inhibitory circuits. The observed energy metabolism has frequently decreased in investigations using agonists of inhibitory transmitters, as seen. Modeling studies have shown that local connectivity, inhibitory connection type, and task type are three variables that may influence how inhibition affects imaging outcomes. If the region is not driven by excitation or if there is little local excitatory recurrence, neural inhibition may cause BOLD rises. A different outcome for active excitation or high recurrence is inhibition, which might result in a drop in BOLD [3]–[5].

Whether fMRI can distinguish between tiny activity changes in vast cellular populations and significant changes in small populations is an additional intriguing and unsolved issue. Typical fMRI scanner resolution ranges from 8 to 50 mm³, or at least neurons. One cortical column including neurons and the maximum resolution. Therefore, using a device with a standard resolution, it is possible to scan many neuronal populations with various activity patterns.

Brain oscillations vs. BOLD

At the macroscopic level, EEG/MEG amplitude mostly depends on the number of neurons operating synchronously, whereas BOLD indicates the number of active neurons. According to Nunez, synchronously acting neurons have activity that is proportional to their number, but asynchronously acting neurons have activity that is proportional to the square root of their number. In the vicinity of a typical EEG electrode, there are almost that many neurons; theoretically all of them are continually active, but only 1% of them act synchronously. The latter will provide $1/\sqrt{}$, or 100 times more to the scalp signal than the 99% nonsynchronized neurons. As a result, in contrast to fMRI, asynchronous brain activity will scarcely be reflected in the EEG. The distinctive EEG rhythms are created by the synchronized activity of neuronal populations and play a special function in how the brain processes information. The synchronization and desynchronization of EEG in particular frequency bands are related to specific tasks, such as movements or perceptions. Therefore, it

is crucial to establish links between fMRI data and electroencephalographic rhythmical activity. Kilner et al. developed a heuristic model that links alterations in hemodynamic status to the spectral character of continuous EEG activity. The model made the assumption that the BOLD signal is inversely correlated with the rate of energy dissipation, where dissipation was calculated as the sum of trans-membrane potential and current. The metabolic reaction, according to the researchers, is inversely correlated with the transmembrane potentials' "effective connectivity" and temporal covariance. A Jacobian was used to express "effective connectivity" in the sense of synaptic efficacies, with the diagonal elements representing effective membrane conductance. The parameter, specified, expresses how effective connectivity has changed [6]–[8].

EEG versus fMRI: A Motor Imagery Comparison

To get beyond some of the constraints of individual measures, more sophisticated multi-modal data fusion is being done in respect to a particular type of brain activity. Examples of single-modality research on a particular cognitive process, namely motor imagery, will be discussed in this section. We will discuss and compare independent EEG and fMRI studies of motor execution, passive movements, and movement imagination in spinal cord damaged (SCI) patients in more detail. In EEG research by Müller-Putz et al. event-related desynchronization/synchronization (ERD/ERS) patterns during attempted (active) and passive foot movements were compared between paraplegic patients (with a full spinal cord damage) and able-bodied controls. The goal was to determine whether patients' attempted foot movements had the same focused beta ERD/ERS pattern as those of normal people. For this, sixteen sintered conventional scalp electrodes were used to record EEG. The findings demonstrated that beta ERD/ERS patterns during passive, active, and simulated foot motions had a mid-central focus in healthy people. In contrast, patients' attempted foot motions display a diffuse and broad ERD/ERS pattern. Only one case displayed an ERD/ERS pattern like that of healthy individuals. Furthermore, in the group of paraplegics, there were no discernible ERD/ERS patterns during passive foot movement. A 3-class Brain-Computer Interface motor imagery screening (left hand, right hand, and feet) was conducted in a group of healthy and spinal cord injured subjects in a subsequent EEG investigation. 15 scalp electrodes were used to record the EEG. We discovered that patients had significantly worse categorization rates than healthy people when comparing the accuracy of the Brain-Computer Interface. According to the results stated above, the ERD/ERS patterns in the patient group are diffuse and dispersed.

It evaluated the imagination of persons with SCI and able-bodied participants' foot motions using fMRI (lesion height from Th3 to L1, range of age was 22–43 years). They discovered that SCI patients had considerably higher levels of BOLD activity (contra-lateral M1 and S1 foot representation; bilaterally SMA, pre-SMA, CMA, and beyond) than participants who were able to move around unassisted. It's interesting to observe that the vividness scores for motor imagery among SCI patients had a strong association. One explanation for the increased activation in SCI patients could be because they were more focused on the task and exerted more mental effort than the subjects with normal physical abilities. In a subsequent fMRI investigation, Enzinger et al. compared the motor imagery BOLD patterns of a remarkable SCI patient who had received significant training over a number of years to a group of healthy controls. In the patient, imagery of repetitive hand and foot movements (versus rest) significantly activated sensorimotor networks (sensorimotor cortex contralateral to side of movement imagination, SMA, pre-SMA, and further); however, in able-bodied subjects, significant activation only happened in relation to hand motor imagery and only in premotor areas (pre-SMA). In the control group, no detectable activation of the sensorimotor cortex could be found. The patient's pattern of activation during motor imaging matched the controls' pattern of activation during actual motor execution [9]–[12].

Experimental factors (such as intersubject variability and variations in experimental circumstances) and biological factors are two potential explanations for the divergent outcomes of the EEG and fMRI research. The elimination of intersession (and hence intermodality) experimental confounds by the use of simultaneous EEG and fMRI acquisitions would allow for deeper biological understanding. For instance, one could determine whether the results show a mismatch between the BOLD effect and the EEG technique that was employed. For ERD, such investigations have already been carried out. For instance, used combined EEG-fMRI across motor regions during finger movements and discovered a negative connection between EEG power fluctuations and BOLD activity contra-lateral to the movement. The anterior and posterior central sulcus in both sensorimotor regions were activated in significant ERD in the alpha and beta frequency bands.

CONCLUSION

Signals can be acquired under identical experimental circumstances thanks to simultaneous multi-modal acquisitions. Continuous acquisition synchronization allows the same events to be recorded and examined across modalities, presuming that data quality is maintained. Because of this, signals connected to events over which one has no experimental control, such as spontaneous brain activity at rest, can be studied using synchronous multi-modal acquisitions.

An notable illustration of this is the ability of the EEG, a crucial clinical and research tool in the field of epilepsy, to record epileptic activity. (And obviously visually in the case of seizures; for instance, there have been several (single-modality) fMRI investigations of Localization of the epileptic activity generators are a crucial topic in the field of epilepsy imaging because of its potential clinical impact in cases with drug-resistant epilepsy that are being considered for surgical resection. The nonunicity of the inverse electromagnetic problem essentially restricts EEG's ability to localize generators, despite the fact that it offers valuable clinical information. However, this restriction does not apply to tomographic modalities like fMRI. Therefore, researchers in Boston began working on combined EEG and fMRI acquisitions as early as 1993, just a few years after the introduction of BOLD fMRI. This methodological advancement is primarily motivated by the absence of overt symptoms during or after an interictal spike (as opposed to seizures, which are less common and generally more challenging to examine using fMRI due to mobility and safety issues). In the case of fMRI, this means that simultaneous EEG recording is the sole way to tag scans according to brain.

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CHAPTER 9

CHANGES IN BIOPHYSICAL SKIN PARAMETERS: AN OVERVIEW

Umesh Daivagna, Professor

Department of ISME, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id- umesh.daivagna@atlasuniversity.edu.in

ABSTRACT:

Understanding the skin's physiology, chemistry, and biophysics enables us to plan an effective strategy for treating skin conditions. This study set out to test six biophysical traits of healthy skin: sebum content, hydration, trans-epidermal water loss (TEWL), erythema index, melanin index, and elasticity in a population of healthy individuals and determine how gender, age, and body location affected these traits. In this study, 50 healthy volunteers were divided into 5 age groups, with 5 men and 5 women in each group. Eight distinct body parts were examined to determine the sebum level, hydration, TEWL, erythema index, melanin index, and flexibility of the skin using a multifunctional skin physiology monitor (Courage & Khazana electronic GmbH, Germany). Different age groups' hydration, melanin indexes, and elasticity all varied significantly. In terms of the locations, the palm had the lowest melanin index and the forehead had the highest. Males had considerably higher mean values for the erythema index, melanin index, and TEWL, and anatomic location was a significant independent factor for each of the six assessed parameters. Diverse genders, age groups, and bodily regions have diverse skin types with varying biophysical characteristics.

KEYWORDS:

Age Groups, Biophysical, Skin Parameters, Skin Types.

INTRODUCTION

Due to population expansion, urbanization and economic development, Indonesia's demand for bioenergy has expanded dramatically with dwindling fossil fuel supplies unable to supply increasing energy demands into the future. Whilst responding to interests in renewable energy and degraded land rehabilitation, bioenergy can give a feasible alternative to fulfil growing energy demand. The Government of Indonesia has legislated to boost renewable energy generation, including bioenergy, with the aim of renewables making up 23% of the national energy mix. However, increase of bioenergy production could cause rivalry with other land uses, such as food production and biodiversity conservation. To avoid such rivalry, degraded land has been highlighted as a viable target for bioenergy production. Central Kalimantan Province has a substantial quantity of degraded land, estimated at around

Forest conversion for other land uses, such as agriculture and open pit mining, is a crucial driver causing land degradation. Frequent forest fire occurrence, particularly in recent years, has prompted an escalation in damaged land, including degraded peatlands. Fires have harmed agricultural land controlled by local farmers, causing production to plummet, resulting in most burned land, including peatland, being abandoned due to its diminished fertility. Central Kalimantan is likewise battling energy deficiencies, with 42% of households in the province having no access to electricity. Consumption of biomass in traditional cooking practices is relatively high. To expand community access to energy, the federal government, through the Ministry of Energy and Mineral Resources (ESDM), in partnership with district and provincial administrations, has begun a bioenergy scheme called Bioenergy Lestari. The strategy comprises planting bioenergy crops on roughly of abandoned land, including degraded land in Pulang Passau and Kitingan districts, with the expectation of improving bioenergy production. However, relatively few studies provide relevant information on bioenergy crops appropriate for cultivation on degraded areas in Central Kalimantan. To bridge this knowledge vacuum, this research project aims to find the most

adaptable bioenergy crops suitable for degraded lands, and measure their performance in agroforestry and monoculture systems. As huge regions, notably peatlands, damaged by deforestation and forest degradation need a sustainable long-term solution for restoration linked to energy security and producing renewable energy, the effectiveness of bioenergy crops in recovering peatlands needed to be studied. This research aims to analyse the performance of possible bioenergy crops, and their potential for recovering burned and damaged peatlands without affecting food security.

Suitability of bioenergy tree species in degraded peatlands in Central Kalimantan, Indonesia Materials and procedures Bantoid Village, located between in the district of Pulang Passau in Central Kalimantan, Indonesia was selected as the study site. Bantoid, with a total land area of 16,261.595 ha, is characterized by forest and agricultural land. Its soils are mostly peat and alluvial. The settlement enjoys a humid tropical climate with temperatures ranging from 26.5 to 27.5°C. The Ministry of Energy and Mineral Resources and the local government has picked Bunti Village as one of a number of places under the Bioenergy Lestari initiative. Buntin has a total population of 2,729, majority of whom depend on farming and rubber and sengon (*Albizia chinensis*) plantations. In late 2015, Bunton Village was heavily damaged by forest and peat fires, which devastated large tracts of farmers' productive land, including around 461 ha of rubber plantations. The burned area has since been abandoned, and farmers are now looking for alternate land uses to suit their living demands. Trials were done between March 2016 and February 2017 on two hectares of damaged peatland.

Having a total of 16 subplots, a split plot design was utilized to examine the performance of four possible biofuel plants under two different treatments: monoculture and agroforestry with a system involving intercropping with pineapple. The two-hectare total area of the plots limited the number of feasible replications to only two. Our research showed mampalon to be the species most adapted to burned and degraded peatlands in Central Kalimantan, followed by kemiri suntan. Both species responded more positively under agroforestry than monoculture treatments. This appears to be a win-win option, as growing biofuel under agroforestry systems can be a better land-use strategy, considering the ability to boost farm productivity and incomes, protect biodiversity and support sustainable development. If the purpose is to persuade local farmers to use their degraded land for biofuel production, it is vital to recognize that tree growing by farmers is typically associated with numerous objectives impacted by subsistence demands and local customs.

Current literature highlights farmers' capacity to accept tree planting being dependent on production technology, suitable physical infrastructure and developed markets for tree products. Improved understanding of these variables is vital for policy improvements to succeed in making tree planting practicable, acceptable and ultimately profitable for local people and related stakeholders Planting millions of square kilometres of biofuel crops might sequester massive amounts of carbon annually while simultaneously providing ample energy stock. Supportive policies could further assist biofuel development on degraded land to avoid compromising agricultural productivity and to escape harmful environmental impacts.

DISCUSSION

A collection of partially decomposed organic material or vegetation is known as peat (/pit/). It only occurs in wetlands, bogs, mires, moors, or muskegs in nature. One of the most frequent ingredients in peat is sphagnum moss, usually known as peat moss, however many other plants can also contribute. A phenomenon known as "habitat manipulation" occurs when the biological characteristics of sphagnum mosses act to generate a habitat that facilitates peat formation. Histosols are soils that mostly include peat. Peat develops in wetland environments when floods or standing water prevents oxygen from the atmosphere

from escaping and slows the pace of decomposition. High spatial heterogeneity can be seen in peat parameters including organic matter concentration and saturated hydraulic conductivity [1]–[3].

The main source of peat is wetlands, notably bogs; but, although less frequently, other wetlands such as fens, porosis, and peat swamp forests also deposit peat. Species like *Sphagnum* moss, ericaceous bushes, and sedges can be found in peat-covered landscapes. Peat deposits offer records of historical vegetation and climate because organic matter accumulates over a long period of time, retaining plant remnants like pollen. This enables the study of changes in land use and the reconstruction of historical landscapes.

In some regions of the world, peat is used by gardeners and for horticulture, but in others, it is prohibited. The total volume of peat in the world is roughly 4 trillion cubic meters. Peat development through time is frequently the initial stage in the geological creation of fossil fuels like coal, especially low-grade coal like lignite. The most effective carbon sink on the earth, the peatland ecosystem has an area of 3.7 million square kilometers (2.3 million square miles) as a result of peatland plants' ability to absorb carbon dioxide (CO₂) that is naturally emitted from the peat, an equilibrium is maintained. However, it takes "thousands of years" for peatlands to develop the deposits of 1.5 to 2.3 m, which is the average depth of the boreal peatlands, which store about 415 gigatons (Gt) of carbon (roughly 46 times 2018 global CO₂ emissions). In natural peatlands, the "annual rate of biomass production is greater than the rate of decomposition." Although peat only makes about 3% of the earth's surface, it holds up to 550 Gt of carbon, or 42% of all soil carbon, more than any other type of plant, including the world's forests.

Peat is not a renewable energy source since it is extracted at a pace in industrialized nations that is much higher than its slow rate of regrowth, which is 1 mm (0.04 in) per year, and because only 30–40% of peatlands are believed to experience renewal. A lot of peatland restoration is required to help slow down climate change since humans have released a lot of CO₂ into the atmosphere through centuries of burning and draining peat. Peat is created when plant material fails to completely decompose in anaerobic and acidic environments. Wetland vegetation, primarily bog plants including mosses, sedges, and shrubs, make up the majority of its composition. The peat traps water as it builds up. This gradually makes the environment wetter, allowing the wetland area to grow. Ponds, ridges, and high bogs are examples of peatland characteristics. Some bog plants actively encourage bog formation due to their traits. *Sphagnum* mosses actively secrete tannins, for instance, which help to retain organic matter. In addition, *sphagnum* has unique water-retaining cells called hyaline cells that may release water, keeping the bogland perpetually moist and aiding in peat production.

After the glaciers retreated at the end of the last ice age, the majority of contemporary peat bogs developed 12,000 years ago in high latitudes. The average rate of peat accumulation is a millimeter each year. 415 gigatons (457 billion short tons) of carbon are thought to be present in northern peatlands, 50 Gt (55 billion short tons) in tropical peatlands, and 15 Gt (17 billion short tons) in South America. the most common type of wetland in the world, accounting for 50 to 70% of all wetlands. They occupy more than 4 million square kilometers (1.5 million square miles), or 3% of the planet's surface in terms of land and freshwater. One third of the worldwide soil carbon and 10% of the world's freshwater supplies are located in these ecosystems. The ability of these ecosystems to gather and store dead organic matter from *Sphagnum* and many other non-moss species as peat under conditions of nearly constant water saturation is what distinguishes them from other ecosystems. Peatlands have evolved to withstand the harsh environment of high water and low oxygen concentration, poisonous substances, and limited plant nutrition availability. Their water is acidic to alkaline in chemistry. Peatlands can be found on every continent, from tropical to boreal and Arctic regions, at sea level to high altitudes [4]–[6].

A GIS shapefile dataset called PEATMAP displays the distribution of peatlands across the entire world. An updated estimate from an improved global peatland map, PEATMAP, based on a meta-analysis of geospatial data at the global, regional, and national levels places global coverage at 4.23 million square kilometres (1.63 million square miles), or roughly 2.84% of the world's land area, slightly higher than earlier peatland inventories. Peatlands cover roughly 515,000 km² (199,000 sq mi) of land in Europe. Peat makes up over 60% of the world's wetlands. The world is home to several peat deposits, notably those in northern Europe and North America. Canada and the northern United States are the main locations of North American peat deposits. The West Siberian Lowland, the Hudson Bay Lowlands, and the Mackenzie River Valley are a few of the largest peatlands in the world. The Southern Hemisphere has less peat, in part because there is less land there. The Democratic Republic of the Congo is in Africa and is home to the largest tropical peatland on earth. Another significant peat-dominated terrain is the immense Magellan Moorland in South America (Southern Patagonia/Tierra del Fuego). In addition to Indonesia Kalimantan Sungai Putri, Danau Siwan, Sungai Tolak, Rasual Jaya (West Kalimantan), and Sumatra), peat is also found on Kerguelen, the Falkland Islands, and New Zealand. More tropical peatlands and mangrove forests exist in Indonesia than any other country on the planet, but Indonesia is losing wetlands at a rate of 100,000 hectares (250,000 acres) annually. Approximately 7% of all peatlands have been used for forestry and agriculture. Peat can eventually transform into lignite coal under specific circumstances and over geologic time.

ecological and environmental issues

The amount of carbon dioxide in the atmosphere has increased and changed in relation to the previous year. Peat wetlands' unique ecological features offer a home to a variety of animals and plants. Whooping cranes, for instance, lay their eggs on North American peatlands, whereas Siberian cranes do it in a peatland in West Siberia. Polar bears in Canada use riparian peat banks as their places to give birth, whereas pals mires in the EU are home to a variety of birds and are a red-listed habitat. There are numerous varieties of wild orchids and carnivorous plants on natural peatlands. See marsh, bog, or fen for further information on biological communities. affects around half of the northern peatlands, which make up about a tenth of the world's permafrost area and contain about a tenth of its carbon content (185 66 Gt), or about half of the carbon in the atmosphere. Dry peat prevents permafrost from thawing because it is a good insulator (it has a thermal conductivity of about 0.25 Wm⁻¹K⁻¹). Dry peat's insulating qualities also make it a crucial component of rare permafrost landforms like palsas and permafrost peat plateaus. The thawing of peatland permafrost tends to increase methane emissions while very slightly increasing carbon dioxide absorption, thus adding to the permafrost carbon feedback. A cumulative 0.7 to 3 PgC of methane might be emitted by 2100 as a result of permafrost peatland thawing with temperatures of +1.5 to 6°C. Under 2°C global warming, 0.7 million km² of peatland permafrost could thaw. The prospective emissions' force would be roughly equal to 1% of anticipated anthropogenic emissions [7]–[9].

The bioaccumulation of metals that are concentrated in the peat is one of its characteristics. Mercury buildup is a serious environmental hazard. To support agriculture, forestry, and peat extraction, large sections of organic wetland (peat) soils are currently drained. The world over, this process is happening. In addition to destroying many species' habitats, this contributes significantly to climate change. The organic carbon, which has been accumulating over thousands of years and is often submerged, is abruptly exposed to the air as a result of peat draining. As it breaks down, carbon dioxide (CO₂) is produced and released into the atmosphere. From 1,058 Mon in 1990 to 1,298 Mon in 2008 (an increase of 20%), the global CO₂ emissions from drained peatlands have grown. This increase has occurred primarily in developing nations, with Indonesia, Malaysia, and Papua New Guinea among the top emitters

with the greatest rate of growth. The emissions from peat fires are not included in this calculation; conservative estimates for south-east Asia are at least 4,000 Mton/CO₂-eq./yr. With 174 Mton/CO₂-eq./yr, the EU is the world's second-largest emitter of drainage-related peatland CO₂ (excluding harvested peat and fires), trailing only Indonesia (500 Mton) and Russia (161 Mton). The 500,000 km² of degraded peatland around the world may produce more than 2.0 Gt of CO₂ in total (including emissions from peat fires), or around 6% of all carbon emissions worldwide. Peat is a significant fire risk and is not put out by light rain. If there is an oxygen supply nearby, peat fires may burn for a very long time or smolder underground and rekindle after the winter.

Peat can fire when there is little moisture present because of its high carbon content. It smolders after becoming ignited by the presence of a heat source (such as a subterranean wildfire). These smoldering flames can spread slowly through the peat layer beneath and continue to burn unnoticed for very long times (months, years, or even centuries). Bogs are inherently prone to flames, and they rely on the wildfires to prevent woody competition from lowering the water table and shading out many bog plants, despite the harm that burning raw peat can inflict. Diverse plant families, including the carnivorous *Sarracenia* (trumpet pitcher), *Dionaea* Venus's flytrap, and *Utricularia* (bladderworts), as well as non-carnivorous ones like the sandhills lily, toothache grass, and numerous species of orchids, are currently threatened and in some cases endangered due to human drainage, negligence, and the absence of fire.

Increases in global carbon dioxide levels have been attributed to the recent burning of peat bogs in Indonesia, whose huge and deep growths contain more than 50 billion tonnes (55 billion short tons; 49 billion long tons) of carbon. By 2040, Southeast Asia's peat reserves might be gone. According to estimates, peat and forest fires in Indonesia caused the release of between 0.81 and 2.57 gigatons (0.89 and 2.83 billion short tons; 0.80 and 2.53 billion long tons) of carbon in 1997. This is greater than the amount of carbon that the earth's biosphere was able to absorb. The acceleration of the rise in carbon dioxide levels since 1998 may be due to these fires. Since 1997, there have been more than 100 peat fires burning in Kalimantan and East Sumatra; each year, these peat fires start fresh forest fires above the ground.

Peat fires can break out during severe droughts everywhere in North America, from Canada's boreal woods to the subtropical southern Florida Everglades' marshes and fens. After a fire has passed through the area, hummocks and hollows in the peat are parched and burnt away, yet they can help *Sphagnum* recolonize the area. A major peat deposit in Central Russia caught fire in the summer of 2010, resulting in the burning of thousands of homes and the toxic smoke blanketing the city of Moscow. The exceptionally high heat wave reached temperatures of up to 40 °C (104 °F). Right up until the end of August 2010, the situation was still dire. Despite the implementation of various forest fire mitigation strategies in June 2014, peat fires in the Arctic released smoke. In Finland, bog and peat bog formation is encouraged by the country's climate, geography, and ecology. Peat is so readily available in large amounts. To generate heat and power, it is burned. About 4% of Finland's annual energy production comes from peat.

Additionally, peat bogs that have been drained for agriculture and forestry actively release more CO₂ each year than Finland's peat energy output does. However, the typical time it takes for a single peat bog to regenerate is long between 1,000 and 5,000 years. In addition, it is typical practice to clear-cut exhausted peat bogs rather than allowing them to regenerate. As a result, less CO₂ is stored than in the original peat bog. Peat emits more carbon dioxide per unit of energy than coal or natural gas (106 g CO₂/MJ vs. 94.6 and 56.1, respectively). According to one study, the emissions may be reduced to 93 g CO₂/MJ by raising the average proportion of wood in the fuel combination from the present 2.6% to 12.5%. Despite this, not

much is being done to make this happen. The Finnish municipal and federal governments were asked in 2006 by the International Mire Conservation Group (IMCG) to safeguard and conserve the country's last unspoiled peatland ecosystems. This entails stopping drainage, peat extraction, and any other groundwater extraction activities that might have an impact on places with intact mires. After a protracted period of consultation, a proposal for a Finnish peatland management strategy was sent to the government in 2011 [10], [11].

CONCLUSION

This study reveals that ambling and kemiri Sunan were the two bioenergy-producing species that were best suited for cultivation on degraded peatlands in Central Kalimantan, with survival rates of 88% and 48%, respectively. Given that none of the seedlings that were planted survived, neither gamely nor kalinda seem to be good alternatives. According to growth performance metrics, mampalon grew better in agroforestry treatment plots than in monoculture ones in terms of tree height and stem diameter. In agroforestry plots, kemiri suman performed better in terms of tree height growth. It is possible to promote the advantages of agroforestry, improve farmers' livelihoods, and assist sustainable development by being aware of how enamelling and kemiri sunan can thrive on damaged peatlands and perform better under agroforestry systems. To augment the results, additional research on the productivity of both species is required. Additionally, more research is required to test various species on various degraded peatlands. More precise extended measurement variables including soil nutrients, peat water table, and peat depth should be included in these. It may be advantageous to increase farmers' incentive to use degraded lands for the production of biofuel by choosing tree species with numerous benefits in terms of livelihoods, familiarity with the local culture, and great market value.

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CHAPTER 10

SCALP SEBORRHEIC DERMATITIS BIOPHYSICAL AND PHYSIOLOGICAL PROFILES IN THAI POPULATION

Rajesh Kumar Samala, Assistant Professor

Department of ISME, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id-rajesh.samala@atlasuniversity.edu.in

ABSTRACT:

The skin condition known as scalp seborrheic dermatitis (SD) is a common and recurrent chronic inflammatory skin condition. Numerous studies describe aberrant biophysical profiles and their correlation with various dermatologic illnesses by assessing the stratum corneum's biophysical properties. The study's objective is to compare scalp SD to healthy controls in order to investigate the biophysical characteristics and skin barrier abnormalities. Supplies and procedures. The link between several biophysical and physiological parameters in scalp SD is examined in this cross-sectional study. In the study, 40 healthy Thai participants served as the control group in addition to 42 Thai patients with scalp SD. The biophysical and physiological parameters of trans epidermal water loss (TEWL), stratum corneum hydration (SCH), skin surface pH, skin surface lipid, and skin roughness were measured once for both the SD and control groups. Results. In comparison to the control group, the mean TEWL of lesioned skin in SD cases was substantially higher ($P < 0.05$). The mean SCH was observed to be substantially lower in SD instances in relation to high mean TEWL ($P < 0.05$). Additionally discovered to be considerably greater in the SD group was skin surface lipid ($P < 0.05$). However, there were no differences in the two groups' skin surface pH ($P = 0.104$) or roughness ($P = 0.308$). When each category was compared on a pairwise basis, it was shown that moderate and severe SD showed significantly higher mean skin surface lipid than the control group ($P < 0.05$). Conclusion. In Thai people, seborrhea may be linked to scalp SD. In individuals with scalp SD, monitoring of SCH, TEWL, and skin surface lipid may be useful in determining the severity and assessing the effectiveness of treatment.

KEYWORDS:

Abnormalities, Category, Effectiveness, Treatment.

INTRODUCTION

Seborrheic dermatitis (SD) is a typical, recurrent, chronic inflammatory skin condition that affects the seborrheic region. 2.35%–11.3% of the general population are impacted. One of the most frequent sites of SD was discovered to be the scalp, where the frequency ranged from 10.16 to 11.6% and as high as 20% to 50% in some investigations. Three main causes, including *Malassezia* proliferation, increased sebum production, and individual predisposition, have been widely suggested as contributing to the onset of SD. Recently, connections between scalp SD and the presence of particular strains of *Malassezia* yeasts and commensal bacteria in the scalp microbiome have been reported. The pathophysiology of scalp SD still has to be further understood, and this information fills in some of the gaps. As the epidermal barrier, the stratum corneum is essential in controlling metabolic processes and functions. Several studies indicate aberrant biophysical profiles and their connection in various dermatologic illnesses, such as atopic dermatitis (AD) and psoriasis, by assessing various stratum corneum biophysical parameters. Patients with these disorders have a variety of aberrant profiles compared to the healthy population, such as an increase in trans epidermal water loss or a decrease in stratum corneum hydration. The intrinsic characteristics of the stratum corneum may play a significant role in the etiology of SD. According to one study, the mean TEWL of neonatal patients with SD was often higher than that of the control group, and following therapy, the mean TEWL of these patients decreased more toward the

value of the control group. The skin on the scalp differs noticeably from the skin on other parts of the body. It has a disproportionate number of hair follicles, sebaceous glands, and blood arteries compared to other body areas, which affects its biophysical characteristics. To our knowledge, no research has ever been done on the biophysical profiles of scalp SD. A better understanding of their characteristics may aid in determining the etiology of the illness, evaluating the effectiveness of the treatments, and enhancing patient care. The study's objective is to compare the physiological and biophysical characteristics of scalp SD to those of healthy controls. An interdisciplinary field of research known as "biophysics" uses techniques and methods often associated with physics to explore biological processes. All levels of biological organization from the molecular to the organismic and population are covered by biophysics. The fields of biochemistry, molecular biology, physical chemistry, physiology, nanotechnology, bioengineering, computational biology, biomechanics, developmental biology, and systems biology all have a great deal in common with biophysical study.

The study of physical quantities (such as electric current, temperature, stress, and entropy) in biological systems is also sometimes referred to as "biophysics" in academic circles. Research on the biophysical characteristics of living things is also done in the fields of molecular biology, cell biology, chemical biology, and biochemistry. typically seeks to understand the physical basis of biomolecular events by addressing biological issues analogous to those in biochemistry and molecular biology. Researchers in this area study the relationships between a cell's numerous processes, including those involving DNA, RNA, and protein production, as well as how these interactions are controlled. Many different methods are employed to provide answers to these queries.

Structures of biological importance are frequently visualized using fluorescent imaging methods in addition to electron microscopy, x-ray crystallography, NMR spectroscopy, atomic force microscopy (AFM), and small-angle scattering (SAS) both with X-rays and neutrons (SAXS/SANS). Neutron spin echo spectroscopy can be used to study protein dynamics. Techniques including circular dichroism, SAXS, and SANS, as well as dual polarization interferometry and SAXS, can be used to measure conformational change in structure. It is also possible to directly manipulate molecules using optical tweezers or AFM to observe biological processes where forces and distances are nanoscale. For example, statistical mechanics, thermodynamics, and chemical kinetics can all be used to understand complicated biological events, according to molecular biophysicists. Biophysicists are frequently able to directly examine, simulate, or even change the structures and interactions of individual molecules or complexes of molecules by combining knowledge and experimental methods from a wide range of disciplines.

Modern biophysics spans an incredibly wide range of studies, from bioelectronics to quantum biology, employing both experimental and theoretical methods, in addition to classic (i.e. molecular and cellular) biophysical themes like structural biology or enzyme kinetics. Biophysicists are increasingly using models and experimental methods that come from physics as well as mathematics and statistics to study larger systems including tissues, organs, populations, and ecosystems. The analysis of neural circuits in tissue and the entire brain, as well as the study of electrical conduction in single neurons, both make substantial use of biophysical models. use of physics to medicine or healthcare, including radiology, microscopy, and nanomedicine, is considered medical physics, a subfield of biophysics. Richard Feynman, a physicist, made predictions regarding the potential of nanomedicine, for instance. He discussed the notion that biological machines might be used in medicine (see nanomachines). As Albert Hibbs and Richard Feynman put it, "swallowing the doctor" might be a possibility in the future because to the size reduction of some repair equipment. In his 1959 essay *There's Plenty of Room at the Bottom*, Feynman explained the concept. Many

colleges and universities do not have university-level biophysics departments, instead having groups in related departments like biochemistry, cell biology, chemistry, computer science, engineering, mathematics, medicine, molecular biology, neuroscience, pharmacology, physics, and physiology. While some colleges and universities have dedicated departments of biophysics, usually at the graduate level. Different focus will be placed on various topics of biophysics at different universities, depending on the department's capabilities. The examples of how each department contributes its efforts to the study of biophysics are listed below. This list is far from exhaustive. Additionally, no particular department has exclusive control over any given subject of study. Each academic institution establishes its own regulations, and departments frequently overlap. The publication of Erwin Schrödinger's book *What Is Life?* increased interest in the subject. The Biophysical Society, which presently has around 9,000 members worldwide, was founded by biophysicists in 1957.

DISCUSSION

Scalp SD and dandruff are both regarded to be symptoms of the same scalp-related dermatological disorder, with SD having a more severe and diffuse expression. Although SD or dandruff is a rather prevalent illness, its pathophysiology is yet unknown. Nevertheless, there is broad agreement that three main factors serve as the key predispositions: first, the *Malassezia* yeasts, particularly *M. second*, the sebum level; and third, individual susceptibility, which may be related to the abnormality of the stratum corneum barrier. The results of the current study show a considerable increase in TEWL and skin surface lipid and a significant drop in SCH, suggesting that patients with scalp SD have impaired skin barrier function. The stratum corneum is made up of many layers of flattened, anucleated corneocytes connected by a continuous, specialized lipidic matrix. diverse body sites' stratum corneums have diverse characteristics, compositions, and organizational structures, which affect the permeability and cohesiveness of the skin. As a result, biophysical characteristics of one place may not apply to the entire body, and values of each characteristic may also vary significantly between body sites. Therefore, scalp measuring should be done routinely in situations involving the scalp[1]–[3].

The corneodesmosome, a unique intercellular protein that binds the corneocytes together, has the most significant role in preserving the integrity of the stratum corneum among these several stratum corneum components. The hydrolytic enzymes that operate on these corneodesmosomes and affect the stratum corneum permeability barrier homeostasis and integrity were discovered to be made easier to work with by skin hydration and pH. It was discovered that increased sebum production interfered with the stratum corneum's lipid structure and disrupted the desquamation process. Increased TEWL in the same range as AD in patients with scalp SD indicates decreased permeability function. Similar to AD, it was discovered that SCH of scalp SD was similarly declining. The lowering value of SCH observed in the AD model correlates with varying levels of inflammation that lead to filaggrin insufficiency and, eventually, insufficient natural moisturizing factor of the epidermis. There is yet no proof connecting SD to filaggrin abnormalities, though. It is more likely that the altered epidermal tight junction barrier function resulting from the skin's inflammatory process is the cause of the aberrant TEWL and SCH in scalp SD. This behavior was seen in a mouse model of dermatitis, and it was discovered to be solely caused by a filaggrin defect. Although not statistically significant in our study, the degree of TEWL and SCH abnormalities appeared to be influenced by the severity of scalp SD, with higher severity indicating higher TEWL and lower SCH. These results might be further justified by a larger study population.

Scalp SD and dandruff demonstrated a substantial positive association between the mean skin surface lipid and the severity of scalp SD illness. Higher mean skin surface lipid was linked to more severe illness. Thus, in contrast to earlier research that were either unclear or

suggested our investigation supports the idea that seborrhea is an etiology of SD. It has been discovered that sebocyte proliferation and sebum production are regulated by hormones, which change in response to the biology of the sebaceous gland. Additionally, the bimodal distribution of SD prevalence at birth and after puberty raises the possibility that SD is influenced by the activity of male sex hormones. Further corroborating the function of testosterone in sebum excretion and SD was a study on seborrhea in Parkinson's disease patients that found a higher prevalence of SD in both normal and parkinsonian male individuals compared to female subjects [38]. It was discovered that an increase in skin surface lipid encouraged the growth of *Malassezia* yeasts, whereas a decrease in sebum production following isotretinoin treatment inhibited this growth and lessened the severity of SD. Alteration in lipid content may contribute to SD pathophysiology in addition to increased sebum production. Free fatty acid was lower and triglyceride was higher in both HIV and non-HIV patients with SD compared to patients without SD while free cholesterol, wax esters, and squalene showed no significant difference. According to a study from India, patients with dandruff have higher mean TEWL and surface lipid levels than the general population. The fact that the mean TEWL in the study was higher than in our study for both the control group and the dandruff patients suggests that various demographic features may have an impact on the scalp's biophysical profile [4]–[7].

Our study's key limitations are its single-center design and limited study sample. Furthermore, a defined range or cut-off point of the biophysical and physiological parameters of scalp SD may be impacted by a variety of contributing factors, including sex, age, and ethnicity. As a result, our subjects might not accurately represent the general public. It is advised to conduct a well-planned study with lots of subjects. Another drawback of our study is that scalp SD patients were tested on their specific regional area whereas control patients were only measured on the occipital area. The outcomes of our investigation may be impacted by the diverse structural, biophysical, and physiological characteristics that various scalp regions may display. Skin irritation known as dermatitis is frequently characterized by itching, redness. In short-term situations, there can be tiny blisters, however in long-term cases, the skin might thicken. The affected skin might range in size from a small patch to the There is no established distinction between eczema and dermatitis, which is frequently used interchangeably.

There is frequently debate over the condition's precise cause. In some cases, there may be a concomitant allergy and impaired venous return. The person's history and the location of the rash typically indicate the type of dermatitis. People who frequently get their hands wet, for instance, usually develop irritating dermatitis on their hands. Allergic contact dermatitis develops as a result of skin hypersensitivity brought on by exposure to an allergen. Cream can be used to treat it. Because side effects are possible, the steroid creams should typically be used for short periods of time—less than two weeks. If there are indications of a skin infection, antibiotics may be necessary. Avoiding the allergen or irritant is the conventional treatment for contact dermatitis. Antihistamines might improve sleep quality and lessen nightly scratching. According to estimates, 245 million individuals, or 3.34% of the world's population, suffered with dermatitis in the most prevalent kind, atopic dermatitis, typically begins in childhood. In the US, it affects 10–30% of the population. Females are twice as likely as males to get contact. Approximately 7% of people will get allergic contact dermatitis at some point in their life. Irritant contact dermatitis is widespread, especially in certain occupational groups; prevalence are unknown.

Symptoms and signs

Atopic dermatitis, contact dermatitis, stasis dermatitis, and seborrheic dermatitis are only a few of the several forms of dermatitis. Various types of dermatitis have various symptoms. Despite the fact that each variety of dermatitis manifests differently, there are several

symptoms that are present in all of them, including redness, swelling, itching, and skin lesions that may occasionally ooze and leave scars. With each type of dermatitis, the skin location where the symptoms manifest, whether on the neck, wrist, forearm, thigh, or ankle, tends to vary. The main sign of this illness is itchy skin, though the location may vary. Rarely, it could show up on the vulva or scrotum, which are genital regions. This kind of dermatitis can have quite severe symptoms that fluctuate. In general, irritant contact dermatitis hurts more than it itches. Although atopic dermatitis symptoms differ from person to person, dry, itchy, and red skin are the most typical symptoms. The folds of the arms, the back of the knees, the wrists, the face, and the hands are typical areas of skin that are affected. A red, raised rash around the mouth is referred to as perioral dermatitis. Vesicles and papules are frequently seen. The red, tiny bumps that are common in this type of dermatitis can be found symmetrically grouped or dispersed around the scalp, neck, shoulders, buttocks, elbows, and knees. They are typically about 1 cm in size. from dandruff to facial scaling, occasionally accompanied by itching but without hair loss. The illness creates a thick, yellowish scalp rash on newborns, which is frequently accompanied by a diaper rash. The hairline, behind the ears, on the eyebrows, around the nose, on the chest, and on the upper back may all exhibit symptoms in severe cases[8]–[10].

Moisturizers

Emollients, which moisturize the skin, may lessen eczema severity and prevent flare-ups, according to low-quality research. Water-based formulations are not advised for use on youngsters; oil-based formulations seem to be preferable. It is uncertain if ceramide-containing moisturizers work better or worse than others. It is not advisable to use anything with colours, fragrances, or peanuts in it. Nighttime occlusive dressings may be helpful. Some moisturizers or barrier creams may lessen irritation in occupational irritant hand dermatitis, a condition of the skin that can afflict persons who work in occupations that frequently involve contact with irritants like water, detergents, chemicals, or other substances. Emollients may help dermatitis sufferers experience fewer flare-ups.

CONCLUSION

As of 2010, 3.5% of the world's population, or around 230 million individuals, were affected by dermatitis. The most frequent occurrence of dermatitis occurs in infancy, while females are more likely to present with eczema between the ages of 15 and 49 when they are fertile. Around 20% of children in the UK and 10% of children in the US are impacted by the illness, respectively. The prevalence of eczema has been discovered to have significantly grown in the latter half of the 20th century, with an increase in eczema in school-aged children being identified between the late 1940s and 2000, despite the fact that there is limited information on eczema rates throughout time prior to the 1940s. Eczema prevalence has increased over time in the developed world. Eczema incidence and lifetime prevalence have been observed to rise recently in England. In 2010, nearly 15 million American employees, or 10% of the workforce, were impacted by dermatitis. In comparison to individuals with only a high school diploma or less, prevalence rates were greater among women than men and among those with some college education or a college degree. The highest reported rates of dermatitis were seen among those working in the healthcare and social support sectors, as well as in the life, physical, and social sciences. A healthcare practitioner linked work-related dermatitis to about 6% of dermatitis cases among U.S. workers, meaning that the prevalence rate of work-related dermatitis among workers was at least 0.6%.

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CHAPTER 11

A BIOPHYSICAL STUDY OF YAM TYROSINASE CATECHOL OXIDASE: BINDING AFFINITY FOR SMALL MOLECULES

Ashwini Malviya, Associate Professor

Department of uGDX, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id-ashwini.malviya@atlasuniversity.edu.in

ABSTRACT:

Due to its simplicity in purifying and wide availability of yam tubers, yam tyrosinase has emerged as an economically crucial enzyme. However, yam tyrosinase has not yet been effectively biochemically and biophysically characterized. Tyrosinase from yam (*Amorphophallus paeoniifolius*) was explored in the present work in relation to compounds like crocin (*Crocus sativus*), hydroquinone, and kojic acid. In order to ascertain the binding affinities and alterations in the secondary and tertiary structures of yam tyrosinase in the presence of four relevant small molecules, the following methods were used: surface plasmon resonance (SPR), fluorescence spectroscopy, and circular dichroism. The binding affinities of hydroquinone and crocin were extremely low, 0.24 M and 0.0017 M, respectively. Competition tests were utilized to more precisely measure the binding affinities because of their ostensibly weak interactions. This work provides a detailed correlation between structure-function correlations, and the findings can be contrasted with those of other tyrosinases that are currently in use. Cytochrome c oxidase, also known as Complex IV, is a large transmembrane protein complex that is present in the mitochondria of eukaryotes, bacteria, and archaea. It was once classed. It is the final enzyme in the membrane-based respiratory electron transport chain of cells. One oxygen molecule and four protons receive an electron from each of the four cytochrome c molecules, which it then transfers to produce two molecules of water. It ferries an additional four protons across the membrane in addition to binding the four protons from the inner aqueous phase. This increases the transmembrane difference of proton electrochemical potential, which is then used by the ATP synthase to create ATP.

KEYWORDS:

ATP Synthase, Biophysical Study, Biochemically, Characterized.

INTRODUCTION

Tyrosinase is an enzyme that can be found in all living things. It is involved in the conversion of monophenols into diphenols through the action of monophenolase and the subsequent conversion of diphenols into quinones through the action of diphenolase. Tyrosinase, together with two additional accessory enzymes known as tyrosinase-related proteins (Trp1 and Trp2), is primarily in charge of producing melanin in mammals. Melasma, freckles, lentigo senilis, and other types of melanin hyperpigmentation are skin conditions that can result from the oversynthesis of melanin. The tyrosinases of plants, as opposed to those of mammals, play a role in the synthesis of phenolic polymers including lignin, flavonoids, and tannins as well as in a number of metabolic processes such cellular respiration, oxidation-reduction potential control, host defense, and wound healing Plant tyrosinases differ from animal tyrosinases in that they do not hydroxylate tyrosine. Tyrosine hydroxylase causes tyrosine to be converted into catecholamines, which differ from tyrosinases by a single amino acid, G241. Designing efficient modulators will be made easier by understanding these variations between animal and plant enzymes. Tyrosinase causes unwelcome browning during fruit and vegetable processing, which lowers their marketability. Tyrosinase inhibitors have thus been researched for a while, and their application in the food, drug, and cosmetic industries has expanded. Numerous tyrosinase inhibitors, both natural and man-made, have been researched. These

include triolein, trilinolein, triolein, flavonoids, polyphenols, oxyresveratrol, hydroxystilbene compounds, quercetin, and polyphenols. Notably, tyrosinase from elephant foot yams has been isolated and biochemically described for use in baking. The food and baking sectors have paid a great deal of attention to yam tyrosinase due to its wide availability, high thermostability, and affordable technique of purification.

Tyrosinase is a commercially significant enzyme, so the food and cosmetics industries will be interested in strategies to block it. Surface plasmon resonance (SPR) is a very reliable and often used biophysical technique for enzyme inhibitor binding interaction studies, despite the fact that many different biophysical techniques can be used. Recently, Patil et al. employed the SPR method to investigate the interactions between small compounds and mushroom tyrosinase. SPR is a binding method based on biosensors that is used to study biomolecular interactions. By observing changes in the local refractive index, it determines the molecular interactions that occur at the metal surface. Real-time measurement, label-free interactions, and a surface-sensitive response are all characteristics of SPR. SPR has many uses, including the investigation of binding sites and concentration, kinetic measurements (k_a , k_d), the screening of pharmacological compounds against enzymes, and specificity studies.

The goal of this research is to comprehend how various analytes interact with the ligand, tyrosinase. The objective was to ascertain the efficacy of inhibitors to modulate yam tyrosinase (either singly or in combination). To investigate the interactions of inhibitors including kojic acid, hydroquinone, and crocin towards yam tyrosinase, a competitive analyte kinetics model technique was used. To explore the binding and synergistic action of these molecules with immobilized yam tyrosinase, a combination of the (inhibitors) kojic acid, hydroquinone, and crocin was used along with its substrate, L-DOPA. Circular dichroism (CD) and fluorescence spectroscopy methods were used to investigate the impact of small compounds on yam tyrosinase. In mammals, the complex is a large integral membrane protein made up of protein subunits and many metal prosthetic sites. In mammals, three of the eleven nuclear-derived subunits are created in the mitochondria. The complex is made up of two copper centers, the CuA and CuB centers, as well as two heme molecules, cytochrome a and cytochrome c. In actuality, the binuclear core formed by cytochrome a₃ and CuB is where oxygen reduction takes place. Cytochrome c, which is oxidized back to cytochrome c carrying Fe³⁺, attaches close to the CuA binuclear center after being reduced by the respiratory chain's initial component (cytochrome bc₁ complex, Complex III). Now, the cytochrome a₃-CuB binuclear center receives an electron from the reduced CuA binuclear center, which then transfers it to cytochrome a. In this binuclear center, two metal ions that are 4.5 Å apart coordinate an entirely oxidized hydroxide ion.

The C6 of Tyr (244) and the -N of His (240) of the cytochrome c oxidase are linked in an uncommon post-translational alteration, according to crystallographic research (bovine enzyme numbering). It is essential for the reduction of molecular oxygen and four protons into water because it enables the cytochrome a₃-CuB binuclear center to take four electrons. The formation of superoxide was assumed to be the end result of a peroxide intermediate presumed to be involved in the reduction pathway. The widely accepted process, however, avoids any intermediate that can create superoxide by using a quick four-electron reduction that requires direct oxygen-oxygen bond breaking. Due to the rapid and irreversible aggregation of hydrophobic subunits that make up the holoenzyme complex as well as the aggregation of mutant subunits with exposed hydrophobic patches, COX assembly in yeast is a complicated process that is not fully understood. Nuclear and mitochondrial genomes both contain COX subunit encoding regions. The mitochondrial genome contains the instructions for the three subunits that make up the COX catalytic core.

Subunits I and II are supplemented with heme and cofactors. Two copper molecules help in the continued flow of electrons from subunit II to subunit I, where the two heme molecules

are located. Assembly is started by subunits I and IV. It is possible for various subunits to work together to create intermediate sub-complexes that eventually join with other subunits to form the COX complex. COX will create a homodimer upon adjustments made after assembly. It is necessary for the activity. A cardiolipin molecule, which connects the dimers, has been revealed to be essential for the holoenzyme complex's stabilization. Cardiolipin removal and the dissociation of subunits VIIa and III lead to a complete loss of enzyme function. It is known that the nuclear genome's subunits contribute to the stability and dimerization of enzymes. These subunits' functions are lost when they undergo mutations. It is known that assembly takes place in at least three different rate-determining processes. Although particular subunit compositions have not been established, the results of these stages have been discovered.

Translational activators, which interact with the mitochondrial mRNA transcripts' 5' untranslated sections, help with the synthesis and assembly of COX subunits I, II, and III. The nucleus contains the encoding for translational activators. The precise molecular methods by which they function are unknown because it is challenging to synthesize translation machinery in a lab setting. However, they can interact directly or indirectly with other translation machinery components. Although interactions between bigenomic subunits contribute more to enzyme stability than interactions between subunits encoded in the mitochondrial genome, subunits I, II, and III are more conserved, suggesting possible unknown functions for enzyme activity.

DISCUSSION

A reagent, also known as an analytical reagent, is a material or compound that is supplied to a system in order to trigger a chemical reaction or check to see whether one has already occurred. Although the terms "reagent" and "reactant" are frequently used synonymously, "reactant" refers to a material that is consumed during a chemical reaction. Despite being a part of the reaction mechanism, solvents are not typically referred to as reactants. Catalysts are not reactants because they are not consumed by the reaction. The reactants in biochemistry are frequently referred to as substrates, particularly in relation to enzyme-catalyzed reactions. The term "reagent" in organic chemistry refers to a chemical component (a compound or combination, often composed of tiny inorganic or organic molecules) added to bring about the desired transformation of an organic substance. The Collins reagent, Fenton's reagent, and Grignard reagents are a few examples. The term "reagent" in organic chemistry refers to a chemical component (a compound or combination, often composed of tiny inorganic or organic molecules) added to bring about the desired transformation of an organic substance. The Collins reagent, Fenton's reagent, and Grignard reagents are a few examples. Reagent-grade refers to chemical substances that meet purity requirements for scientific accuracy and dependability in chemical analysis, chemical reactions, or physical testing when used in commercial or laboratory preparations. Organizations like ASTM International or the American Chemical Society set purity requirements for reagents. For instance, reagent-quality [1]–[3] water must have very high electrical resistivity, very low concentrations of bacteria, silica, salt and chloride ions, and other contaminants. Technical, practical, or crude grade designations can be used to distinguish laboratory items from reagent versions that are less pure but still practical and affordable for tasks that don't require much of them. The creation of reagents that could be used to identify and control the chemical substances in and on cells sparked the biotechnology revolution in biology in the 1980s. These substances comprised oligomers, various model organisms and immortalized cell lines, polyclonal and monoclonal antibodies, reagents and techniques for molecular cloning and DNA replication, among many more.

Tool compounds, which are small molecules or biochemicals like siRNA or antibodies that are known to affect a specific biomolecule—for example, a drug target—but are unlikely to

be useful as drugs themselves, are also important reagents in biology. These compounds are frequently used as starting points in the drug discovery process. Many natural chemicals, including curcumin, are considered "pan-assay interference compounds" by medicinal chemists because they produce hits in virtually every assay in which they are evaluated and are not effective tool compounds.

Test for Diphenols Activity

The chemical compound phenol, also known as benzenol, has the molecular formula C_6H_5OH . It is also referred to as carbolic acid or phenolic acid. It is a volatile white crystalline substance. A hydroxy group (OH) is joined to a phenyl group (C_6H_5) to form the molecule. It is mildly acidic and should be handled carefully because it can result in chemical burns. Originally extracted from coal tar, phenol is now produced in enormous quantities (about 7 million tonnes annually) from feedstocks obtained from petroleum. Due to its role as a precursor to numerous minerals and beneficial chemicals, it is a crucial industrial commodity. Plastics and related materials are largely created using it. The manufacture of polycarbonates, epoxies, Bakelite, nylon, detergents, herbicides like phenoxy herbicides, and several pharmaceutical medications all depend on phenol and its chemical derivatives. Aliphatic alcohols are less acidic than phenol. Resonance stabilization of the phenolate anion is the cause of its increased acidity. In this manner, the pi system allows the oxygen's negative charge to be delocalized and transferred to the ortho- and para-carbon atoms. The sigma framework offers a different explanation, postulating that the dominant effect is the induction from the more electronegative sp^2 hybridized carbons; the oxyanion is greatly stabilized by the comparatively more potent inductive withdrawal of electron density provided by the sp^2 system as compared to an sp^3 system. The second theory is supported by the fact that the enol of acetone in water has a pK_a of 10.9, which is just marginally less acidic than phenol (pK_a 10.0)[4]–[6].

The fact that phenoxide has more resonance structures available to it than acetone enolate does not appear to have much of an impact on its stability. However, when solvation effects are taken into account, the picture is different. With its unstable keto tautomer cyclohexadienone, phenol displays keto-enol tautomerism, however the effect is essentially nonexistent. Since the equilibrium constant for enolization is roughly 10^{13} , hardly one in ten trillion molecules are ever in the keto state. The slight stabilization that results from switching a $C=C$ bond for a $C=O$ bond is more than balanced by the significant destabilization brought on by the loss of aromaticity. As a result, enol is practically the only form of phenol. In acidic conditions, substituted cyclohexadienone can go through a dienone-phenol rearrangement and produce stable 3,4-disubstituted phenol. For substituted phenols, a number of processes, including extra hydroxy groups annulation, which results in naphthols, and deprotonation, which results in phenolate, can prefer the keto tautomer. Enolates stabilized by aromaticity are phenoxides. As a rule, phenoxide is more reactive at the oxygen position, although this is because oxygen is a "hard" nucleophile while alpha-carbon locations are more commonly "soft"

Immobilization of Enzymes

An enzyme that has been immobilized has limited mobility and is bound to an inert, insoluble substance, such as calcium alginate, which is created by combining a solution of sodium alginate and an enzyme solution with calcium chloride. Increased resistance to alterations in circumstances, such as pH or temperature, may result from this. It also enables the retention of enzymes during the reaction, making it easier for them to be separated from the products and used once more. As a result, it is a method that is frequently employed in industry for enzyme-catalyzed reactions. Whole cell immobilization is an alternative to enzyme

immobilization. Enzymes that have been immobilized are simple to handle, may be reused, and can be easily separated from their byproducts

Enzymes are bio-catalysts that are crucial for accelerating chemical reactions within cells without causing long-term modification, waste, or a loss of chemical reaction equilibrium. Even though enzymes have incredibly distinctive qualities, their use in the industry is limited because to their poor reusability, instability, and expensive production costs. In the 1950s, the first synthetic immobilized enzyme was created by incorporating the enzyme into polymeric matrices or binding to carrier materials. Additionally, the cross-linking process was used to cross-link proteins either on their own or in combination with innocuous substances. Various immobilization techniques have been developed over the past ten years. The most popular approach to date is binding the enzyme to previously produced carrier materials, for instance. The process of cross-linking enzyme crystals is now regarded as an interesting replacement. Immobilized enzyme utilization is increasing steadily [7]–[9].

Considerations

Several considerations need to be taken into consideration before using any immobilization procedures. Understanding an enzyme's physical and chemical reactions after immobilization is crucial. When an enzyme is trapped, attached to a support material, or produces an enzymatic reaction, for example, its microenvironment circumstances can change, which can affect the enzyme's stability and kinetic properties. Prior to immobilizing an enzyme, it's crucial to take into account retaining the tertiary structure in order to have a working enzyme. The active-site of an enzyme is also a critical location for its functionality, and it must be preserved. To prevent creating an immobilized but malfunctioning enzyme, a selective approach for the attachment of surface/material is necessary when an enzyme is being connected to a surface for immobilization. In order to produce functioning immobilized enzymes, three fundamental considerations must be made: immobilization supports selection, circumstances, and techniques of immobilization [10]

Support choice

An ideal support material would be hydrophilic, inert to enzymes, biocompatible, resistant to microbial attack and compression, and reasonably priced. Since support materials are ultimately biomaterial types, they can be either organic or inorganic, synthetic or natural (depending on the composition). There isn't a single type of support material that can be utilized to immobilize all enzymes. There are, nevertheless, a few widely utilized supports, including carriers made of silica, acrylic resins, man-made polymers, active membranes, and exchange resins. The choice of support material is one of the most challenging steps before immobilization since it depends on the type of enzyme, media's reaction, safety rules for hydrodynamics, and reaction conditions. Because different types of supports have varied physical and chemical traits, such as hydrophilicity and hydrophobicity, surface chemistry, and pore size, these traits can affect how well an enzyme works [11]–[13].

CONCLUSION

Tyrosinase has developed into a key therapeutic target, and effective inhibitors will be widely used in the food, cosmetic, and pharmaceutical industries. Tyrosinases from plants, fungi, animals, and humans differ greatly from one another, and each tyrosinase needs a specific inhibitor to be effective. Tyrosinases have been the subject of numerous reports, but they have not yet been thoroughly characterized, and high-affinity inhibitors have not yet been found. Hydroquinone, kojic acid, arbutin, ascorbic acid, oxyresveratrol, hydroxystilbene, ellagic acid, and gallic acid are only a few of the chemically created tyrosinase inhibitors that are currently being used as skin-whitening ingredients in cosmetics with little to no negative side effects. Thioguanine and other thiopurine medications have recently been developed as

tyrosinase inhibitors The stem bark powder of *Hesperethusa crenulata*, *Naringi crenulata*, and *Limonia acidissima* has demonstrated antityrosinase properties since ancient times and is traditionally used in skin-whitening treatments in Southeast Asia and India. Similar to *Podocarpus elongatus*, *Podocarpus falcatus*, *Podocarpus henkelii*, and *Podocarpus latifolius*, extracts from their leaves and stems demonstrated tyrosinase inhibition and have also been utilized in traditional medicine in Southern Africa. As was already said, SPR spectroscopy can assess how molecules connect to one another. The binding affinities and kinetics of yam tyrosinase to inhibitor compounds were investigated in this study using SPR methods. Surface plasmon resonance is a biosensor-based method that can be employed extensively in drug development.

It offers important benefits like quick response times and the capacity to detect multiple analytes at once. SPR is widely used in biochemistry and bioanalytical chemistry to characterize the interactions between biological molecules, such as in antigen-antibody interactions and RNA-DNA hybridizations, in the diagnosis of bacteria and virus-induced diseases, in the determination of biosimilarity, in the quantification of serum, and in the study of hormones, steroids, immunoglobulins.

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CHAPTER 12

EFFECT OF SN AND PB CHLOROPROPENE DERIVATIVES ON MEMBRANE BIOPHYSICAL PROPERTIES

Suresh Kawitkar, Professor

Department of ISME, ATLAS SkillTech University, Mumbai, Maharashtra, India

Email Id-suresh.kawitkar@atlasuniversity.edu.in

ABSTRACT:

Triphenyltin chloride (TPhT) and Triphenyllead chloride (TPhL), two twin organometallic compounds, were studied for their biophysical activity in their interactions with yeast cells (*Saccharomyces cerevisiae*) and model membranes. Four measuring techniques were utilized in the experiments: the yeast survival test, the minimum inhibitory concentration (MIC), and two physical techniques (the spin probe method and the electric technique). It has been discovered that TPhT exhibits noticeably higher activity than TPhL when interacting with model membranes and yeast cells. At a concentration of 5, the activity completely inhibits the growth of yeast cells while also significantly increasing the fluidity of the middle part of the liposome bilayer and changing the direction of the polarization of the transmembrane voltage of filters impregnated with lauric acid. A thin polar membrane comprised of two layers of lipid molecules is known as a lipid bilayer (or phospholipid bilayer). These membranes are flat sheets that surround every cell in a continuous barrier. The nuclear membrane enclosing the cell nucleus and the membranes of the membrane-bound organelles in the cell are all made of a lipid bilayer, as are the cell membranes of practically all animals and many viruses. The lipid bilayer serves as a barrier, retaining ions, proteins, and other molecules where they are required while preventing their diffusion into unintended locations. Even though they are only a few nanometers wide, lipid bilayers are best suited for this function since they are impermeable to the majority of water-soluble (hydrophilic) compounds. Because bilayers are so impermeable to ions, cells may control salt concentrations and pH by moving ions across their membranes with the help of ion pump proteins.

KEYWORDS:

Chloride, Experiments, Impregnated, Retaining.

INTRODUCTION

Due to their high biological activity, biochemists, biophysicists, biologists, and geneticists have all been conducting extensive study on organometallic compounds. The research largely focuses on the hazardous qualities of derivatives of lead, mercury, and cadmium which are metals that were often used in industrial operations in the past century. However, due to the rapid advancement of our civilization and the globalization of information, the electronic sector has been expanding quickly and producing new technologies, which has resulted in the emergence of a new source of environmental contamination with hazardous metal compounds. Tin is one of them; it is frequently used in the electrical sector and is typically regarded as a metal with low toxicity. Tin can, however, cause serious poisonings because of its propensity to accumulate in living things and frequent occurrence in numerous items. According to several studies tin organic compounds hinder, among other things, the process of oxidative phosphorylation, speed up erythrocyte hemolysis, and change the physical characteristics of model lipid membranes. Tin compounds that have been ionized exhibit a specific action that affects lipid membranes (e.g., chlorides).

Man reported on a very high activity of tin chloride (Triphenyltin chloride-TPhT) impacting the middle section of lipid bilayer and made up of three aromatic rings. After entering the liposomes, this substance significantly fluidizes their structure, which, in terms of biological

membranes, means an adverse influence on their functions, i.e., cell death. It has been demonstrated that TPhT reduces pig testicular 17 beta-hydroxysteroid dehydrogenase activity and lowers testicular testosterone synthesis, while the compound causes the appearance of apoptosis in Leydig cells (LC-540) from rats. Additionally, pig erythrocytes are hemolyzed by triphenyl chloride when utilized in micromolar amounts. The biological activity of TPhT and its twin lead molecule, triphenyllead chloride (TPhL), in model membranes and in living organisms' cells should thus be thoroughly compared. Such a comparison can clarify the role that the molecule's structure plays in the activity of chemicals as well as the function of the metal ion that is carried by the molecule to the membrane. Additionally, we hope to learn more about the interaction that an admixture causes in the membrane in order to determine its hazardous qualities.

The experiments employed four measuring techniques: two physical (the spin probes method and the electric method) and two biologicals (the minimal inhibitory concentration/MIC/ and test of yeast survival) for the research of the model membranes and the *Saccharomyces cerevisiae* cells, respectively. Using the spin probes method (ESR), it was determined how TPhT and TPhL chemicals affected the dynamic characteristics of liposome membranes made from Egg Yolk Lecithin (EYL). The transmembrane voltage produced by these substances on the filters coated with a lauric acid ester was investigated using the electric technique. On the other hand, the MIC method and the test of yeast survival were used to assess how the tested substances affected living things. The model organism *Saccharomyces cerevisiae* was employed to research the impact of the aforementioned chemicals on the cellular viability of those organisms' cells. Amphiphilic phospholipids with a hydrophilic phosphate head and a hydrophobic tail made up of two fatty acid chains often make up biological bilayers. For example, phospholipids with specific head groups can act as signals and "anchors" for other molecules in cell membranes, changing the surface chemistry of a bilayer. Lipid tails, like lipid heads, can influence membrane characteristics by, for example, affecting the bilayer's phase. The chemical characteristics of the lipids' tails affect the temperature at which this happens. The bilayer can adopt a solid gel phase state at lower temperatures but phase transition to a fluid state at higher temperatures. The bilayer's mechanical characteristics, such as its resistance to stretching and bending, are also influenced by how the lipids are arranged within it. Artificial "model" bilayers made in a lab have been used to study many of these features. Drug delivery has also been done therapeutically using vesicles created by model bilayers.

In addition to the phospholipids that make up the bilayer that forms the structure of biological membranes, various other types of molecules are often present. Cholesterol, which helps to reinforce the bilayer and lessen its permeability, is a particularly significant example in animal cells. Additionally, cholesterol influences how some essential membrane protein's function. An annular lipid shell serves to firmly anchor integral membrane proteins to a lipid bilayer, which is necessary for their function. These membrane proteins are engaged in a variety of intra- and intercellular signaling activities because bilayers establish the boundaries of the cell and its compartments. The joining of two bilayers occurs as a result of specific membrane proteins. The combining of two separate structures is made possible by this fusion, as in the acrosome response during sperm fertilization of an egg or the entry of a virus into a cell. Lipid bilayers are difficult to investigate due to their fragility and invisibility under a conventional microscope. Advanced methods like atomic force microscopy and electron microscopy are frequently needed for experiments on bilayers. Phospholipids form a two-layered sheet when they are in contact with water, with their hydrophobic tails pointing in its direction. Two "leaflets" made up of a single molecular layer each are the consequence of this arrangement. Nearly all water and water-soluble compounds like sugars and salts are absent from the middle of this bilayer. The hydrophobic effect, also known as the aggregation of hydrophobic molecules, is what propels the assembly process. Non-covalent interactions

including van der Waals forces, electrostatic interactions, and hydrogen bonds are all a part of this intricate process. A typical lipid bilayer's cross-sectional profile is shown schematically. The totally hydrated headgroups, the fully dehydrated alkane core, and a brief intermediate area with partial hydration make up the three different zones. Despite being neutral, the head groups contain sizable dipole moments that affect the molecular configuration. When compared to its lateral dimensions, the lipid bilayer is incredibly thin. The lipid bilayer that makes up the plasma membrane is about the thickness of a piece of office paper if a typical mammalian cell (diameter 10 micrometers) were enlarged to the size of a watermelon (1 ft/30 cm). The bilayer is made of multiple unique chemical regions across its cross-section while being only a few nanometers thick. X-ray reflectometry, neutron scattering, and nuclear magnetic resonance techniques have been used during the past few decades to characterize these zones and their interactions with the surrounding water.

The hydrophilic headgroup is the initial area on each side of the bilayer. This region of the membrane is typically 0.8–0.9 nm thick and fully hydrated. The phosphate group in phospholipid bilayers is situated in this hydrated area, roughly 0.5 nm outside the hydrophobic core. The hydrated area may extend considerably further in particular circumstances, such as in lipids with a big protein or long sugar chain attached to the head. The lipopolysaccharide coating on a bacterial outer membrane, which aids in maintaining a water layer around the bacterium to prevent dehydration, is a typical illustration of such a change in nature.

DISCUSSION

During the sonification procedure, liposomes were created from EYL in distilled water. A single sample (1.5 ml) was subjected to 5 minutes of sonification in total, which was done in cycles of 30 seconds of sonification and 30 seconds of cooling. The EYL content in the sample was 0.04M, and the spin probe concentration, which was introduced to the liposomes while they were being created, was 0.05% in relation to the lecithin. For the experiment, two twin compounds were used: TPhT, which contains tin, and TPhL, which contains lead. After the synthesis of liposomes in a solution of dimethylformamide (DMF), mixtures of the chemicals under investigation were added to the samples, and their concentrations in relation to the EYL ranged between 1% and 10% (molar). 180 hours at a steady temperature of 297 were spent collecting the measurements. The pace at which red blood cells in anticoagulated whole blood decelerate in a standardized tube over the course of an hour is known as the erythrocyte sedimentation rate (ESR or sed rate). It is a typical hematological examination and a general indicator of inflammation. In order to do the test, anticoagulated blood is typically placed in an upright tube called a Westergren tube. After one hour, the red blood cells' fall distance is measured and reported in millimeters[1]–[4].

The ESR test has been carried out automatically ever since automated analyzers were introduced into clinical laboratories. The aggregation of red blood cells affects the ESR; blood plasma proteins, particularly fibrinogen, encourage the creation of bigger structures (interconnected rouleaux, irregular clusters) of aggregating red blood cells. Larger aggregates settle more quickly because, in accordance with Stokes' Law, the sedimentation velocity varies as the square of the object's diameter. Even though aggregation already occurs at normal physiological fibrinogen levels, it tends to get worse when there is inflammation, which raises ESR. Inflammation, pregnancy, anemia, autoimmune diseases (including lupus and rheumatoid arthritis), infections, some renal diseases, and some malignancies (like lymphoma and multiple myeloma) all result in elevated ESR levels. Polycythemia, hyperviscosity, sickle cell disease, leukemia, chronic fatigue syndrome, low plasma protein (caused by liver or kidney illness), and congestive heart failure all result in a reduced ESR. Although increases in immunoglobulins often cause the ESR to rise, extremely high levels may cause it to fall because of the plasma's hyperviscosity. IgM-class paraproteins and, to a

lesser extent, IgA-class paraproteins are particularly likely to exhibit this. Females have a somewhat greater basal ESR than males.

Diagnosis

Multiple myeloma, temporal arteritis, polymyalgia rheumatica, various autoimmune illnesses, systemic lupus erythematosus, rheumatoid arthritis, inflammatory bowel disease, and chronic kidney disorders are a few examples of conditions for which ESR can occasionally be helpful in the diagnosis. The ESR may be greater than 100 mm/hour in several of these situations. It is frequently used to distinguish Kawasaki's disease from Takayasu's arteritis, which has a noticeably raised ESR. It may also be elevated in some chronic infectious diseases, such as tuberculosis and infective endocarditis. Additionally, it is increased in DeQuervain's subacute thyroiditis[5].

According to an American study, infection causes a considerably elevated ESR of ≥ 100 mm/h in 33% of cases, followed by cancer (17%), kidney disease (17%), and non-infectious inflammatory illnesses (14%). However, the ESR remains below 100 in pneumonia. Some have questioned the ESR's relevance in modern practice because it is a test that, when compared to other diagnostic options, is somewhat non-specific and imprecise. An ESR should, according to recent literature, be "obtained on all patients over the age of 50" who are experiencing severe headache

Electric Approach

A Synpor filter impregnated with lauric acid was employed as the membrane to divide the two chambers of the experimental apparatus (the measuring and the reference ones). The measuring system's chambers were submerged in a 10 mM solution of Ag/AgCl measuring electrodes that were connected to the electrometer, and the intermediate chambers were connected to the measuring system's chambers via salt bridges. An interaction between the measuring electrode and the substance added to the chamber is prevented by such a system. The temporal dependence of the transmembrane voltage (TMV), generated by the presence of admixtures of the investigated chemicals, was determined using the Keithley 6517 electrometer. The examined compounds were dissolved in DMF and introduced to the measuring chamber in the same form as in the ESR procedure. For two different admixture amounts, 1% and 10% (molar) in relation to lauric acid, measurements were made. The admixture concentrations roughly matched the levels used in the ESR-based assessments[6]–[9].

The results are the arithmetic means of the five times that each of the ESR and electric measurements were repeated. Relative measurement errors for the parameter, parameter, and electric method were each 1.5%, 2.5%, and 2%, respectively. The collection of physical phenomena known as electricity are those that are connected to the presence and movement of matter that possesses an electric charge. Maxwell's equations describe the phenomenon of electromagnetism, which includes both magnetism and electricity as components. Lightning, static electricity, electric heating, electric discharges, and many other common phenomena have an electrical component. An electric field is created when there is an electric charge, either positive or negative. Electric current, which results from the movement of electric charges, also creates a magnetic field. In the majority of cases, a force acting on a charge has an intensity determined by Coulomb's law. Volts are commonly used to measure electric potential.

electric power, which energizes equipment via electric current

Electronics is the study of electrical circuits containing transistors, integrated circuits, vacuum tubes, and other active electrical components, along with related passive connecting techniques. Since antiquity, electrical phenomena have been researched, but until the 17th and

18th century, theoretical knowledge of these phenomena remained sluggish. By the end of the 19th century, electrical engineers had applied the electromagnetic theory to the usage of electricity in both industrial and domestic settings. Electrical technology was rapidly developing during this period, transforming society and industry and serving as a catalyst for the Second Industrial Revolution. Due to electricity's exceptional adaptability, it may be used for a virtually infinite number of purposes, including transportation, heating, lighting, communications, and computation. Modern industrial society is now supported by electrical power[10]–[12].

History

People were aware of electric fish shocks long before they had any awareness of electricity. These fish were referred to as the "Thunderer of the Nile" and described as the "protectors" of all other fish in ancient Egyptian writings from 2750 BCE. Ancient Greek, Roman, and Arabic naturalists and medics once more mentioned electric fish thousands of years later. A number of early authors, including Pliny the Elder and Scribonius Largus, attested to the numbing effects of electric shocks given by electric catfish and electric rays, and they were aware that such shocks may travel along conducting objects. In the hopes that the strong shock would heal them, patients with conditions like gout or headaches were instructed to contact electrified fish. Ancient societies in the Mediterranean region were aware that some items, such as amber rods, might be attracted to feathers by rubbing them with cat fur. Around 600 BCE, Thales of Miletus made a number of studies regarding static electricity, and as a result, he came to the conclusion that amber was magnetic due to friction, unlike minerals like magnetite, which required no rubbing though subsequent research would demonstrate a connection between magnetism and electricity, Thales was mistaken in his assumption that the attraction was caused by a magnetic influence. The 1936 discovery of the Baghdad Battery, which resembles a galvanic cell, has given rise to the contentious hypothesis that the Parthians may have been familiar with electroplating. However, it is unclear whether the item was electrical in origin.

A bald, slightly chubby man in a three-piece suit is portrayed in a half-length portrait. Joseph Priestley's *History and Present Status of Electricity*, published in 1767, details Benjamin Franklin's considerable research on electricity during the 18th century. Franklin and Priestley had a long relationship. Until the English scientist William Gilbert wrote *De Magnete* in 1600, electricity would have remained little more than a scientific curiosity for millennia. In it, he made a careful study of electricity and magnetism and distinguished the lodestone effect from static electricity created by rubbing amber. He created the Neo-Latin word *electricus*, which means "of amber" or "like amber" and comes from the Greek word *elektron*, which means "amber," to describe the ability to attract small things when rubbed. The English words "electric" and "electricity" originated from this relationship and were first used in literature in Thomas Browne's *Pseudodoxia Epidemica* in 1646. In the 17th and early 18th centuries, Otto von Guericke, Robert Boyle, Stephen Gray, and C. F. du Fay carried out additional research. Benjamin Franklin spent a significant amount of the latter half of the 18th century researching electricity, raising money by selling his valuables. He is said to have flown a kite in a storm-threatened sky in June 1752 while fastening a metal key to the bottom of the dampened string. Lightning was electrical in nature, as evidenced by the series of sparks that flew from the key to the palm of his hand. He also used electricity, which consists of both positive and negative charges, to explain the seemingly counterintuitive behavior of the Leyden jar, a device for storing significant amounts of electrical charge.

Hugh Williamson presented a number of tests to the Royal Society in 1775 regarding the electric eel's shocks, and the same year, surgeon and anatomist John Hunter provided a description of the design of the fish's electric organs. Luigi Galvani's discovery of bioelectromagnetics, which showed that electricity was the medium by which neurons

conveyed impulses to the muscles, was published in Scientists had a more dependable source of electrical energy before Alessandro Volta's battery, or voltaic pile, of 1800, which was comprised of alternating layers of zinc and It was Hans Christian Arrsted and André-Marie Ampère who first recognized electromagnetism, the unification of electric and magnetic phenomena, in 1819–1820. The electric motor was created in 1821 by Michael Faraday, and the electrical circuit was mathematically analyzed in 1827 by Georg Ohm. James Clerk Maxwell established a clear connection between electricity, magnetism, and light, particularly in his "On Physical Lines of Force Although electrical science had advanced quickly in the early 19th century, electrical engineering would advance most significantly in the latter half of the century. Electricity was transformed from a scientific curiosity into a necessary tool for modern life by individuals like Alexander Graham Bell, Ottó Bláthy, Thomas Edison, Galileo Ferraris, Oliver Heaviside, nyos Jedlik, William Thomson, 1st Baron Kelvin, Charles Algernon Parsons, Werner von Siemens, Joseph Swan, Reginald Fessenden, Nikola Tesla, and George Westinghouse.

Heinrich Hertz observed that electrodes irradiated with UV light produce electric sparks more quickly Albert Einstein wrote a paper in 1905 in which he proposed the explanation of experimental data from the photoelectric effect: light energy is transmitted in discrete quantized packets, energizing electrons. The quantum revolution was sparked by this finding. In 1921, "his discovery of the law of the photoelectric effect" earned Einstein the Nobel Prize in Physics. Photocells, like those found in solar panels, use the photoelectric effect as well.

The "cat's-whisker detector," used in radio receivers for the first time in the 1900s, was the first solid-state component. To use the contact junction effect to detect a radio signal, a whisker-like wire is placed lightly in touch with a solid crystal (such as a germanium crystal). The current is limited to solid elements and compounds designed particularly to switch and amplify it in a solid-state component. Positively charged electron deficits, often known as holes, and negatively charged electrons are the two ways that current flow can be conceptualized. Quantum physics is used to interpret these charges and holes. Crystalline semiconductors are most frequently used as the building material. Transistor technology's development ushered in the era of solid-state electronics. John Bardeen and Walter Houser Brattain at Bell Labs created the first functional transistor, a germanium-based point-contact transistor, in 1947. The bipolar junction transistor was created in 1958.

CONCLUSION

It also appears surprising that the type of ion contained within a big molecule has a significant impact on the biological activity of the latter when interacting with both biological and model membranes. Similar findings may be found in, which reports the findings of research into the family of metalloporphyrins that varied depending on the metal ion contained within the molecule.

The information in shows that while the general nature of metalloporphyrins' influence on membranes is quite similar (they all fluidize the membrane's interior), the efficiency of their interaction is strongly dependent on the metal ion. It is also quite surprising that the compound containing tin has a much higher toxicity than the compound containing lead; this fact alone requires a fresh perspective on the issue of environmental metal pollution and forces us to reconsider our previous assumptions about how "low-harmful" tin is in municipal and industrial waste. The fact that other organic tin compounds studied using the ESR approach also exhibit a significant activity when interacting with EYL liposome membranes makes it even more likely that it will prevent us, in the era of widespread society-wide electronization, from experiencing an unanticipated ecological catastrophe. A future study will describe the findings of comparative examinations of these compounds and related ones containing lead.

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CHAPTER 13

A PROMISING METHOD IN STUDY OF MECHANISM OF PROPOFOL

Swarna Kolaventi, Assistant Professor
Department of uGDX, ATLAS SkillTech University, Mumbai, Maharashtra, India
Email Id-swarna.kolaventi@atlasuniversity.edu.in

ABSTRACT:

We know relatively little about the physiological and neuroregulatory mechanisms of propofol. It is one of the key conundrums in anesthesiology and has significant therapeutic and scientific value. It is known that the anesthetic mechanism may entail neural networks made up of several brain circuits. But more explanation of this hypothesis' mechanism is required. It is increasingly likely that this issue will be resolved as artificial neural networks are used to analyze temporal waveform data and build biophysical computational models as artificial intelligence advances. By building biophysical computational models, this review concentrates on the most recent understanding of the anesthetic mechanism of the intravenous general anesthetic propofol. Propofol, also known as 2,6-Diisopropylphenol and sold under the brand names Depivering among others, is a fast-acting drug that causes a loss of consciousness and short-term memory loss. Sedation for individuals who are mechanically ventilated, procedural sedation, and the induction and maintenance of general anesthesia are some of its applications. If other drugs have failed to control status epilepticus, it is also utilized the maximal effect occurs within two minutes and normally lasts between five and ten minutes. It is administered by injection into a vein. Euthanasia is another usage of propofol in Canada. Although it has not been well researched for usage in this situation, the medicine seems safe for use during pregnancy. Using it during a cesarean procedure is not advised. Opioids like morphine may also be utilized because it is not a pain reliever; nevertheless, it is unclear if they are always necessary. It is thought that propofol functions at least in part through a GABA receptor.

KEYWORDS:

Anesthesiology, Biophysical, Computation, Propofol.

INTRODUCTION

A popular short-acting intravenous anesthetic for sedation and induction of general anesthesia in adult intensive care unit (ICU) patients is propofol. After intravenous injection, the impact takes around two minutes to reach its peak and lasts for five to ten minutes. For more than 30 years, propofol has been utilized in clinical anesthesia. Propofol misuse is commonly acknowledged to increase the risk of injection discomfort, respiratory depression, and circulatory inhibition. The most frequent side effect of propofol is injection discomfort, which is mostly caused by the drug's activation of blood vessel walls during intravenous administration. However, after the patient is drugged, the pain will go away, and when the patient wakes up, the pain at the injection site won't be there. One of the serious side effects that prevent propofol from being used more widely is respiratory suppression. The administration of propofol would reduce the patients' respiratory rate and amplitude, and in severe circumstances, could result in respiratory arrest. The patient's life will be in risk at any time if the anesthesiologists are unable to responsibly control the dosage and indication of propofol while continuously monitoring the patient's vital signs. The propofol adverse effect of circulatory inhibition is another dangerous one. In addition to its sedative effects, propofol also inhibits the circulatory system. Propofol overuse may cause a reduction in blood

pressure, cardiac arrhythmia, and other problems. The patient's life will be in danger without continuous electrocardiogram (ECG) monitoring. Therefore, it is crucial for safe and effective use that the administration of propofol is monitored using a method based on the drug's mechanism. Propofol's method of action is yet unclear. Numerous studies have revealed that propofol causes general anesthesia by controlling a range of brain transmitters and ion channels and. Propofol has anesthetic effects on interactions between various neurons in each layer of the brain, although the precise mechanism underlying this effect is still completely unclear. It is difficult to explain the precise anesthetic mechanism of propofol as a result. The mechanism of general anesthesia has been studied previously from six angles, including molecular, synaptic cellular, neural microcircuit systematic (brain regions), and behavioral levels. The fact that these neural networks are made up of several neuronal circuits implicated in the anesthetic mechanism is well recognized. This review employs biophysical modeling to highlight current understanding of the anesthetic mechanism of propofol.

Patients who undergo general anesthesia experience consciousness, drowsiness, and arousal after receiving anesthetics. Since general anesthesia was first in 1846, one of the most significant scientific subjects has focused on its mechanism. The study of general anesthetics' mechanisms has increased dramatically over the past few decades. The most alluring of these hypotheses has been the notion of network regulation in the mechanism of general anesthesia based on neural microcircuit and systematic levels. Alkire et al. studied anesthesia-induced loss of consciousness and described substantial alterations in the brain processes using slow imaging techniques including Positron Emission Computed Tomography (PET) and statistical parametric mapping (SPM). The "thalamic consciousness switch" was termed after their discovery that the thalamus decreased in activity while under general anesthesia. Contrary to the conventional idea, Ching et al. discovered that the thalamus was not entirely dormant under general anesthesia. Instead, a few thalamic subsets organized their activity into a highly organized γ -rhythm. These demonstrated that propofol can produce anesthesia through thalamic rhythm inhibition.

Additionally, propofol prevents the transmission of auditory signals by preventing the thalamic rhythm. Propofol decreased auditory signal transduction while also inducing distinctive changes in patients' brain physiological processes, according to Purdon et al.'s research [23]. They discovered that as the dosage of propofol increased, the correct response seen in the auditory tone discrimination task gradually decreased, followed by a complete disappearance of the correct responses and a decrease in activities of the secondary auditory cortex, with activities of the primary auditory cortex remaining unchanged. This was discovered using functional magnetic resonance imaging (fMRI) and electroencephalogram (EEG). This proved that general anesthetics might make their victims unconscious and impede their auditory transduction. Propofol may boost GABAA receptor function or GABAergic neurotransmission by possibly making it easier for GABAA receptors to bind to GABA, which is the fundamental mechanism for propofol's inhibition of auditory signal transduction [25, 26]. Gamma rhythm synchronization depends on inhibitory synapses such GABAA ligand-gated channels, which are both required and sufficient.

This is in line with the findings of Paik and Wang, who found that the primary source of the high-frequency rhythmic activity of gamma oscillation is neural networks made up of inhibitory interneurons. Using EEG, intracranial EEG (iEEG), magnetoencephalography (MEG), and other methods, studies on humans and animals have shown that synchronized gamma oscillation is connected to auditory perception. A number of mammalian and human brain areas, including the thalamus, somatosensory cortex, and the hippocampus, exhibit gamma oscillation. Propofol's chemical mechanism has been extensively studied, but little is known about the brain process that inhibits auditory signal transduction. Combining computer modeling of biophysical processes with investigations of brain circuits may be able

to resolve this. According to Lee et al.'s research, brain rhythms can coordinate and plan neural circuits across cortex layers and cortical areas, adding support to the notion that propofol inhibits auditory transduction by modifying gamma oscillation.

Propofol, which has essentially supplanted sodium thiopental, is the medication that is usually always used to induce general anesthesia. Additionally, it can be delivered as a component of the complete intravenous anesthesia maintenance approach, which uses either manually programmed infusion pumps or computer-controlled infusion pumps in a procedure known as target-controlled infusion (TCI). Additionally, patients in intensive care units who are receiving mechanical breathing but are not undergoing surgery can be sedated with propofol. Propofol outperforms lorazepam in critically ill patients in terms of both effectiveness and overall cost. Due to its shorter ICU stay, propofol is comparatively affordable when compared to drugs with comparable uses. Because benzodiazepines like midazolam and lorazepam tend to build in critically ill patients, extending sedation, research have revealed that propofol is regarded to be more effective than lorazepam (even though it has a longer half-life than lorazepam). The effectiveness of propofol in simulating the mental and physical aspects of sleep for patients in the ICU is unclear, but it has been suggested as a sleep aid for critically ill adults in the ICU.

A central IV line or a peripheral IV can be used to administer propofol. In sedated and intubated patients, propofol is frequently used with fentanyl for pain treatment. In IV form, the two medications are compatible. In order to treat laryngospasm, propofol is also used to deepen anesthesia. It can be used either on its own or after succinylcholine. Its use can prevent the need for paralysis and, in some cases, succinylcholine's potential negative effects.

DISCUSSION

Research on brain shape and function has been exploding by combining neuroscience and bioinformatics technologies as a result of the quick development of current informatics tools. For instance, the mesoscopic mapping of brain circuits and their activity patterns can be finished, and the underlying process can be investigated in animal models. This also holds true for computer modeling-aided research on the mechanism of propofol. Ching et al. discovered a connection between consciousness loss and the propofol-induced γ -rhythm. They combined it with the established thalamus and cortical dynamics models to create a thalamocortical model to simulate the effects of propofol. Additionally, they discovered that dynamic system models could be used to replicate highly structured brain rhythmic processes and that the level of consciousness of patients was closely related to the highly structured EEG produced by propofol. They observed that propofol may affect GABAergic neuronal networks in the brainstem, cortex, and thalamus to cause dramatic alterations in brain dynamics that result in shifts from sedation to loss of consciousness. Synchronous rhythms generated by the cerebral cortex may limit reactions to external stimuli due to the involvement of the thalamus, sustaining an unconscious state[1]–[3].

By developing a biophysically based computer model, Lee et al. were able to mimic the interactions between the main auditory cortex (A1) and the secondary somatosensory cortex as shown in vitro. They suggested that the coordination between the top-down gamma and beta rhythms is one of the most significant variables controlling the gating process that controls the bottom-up sensory signaling from A1 to Par2. Cholinergic modulation between the cortices controlled this coordination. This provides a nice illustration of how biophysical computational modeling can be used to understand propofol's mechanism of action.

Important Techniques for Studying Neural Networks Include Biophysical Modeling and Computational Simulation Due to the complexity of biological neural networks and the constraints of experimental settings, it is challenging to study the mechanism of interactions within and across neural networks. Researchers may now study biological brain networks

using a variety of methodologies, rather than just depending on biological studies, thanks to the quick growth of information technology. The dynamic processes of different neurons and brain regions can be easily simulated using mathematical modeling and computer simulation to study neural networks under various conditions, particularly to describe the electrophysiological activities of individual or collectively recorded neurons in large neural networks. Neuroscience explains how the brain works by looking at all of its components, including how chemicals interact and how that influences behavior. In explaining and interpreting a wide range of brain processes, mathematical techniques and statistical concepts are crucial. The ability to record the electrical activity of neurons in great detail has also been made possible by improvements in measurement and storage technologies, which therefore aid neuroscientists in managing massive experimental databases[4]–[6].

Hodgkin and Huxley had investigated the ionic current in the squid large axon in the 1950s. They discovered that the conductivity change of the calcium and potassium channels in the axon membrane is the cause of the current production through a series of carefully thought-out experiments. They developed the traditional Hodgkin-Huxley model (also known as the H-H model), which describes how the conductivity of calcium and potassium varies across time and membrane potential. The shape of the action potential, morphological changes in the action potential with sodium concentrations, the number of sodium ions involved in the inward flux across the membrane, the speed at which the action potential propagates, and the voltage curves of sodium and potassium ions were all accurately predicted by this model. In the field of computational neuroscience, the H-H model has numerous extensions. These include models that incorporate extra ion currents and various aspects of the extracellular environment of neurons both of which add new fast and slow time scales to the dynamic equation.

The H-H model continues to serve as the foundation of computational neuroscience even if it is important to take into consideration the complexity of biological situations and use more intricate mathematical reasoning when modeling when analyzing a significant number of neuronal events. The groundwork is laid for electrophysiological modeling. It served as the foundation for the development of more precise models, like the calcium-dependent channel model the single-ion channel Markov model the multicompartment model, and others, that describe variations in the membrane potential of neurons. A synaptic model was also developed to explain how neurons communicate with one another. A neural network model can be made directly by mixing these models. For instance, the cell bodies, axons, and dendrites of neurons are described using a multicompartment model, and compartment models are connected using a synaptic model. It is possible to mimic dynamic changes in the neural network after translating the mathematical model into the matching computer program.

It is typical to examine the gamma-band oscillation by building a biophysical computational model based on the concepts discussed above. In order to show connections between cholinergic modulation, gamma-band oscillation, and selective attention, Borgers et al. constructed a computational model that mimicked the local circuit made up of a few inhibitory and excitatory neurons. In order to investigate the mass phenomena over the entire thalamus cortex, Traub et al built a computational model with extensive networks made up of diverse neurons. Gamma oscillation in the auditory transmission channel has received a lot of attention recently, prompting substantial research into the phenomenon. To show the correlation between gamma oscillation and information transmission between these two regions, Lee et al. developed a computer model on interactions between the primary auditory cortex and the secondary somatosensory cortex. This model is capable of properly simulating biological experiment results and forecasting experimental phenomena[7]–[9].

The computing models can be employed in clinical settings in addition to directly replicating biological processes under experimental conditions. Recurrent Neural Networks (RNN), for

instance, are a particular class of neural network with memory capabilities that may efficiently utilize time information for time series analysis. The Long Short-Term Memory (LSTM) model, a modification of the RNN model, is frequently used to track the level of anesthesia. The gradient disappearance or explosion issue affects the conventional RNN paradigm. By merely including a number of gates to efficiently handle serial input, the LSTM model, an upgraded version of the RNN model, can simulate nerve cells and so partially address this issue. Li et al. suggested a technique for LSTM and sparse denoising autoencoder (SDAE) paired with EEG inputs for monitoring the depth of anesthesia. This model has a higher probability of being able to predict the depth of anesthesia properly than models that only use one feature. An RNN model was created by Sun et al. utilizing a clinical dataset of 154 patients receiving anesthesia. End-to-end training is used to separate non-sedating from depth of anesthesia utilizing the original EEG spectrum without any feature extraction. Their RNN model can continually give a better and more reliable assessment of the sedative level compared to the straightforward and smooth feedforward approach.

Optimization of anesthesia and artificial intelligence (AI)

Artificial intelligence is being used increasingly in the fields of medicine and health care, including image identification, new medication research and development, medical robots, assistive diagnosis, and more. The evaluation of anesthetic depth, the creation of prediction models, the development of clinical decision support tools, and intelligent drug delivery systems are all possible because to anesthesiology's data-intensive field. Anesthesiologists can judge the state of anesthesia and prevent adverse events using patient health information collected before and after surgery as well as a large amount of monitoring data generated during surgery. However, it is frequently challenging to accurately manage each patient due to the variety of individual patients' medical conditions, which is the main cause of anesthesia, perioperative complications, and even death. AI has many benefits, including excellent data processing and self-learning capabilities. We can efficiently integrate and manage the complex clinical big data through machine learning, summarize the rules, and then optimize the anesthetic strategy to produce correct anesthesia. Integrating perioperative monitoring data based on AI convolutional neural network modeling will provide precise anesthetic depth/state monitoring.

Through machine learning, Sahrawi et al. use the subjects' EEG, EMG, heart rate, blood pressure, pulse, and signal quality index as input signals. In comparison to the current depth of anesthesia monitoring, the artificial neural network model can monitor anesthesia depths that are substantially higher. With an accuracy of 92.2% and a delay time of only 1 s, Saadeh [68] et al. have further enhanced the anesthetic depth monitoring system based on AI analysis EEG, which can be used under challenging circumstances such as different ages and different drugs. Second, the clinical decision support system and anesthesia closed-loop system developed on this foundation can assist in achieving accurate anesthesia and optimizing anesthesia management, thereby significantly reducing the workload of anesthesiologists. Although ultrasound-guided nerve blocks are a crucial technical tool for precise anesthetic, it is challenging to guarantee their popularity and blocking effectiveness due to their complexity and variety. By learning from big data, Bowness et al [10], [11].

developed a clinical support system for nerve block based on the Anatomy Guide system that can help doctors detect nerve block, operate, and fulfill the duty of optimizing anesthesia management. Numerous studies have demonstrated that closed-loop management based on anesthetic depth can more safely direct clinical anesthetic medications to achieve precise anesthesia during general anesthesia. Anesthesiologists must collect and measure data on the control of cardiac output, blood pressure, and blood glucose during the perioperative period. According to the sub journal Lancet perioperative closed-loop insulin based on deep learning and norepinephrine management system can optimize the current anesthetic regimen from

multiple dimensions and eradicate the possibility of human error. The complex process of judgment and regulation is frequently lagging. Additionally, it might offer a better treatment strategy for enhancing patients' prognoses. The prediction and management of perioperative adverse events, such as hypoxemia, hypotension, etc., may inflict some degree of harm on the function of the patient's brain and other peripheral organs and may even result in death. This is another problem confronted by anesthesiology. With early prediction of perioperative adverse reactions and early notification of anesthesiologist intervention, the machine learning model created by Lundberg.

It could predict the oncoming hypoxemia more correctly than anesthesiologists and point out the reasons of hypoxemia. This can increase the effectiveness of anesthesiologists' preoperative assessments while also enhancing postoperative patient management and ensuring patient safety. In the areas of anesthesia and perioperative medicine, AI has also been progressively improved. By combining a video laryngoscope with a robotic arm, McGill University in Canada has created the first Kepler remote artificial intelligence intubation system. Anesthesiologists can utilize AI to uncover more hidden information and enhance postoperative outcomes in addition to fully comprehending the prior clinical diagnosis and treatment information of patients and performing quick preoperative evaluations. Infant pain was automatically determined by Cheng using machine learning of facial expressions. Through the use of functional magnetic resonance imaging (fMRI) and artificial intelligence (AI). It was discovered that alterations in autonomic nerve activity in the human body are strongly correlated with the intensity of pain. With an accuracy of 92.4%, doctors may assess pain in patients who are unable to speak by observing autonomic nerve activity. This considerably reduces the risk that these patients would develop chronic pain after surgery.

CONCLUSION

Most computational simulation models for studying propofol concentrate on a tiny local network with a few neurons. Traditional models may not effectively simulate neural networks with more neurons or with greater complexity. Brain-inspired information processing models could offer solutions to this problem. On the one hand, the power of artificial intelligence models has been greatly boosted by parallel computation based on GPU. Similar to this, parallel computational platforms can also be used to run the simulation models. Given that neurons have a distributed structure, it is possible to simulate and update each neuron in parallel using arithmetic units. According to theory, as the number of neurons increases, so does the computational complexity of parallel computation. The computational complexity even grows exponentially for serial computation. As a result, far more intricate structures and a wider variety of neuronal types are effectively stimutable. On the other hand, models of artificial intelligence offer superior modeling approaches for replicating actual neurons. As demonstrated, the popular H-H model accurately depicts the relationship between a neuron's input and output.

The parameters are calculated using information gathered from in vivo tests. But since there are so many different kinds of neurons in the brain, it is challenging for a model to represent them all. Artificial intelligence models, like the aforementioned artificial neural networks, may also learn the relationship between input and output. A two-layer neural network can theoretically model any function. illustrates how well the RNN model handles time series data, which can be used to simulate how neurons work. Data gathered from in vivo trials is used to teach the RNN's parameters. Learning RNNs allows for the simulation of every neuron. One neural network can also imitate a collection of neurons, such as a local cortical area, because to the ability of neurons to model in several dimensions. As a result, many artificial neural networks can imitate a bigger portion of the brain.

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