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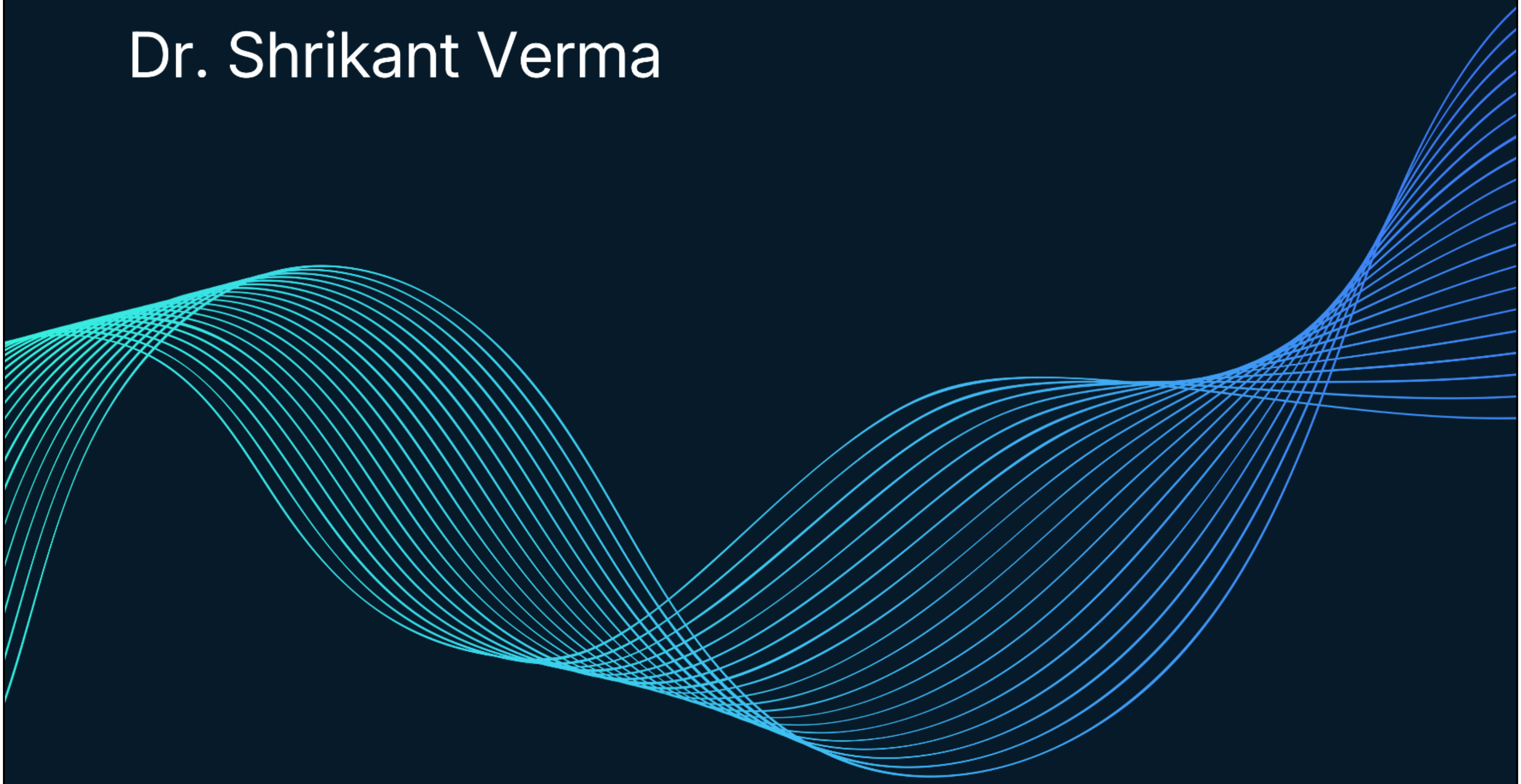
Progressive Pathways in Science and Technology Research

Volume II

Editors:
Dr. Archana Ramteke
Dr. Pradip D. Satav
Dr. Ashwini V Yankati
Dr. Shrikant Verma



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Editors

Dr. Archana Ramteke

Department of Chemistry,

K. D. K. Engineering College,

Nagpur, Maharashtra

Dr. Pradip Duryodhan Satav

Department of Botany,

Microbiology and Biotechnology,

Science College, Nanded, M.S.

Dr. Ashwini V Yankati

Department of Home Science,

B.V.V.S Akkamahadevi Women's Arts, Science

and Commerce College, Bagalkot

Dr. Shrikant Verma

Department of Personalized and

Molecular Medicine,

Era University, Lucknow, U.P.

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PREFACE

The rapid advancement of science and technology continues to redefine the boundaries of knowledge, innovation, and human potential. *Progressive Pathways in Science and Technology Research* is a thoughtful compilation that reflects the dynamic evolution of modern scientific inquiry and its transformative impact on society. This volume brings together diverse perspectives from researchers, academicians, and professionals, offering valuable insights into emerging trends, interdisciplinary approaches, and novel methodologies shaping the future.

In an era driven by innovation, the integration of science and technology has become essential for addressing global challenges such as climate change, healthcare disparities, sustainable development, and resource management. The chapters presented in this book explore a wide spectrum of disciplines, including life sciences, chemical sciences, environmental studies, information technology, and applied research. Each contribution highlights not only theoretical advancements but also practical applications, emphasizing the relevance of research in real-world problem-solving.

This book aims to serve as a platform for knowledge exchange and intellectual growth, encouraging collaboration across disciplines. It underscores the importance of progressive thinking, critical analysis, and innovation in advancing scientific frontiers. The contributors have made commendable efforts to present their research in a clear and comprehensive manner, making it accessible to students, educators, researchers, and industry professionals alike.

We believe that this volume will inspire readers to explore new research directions, adopt innovative approaches, and contribute meaningfully to the ever-expanding domain of science and technology. It is our hope that *Progressive Pathways in Science and Technology Research* will not only enrich academic discourse but also foster a spirit of inquiry and discovery among its readers.

We extend our sincere gratitude to all authors, reviewers, and collaborators whose dedication and scholarly contributions have made this publication possible.

- Editors

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MITOCHONDRIAL DYSFUNCTION AS AN EARLY CELLULAR MARKER OF EXOGENOUS CORTICOID TOXICITY

Ranjana
Department of Zoology,
Patna Science College, Patna University, Patna, Bihar, 800005, India.
Corresponding author E-mail: ranjana.prakash81@gmail.com, ranjanazoolpsc@pup.ac.in

Abstract

Exogenous corticosteroids remain among the most widely prescribed drug classes globally, employed across a spectrum of inflammatory, autoimmune, and neoplastic conditions. However, their chronic administration is associated with a constellation of metabolic and cellular toxicities that extend far beyond the well-documented systemic effects such as hyperglycaemia, osteoporosis, and hypothalamic-pituitary-adrenal axis suppression. Among the earliest and most mechanistically consequential events in corticoid-induced cellular injury is dysfunction of the mitochondrion — the central hub of bioenergetics, reactive oxygen species homeostasis, and apoptotic signalling. This chapter synthesises the expanding body of evidence demonstrating that mitochondrial dysfunction precedes overt histopathological changes and clinical biomarker alterations in multiple tissue types, including skeletal muscle, hepatic parenchyma, cardiomyocytes, and neurons. We review the molecular mechanisms underpinning glucocorticoid-induced perturbations in oxidative phosphorylation, mitochondrial membrane potential, biogenesis pathways, and mitophagy. The potential utility of mitochondria-derived biomarkers — including circulating mitochondrial DNA, cardiolipin oxidation, and bioenergetic indices — as early sentinels of corticoid toxicity is critically appraised. Understanding mitochondrial dysfunction as an inaugural cellular event in glucocorticoid toxicity opens avenues for targeted monitoring, novel therapeutic co-intervention, and personalised dosing strategies.

Keywords: Glucocorticoids, Mitochondria, Oxidative Stress, Bioenergetics, Corticosteroid Toxicity, Mitochondrial DNA, Reactive Oxygen Species, Apoptosis.

1. Introduction

Glucocorticoids (GCs) are steroid hormones synthesised and secreted by the zona fasciculata of the adrenal cortex, playing indispensable physiological roles in metabolic regulation, immune modulation, stress adaptation, and circadian rhythmicity. Since the landmark isolation of cortisone by Kendall and Reichstein in the 1940s and its first therapeutic application by Hench, exogenous corticosteroids have been synthesised in increasing pharmacological potency and prescribed with mounting frequency. Contemporary estimates suggest that approximately 1–3% of the general population in developed countries is receiving long-term systemic glucocorticoid therapy at any given time, with prevalence rising sharply among elderly cohorts and those with chronic inflammatory diseases.[1]

The clinical pharmacology of exogenous corticosteroids is inseparable from a portfolio of adverse effects that accrue with dose and duration. Recognised toxicities encompass the hypothalamic-pituitary-adrenal (HPA) axis suppression, Cushing syndrome phenotype, hyperglycaemia and steroid-induced diabetes mellitus, osteoporosis, growth retardation in children, immunosuppression, neuropsychiatric disturbances, myopathy, and dyslipidaemia.[2] These sequelae reflect glucocorticoid receptor (GR)-mediated transcriptional reprogramming of gene networks governing intermediary metabolism, bone remodelling, immune function, and neuroendocrine regulation. Yet underlying all these organ-level manifestations is a layer of cellular and subcellular disruption that has historically received comparatively less investigative attention: the early impairment of mitochondrial function.[3]

Mitochondria are double-membrane organelles occupying 15–25% of cellular volume in metabolically active tissues and serving as the primary sites of adenosine triphosphate (ATP) generation through oxidative phosphorylation (OXPHOS). Beyond bioenergetics, they regulate calcium homeostasis, orchestrate intrinsic apoptotic pathways, participate in steroidogenesis and haem biosynthesis, and are central nodes in reactive oxygen species (ROS) signalling.[4] The intimate relationship between glucocorticoid exposure and mitochondrial pathophysiology has become increasingly apparent over the past two decades, fuelled by advances in high-resolution respirometry, mitochondrial proteomics, and in vivo imaging techniques.

A defining feature of mitochondrial dysfunction in corticoid toxicity is its temporal priority: experimental models consistently demonstrate measurable alterations in mitochondrial membrane potential (MMP), electron transport chain (ETC) complex activity, and mitochondrial DNA (mtDNA) integrity before conventional hepatocellular, myocyte, or neuronal injury markers become abnormal.[5] This chronology positions mitochondrial dysfunction not merely as a secondary consequence of cellular damage but as an initiating and amplifying mechanism. Consequently, mitochondria-derived parameters hold promise as early biomarkers enabling pre-emptive clinical intervention.

This chapter provides a comprehensive mechanistic account of how exogenous corticosteroids compromise mitochondrial integrity, surveys the tissue-specific manifestations of this dysfunction, and critically evaluates the translational potential of mitochondrial biomarkers in clinical monitoring of patients on glucocorticoid therapy. The chapter also addresses emerging pharmacological strategies targeting mitochondrial protection as adjuncts to corticosteroid treatment regimens.

2. Glucocorticoid Receptor Signalling and Mitochondrial Cross-Talk

2.1 Classical Genomic Pathway

The canonical mechanism of glucocorticoid action involves diffusion of lipophilic GC molecules across the plasma membrane and binding to the cytoplasmic glucocorticoid receptor alpha (GRα). Upon ligand binding, GRα undergoes conformational change, dissociates from chaperone proteins (heat shock protein 90, heat shock protein 70, and immunophilin), and translocates to the nucleus where it binds glucocorticoid response elements (GREs) within promoter regions, activating or repressing target gene transcription.[6] Pharmacological GCs such as dexamethasone, prednisolone, and methylprednisolone engage this pathway with high affinity, exerting transcriptional effects on hundreds to thousands of genes in a cell-type-specific manner.

Key transcriptional targets relevant to mitochondrial biology include peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC-1α), a master regulator of mitochondrial biogenesis; uncoupling proteins (UCPs); pyruvate dehydrogenase kinase 4 (PDK4), which suppresses mitochondrial glucose oxidation; and components of the ETC. GC-driven upregulation of PDK4 redirects metabolic flux away from mitochondrial oxidative phosphorylation toward glycolysis and gluconeogenesis, creating a bioenergetic context inherently predisposed to mitochondrial stress.[7]

2.2 Non-Genomic Mitochondrial Actions

Beyond nuclear transcriptional effects, glucocorticoids exert rapid, non-genomic actions directly at the mitochondrial membrane. Mitochondria express mitochondrial GR (mtGR), a variant of GRα that localises to the matrix and inner mitochondrial membrane, where it interacts directly with mtDNA regulatory sequences and ETC complexes.[8] Studies employing confocal immunofluorescence and mitochondrial fractionation have confirmed mtGR localisation in hepatocytes, cardiomyocytes, and neurons, with receptor levels upregulated by GC pre-treatment.[9] Binding of dexamethasone to mtGR acutely modulates the transcription of mitochondrially encoded ETC subunits (ND1–ND6 of Complex I, cytochrome b of Complex III, and the three cytochrome c oxidase subunits of Complex IV), contributing to an immediate bioenergetic perturbation independent of nuclear gene regulation.

Additionally, glucocorticoids have been shown to alter the physicochemical properties of the inner mitochondrial membrane (IMM), increasing its permeability to protons and thereby uncoupling electron transport from ATP synthesis. This effect has been attributed to GC-induced changes in membrane lipid composition, specifically the oxidation and depletion of cardiolipin — a phospholipid exclusive to the IMM that stabilises respiratory supercomplexes and maintains cytochrome c anchoring.[10]

3. Molecular Mechanisms of Mitochondrial Dysfunction

3.1 Impairment of Oxidative Phosphorylation

The electron transport chain (ETC), comprising four multi-subunit complexes (I–IV) embedded in the IMM plus ATP synthase (Complex V), is exquisitely sensitive to GC-induced perturbations. Complex I (NADH: ubiquinone oxidoreductase) represents the primary entry point for electrons derived from the tricarboxylic acid (TCA) cycle and is the most frequent site of mitochondrial superoxide generation under pathological conditions. Multiple lines of experimental evidence demonstrate that dexamethasone exposure reduces Complex I activity in a dose- and time-dependent fashion in hepatic and muscular mitochondria.[11]

Spectrophotometric enzyme assays in isolated mitochondria from dexamethasone-treated rats reveal decrements in Complex I (NADH-ubiquinone reductase), Complex II (succinate dehydrogenase), and Complex IV (cytochrome c oxidase) activities within 24–72 hours of GC administration, timepoints at which serum transaminases and creatine kinase levels remain within normal reference ranges.[12] High-resolution respirometry using the Oroboros O2k oxygraph system has further demonstrated that GC exposure reduces State 3 (ADP-stimulated) respiration, diminishes respiratory control ratios, and decreases the P/O ratio (ATP produced per oxygen consumed), collectively indicating impaired coupling efficiency rather than simple substrate limitation.[13]

3.2 Mitochondrial Membrane Potential Dissipation

The mitochondrial membrane potential ($\Delta\Psi m$), maintained by proton pumping activities of Complexes I, III, and IV, is fundamental to ATP synthesis and the driving force for mitochondrial protein import. Flow cytometric and confocal fluorescence studies employing voltage-sensitive dyes such as JC-1, TMRM (tetramethylrhodamine methyl ester), and DiOC6 consistently demonstrate that GC treatment causes a concentration-dependent decline in $\Delta\Psi m$ preceding any decrease in cellular ATP content or viability.[14]

The mechanism involves at least two interconnected processes: direct proton leak through GC-modified IMM lipid bilayers, and the opening of the mitochondrial permeability transition pore (mPTP). The mPTP is a non-selective channel formed at the contact sites between the IMM and outer mitochondrial membrane (OMM), whose sustained opening causes matrix swelling, rupture of the OMM, and release of pro-apoptotic factors including cytochrome c, Smac/DIABLO, and apoptosis-inducing factor (AIF). Dexamethasone-induced mPTP sensitisation has been demonstrated in hippocampal neurons, cardiomyocytes, and thymocytes, and has been implicated as a key mechanism of glucocorticoid-induced apoptosis.[15]

3.3 Reactive Oxygen Species Generation and Oxidative Stress

Mitochondria are the principal source of cellular ROS, generating superoxide anion (O2•−) primarily at Complex I and III as a byproduct of electron transport. Under conditions of ETC dysfunction, electron leak increases disproportionately, amplifying ROS production. Glucocorticoid-induced Complex I impairment creates precisely such a situation. The resultant oxidative stress is further compounded by GC-mediated downregulation of endogenous antioxidant defences, including manganese superoxide dismutase (MnSOD), catalase, and glutathione peroxidase.[16]

The consequences of excessive mitochondrial ROS generation are multifaceted. Superoxide rapidly dismutates to hydrogen peroxide (H2O2), which in the presence of transition metals generates the highly reactive hydroxyl radical (OH•) via Fenton chemistry. These ROS species inflict oxidative damage on mtDNA (which lacks protective histones), ETC protein subunits, and cardiolipin. Accumulation of 8-hydroxy-2'-deoxyguanosine (8-OHdG) — a biomarker of oxidative mtDNA damage — has been documented in hepatic tissue of glucocorticoid-exposed animals at timepoints preceding elevation of serum liver enzymes.[17] Furthermore, ROS-mediated lipid peroxidation generates malondialdehyde (MDA) and 4-hydroxynonenal (4-HNE), which adduct and inactivate ETC proteins, establishing a self-amplifying cycle of bioenergetic collapse.

3.4 Disruption of Mitochondrial Biogenesis

Mitochondrial biogenesis — the process by which new mitochondria are assembled through coordinated expression of nuclear-encoded and mitochondrially encoded genes — is centrally regulated by the PGC-1α/NRF1/NRF2/TFAM axis. PGC-1α serves as a transcriptional coactivator that integrates signals from AMP-activated protein kinase (AMPK) and sirtuin-1 (SIRT1) to drive mitochondrial mass expansion in response to energetic demand. Exogenous glucocorticoids exert a dual, tissue-specific effect on this pathway.[18]

In skeletal muscle, prolonged GC exposure suppresses PGC-1α expression through GR-mediated transcriptional repression, reducing mitochondrial biogenesis and contributing to the characteristic myopathy of glucocorticoid excess. Paradoxically, some studies in hepatic tissue report transient PGC-1α upregulation with acute GC exposure, driving gluconeogenic gene transcription rather than mitochondrial expansion per se. Regardless, sustained pharmacological GC treatment results in a net reduction in mitochondrial density, mtDNA copy number per cell, and cellular respiratory capacity across multiple tissue types studied, including cardiac muscle.[19]

3.5 Impaired Mitophagy and Mitochondrial Quality Control

Mitophagy — the selective autophagic elimination of damaged or dysfunctional mitochondria — constitutes a critical quality control mechanism preventing the accumulation of ROS-generating defective organelles. The PINK1/Parkin pathway represents the best characterised mitophagy axis: damaged mitochondria with collapsed ΔΨm fail to import and process PINK1 (PTEN-induced kinase 1), allowing its accumulation on the OMM where it recruits and phosphorylates

Parkin, triggering polyubiquitination of OMM proteins and subsequent recognition by autophagy adaptors p62/SQSTM1 and NDP52.[20]

Glucocorticoid exposure has been shown to impair mitophagy through multiple mechanisms: suppression of autophagy gene expression (including Beclin-1 and ATG7), reduction of PINK1 protein stability, and impairment of lysosomal acidification necessary for cargo degradation. The net result is the pathological retention of dysfunctional, ROS-generating mitochondria within cells, compounding the bioenergetic deficit and amplifying oxidative injury. This failure of mitochondrial quality control has been specifically implicated in glucocorticoid-induced osteocyte dysfunction and hippocampal neuronal injury.[21]

4. Tissue-Specific Manifestations of Glucocorticoid-Induced Mitochondrial Dysfunction

4.1 Skeletal Muscle

Glucocorticoid myopathy is among the most prevalent adverse effects of chronic steroid therapy, affecting up to 60% of patients receiving long-term systemic GC treatment. Clinically manifest as proximal muscle weakness and wasting, its cellular basis involves not only GR-mediated transcriptional upregulation of the muscle atrophy ubiquitin E3 ligases MuRF1 and MAFbx (atrogin-1) but also early mitochondrial bioenergetic failure.[22] Electron microscopy of skeletal muscle biopsies from GC-treated patients and animal models reveals ultrastructural mitochondrial abnormalities — cristae disorganisation, matrix vacuolisation, and inter-myofibrillar mitochondrial loss — that precede the fibre atrophy detectable by standard histopathology.

At the biochemical level, mitochondrial oxygen consumption rates in skeletal muscle fibres from dexamethasone-treated rodents are significantly reduced within 3–5 days of treatment, with parallel declines in Complex I and IV activities and a fall in the mitochondrial ATP/ADP ratio. Reduced ATP availability impairs the actomyosin cross-bridge cycle and Ca2+ re-uptake by the sarcoplasmic reticulum, directly contributing to the clinical weakness phenotype.[23] Furthermore, mitochondria-derived ROS in GC-exposed muscle activate the nuclear factor kappa-B (NF-κB) pathway, upregulating the ubiquitin-proteasome system and accelerating protein catabolism — a mechanistic link between bioenergetic failure and the catabolic phenotype.

4.2 Liver

The liver, as the primary organ of glucocorticoid metabolism and gluconeogenesis, displays a complex mitochondrial response to exogenous GC administration. Hepatic glucocorticoid-induced steatosis — characterised by triglyceride accumulation in perivenular hepatocytes — results in part from mitochondrial dysfunction that impairs fatty acid beta-oxidation while diverting lipid substrates toward esterification.[24] This mirrors the mitochondrial lipotoxicity observed in non-alcoholic fatty liver disease, albeit with a distinct regulatory mechanism centred on GR/PGC-1α interaction.

Studies in primary rat hepatocytes and HepG2 cells exposed to dexamethasone demonstrate a sequential mitochondrial injury pattern: within 6 hours, ΔΨm begins to decline; by 12–24 hours, Complex I activity is measurably impaired and mitochondrial superoxide production increases; by 48–72 hours, cytochrome c release into the cytosol is detectable, initiating caspase-9/caspase-3 apoptotic cascades.[25] Throughout this timeline, serum alanine aminotransferase (ALT) and aspartate aminotransferase (AST) — the conventional markers of hepatocellular injury — may remain within normal limits, underscoring the temporal priority of mitochondrial dysfunction as a herald of hepatotoxicity.

4.3 Cardiac Muscle

The myocardium is exceptionally dependent on mitochondrial oxidative phosphorylation, deriving approximately 95% of its ATP from this pathway. Cardiomyocyte mitochondria are densely packed, occupying nearly 30% of cell volume, and any reduction in OXPHOS efficiency rapidly translates into contractile dysfunction. Chronic glucocorticoid excess — whether from endogenous hypercortisolism in Cushing syndrome or exogenous pharmacotherapy — is epidemiologically associated with left ventricular hypertrophy, diastolic dysfunction, and increased cardiovascular mortality.[26]

Experimental cardiomyocyte models treated with clinically relevant dexamethasone concentrations show early reductions in mitochondrial respiratory reserve capacity, the fraction of maximal respiratory capacity not utilised under basal conditions. Loss of respiratory reserve impairs the cardiomyocyte's ability to upregulate ATP production during increased haemodynamic demand, providing a mechanistic basis for stress-induced cardiac dysfunction. Glucocorticoid-induced cardiolipin peroxidation — quantifiable by mass spectrometric lipidomic analysis — has emerged as a particularly sensitive early indicator of GC-mediated cardiac mitochondrial injury.[27]

4.4 Central Nervous System

The hippocampus, a brain region particularly rich in glucocorticoid receptors, is vulnerable to GC-mediated neurotoxicity. Volume reductions in the hippocampus are consistently documented in patients with Cushing syndrome and in individuals receiving prolonged high-dose corticosteroid therapy, correlating with deficits in declarative memory and spatial navigation. At the cellular level, hippocampal neuronal mitochondria are early targets of glucocorticoid toxicity.[28]

Mitochondria in hippocampal neurons maintain a particularly critical role in dendritic ATP supply, Ca2+ buffering, and the regulation of synaptic plasticity through BDNF-TrkB signalling — all functions compromised by GC-induced bioenergetic failure. Cortisol-exposed hippocampal neurons exhibit decreased ΔΨm, reduced OXPHOS capacity, elevated mitochondrial superoxide, and increased susceptibility to mPTP opening within timeframes preceding any detectable synaptic loss or neuronal apoptosis.[29] These findings implicate mitochondrial bioenergetic vulnerability as an early mechanism translating glucocorticoid excess into the structural hippocampal changes observed clinically.

4.5 Adipose Tissue and Endocrine Pancreas

Glucocorticoid-induced metabolic syndrome involves impaired insulin sensitivity in both adipose tissue and the endocrine pancreas, with mitochondrial dysfunction playing a contributory role in both. In white adipose tissue, GCs promote mitochondrial fragmentation through upregulation of the fission GTPase DRP1 and downregulation of the fusion protein MFN2, creating a fragmented mitochondrial network with reduced OXPHOS capacity and increased lipogenesis.[30] In pancreatic beta cells, GC-induced mitochondrial dysfunction impairs the glucose-stimulated ATP surge that normally triggers insulin exocytosis, providing a mitochondrial explanation for the impaired first-phase insulin secretion characteristic of steroid diabetes.

5. Mitochondrial Dysfunction as an Early Biomarker: Translational Considerations

5.1 Circulating Mitochondrial DNA

Circulating cell-free mitochondrial DNA (cf-mtDNA) in plasma has emerged as a promising damage-associated molecular pattern (DAMP) and biomarker of mitochondrial injury. mtDNA lacks the protective histones of nuclear chromatin and is released into the circulation upon mitochondrial outer membrane permeabilisation — an event occurring before cell death. Several studies have documented elevated plasma cf-mtDNA levels in glucocorticoid-treated subjects, including patients receiving pulse methylprednisolone therapy, at timepoints where conventional organ function markers remain normal.[31]

Quantitative PCR-based measurement of specific mitochondrial gene loci (most commonly the mitochondrially encoded NADH dehydrogenase 1 gene, ND1) normalised against nuclear reference genes provides a reproducible cf-mtDNA index that correlates with the degree of mitochondrial injury. The clinical utility of serial cf-mtDNA monitoring in patients receiving long-term GC therapy for conditions such as systemic lupus erythematosus, inflammatory bowel disease, or vasculitis warrants prospective evaluation in well-designed cohort studies.

5.2 Cardiolipin Oxidation Products

Cardiolipin, a bis-phosphatidyl glycerol phospholipid exclusively localised to the IMM, is uniquely susceptible to peroxidation owing to its high content of linoleic acid side chains and proximity to ROS-generating sites within the ETC. Cardiolipin oxidation products, including acyl hydroperoxides and truncated species detectable by liquid chromatography-mass spectrometry (LC-MS), have been identified in biofluids and tissues as early markers of mitochondrial membrane injury.[32] In animal models of GC toxicity, cardiolipin oxidation is measurable in cardiac and hepatic tissues before morphological mitochondrial changes are evident by transmission electron microscopy, suggesting its potential utility as a liquid biopsy marker.

5.3 Urinary Bioenergetic Indices

The ratio of urinary organic acids reflecting the TCA cycle (citrate, isocitrate, alpha-ketoglutarate, succinate, fumarate, malate) to those reflecting cytoplasmic glycolysis (lactate, pyruvate) provides a non-invasive index of mitochondrial metabolic flux that can be assessed by gas chromatography-mass spectrometry or nuclear magnetic resonance (NMR) spectroscopy. Perturbations in this urinary organic acid pattern indicative of reduced mitochondrial engagement have been reported in glucocorticoid-treated subjects and animal models.[33] While analytical standardisation and reference intervals remain to be established for clinical application, the approach represents a promising non-invasive window into in vivo mitochondrial function.

5.4 Platelet and Peripheral Blood Mononuclear Cell Mitochondrial Function

As easily accessible cellular proxies for systemic mitochondrial bioenergetic status, platelets and peripheral blood mononuclear cells (PBMCs) have been evaluated for mitochondrial function in clinical research. The Seahorse XFe96 analyser and Oroboros O2k respirometer enable high-throughput assessment of oxygen consumption rates (OCR) and extracellular acidification rates (ECAR) in isolated platelets and PBMCs, providing a real-time cellular bioenergetic profile. Reduced basal OCR, spare respiratory capacity, and ATP-linked respiration in PBMCs have been reported in patients with pharmacological hypercortisolism and Cushing syndrome.[34] Translating this to routine clinical monitoring of GC-treated patients, while technically demanding, would offer a dynamic and early window into GC-induced cellular mitochondrial compromise.

6. Clinical Implications and Emerging Therapeutic Strategies

6.1 Risk Stratification and Monitoring Frameworks

Recognition of mitochondrial dysfunction as a preclinical harbinger of corticoid toxicity suggests that conventional monitoring frameworks — which rely on organ-function surrogates (serum electrolytes, glucose, liver enzymes, bone density scans, blood pressure) — may be insufficiently sensitive for early intervention. A mitochondria-centred monitoring strategy, incorporating cf-mtDNA quantification, PBMC bioenergetic profiling, or urinary organic acid panels, could identify patients on a trajectory of cellular injury before irreversible tissue damage ensues.[35]

Stratification by genetic risk may refine this approach: single nucleotide polymorphisms in mitochondrial biogenesis regulators (PGC-1α codon 482 Gly/Ser polymorphism), antioxidant enzyme genes (MnSOD Val16Ala), and mitochondrial haplogroups have been associated with differential susceptibility to oxidative stress and may predict inter-individual variability in GC-induced mitochondrial injury. Pharmacogenomic integration of such markers into GC prescribing decisions represents a forward-looking personalised medicine objective.

6.2 Mitochondria-Targeted Antioxidant Strategies

Given that mitochondrial ROS overproduction is a central mechanism of corticoid-induced cellular injury, mitochondria-targeted antioxidants have attracted significant investigative interest as GC adjuncts. MitoQ (mitoquinone mesylate), a coenzyme Q10 derivative conjugated to the triphenylphosphonium (TPP+) cation that accumulates several-hundred-fold within the mitochondrial matrix, has demonstrated protection against dexamethasone-induced mitochondrial dysfunction in skeletal muscle and hepatic cell models, reducing ETC impairment, normalising $\Delta\Psi m$, and attenuating apoptosis.[36]

SKQ1 (plastoquinonyl-decyltriphenylphosphonium), MitoTEMPO, and SS-31 (Szeto-Schiller peptide) represent additional mitochondria-targeted antioxidant platforms under preclinical investigation for GC mitochondrial toxicity. SS-31 is of particular interest given its selective binding to cardiolipin, thereby protecting the structural integrity of respiratory super complexes and preventing cytochrome c release, directly counteracting two cardinal mechanisms of GC-induced mitochondrial injury.[37]

6.3 Modulation of Mitochondrial Biogenesis

Pharmacological activation of the AMPK-PGC-1α axis offers a rational strategy to counteract GC-induced impairment of mitochondrial biogenesis. Metformin, a biguanide widely used in steroid diabetes management, activates AMPK through Complex I inhibition and mitochondrial uncoupling, thereby driving PGC-1α expression and mitochondrial biogenesis. Beyond glycaemic management, metformin's mitochondrial biogenesis-promoting effect may offer a mechanistic rationale for its observed attenuation of GC myopathy in clinical studies.[38]

Sirtuin-1 (SIRT1) activators, including resveratrol and synthetic agonists such as SRT2104, deacetylate and activate PGC-1α, promoting mitochondrial biogenesis and OXPHOS gene expression. In experimental models of GC-induced myopathy, resveratrol supplementation partially restores mitochondrial density, Complex I activity, and muscle force-generating capacity, suggesting additive protective benefit when combined with GC tapering strategies.[39]

6.4 Optimisation of Corticosteroid Dosing and Formulation

The circadian biology of glucocorticoid signalling has mitochondrial implications. Endogenous cortisol follows a pronounced diurnal rhythm peaking in the early morning hours, and mitochondrial OXPHOS capacity fluctuates in phase with this rhythm through clock gene-regulated expression of ETC subunits. Modified-release prednisolone formulations designed to mimic physiological diurnal cortisol profiles (evening administration with delayed release to produce an early morning peak) have shown reduced metabolic adverse effect profiles compared with conventional immediate-release preparations in controlled trials.[40] Whether this extends to reduced mitochondrial toxicity is a mechanistically plausible and clinically testable hypothesis.

7. Future Directions and Research Priorities

The field of glucocorticoid-induced mitochondrial toxicity is at an inflection point, transitioning from mechanistic characterisation in cell and animal models to translational clinical application. Several key research priorities merit emphasis. First, prospective longitudinal clinical studies in well-defined patient cohorts — such as newly commenced prednisolone for rheumatoid arthritis or pulse methylprednisolone for multiple sclerosis relapses — are needed to validate mitochondrial biomarkers against hard clinical endpoints including myopathy severity, metabolic complications, and cardiovascular events.

Second, advanced single-cell and spatial metabolomics technologies offer the prospect of mapping mitochondrial bioenergetic heterogeneity across cell populations within tissues, providing granular insight into which cell types and metabolic niches are most vulnerable to GC-induced mitochondrial injury at any given dose and time point. Third, the development of standardised, clinically applicable assays for PBMC bioenergetic profiling or cf-mtDNA quantification, analogous to the standardisation achieved for troponin in acute myocardial injury or NT-proBNP in heart failure, would be a transformative advance enabling routine incorporation of mitochondrial surveillance into GC management protocols.

Fourth, the intersection of glucocorticoid pharmacology with mitochondrial genetics — including the role of mitochondrial haplogroups and somatic mtDNA mutation burden in modifying susceptibility to GC-induced bioenergetic failure — represents an understudied but potentially clinically significant frontier. Finally, the evaluation of combination regimens pairing low-dose GC with mitochondria-targeted interventions (MitoQ, SS-31, AMPK activators) in phase II randomised trials is a therapeutically compelling priority that could fundamentally alter the risk-benefit calculus of corticosteroid therapy.

Conclusion

The mitochondrion occupies a privileged position at the intersection of glucocorticoid pharmacology, cellular bioenergetics, and organ toxicity. The totality of current evidence establishes that exogenous corticosteroids induce a temporally early, mechanistically diverse, and functionally consequential impairment of mitochondrial function — encompassing disruption of oxidative phosphorylation, dissipation of membrane potential, amplification of reactive oxygen species, suppression of biogenesis, and failure of mitophagy-mediated quality control. These events unfold across multiple tissue types that are major targets of corticoid adverse effects, including skeletal muscle, liver, heart, and hippocampus, and they precede the clinical and biochemical markers by which toxicity is conventionally identified.

This temporal priority renders mitochondrial dysfunction not a consequence but a catalyst of corticosteroid toxicity — an early cellular marker with both mechanistic primacy and biomarker potential. The development of sensitive, specific, and clinically applicable mitochondrial biomarkers, coupled with mitochondria-protective pharmacological co-interventions, represents a scientifically grounded and therapeutically urgent agenda. As glucocorticoid therapy continues to be prescribed across an enormous clinical breadth, a mitochondria-centred approach to early toxicity detection and mitigation holds genuine promise for improving the safety profile of one of medicine's most powerful and enduring pharmacological tools.

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DIMETHYL ETHER IN THE ENERGY TRANSITION: A SYSTEMS PERSPECTIVE ON DEPLOYMENT, INFRASTRUCTURE, AND POLICY

Kuldeep Singh and Raman Singh*
Department of Applied Chemistry,
Amity University Madhya Pradesh, Gwalior, Madhya Pradesh, India
*Corresponding author E-mail: bhadauria.raman@gmail.com

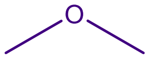
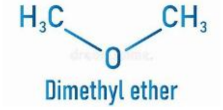
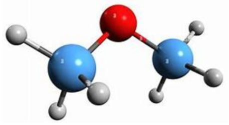
Abstract

The physicochemical and combustion properties of dimethyl ether (DME) have been extensively characterized in the peer-reviewed literature. This chapter moves beyond those fundamentals to examine what deployment at scale would actually require: how DME fits within existing and planned energy infrastructure; what a hydrogen-economy transition pathway looks like when DME serves as an intermediate energy carrier; how national and regional regulatory frameworks either enable or constrain DME adoption; and how life cycle greenhouse gas accounting should be applied consistently across competing feedstock routes. Drawing on techno-economic analyses, life cycle assessments, infrastructure case studies, and policy reviews, this chapter argues that DME's transition from a technically validated fuel to a widely deployed energy commodity depends less on further laboratory work and more on coordinated decisions at the infrastructure, regulatory, and investment levels.

Keywords: Dimethyl Ether, Energy Transition, Alternate Fuel, Energy Carrier.

Introduction

The case for dimethyl ether as an alternative fuel has been rigorously made on technical grounds. A comprehensive review of the literature covering cetane characteristics, soot-free combustion, spray dynamics, blending strategies, fuel cell integration, and gas turbine performance confirms that dimethyl ether (DME) satisfies the core combustion engineering requirements for a modern energy carrier (Sharma, 2026). However, the studies do not address the equally important question of how a fuel with these properties is transported from a synthesis reactor to an end user's vehicle or stove, as it lies outside the domain of combustion science.

Dimethyl Ether-Structural Representation		
 Di Methyl Ether		 **3D Structure**

This chapter addresses this gap. The systems-level challenge of deploying DME involves at least four interlocking problems that are qualitatively different from the engineering questions resolved in laboratory and engine test-bench studies. First, there is an infrastructure problem:

DME must be stored, transported, and dispensed through supply chains designed for other fuels that carry substantial sunk costs. Second, there is a life cycle accounting problem: the environmental benefit of DME relative to diesel, liquefied petroleum gas (LPG), or natural gas is highly sensitive to the source of carbon in the DME, the method of synthesis energy generation, and the system boundary chosen for the comparison. Third, there is a regulatory and standardization problem: without harmonized fuel quality standards, safety classifications, and vehicle-type approvals, no investor will commit to the large fixed assets required for a national DME supply chain. Fourth, there is a political-economy problem: incumbent fuel industries have lobbying power, and new fuels must navigate that landscape as well as the technical landscape.

The chapter is structured to address each of these problems in turn and concludes with a discussion of the most promising near-term deployment pathways—the contexts in which the infrastructure, economic, and regulatory conditions are already most favorable for DME introduction.

Infrastructure Realities: Storage, Distribution, and Refueling

Leveraging existing LPG infrastructure

DME's vapor pressure of DME at ambient temperature is approximately 0.5 MPa, which is in the same pressure range as LPG (predominantly propane and butane). This physical similarity is arguably the greatest infrastructure asset of the DME. LPG infrastructure—including pressurized road tankers, cylindrical storage vessels, dispensing pumps, and regulatory frameworks for handling flammable compressed gases—exists in a mature form across much of Asia, Europe, and the Americas. Repurposing this infrastructure for DME requires significant but not fundamental modifications, such as material compatibility assessments (DME attacks certain elastomers and polymers that LPG does not (Qui *et al.* , 2022; Wang & Wang, 2008)), recalibration of metering equipment to account for DME's different density and vapor pressure curve, and replacement of any seals or gaskets found to be incompatible.

By the mid-2000s, the country had established a substantial coal-to-DME production base and was distributing DME–LPG blends through existing cylinder networks (Larson & Yang, 2004; Matsuda, 2005). The blend proportions were constrained not primarily by combustion performance—DME performs well in LPG appliances at moderate blend fractions—but by the physical compatibility of existing cylinder valve seats and the settling behavior of unmixed DME–LPG blends in cylinders, which can lead to variable composition at the point of use. These are engineering problems with known solutions: valve redesign, additive mixing, and cylinder orientation guidance. They are not barriers in principle, but they do require coordinated action across appliance manufacturers, cylinder owners, and gas distributors, a coordination challenge that is fundamentally institutional rather than technical (Figure 1).

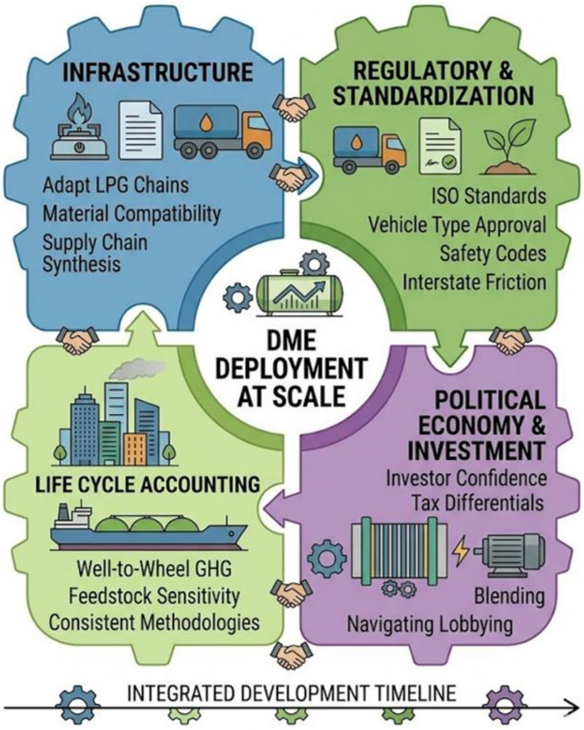


Figure 1: The Interlocking Dimensions of DME Deployment: A Systems Framework

Vehicle Refueling Infrastructure

For transportation applications, the refueling infrastructure question is more demanding than that for stationary or domestic use. Vehicles must be refueled rapidly (within minutes), reliably, and at locations distributed across road networks. An analogous challenge has been faced and partially overcome for compressed natural gas (CNG) and LPG vehicles in several markets, and the lessons from these transitions are directly applicable to DME.

Key requirements for a DME vehicle refueling station include a bulk storage vessel (likely a horizontal cylindrical tank at 0.7–1.0 MPa), a dispensing pump compatible with DME’s low viscosity and high vapor pressure, and a nozzle and coupling system that prevents vapor release during disconnection. The low viscosity of DME, which is a lubrication challenge for vehicle injection systems (Qui *et al.* , 2022; Wang & Wang, 2008), is advantageous at the dispensing interface, as it reduces the pressure drop through the dispensing lines and permits rapid flow rates with modest pump power. Vapor recovery at the nozzle, which is already a standard practice at many CNG and LPG stations, is also applicable to DME.

Fleet-based deployment models, in which vehicles return to a central depot for refueling, substantially reduce the infrastructure investment required in the early stages of the DME transition. Municipal bus fleets, refuse collection vehicles, agricultural tractors, and short-haul freight vehicles are candidates for this model. Their operators are familiar with alternative fuel infrastructure, often have sustainability mandates, and operate predictable duty cycles that simplify onsite storage sizing. The Global DME Forum and several national pilot programs have identified these fleet segments as natural entry points for DME in transportation (Global DME Forum & DME, n.d.).

Supply Chain Economics

The economics of a DME supply chain are shaped by three cost components: production cost (dominated by feedstock and synthesis energy), transport and storage cost (driven by the need for pressure vessels and the relatively low energy density of DME per unit volume compared to diesel), and the capital cost of adapting end-use equipment. Table 7.1 illustrates how these components compare across various deployment scales and feedstock scenarios.

Table 1: Indicative supply chain economics and GHG intensity for the three DME production pathways. The values are illustrative ranges drawn from the techno-economic literature (Semelsberger *et al.*, 2006; Trippe *et al.*, 2013; Yadav *et al.*, 2025).

Supply chain element	Coal-to-DME (large scale, China)	Natural Gas-to-DME (Midscale, global)	Bio-DME (small-scale biomass)
Production cost (USD/GJ)	6–8	8–12	14–22
Transport and storage premium over diesel	moderate (+15–25%)	moderate (+15–25%)	similar
Infrastructure adaptation cost	high (purpose-built)	medium	low (modular)
GHG intensity (g CO_2e/MJ, well-to-wheel)	180–220	90–130	10–40
Commercial readiness	established (China)	near-term	pilot stage

Abbreviations: DME-dimethyl ether.

The table highlights a tension that runs through much of the DME policy debate: the most economically mature pathway (coal-to-DME) carries the highest carbon intensity, whereas the lowest-carbon pathway (bio-DME) remains expensive and commercially unproven at scale. This tension is not unique to DME; it equally applies to hydrogen, synthetic methane, and biomass-derived liquid fuels. However, it is important to frame this honestly when evaluating policy support mechanisms.

Life Cycle Greenhouse Gas Accounting: Method Matters

System Boundary Choices and Their Consequences

The claim that DME is a "low-carbon" fuel requires careful consideration. At the tailpipe, DME combustion produces lower CO_2 per unit of energy delivered than diesel because of DME's lower carbon-to-hydrogen ratio. However, the tailpipe is only part of the story, and in the case of fossil-feedstock DME, it is a relatively small part. The energy-intensive synthesis of DME from coal or natural gas, methane venting and flaring associated with coal mine gas, and CO_2 co-produced in the water-gas shift reactions integral to syngas chemistry all contribute to upstream emissions that can, in unfavorable scenarios, make fossil DME worse than the diesel it displaces on a well-to-wheel basis (Trippe *et al.* , 2013).

This sensitivity to system boundary choice is not a reason to dismiss DME as a climate policy instrument; rather, it is a reason to be rigorous about the conditions under which public support or regulatory preference is appropriate. The life cycle framework established in the Renewable Energy Directive in the European Union and its equivalents in other jurisdictions provides a starting point, but DME presents specific accounting challenges: the allocation of emissions between DME and coproducts (methanol and LPG fractions) in direct synthesis, the treatment of biogenic carbon in bio-DME, and the counterfactual use of the biomass feedstock, all of which require explicit methodological choices.

The Bio-DME and eCO_2-DME Pathways

Bio-DME, produced from lignocellulosic biomass, agricultural residues, or municipal solid waste via gasification and synthesis, represents the pathway with the greatest potential for deep decarbonization. Life cycle assessments of bio-DME production from waste biomass in India have estimated well-to-wheel GHG emissions below 20 g CO_2e/MJ, compared to approximately 90 g CO_2e/MJ for fossil diesel (Gröve *et al.* , 2018). However, the uncertainty range around these estimates is substantial, reflecting variability in feedstock supply chain emissions, synthesis plant efficiency, and the assumptions made about land-use change.

An emerging variant of the bio-DME concept combines CO_2 captured from industrial point sources with green hydrogen (produced by electrolysis using renewable electricity) to synthesize methanol, which is then dehydrated to form DME. This eCO_2-DME pathway—sometimes described as Power-to-DME or e-DME—offers the prospect of near-zero or even negative life cycle emissions if the electricity used for electrolysis is genuinely generated from renewable sources. Techno-economic assessments of Power-to-DME in the Chinese context, which has both large CO_2 point sources and rapidly falling renewable electricity costs, have shown that the pathway is approaching economic viability at the scale of a regional pilot project (Tomatis *et al.* , 2019). The key cost driver is the electrolyzer capital cost, which has fallen by more than 60% since 2015 and is projected to continue to decline. DME becomes competitive with fossil diesel at green hydrogen costs below approximately 2–2.5 USD/kg.

Integrating DME into Carbon Accounting Frameworks

For DME to receive policy support—blending mandates, fuel tax exemptions, and carbon credits—that would accelerate its deployment, it must be incorporated into national and international carbon accounting frameworks in a technically coherent manner. This requires standard methodologies for attributing the GHG intensity of DME from different production routes, analogous to the pathway-specific emission factors already established for biodiesel, bioethanol, and biomethane in EU and U.S. renewable fuel regulations. The ISO fuel quality standards for DME, finalized in 2015 (Oguma, 2017), provide a foundation for quality specifications, but they do not address GHG intensity. Developing a parallel set of DME life cycle assessment standards, potentially under ISO TC 28 (Petroleum and related products, fuels, and lubricants) or the IEA Bioenergy Task framework, is a priority for enabling policy integration.

Regulatory and Policy Environment

Fuel Quality Standards and Vehicle Type Approval

Fuel standardization is not merely a technical housekeeping matter; it is a precondition for market development. Without a harmonized DME fuel specification, vehicle manufacturers cannot certify engine warranties for DME operation, fleet operators cannot obtain insurance, and regulators cannot establish emissions compliance thresholds. The five ISO standards for DME fuel quality published in 2015 represented a significant milestone; however, their geographic uptake has been uneven (Oguma, 2017). The standards are formally recognized in Japan and South Korea, which have the most developed DME vehicle programs, but have not been adopted into the EU or U.S. regulatory frameworks.

Vehicle type approval for DME-fueled vehicles, the process by which a vehicle design is certified as meeting safety and emissions requirements, has been completed for commercial vehicles in Japan and for a limited range of passenger vehicles in South Korea. In the EU, DME falls outside the standard fuel definitions used in the Euro emissions framework, requiring manufacturers to seek individual type approval, which is expensive and commercially uncertain. By updating current laws to allow cars to run on a mix of LPG and DME fuel, Europe can quickly and cheaply introduce this cleaner fuel to the public without needing to invent entirely new safety rules.

Safety Regulation and Transport Classification

DME is classified as a transport classification of DME under the UN Model Regulations and the ADR (European Agreement concerning the International Carriage of Dangerous Goods by Road), the same class as LPG. This classification is technically appropriate and indicates that DME road transport is governed by existing regulations designed for LPG tankers and cylinders. No fundamental changes to the transport safety framework are required. However, because DME is newer, some national implementations of the ADR and equivalent regulations include specific provisos or exclude DME from general LPG provisions, creating administrative friction that adds cost without enhancing safety. A systematic audit of national derogations and their technical justifications, with a view to harmonizing them at the international level, would reduce compliance costs for DME distributors operating across borders.

Policy Mechanisms that have worked for Analogous Fuels

The history of alternative fuel deployment offers several relevant examples. Natural-gas vehicles achieved commercial scale in Italy and Pakistan through a combination of favorable fuel tax differentials and government-backed vehicle conversion programs in both countries. LPG autogas achieved high market penetration in the Netherlands and Poland through a combination of tax advantages and infrastructure requirements. Compressed biomethane achieved strong growth in Sweden through green gas certificate schemes that provided revenue certainty to gas injection operators.

The common elements across successful alternative fuel transitions are a price signal that makes the alternative fuel economically attractive to end users over the medium term, a mechanism for internalizing the infrastructure investment risk that no single private actor will bear alone, and a regulatory framework that is stable enough to support long-lived capital commitments. In the case of DME, a carbon price that correctly prices the life cycle GHG benefits of bio-DME or eCO_2-DME relative to fossil diesel would be the most efficient policy instrument. In the absence of an adequate carbon price—which remains the situation in most jurisdictions—targeted fuel tax differentiation, blending mandates, and accelerated depreciation for DME infrastructure investment are the second-best instruments with demonstrated effectiveness (Table 2) (Figure 2).

Table 2: Policy instruments applicable to DME deployment with analogous precedents from other alternative fuel transitions

Policy instrument	Mechanism	Relevant DME context	Precedent
Fuel tax differentiation	lower excise duty on DME than diesel	passenger and freight DME vehicles	LPG autogas (Netherlands, Poland)
Blending mandate	require X% DME in LPG supply	domestic cooking, heating	biodiesel mandates (EU, India)
Carbon credits/LCFS	award credits per tonne of CO_2e avoided	bio-DME, eCO_2-DME	LCFS California, EU ETS
Infrastructure grants	capital support for refueling stations	fleet operators, depots	CNG station programs (Italy, India)
Type approval simplification	Extend LPG approval to cover DME blends.	vehicle manufacturers	CNG vehicle approvals (EU)
Green procurement mandates	Government fleets must consider DME.	early demand signal	various EV mandates

Abbreviations: CNG-compressed natural gas, DME-dimethyl ether, LPG-liquefied petroleum gas.

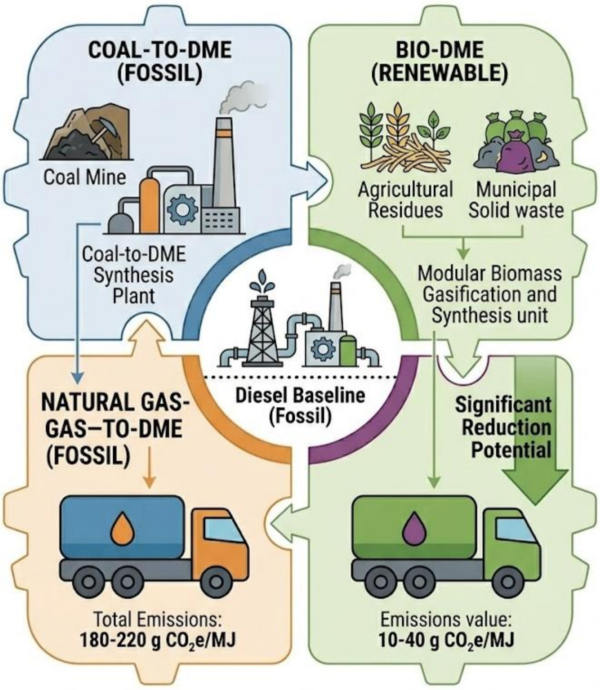


Figure 2: Well to Wheel GHG Intensity of DME Across primary feedstock Pathways

DME as a Hydrogen Energy Carrier: Bridging Transition

Much of the long-term decarbonization discourse focuses on molecular hydrogen (H_2) as the ultimate clean energy carrier for the future. The practical challenge of hydrogen is that it is a gas at ambient conditions with a very low volumetric energy density, requiring either high-pressure compression (700 bars for automotive applications) or cryogenic liquefaction (−253 °C) for storage and transport, both of which involve significant energy penalties and infrastructure costs. Chemical hydrogen carriers, which are molecules that can store and release hydrogen through reversible chemical reactions, have attracted growing interest as a more practical route to a hydrogen economy.

DME is an attractive chemical hydrogen carrier for several reasons. It can be produced from green hydrogen (via CO_2 hydrogenation to methanol and dehydration) and stored and transported as a liquid under modest pressure using the existing LPG infrastructure. It can then release hydrogen through steam reforming at 250–300 °C, a reaction that is thermodynamically feasible at temperatures accessible from waste heat in industrial processes or fuel cell exhaust streams (Sharma, 2026). The hydrogen-to-total-weight ratio of DME (approximately 13.0 wt% H) is comparable to that of methanol (12.5 wt%) and superior to that of methylcyclohexane (6.2 wt%) or liquid organic hydrogen carriers such as dibenzyltoluene (6.2 wt%), making it competitive within the chemical carrier class.

The concept of a distributed hydrogen supply chain based on DME, where centralized renewable electricity-driven electrolyzers produce green hydrogen, which is combined with captured CO_2 to make DME, shipped as a pressurized liquid via road or sea, and then reformed on-site or onboard to hydrogen for fuel cell use, has been assessed for several regional contexts. In island economies and remote industrial sites where pipelines are impractical, DME's combination of energy density, handleability, and reformability of DME makes it more practical than compressed or liquefied hydrogen (Tomatis *et al.* , 2019). The onboard DME steam reformer coupled to a polymer electrolyte membrane fuel cell represents a specific realization of this concept that has been validated at the laboratory scale and is approaching vehicle integration (Zhang *et al.* , 2018).

Priority Deployment Contexts: Where DME Should Be Introduced First

Given the preceding research, it is feasible to identify the situations in which infrastructure, economic, and regulatory conditions are most conducive to near-term DME implementation. These are not the circumstances in which DME's technical performance is most impressive—that has already been established—but rather those in which the system-level prerequisites for commercial implementation are closest to being met.

Domestic Cooking in LPG-Dependent Markets

In countries where LPG is the primary domestic cooking fuel, including India, Indonesia, and much of sub-Saharan Africa, DME blending offers a route to emissions reduction and energy security without requiring consumers to change their appliances or behavior. At blend fractions below approximately 20% DME by mass, existing LPG stoves can operate without modification. The Indian Government's Pradhan Mantri Ujjwala Yojana program, which has distributed hundreds of millions of LPG cylinders, provides an existing distribution network into which DME can be introduced as a blending component. Domestic DME production from agricultural residues and municipal solid waste simultaneously addresses cooking fuel import dependence and waste management challenges (Gröve *et al.* , 2018; Panigrahy & Mishra, 2018).

Urban Bus and Fleet Vehicle Operations

Municipal and intercity bus fleets represent the transport segment in which DME deployment conditions are most favorable. Buses are refueled at central depots, enabling the DME storage infrastructure to be concentrated at a small number of sites rather than being distributed across a public refueling network. Bus operators are experienced in managing alternative fuel infrastructure (many already operate CNG or electric buses), and many are subject to sustainability and air quality mandates from the municipal authorities. The near-zero particulate emissions of DME combustion (Sharma, 2026) are particularly relevant in urban air quality contexts, where diesel particulate matter (DPM) is a major public health concern. Several Asian cities, including Seoul and Osaka, have operated DME bus pilot programs with encouraging results for both emissions performance and operational costs.

Distributed Power Generation in Energy-Poor Regions

In regions with weak grid infrastructure, such as rural South and Southeast Asia, much of sub-Saharan Africa, and numerous island systems, distributed power generation using small diesel generators is common. The fuel supply chains for these generators are expensive, unreliable, and highly carbon intensive. DME, produced locally from biomass or waste, could substitute diesel in modified generator sets while substantially reducing both GHG emissions and local air pollution. The modular nature of biomass gasification and DME synthesis technology makes this scenario technically feasible at the village or small-town scale, provided that appropriate financing mechanisms and technical support infrastructure are in place.

Outstanding Knowledge Gaps and Research Priorities

The analysis presented in this chapter also reveals areas where the evidence base is weaker and where further research is needed before confident policy or investment recommendations can be made.

Durability of DME-Adapted Injection Hardware in Real Fleet Conditions

While laboratory studies have established the failure modes of conventional diesel injectors when exposed to DME (Qui *et al.* , 2022; Wang & Wang, 2008), and purpose-designed DME injectors have been demonstrated, long-term durability data from real fleets operating over multiple maintenance cycles are sparse. The availability of such data is a prerequisite for vehicle manufacturers to extend engine warranties to DME operations.

Integrated Well-To-Wheel Accounting for Blended Fuels

Most life cycle analyses treat neat DME; GHG accounting for DME–LPG or DME–diesel blends, where both components may have different production provenance and life cycle intensities, has not been standardized. Blended fuels are likely to be the dominant commercial form of DME in the early deployment phase, creating a practical gap.

Social and Behavioral Dimensions of Domestic DME Adoption

Consumer acceptance of DME–LPG blends in domestic cooking markets has received limited systematic attention to date. The transition experience in China suggests that cylinder labeling, appliance compatibility information, and the perceived similarity of DME flames to LPG flames are determinants of consumer acceptance. Rigorous social science research on these factors in target markets—India, Indonesia, and Nigeria—would support the design of more effective introduction programs.

Techno-Economic Optimization of the eCO_2-DME Pathway at Scale

Power-to-DME via CO_2 hydrogenation is technically validated but economically marginal in most scenarios. Systematic analysis of cost reduction pathways, such as electrolyzer learning rates, CO_2 capture cost trajectories, DME synthesis catalyst lifetimes, and optimal plant scale, would enable more confident projections of when and where this pathway becomes commercially viable without subsidies.

Conclusion

Dimethyl ether is a fuel with well-established technical merits. The combustion, emissions, spray, and fuel cell performance characteristics of DME have been documented in detail in a substantial body of peer-reviewed literature and reviewed comprehensively by Sharma (2026). This chapter argues that translating these technical merits into commercial deployment is a systems-level challenge that requires simultaneous progress in infrastructure, life cycle accounting, regulatory harmonization, and policy design.

None of the identified barriers are insurmountable. The LPG infrastructure can be adapted. ISO fuel quality standards exist and can be extended to GHG intensity accounting in the future. The regulatory frameworks for LPG vehicles provide a template for DME type approval. Policy instruments with proven track records for analogous fuels are also available. The economics of bio-DME and eCO_2-DME are improving as the costs of renewable energy decrease. The question is not whether DME can be commercially deployed, but whether the institutional coordination required to deploy it at scale will occur quickly enough to contribute meaningfully to decarbonization targets in the 2030–2040 timeframe.

The most promising near-term strategy is a sequenced deployment approach: beginning with LPG blending in domestic cooking markets in Asia, where infrastructure overlap is greatest and public health co-benefits are largest; scaling fleet vehicle programs in urban environments where air quality regulation creates a pull for near-zero particulate fuels; and using the resulting experience base and supply chain maturation to reduce the cost of the green DME pathway over the course of the decade. Concurrently, investment in eCO_2-DME pilot plants and onboard DME reformer development for fuel cell vehicles would position DME to play a role in the hydrogen carrier economy in the 2040s and beyond.

The energy transition is not a single technology problem but a portfolio management problem, in which diverse fuels and vectors serve different end uses with different lead times for deployment. DME’s portfolio role—as a clean near-term substitute for LPG and diesel in markets where its physical properties and production routes are already advantageous, and as a bridge toward a hydrogen economy in the longer term—is both technically coherent and practically achievable.

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CRISPR-CAS9:
APPLICATIONS, ETHICAL ISSUES, AND FUTURE PROSPECTS

Josna Victoria K Johnson

Department of Zoology,
Vimala College (Autonomous), Thrissur, Kerala
Email id: josnajohns46@gmail.com

Abstract

CRISPR-Cas9 is a powerful genome editing technology derived from a natural bacterial immune system. It allows precise modification of DNA by using a guide RNA to direct the Cas9 enzyme to a specific genetic sequence, where it makes a targeted cut. The cell's natural repair mechanisms then enable the addition, removal, or correction of genes. Due to its simplicity, accuracy, and efficiency, CRISPR-Cas9 has become a revolutionary tool in genetics and biotechnology. It is widely used in research, medicine, and genetic engineering, particularly for studying gene function and developing potential treatments for genetic disorders.

Keywords: CRISPR Cas9, Gene Editing, Cancer Theraphy, Mutations.

Overview of CRISPR Cas9

CRISPR-Cas9 is a genome editing tool that has created great interest in the scientific community because it is faster, cheaper, more accurate, and more efficient than earlier methods of DNA editing (Hsu *et al.* ,2014). It is a powerful technology that allows scientists to modify the genome by adding, removing, or altering specific DNA sequences (Yin *et al.* ,2014). It is currently one of the simplest, most versatile, and precise methods of genetic manipulation and has wide applications in biomedical research and medicine. CRISPR-Cas9 was developed from a natural immune defense system found in bacteria and archaea. When viruses infect bacteria, the bacteria capture small fragments of viral DNA and store them in their genome in specific patterns called CRISPR arrays (Liang *et al.* ,2015). These arrays act as a genetic memory, helping bacteria recognize the same virus if it attacks again. During reinfection, the bacteria produce RNA molecules from these arrays, which guide a protein to the matching viral DNA. This protein then cuts and destroys the viral DNA, protecting the bacteria.

The CRISPR-Cas9 system mainly consists of two components: the Cas9 enzyme and the guide RNA (gRNA). Cas9 acts as molecular scissors that cut both strands of DNA at a specific location. The guide RNA is a short, synthetic RNA sequence of about 20 bases designed to match a target DNA sequence. It has a scaffold region that binds to Cas9 and a guide sequence that directs Cas9 to the correct position in the genome (Schwank *et al.* ,2013). The guide RNA binds to a complementary DNA sequence, ensuring that Cas9 cuts at the intended site. In addition, a short DNA sequence known as PAM (Protospacer Adjacent Motif) is required for Cas9 to recognize and bind to the target region.Once the guide RNA directs Cas9 to the target DNA, Cas9 makes a double-stranded break in the DNA. The cell then detects this as damage and activates its natural repair mechanisms. During this repair process, genes can be disrupted, deleted, or replaced. If the cell repairs the break without a template, small insertions or deletions may occur, which can inactivate the gene. If a repair template is provided, precise modifications or corrections can be made to the DNA sequence (Redman *et al.* ,2016).

CRISPR-Cas9 is widely used in scientific research because it allows the rapid development of cell and animal models, helps in studying gene functions, and supports genome analysis. It is considered a major breakthrough in biotechnology as it enables scientists to correct genetic errors, regulate gene activity, and modify organisms in a fast, cost-effective, and efficient way.

Applications of CRISPR Cas 9

Medicine

CRISPR-Cas9 technology has become a transformative tool in modern medicine due to its precision and versatility in editing genetic material. One of its primary applications is in understanding gene function and disease mechanisms. By selectively modifying or “knocking out” genes in human cells or model organisms, researchers can identify the roles of specific genes in health and disease. For example, genome-wide CRISPR screening has enabled scientists to identify genes essential for cancer cell survival, providing valuable insights into potential therapeutic targets. Another major application of CRISPR-Cas9 is in gene therapy. It offers the ability to directly correct disease-causing mutations within the DNA of patient cells. This approach has shown promise in treating genetic disorders such as β-thalassemia, where mutations have been successfully corrected in patient-derived stem cells. Such advances highlight the potential of CRISPR to provide long-term or even permanent cures for inherited diseases. In oncology, CRISPR-Cas9 is being explored to improve cancer treatment strategies. It can be used to disrupt genes that contribute to tumor growth or chemotherapy resistance, thereby enhancing the effectiveness of existing treatments. Additionally, CRISPR-based approaches are being investigated to engineer immune cells, making them more effective at recognizing and destroying cancer cells. CRISPR technology also plays an important role in diagnostics. Furthermore, CRISPR facilitates research into both single-gene and complex disorders by allowing scientists to test whether specific genetic variants cause disease (Ansori *et al.* ,2023). This is done by introducing suspected mutations into healthy cells or correcting them in diseased cells and observing the resulting effects. Overall, CRISPR-Cas9 has wide-ranging applications in medicine, including disease modeling, gene therapy, cancer treatment, and diagnostics. As the technology continues to advance, it holds great promise for improving patient outcomes and driving the development of personalized medicine.

Agriculture

CRISPR-Cas9 is revolutionizing agriculture and biotechnology by enabling precise, rapid, and cost-effective gene editing to improve crop yield, quality, and resilience. Its key applications include enhancing resistance to pests, diseases, and environmental stresses such as drought, salinity, and heat, along with improving nutritional value and promoting agricultural sustainability. Abiotic stress tolerance is achieved by developing crops such as drought-tolerant soybean, salt-tolerant rice, and heat-resistant varieties, ensuring food security under changing climate conditions. Biotic stress resistance is also improved by engineering crops resistant to pathogens and pests, including virus-resistant potatoes and cucumber, and powdery mildew-resistant wheat and tomatoes. CRISPR is further used to enhance nutritional quality and food properties, producing crops such as high-amylose or high-protein wheat, low-gluten wheat, improved oil compositions, and fruits with extended shelf life. It also supports accelerated domestication and crop improvement by editing key traits in wild plants like groundcherry and reducing anti-nutritional compounds in crops such as cassava. Herbicide resistance has been developed in crops like oilseed rape, aiding effective weed management. Characterized by high precision, specificity, and programmability, CRISPR-Cas enables targeted modification of plant DNA without introducing foreign genes, often resulting in changes similar to natural variations and subject to fewer regulatory restrictions. It is a powerful tool for developing climate-resilient, high-yielding, and sustainable crops, helping to address global challenges in food security and environmental sustainability.

Biomedical Research

CRISPR-Cas9 is a transformative tool in biomedical research, enabling precise gene editing for developing gene therapies, modeling diseases, and conducting high-throughput genetic screens. Its key biomedical applications include the treatment of genetic disorders, where it allows deletion, insertion, or correction of deleterious mutations responsible for hereditary diseases, with notable examples such as β-thalassemia and sickle cell disease, including the FDA-approved therapy CASGEVY™. In cancer immunotherapy, CRISPR-Cas9 is used in CAR T-cell therapies to knock out inhibitory genes such as PD-1 or to engineer universal immune cells with improved tumor-targeting ability (Bharti and Mudge, 2025). It also plays an important role in infectious disease management by targeting and degrading viral genomes, including HIV-1 in human cell models and HPV-associated cancers. In addition, CRISPR is widely used in drug target discovery and disease modeling by creating accurate experimental models in animals and enabling high-throughput genetic screens to identify potential therapeutic targets (Singh *et al.* ,2024). Furthermore, in vivo gene therapy approaches involve direct delivery of CRISPR components into patients to treat diseases such as Leber's congenital amaurosis 10, a rare form of inherited blindness, by editing genes within the body.

Ethical Issues

The ethical issues surrounding CRISPR-Cas9 are complex and involve human health, social justice, and environmental concerns. While the technology has great potential to treat genetic diseases, its ability to permanently change genomes raises serious moral questions. One of the most controversial uses is germline editing, which involves modifying embryos, eggs, or sperm. These changes are heritable, meaning they are passed on to future generations. This raises concerns about unknown long-term effects that could permanently affect the human gene pool. A major issue is informed consent because future generations cannot agree to the genetic changes they inherit. Another concern is the difference between therapy and enhancement. Using CRISPR to cure diseases is generally accepted, but using it to improve traits like intelligence, height, or appearance is controversial (Chin, 2015). Critics fear this could lead to eugenics or "designer babies".

CRISPR technology is not always fully accurate, which leads to safety concerns. Off-target effects occur when DNA is cut at the wrong place, which may cause harmful mutations or diseases like cancer. On-target effects happen when unwanted changes occur at the correct target site. Mosaicism can also occur when only some cells in an embryo are edited, leading to unpredictable outcomes. In addition, long-term effects are still unknown because the technology is relatively new. CRISPR treatments are expensive, which may increase inequality. If only wealthy people can access genetic enhancements or treatments, it could create a gap between different social groups and lead to a "genetic divide" in society. Some disability rights groups also worry that removing certain genetic conditions could increase discrimination against people living with those conditions.

Environmental concerns also exist, especially in agriculture and ecosystems. Gene drives can spread traits through entire species, such as eliminating malaria-carrying mosquitoes, but this may disturb ecological balance (Liao *et al.* ,2015). There is also a risk that modified genes from crops could spread to wild plants, creating invasive species or reducing biodiversity. In addition, issues related to governance and ownership arise because companies and institutions compete for patents over CRISPR technology, raising concerns that profit may be prioritized over public good. There is also a risk of misuse, as CRISPR could potentially be used for bioterrorism or creating harmful biological agents.

Most concerns arise from germline genome editing, which affects future generations. It raises issues such as unintended genetic changes, lack of consent, and ethical worries about eugenics. In general, risks include off-target effects, where changes occur in the wrong part of DNA, and on-target effects, where unwanted changes occur at the correct site. These changes may harm health or sometimes have no noticeable effect.

Future Prospects

The future prospects of CRISPR-Cas9 are highly promising and are expected to transform medicine, agriculture, and biological research. In medicine, CRISPR may lead to the development of permanent cures for many genetic disorders such as sickle cell anemia, cystic fibrosis, and muscular dystrophy by directly correcting faulty genes. It is also expected to play a major role in cancer treatment by engineering immune cells to better recognize and destroy cancer cells. In addition, CRISPR could be used to treat viral infections by targeting and disabling viral genetic material inside human cells.

In the future, improvements in precision and safety are likely, especially with advanced techniques like base editing and prime editing, which allow more accurate and controlled DNA modifications. These developments may reduce errors such as off-target effects and make gene editing safer for clinical use. Personalized medicine is another important prospect, where treatments are designed based on an individual's genetic makeup, making therapies more effective and targeted.

In agriculture, CRISPR is expected to create crops that are more resistant to drought, pests, and diseases, while also improving nutritional value and crop yield. This could help address global food security challenges, especially in the face of climate change. It may also reduce the need for chemical pesticides and fertilizers, supporting more sustainable farming practices.

In research and biotechnology, CRISPR will continue to be a powerful tool for understanding gene function, creating disease models, and developing new drugs. It may also contribute to synthetic biology, where organisms are engineered for useful purposes such as producing biofuels, cleaning pollution, or manufacturing medicines.

However, the future of CRISPR will also depend on strong ethical guidelines and global regulation to ensure its safe and responsible use. As the technology advances, balancing innovation with safety, fairness, and ethical responsibility will be essential for its successful application.

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HISTORICAL DEVELOPMENT OF DYE SENSITIZED SOLAR CELL

M. Srimathi, S. Dorothy*, V. Kanchana and T. Rajesh Kumar

Department of Chemistry,

Academy of Maritime Education and Training (AMET University),

135, East Coast Road, Kanathur - 603 112, Tamil Nadu, India

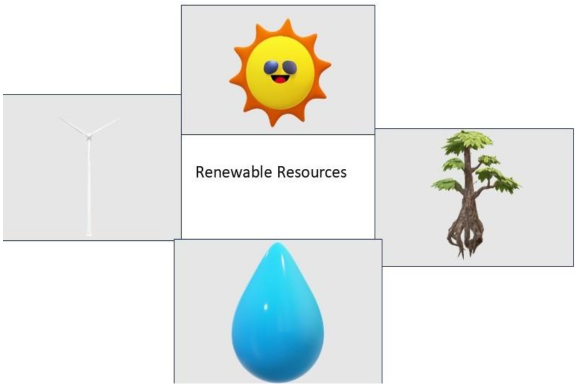
*Corresponding auhor E-mail: dorothys@ametuniv.ac.in

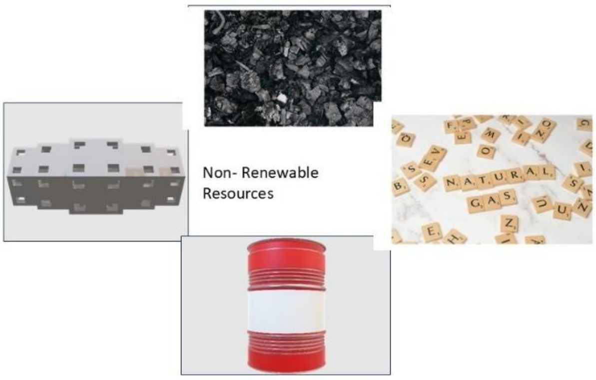
Abstract

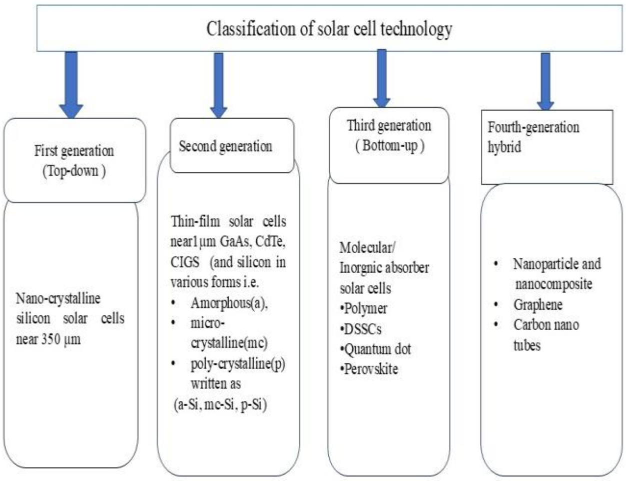
The world is continuously moving forward towards sustainable development with eco-friendly sources of material. Energy demand is increasing every day with a wide range of population rising every day. Storage of energy in further needs, it's difficult to sustain development to avoid non-renewable energy sources because they cause serious health hazards, and create greenhouse gases to be overcome. To use renewable source materials like Solar light has wide benefits compared to other methods to produce huge amounts of electricity. The conventional period involving p-n junctions of semiconductors is inefficient, and is also used for photoelectrochemical studies, but it cannot be flexible for a long time. So the researchers are strenuous tried to develop by every generation, and finally, the 21st century modern third generation of Dye-Sensitized Solar cells (DSSCs), is conversion of natural sunlight into electricity, shows more efficiency than others without suffering environmental harm. DSSCs have metal dye sensitizers, metal -free organic dyes, or natural dyes, including donor, spacer, or acceptor, are low -cost, long-term stability, non-toxicity, easy to manufacture, and work efficiently under low-light conditions such as indoor lighting. Additionally, trends such as surface morphology control, doping, designing, and representation of forward. This part highlights the generation of historical development stages and their fundamentals.

Introduction

The ever-growing world population is increasing day by day, so global energy demand is continuously raising, so immediately address and develop the global energy demand. While fossil fuels still supply 90% of energy to the environment, the world suffers a high reduction in natural resources by involving non-renewable source creates toxic gases such as carbon dioxide, mixed with a clean environment, aggravate green house effects to cause air pollution, acid rain, eruption etc[1].To move into alternative natural renewable sources of energy such as wind, biomass, solar, etc. [2][3].Among these, naturally getting free sunlight provides large amount of solar radiation which is get easily, that can be converted into electricity used for all sector sources [4]. Light from the sun incident on the semiconductor metal surface, the lower level of electron ejected and moves towards the conduction band, and it regenerated is called a solar cell or photovoltaic technology. It is plentiful, naturally replenished, and essentially inexhaustible. This radiation can produce a huge amount of heat, light, and electricity to drive photochemical reactions, and generate electricity through photovoltaic systems (PV) [5].Because of the advantages, solar energy has become a key sustainable source for meeting the growing global energy demand. Therefore, the sustainable development of clean and renewable energy technologies has become essential[6].The development of renewable energy has deep roots, going on in 1887, when Heinrich Hertz first studied the photoelectric, he also observed that ultraviolet light is more effective than visible light in this process. The early first generation of solar cells was based on a nanocrystalline silicon p-n junction and photogenerated following charge carrier created by using bulk material, and to achieve this conversion [7][[8]. In 1980, the second stage of DSSCs based on amorphous silicon (α-Si), cadmium telluride (CdTe), and copper indium gallium selenide (CIGS) had a direct-band gap energy[9] and absorbed sunlight immediately, electrons formed an excitation and were jointly grasped by Coulombic attraction (weakly bonded) and required recombination instead of forming a charge-transfer carrier[10]. The (α-Si) used in electronics devices such as watches, calculators etc are lower absorption efficient and less toxic than conventional silicon photovoltaic and photoelectron chemical performance and reaches maximum efficiency, but its working is complex [11, 12]. Reducing the cost of thin-film solar cells is therefore important to make solar electricity competitive with conventional energy sources. O Vigil-Gala'n *et al.* reported that, instead of using only Indium, which is high cost to overcome, a buffer layer of n-type combined with p-type semiconductor excitation electrons takes place and shows effective absorption compared to conventional crystalline silicon[13].The Ru(II) photoanode attainable dye compound absorbed the solar light radiation from natural sunlight, and excitation occurred to produce electrons, which were injected into another TiO_2 layer as a charge transport. At the same time, holes also approached the counter electrode by using I^-/I_3^- suitable aqueous electrolyte. The thick TiO_2 nanostructured thin -film around 20μm, so absorption of light and dye is sufficient, but scattering of light is very poor due to the thickness of TiO_2. To control this limitation, combined with large nanostructured TiO_2 or other metal oxide can enhance high light scattering more than previously [14, 15]. Among various types of solar cells, Modern DSSCs with low-cost and operate based on this principle to convert sunlight into power conversion efficiency the new third generation of hybrid light gathering PV systems is known as DSSCs[16] includes perovskite solar cells, quantum dots, have high surface area and control band gap, improve catalytic performance major extended into visible region of red wavelength, high excitation occurred regions emerged, easy production with low cost and simple fabrication methods with high durable efficiency as a promising alternative to conventional two generation[17][18][19][20]. In terms of first and second generation, followed by p-n junction devices, the liquid part of the materials is not involved. Compared to the third and fourth generation of PV systems, which are particularly based on mesoporous and nano particles based structured, are more advanced than general solid-state systems [21][22]. DSSCs involved in various field of groups are organic, polymer (polyaniline), metal oxide(TiO_2-workingelectrode), different inorganic materials (V_2O_5), selenides($ZnSe_2$), quantum dots[23] [24] perovskite forms etc[25][26] it is all environmentally less toxic than previous invention materials and driven into photovoltaic performance of DSSCs are versatile features have high pliability in colour, shape, visibility and opportunity to intergrated into many application. DSSC contains some important parts are transparent conductive substrate, photosensitizer (PS), the photoanode, electrolyte, and counter electrode (CE) act as catalysts to enhance the fast reactions. It performs better in light and heat conditions compared to other PV solar cells [27] enactment of redox potential solar energy is, by nature, dispersed and needs large collector areas to raise significant power. However, photovoltaic systems lack effective energy storage for night-time use and transportation purposes. offering towards low-cost and efficient converting solar energy directly into chemical fuels with light absorbing into dye and metal catalysts, particularly through photocatalytic or photoelectrochemical water splitting to produce hydrogen, offers a promising solution, which is a major scientific challenge[28] [29]. While absorption of solar light onto the metal oxide sensitizer and electrons immediately react and are transferred from the valence band (VB) into the conduction band (CB-n -type), oxidation again directly recombination occurred into the positive charge of h^+ containing VB or begins charge transfer with the help of a catalyst, simultaneously electrons move from the conduction band through the platinum metal oxide layer[30]. Mina Soltanmohammadi *et al.* reported using ternary composites of Cu_2ZnSnS_4 (CZTS) thin films as a counter electrode with N719 dye, reaching a maximum of 50% efficiency of electrocatalytic performance compared to a costly platinum material [31]. quantum dots of SnS/CdS Co-sensitized TiO_2 photoelectrodes for quantum dots sensitized solar cells and their band gap 1.5 eV absorb high light absorption control recombination[32][33][34].Ternary perovskite form of nano fiber morphology of $Ba_3Ti_4Nb_4O_{21}$ exhibits tunable optical and structural properties, which are prepared from $BaO–TiO_2–Nb_2O_5/Ta_2O_5$ and move extended towards the optical red region, and more absorption takes place in the solar spectrum[35].DSSCs have also exhibited robust stability by showing no performance loss when subjected to long-term stability tests under various simulated stability conditions.







Early Historical Development of Dye-sensitized Solar Cell

The rapid development of solar energy from the period of 18th century. In the 19th century of 1887 reported the concept of photoelectric sensitization was reported by Moser[36]. In 1893, Edmond Becquerel found that voltage was produced by using two platinum electrodes immersed in a metal halide salt electrolyte with a huge solar light source passing into the solid surface containing an oxide group, and immediately, excitation occurred[37]

1954 at Bell Laboratories[38] In this case, the first generation of silicon solar cell (p-n junction of electron-hole material redox behaviour) with dye using a light source, energy conversion efficiency was only approximately 7%, this limitation was overcome with the help of semiconductor materials, which had photovoltaic technology in the semiconductor electrodes in the electrochemical cells during the period of 1960.

During 1968, Heinz Gerischer introduced the concept model and experimental model of n-type zinc oxide and p-type perylene for dye sensitization of photocurrent at the electrode, which was presented during his period, using dyes like cyanine and rose Bengal to perform photoelectric power generation[39]

In 1970, converting sunlight directly into electricity, following up later, the preliminary investigation was done in semiconductors, starting with the representation of photoexcitation with photosynthesis assisted chlorophyll of single metal oxide photo anode replace electron - transfer electrode with an electrochemical cell, was first examined at the University of California [40]

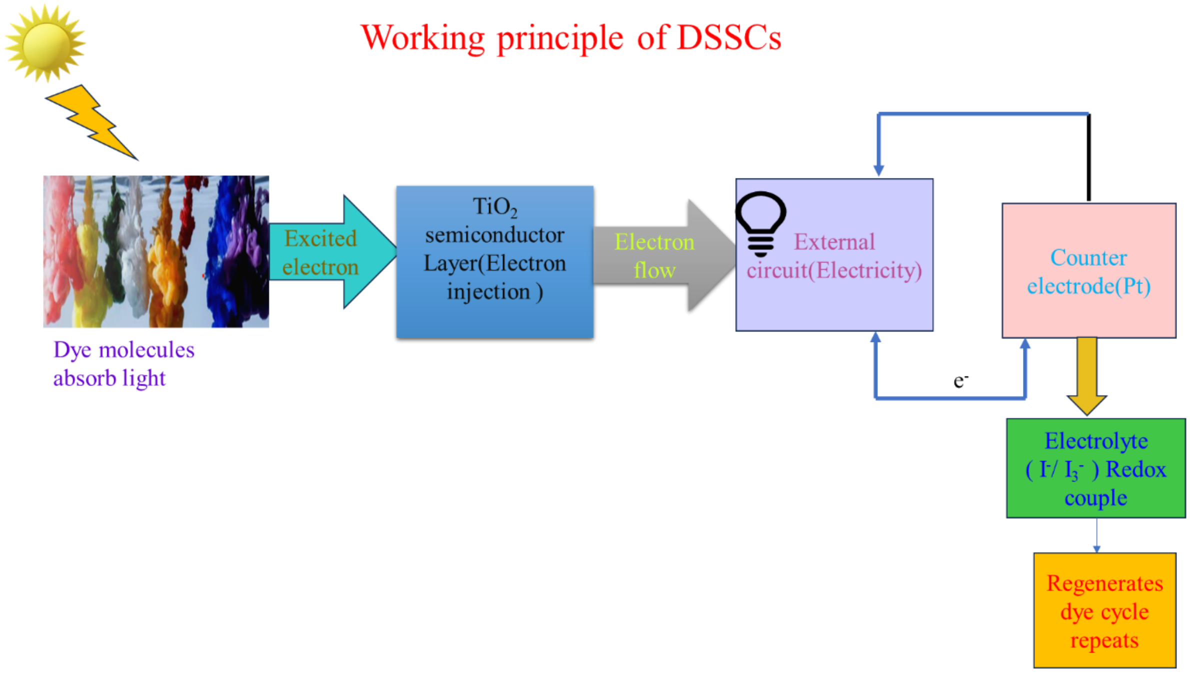
To develop an investigation of the DSSc in 1971, the behaviour of semiconductor electrodes must have a high internal surface area, smooth and well-defined semiconductor surfaces were suitable for photovoltaic applications, so capable of entering into the field of photovoltaics and photo electrochemistry

In 1972, the first reported chlorophyll-assisted ZnO was synthesized by Helmut Tributsch with exposure of dye to produce electricity [41]. The aim of the photosynthesis mechanism is to extract the chlorophyll pigment from green sources like spinach using a single ZnO[42]. At the same time, the invention of hydrogen from water was confirmed in water splitting performance done by using a TiO_2 photoanode. After excitation of electrons, the holes react to move to the photoanode side and help to form the oxygen evolution reaction, further improvement easy to formation of commercial hydrogen gas. This performance can convert solar light into photoelectrochemical water splitting[43]

In 1973, Joseph Lindmayer and Peter Varadi founded Solarex Corporation with the aim of expanding photovoltaic (PV) technology from space applications to terrestrial and public-sector energy systems. Although the patents for high-efficiency silicon solar cells, known as the "Violet Cell," were owned by Communications Satellite Corporation (COMSAT), Solarex successfully commercialized the technology.

In 1976, Tsubomura developed dye-sensitized solar cells from the past to the present. The photocurrent of dye-sensitized photocells with liquid electrolytes, acting as an organic solvent, an ionic liquid electrolyte, and using different electrodes, was studied [44]

By 1980, the company had captured nearly 50% of the global photovoltaic market, contributing significantly to the steady growth of the PV industry that began in the early 1970s. Many PV improvements include important parts such as inverters, batteries, and electrical interconnection to enhance overall performance and energy conversion efficiency[45][46].Earlier attempts to improve light absorption by using multiple layers of dye molecules were generally unsuccessful Matsumura *et al.* and Alonso *et al.* worked with ZnO electrodes using organic dye to increase the efficiency using two dyes rose bengal and other related dyes, resulted below 1% in the 1st attempt due to some drawbacks are inefficient electron injection, rapid recombination of electron, poor charge carriers and un stability of dye compound only showed from conversion of solar light into photo electro chemical reaction based electricity [47]. The structure of a single-layer semiconductor absorbs the organic dye compound when hit by a light source and starts to undergo photoexcitation from the valence band and injects an electron into the conduction band to produce maximum charge efficiency with a large band gap, low efficiency in a photoelectrochemical cell, so fast recombination occurs[48][49]. To develop the DSSC enhanced power conversion efficiency (PCE), doping ZnO with heterojunction-based other metal oxides or transition metal Sulphides (MX_2-M- transition metals) groups to control the band gap energy value from 0.3-1.5 eV and improve charge efficiency [51][52].During the same period, 1980, ZnO/rose Bengal dyes with reducing compound improved the same quantum efficiency level compared to the first and second generation reports. The improved quantum efficiency does not reach high- energy conversion efficiency because of rea using a single dye and a single nanocrystalline metal oxide compound [53] easy to modify the drawbacks has helped to further development, resulting in significantly improved functional groups. The development enhanced dye capacity and reduced the loss of electron recombination by adding new electrolytes, such as ionic liquids, polymer-based gel electrolytes, into the ruthenium-based material, preventing electrolyte damage and improving their stability and certified efficiencies of solar cells 7005A 10% under solar light conditions[54][55]. Only while using TiO_2 is fast recombination occurs because of required suitable more dye with different components, so prevent more absorption durations.



Obaidullah Mohiuddin *et al.* (2018 reported that in the period of 1984, double-bonded compounds containing chromophores, such as Ru $(bpy)_3^{+2}$ with $SrTiO_3$, were introduced into the DSSCs[56][57]. Further researchers diagonised 75% absorption of dyes utilised solar light and extended in the maximum visible region of TiO_2, which contains a high surface crystalline film and $_{\text{high}}$ photochemical performance.

In 1989, many improvements in the field of dye absorption of solar cells reached higher conversion efficiency upto 7%. Developed early before the Gratzel cell, the nano-morphology of TiO_2 in aqueous electrolyte with ruthenium involved, but inefficient absorption of visible light without a correct electrolyte was presented. To overcome this problem, Gratzel's team chose an organic electrolyte. Cao *et al.* reported DSSCs in mesoporous TiO_2/Poly 3,4-ethylenedioxythiopene catalyst counter electrode (PEDOT)[58][59][[60]. To decrease the high cost of metals like titanium/ruthenium, working with organic compounds creates toxic compounds to the environment. Following researchers modified with stable inorganic materials.

Modern DSSCs Materials Development in Gratzel Cells

As a result, improved by enhanced in third generation of Modern DSSCs at 1991 was inventioned by Michae Gratzel so it also called Gratzel cell with minimum 7 % efficiency and new perovskite (ABO_3) solar cells (PSCs) reached high durability, and swift in high power conversion efficiency (PCE) of 22.1 % is verified by the alone National Renewable energy Labortories are low-cost creation with used in PV applications. But still, the third generation is less efficient than the first and second generations. So, Michael Gratzel planned an idea combined modern device with PSC, SSC evaluated the maximum efficiency value is 44%, and it is an extensive process [61][62]. When Brian O′Regan and Michael Gratzel reported broad absorption, higher efficiency nanoporous materials with diameters of 1 and 100 nm. Mesoporous Titanium dioxide (TiO_2) is a nanocrystalline semiconductor had thin film and an extremely large surface area with photo electrode. In 1993, Grätzel *et al.* reported that under solar illumination, improvements happened continuously by combining several important factors such as different material structures, such as glass substrate CE, electrolytes, roughness and surface structure, catalyst, dye, organic dye sensitizers. Ru-based D-π-A, D-A-π-A, D-π-A-A, D-D-π-A, etc., semiconductor photoanodes and redox electrolyte are a pair of (I^-/ I_3^- or CO(II)/ CO(III)), counter electrode (platinum) is a catalyst thin -film[63]. Incident of solar radiation, the absorbed N719(di-tetrabutyl ammonium cis-bis (isothiocyanato)bis(2,2′-bipyridyl-4,4′-dicarboxylato) dye are high cost efficient, so involved or $MAPbI_3$ perovskite that generates electrons that are injected into the conduction band of the mesoporous TiO_2 layer, while the holes are transferred to a solid-state hole transport material, typically spiro-OMeTAD [64]. It has all improved the quality of visible light efficiency as a thermoplastic foil or insulator to avoid short circuit damage without any loss, and improved long-term stability [65]. Ionic liquid–sulfolane composite electrolytes for high-performance and stable dye-sensitized solar cells[66]. Electrochemical and photoelectrochemical properties of nickel oxide (NiO) with nanostructured morphology for photoconversion applications. Before the Gratzel invention, stage wise improved the progress in these aspects. By altering the catalyst, in 2003, Ruthenium (organometallic groups) based dyes such as N3 and N719[67]. Some limitations of Pt catalytic activity are high expense, researchers have involved other than Pt catalyst such as Co and Cu based redox catalysts [68][69] show good performance, high efficiency, with the addition of electrolyte to eliminate charge transport between the electrodes and photovoltaic performance concerns. applications such as indoor electronic and large-scale outdoor energy generation [70] using various metal catalyst contains some amount of toxicity presented so move into carboneous eco-friendly mostly used strong solar light absorption into the visible region and low-cost, also absorbing many dye molecules on the semiconductor surface and emits photo excitations so it reaches enhance light efficiency is developed than previous one. Cu- carbon substrate like nanoplates exhibit increased charge efficiency and high performance[71][72]. PEDOT with graphene nanoplates is not suitable for large areas because they not correctly model to raise the photovoltaic performance and photochemical stability, and in this period various shows different nano morphology categories, such as nanoparticles, nanotubes, nanorods, quantum dots they overall increase the high surface area and improve electron transport occurred with in photo anode (metal oxide). Syed Ghufran Hashmi *et al.* reported the single walled carbon nanotube (SWCNT) is the counter electrodes, similar to graphene nanoplates these SWCNT displayed excellent enactment contrasted to conventional platinum and copper catalysts with only lesser charge transfer resistance 2-2.5 Ω cm^2[73] In the period of 2008 DSSCs with light absorption by the sensitizer produces an excited state through metal-to-ligand charge transfer (MLCT), which injects electrons into the conduction band of the semiconductor. The oxidized dye is control the regenerated by electron donation from the new addition of electrolyte solvent enhance ionic conductivity of iodide and triiodide redox electrolyte, while the injected electrons allowing continuous travel through the semiconductor device to the external circuit and improves photo-current stability and worked to control corrosive nature of silver, copper metals are used as current collectors triiodide is reduced back to iodide, completing the circuit and allowing high redox latent, controlled recombination, continuous electron flow with in the cell of exhibit electrocatalytic behaviour in DSSCs because of NiO contains have large surface area, improving catalysing property, low band gap energy specifically reduced triiodide ions and shows high-performance and reach efficiency photovoltaic energy conversion upto 11-15% [74]. Common metal oxide TiO_2 has very poor light absorption, already many reported due to its large band gap. Combined with transition metal, especially Ni, improved high dye absorption, recombination control, and further other tactics metal -organic framework (MOFs) improved photoanode light harvesting efficiency (LHE), also the best of energy storage application[75]

In 2009, mass production of the first industrial-scale G24 power source was used in DSSCs the higher potential of efficiency reach11- 12% better than Si diffuse light efficiency in the United Kingdom

Advance in Metal-Free

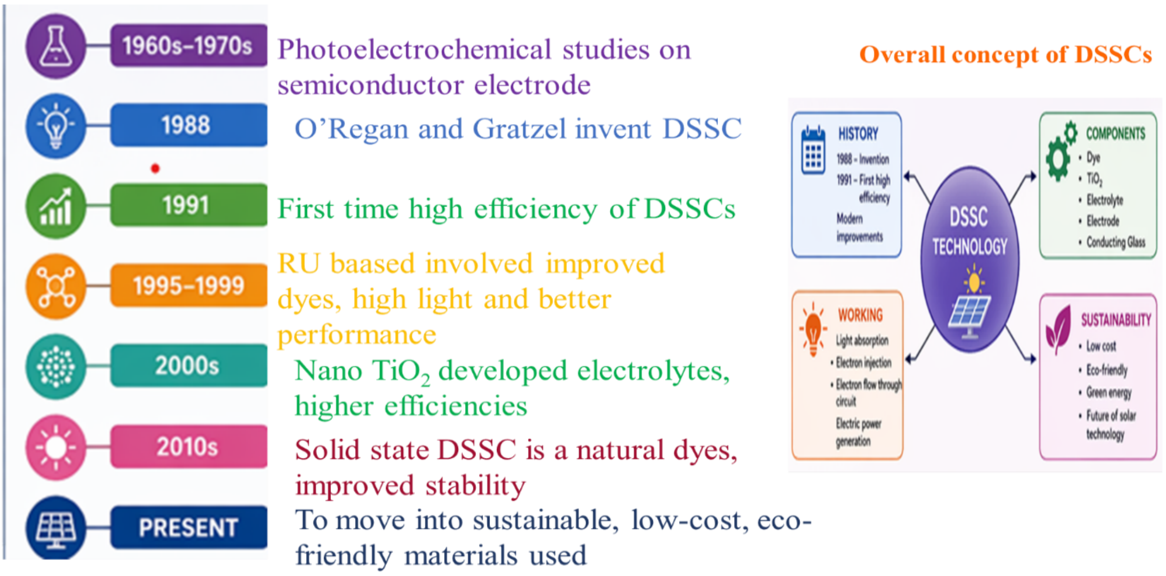
Further researchers introduced metal-free sensitizers to avoid the expensive elements like ruthenium, and when improve the electronic properties of the device, high molar extinction but still low efficiency compared to ruthenium. In 2014, the involvement of a different composition ratio of Cobalt-based Co^{2+} and Co^{3+} and zinc porphyrin redox dye electrolyte redox mediator was used instead of the conventional material[76] Special focus on Pt-TCO (transparent conductive oxide) coated with a PET sheet shows high stability. The cathode nature of the counter electrode and photo anode is dye, the nature of the metal oxide is working electrode are designed with transparent glass sheet material like ITO or FTO(fluorine-doped tin oxide), and allows light to pass inside the semiconductor coated with a strong Platinum catalyst, because its ability to conduct efficient electricity shows an arrangement of sandwiched morphology [77].Andery Lim *et al.* verified that before heteroform, the first step is to analyse whether the

FTO layer may be working or not made up of DSSCs, while doping with Mesoporous TiO_2 film derived from Senna plant is a photo-sensitizer dye, which improved photo-voltaic current performance than crystalline films. FTO-SnO/mesoporous TiO_2 has less electron transport and fast diffusion with similar mesoporous size, so it reduces the recombination and improves solar-to-electrical conversion efficiency upto 14% [78][79]. In 2015, combined with two metal-free sensitizers, an organic dye absorbed with the help of solar irradiation and Co(II)/Co(III) tris (bipyridine) exhibits 14% conversion efficiency[80][81][82].

Highly concentrated dye molecules like inkjet printing dye allow precise high dispersal onto the nanoporous TiO_2 surface, and long-term drying capacity compared to macro porous materials before solvent evaporation, so it shows high absorption within the spongy morphology[83][84]. The main drawback of some dyes and also using strong solvent shows poor chemical compatibility, which may hinder the nozzles. Other than alternate solvents such as dimethylformamide (DMF) and dimethyl sulfoxide (DMSO) have been used gratefully [85]. Recently, Abdullah Yildiz *et al.* (2026 reported that the present low-cost iron phosphide earth-abundant material is an outstanding catalyst of counter electrode. The J_{sc} range of PV-based Fe2 3L of counter electrode 12.3 ± 0.07 mA cm^{-2} was larger than the older Pt catalyst (9.32 ± 0.04 mA cm^{-2}), and overall power conversion Fe_2P3L counter electrode is (3.96 ± 0.06%) [76]. Most famous TiO_2 has some limitations, low electron mobility, so interaction with dyes recombination occurred, to rectify involved spinels oxides and inorganic perovskite to adopt TiO_2 properties and reach above 15% efficiency, and different combinations of ABO_2 and A_2BX_2 improve the photochemical performance[86].

The electrochemical deposition methods recently found that PEDOT acts as a counter electrode, showing higher diffusivity, ionic conductivity onto another FTO applicable for indoor light, using Y123 dye with different intensity was calculated by using CO redox electrolyte, and a high efficiency 26%[87]. The upcoming generation of assess DSSC are altered and improved for indoor application is mostly used in many buildings with a wide scope of artificial light are low-cost, stable, energy efficiency and their sources are LEDs, sodium lamps, halide lamps, and fluorescent lamps and indoor situation are very low temperature range compared to outside temperatures. While regular transportation, usage, and storage of solar panels always result in erratic issues between different climatic situation. so overall affecting stability and enactment. Mojeed A *et al.* (2024 reported that FTO-TiO_2/CoS/SnS, a single quantum dot (counter electrode), could not reach stability due to lower electrical conductivity. Combining the metal sulphide semiconductor catalyst improved both the band gap value, cell effectiveness, and charge transfer process with the addition of a light source[88]. The transparency of DSSCs is sometimes changed during the manufacturing period to control these issues. The semi-transparency of

DSSCs involved working with different applications, which developed the efficiency and transparency of the photovoltaic cell [89]



Early-wise History of DSSCs

Conclusion

The performance of DSSCs' nanostructured role is better than that of early photosensitizers. The history of DSSCs traces a gradual transformation of basic principles of photochemical processes to a potential low-cost technology of photovoltaics. The scientific basis of light-induced chemical reactions was established early in the 19th century, but it was not until the late 20th century that DSSCs became a practical solar energy generator. In 1991, Michael Gratzel and Brian O'Regan made a significant breakthrough in creating the modern DSSC, which has much better efficiency with a nanocrystalline titanium dioxide (TiO2) electrode sensitized with ruthenium-based dyes. This design has surpassed the shortcomings of previous photoelectrochemical cells, especially in their low stability and low-light absorption. Further research was aimed at enhancing every aspect of the DSSC system, including sensitizers, electrolytes, and counter electrodes. Improvements in dye chemistry, such as metal-free organic dyes, porphyrin-based sensitizers, and others, increased the light absorption and extended the spectral response. Liquid iodide/triiodide redox couples were developed into quasi-solid and solid-state hole transport materials, which overcame the leakage and stability problems. Moreover, nanostructured semiconductors like ZnO and SnO_2, as well as carbon-based materials like graphene, have also been considered in order to enhance the electron transport and performance of the device further. Although DSSCs have moderate power conversion efficiencies relative to conventional silicon solar cells, these cells have several distinct advantages, such as low cost of production, simple fabrication, transparency, and low light performance. These characteristics render them especially useful in interior applications and building-integrated photovoltaics. To sum up, the creation of DSSCs is one of the most important advancements in the sphere of renewable energy, as it shows how interdisciplinary research could result in the creation of innovative and sustainable technologies. Although they still have long-term stability, scalability, and efficiency issues, continuous research is still going on to overcome these shortcomings. DSSCs have a great potential as an alternative photovoltaic technology, particularly in specialised markets where flexibility, aesthetics, and economic considerations are crucial. DSSCs are experiencing rapid growth in material design, device performance, and interfacial charge transfer process. The main aim of DSSCs is to reach long-term stability and large-scale production of electricity via bio way. The development of various materials, dyes, catalyst etc are predictable highly efficient, and durable. The overall cost of manufacturing DSSCs has decreased period-wise from the 18th century to the upcoming 2030 because of working with renewable energy to develop sustainable energy

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MICROBIAL SPOILAGE OF PHARMACEUTICAL PRODUCTS

Anesh Sagar*[1], Mhaveer Singh[1], Dinesh Kumar[1],
Sushil Kumar[1], Rajat Saxena[2] and Tribhuwan Kumar Vashishtha[2]
[1]School of Pharmaceutical Sciences,
[2]Pharmacy Academy,
Faculty of Pharmacy, IFTM University, Moradabad, Uttar Pradesh, 244102
*Corresponding author E-mail: aneshsagar333@gmail.com

1. Introduction

Microbial spoilage of pharmaceutical products is a significant barrier to ensuring the quality, safety, and therapeutic efficacy of pharmaceuticals. In pharmaceutical formulations, particularly aqueous systems like syrups, suspensions, emulsions, and ophthalmic therapies, microorganisms such as bacteria, fungi, and yeasts flourish. These bacteria can proliferate and produce metabolic byproducts, including gases, acids, and enzymes, after being added to a product. These byproducts lead to the degradation of the excipient and active pharmaceutical ingredients (APIs). The impacts of microbial breakdown include physical, chemical, and biological deterioration. Turbidity, staining, precipitation, and a foul odor are examples of observable alterations that may occur in addition to non-visible ones like pH shifts and diminished drug potency. More importantly, microbial contamination poses major health dangers, particularly in sterile objects and immune compromised patient-use objects, where it may cause dangerous reactions or severe infections.

Microbial contamination can come from a variety of sources, including humans, equipment, manufacturing settings, water systems, and raw materials. The amount of rotting is influenced by several factors, including pH, temperature, water activity, and the presence of preservatives. Therefore, strict application of Good Manufacturing Practices (GMP), effective sterilization processes, and robust quality control procedures are essential to minimize microbial contamination and ensure product stability throughout its shelf life.

Figure 1: Microbial contamination

Definition

"Microbial spoilage refers to unwanted changes occurring in medicinal products due to contamination and proliferation of bacteria, fungi, or yeasts, resulting in physical, chemical, or biological deterioration."

2. Types of Spoilage in Pharmaceutical Products

The following types of pharmaceutical deterioration can be generally categorized:

2.1 Physical Spoilage

- Changes in physical appearance without chemical alteration
- Examples:
    - ➢ Phase separation in emulsions
    - ➢ Precipitation in solutions
    - ➢ Caking of powders
- Impact: Affects drug uniformity and patient acceptability

2.2 Chemical Spoilage

- Degradation of active pharmaceutical ingredients (API) or excipient
- Mechanisms:
    - ➢ Hydrolysis
    - ➢ Oxidation
    - ➢ Photolysis
- Impact: Loss of potency and formation of toxic products

2.3 Microbial Spoilage

- Caused by growth of microorganisms in formulations
- Manifestations:
    - ➢ Turbidity in liquids
    - ➢ Mold growth
    - ➢ Gas production
- Impact: Infection risk and product recall

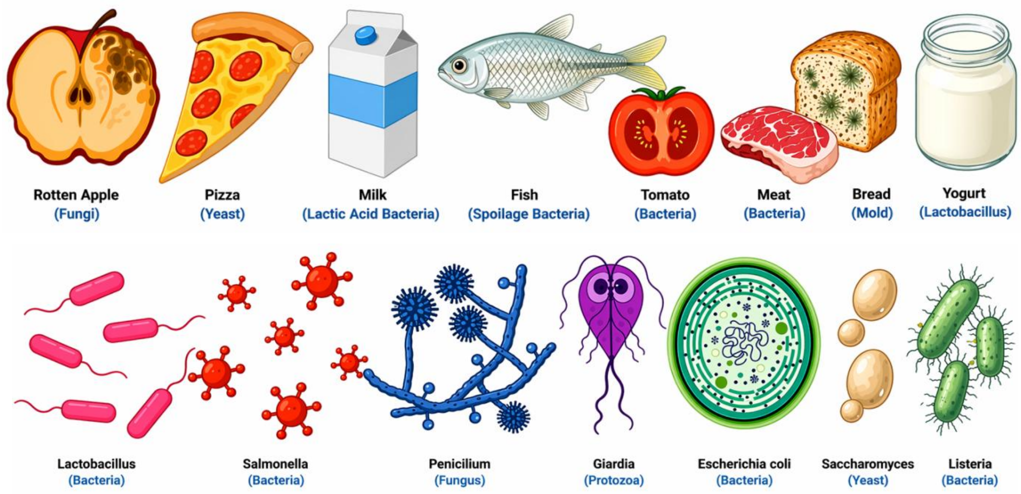

Figure 2: Microbial Spoilage

2.4 Physico-chemical Spoilage

- Combined effect of microbial activity and chemical degradation
- Example: Enzyme-mediated breakdown of excipient

2.5 Biological Spoilage

- Production of microbial toxins and metabolites
- Example: Endotoxin from Gram-negative bacteria

3. Factors Affecting the Microbial Spoilage

Microbial spoilage depends on various intrinsic and extrinsic factors:

3.1 Intrinsic Factors

a) Nutritional Factors

- Microorganisms utilize carbon, nitrogen, and minerals from formulation
- Crude plant/animal materials increase susceptibility

b) pH

- Neutral pH favors bacterial growth
- Acidic pH favors fungi and yeasts

c) Water Activity (Aw)

- Essential for microbial growth
- High Aw → more spoilage risk
- Reduced by sugars, salts, or drying

d) Redox Potential

- Determines aerobic/anaerobic growth conditions
- Oxygen-rich environments support aerobes

e) Preservatives

- Inhibit microbial growth
- Effectiveness depends on concentration and type

3.2 Extrinsic Factors

a) Temperature

- Higher temperature accelerates microbial growth
- Refrigeration reduces spoilage

b) Packaging Design

- Prevents contamination during storage and use
- Examples: Sealed vials and Narrow-mouth containers
- **c) Storage Conditions**
- Humidity, light, and handling influence contamination

d) Size of Inoculum

- Larger microbial load → faster spoilage

4. Sources and Types of Microbial Contaminants

4.1 Sources of Contamination

- Microorganisms may enter pharmaceutical products from:

a) Raw Materials

- Natural products (plant/animal origin) carry microbes

b) Water

- Major source of Gram-negative bacteria

c) Air and Environment

- Dust particles carry spores and bacteria

d) Personnel

- Skin flora, respiratory droplets

e) Equipment and Facilities

- Poor sanitation, biofilms

f) Packaging Materials

- Improper sterilization

g) Manufacturing Process

- Cross-contamination during production

4.2 Types of Microbial Contaminants

a) Bacteria

- Pseudomonas aeruginosa – eye infections
- Salmonella – gastrointestinal infections

b) Fungi

- Molds: Aspergillus, Penicillium
- Yeasts: Candida

c) Spore-forming organisms

- Highly resistant to heat and preservatives

d) Pathogens

- Cause serious infections in sterile preparations

5. Assessment of Microbial Contamination and Spoilage

Microbial load detection, counting, and assessment are all part of assessment.

5.1 Indicators of Microbial Spoilage

- Change in color, odor, and taste
- Gas production and turbidity

- pH variation
- Slimy or viscous texture

5.2 Microbial Limit Tests

- Determines permissible microbial load
- Acceptable limits:
    - 10^2–10^3 CFU/g or ml (depending on product)

5.3 Sterility Testing

- For parenteral and ophthalmic preparations

5.4 Preservative Efficacy Testing

- Evaluates effectiveness of antimicrobial preservatives

5.5 Environmental Monitoring

- Air, surface, and personnel monitoring in manufacturing areas

5.6 Identification of Microorganisms

- Culture methods
- Biochemical tests
- Molecular techniques

6. Prevention and Control of Microbial Spoilage of Pharmaceutical Products

1. Preservative use

Preservatives are chemicals that are added to pharmaceutical formulations in order to prolong shelf life and prevent the growth of germs. They are particularly crucial in multi-dose formulations such as creams, syrups, and eye drops.

Common preservatives include:

- Parabens (methylparaben, propylparaben)
- Benzalkonium chloride
- Phenol and chlorobutanol

An ideal preservative should be:

- Effective against a wide range of microorganisms
- Stable over a wide pH and temperature range
- Non-toxic and non-irritant

However, variables including pH, concentration, and compatibility with formulation ingredients affect how effective preservatives are. Resistance or decreased efficacy could result from improper use.

2. Methods for Sterilization

The process of sterilization eliminates all germs, including spores.

a) Heat Sterilization

- Moist heat (autoclaving at 121°C for 15 minutes)
- Dry heat (hot air oven at 160–170°C)
- Widely used for glassware, media, and heat-stable drugs

b) Filtration

- Used for heat-sensitive liquids (e.g., injections)
- Membrane filters (0.22 µm) remove microorganisms

c) Radiation

- Gamma radiation and UV radiation
- Used for sterilizing disposable medical products

Each method is selected based on the nature and stability of the product.

3. Good Manufacturing Practices (GMP)

GMP ensures that pharmaceutical products are consistently produced and managed in compliance with quality standards.

Key aspects include:

- Clean and controlled manufacturing environment
- Trained personnel
- Proper sanitation and hygiene
- Validation of processes and equipment
- Documentation and quality control

GMP reduces the risk of contamination during production and ensures product safety.

4. Proper Packaging and Storage

Packaging plays an important role in preventing contamination from microorganisms.

Packaging:

- Use of airtight, tamper-proof containers
- Single-dose packaging reduces contamination risk
- Use of sterile containers for parenteral

Storage:

- Controlled temperature and humidity
- Protection from light and air
- Proper labeling and handling instructions

Microbial development and spoiling might be accelerated by improper storage conditions.

5. Hygienic Handling

Pharmaceutical contamination is mostly caused by human handling.

Preventive measures include:

- Use of gloves, masks, and protective clothing
- Regular hand washing and sanitization
- Avoiding direct contact with products
- Maintaining clean working surfaces

To reduce the risk of infection, staff training and strict hygiene practices are crucial.

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EMERGING TECHNOLOGIES AND INTERDISCIPLINARY INNOVATIONS IN ANIMAL SCIENCE

Vishal K. Moholkar

Department of Zoology,

Maharashtra Mahavidyalaya, Nilanga Dist. Latur-413512, (Maharashtra), India.

Corresponding author E-mail: vishalmoholkar20@gmail.com

Abstract

Zoology, as a fundamental branch of life sciences, has undergone remarkable transformation through the integration of advanced science and technology. Modern research pathways in zoology are increasingly shaped by interdisciplinary approaches, including biotechnology, molecular biology, artificial intelligence, and environmental science. These innovations have significantly enhanced our understanding of animal physiology, genetics, behavior, and ecological interactions. Advanced tools such as genomics, proteomics, bioinformatics, and imaging technologies have revolutionized species identification, disease diagnosis, and biodiversity conservation. Additionally, emerging areas like nanotechnology, synthetic biology, and computational modeling are expanding the frontiers of zoological research. This chapter explores progressive pathways in science and technology that are redefining zoology, with a focus on their applications in animal health, aquaculture, conservation, and environmental sustainability. It also highlights challenges, ethical considerations, and future perspectives for integrating technological advancements into zoological research for global benefit.

Keywords: Zoology, Biotechnology, Genomics, Artificial Intelligence, Aquaculture, Biodiversity.

1. Introduction

Zoology is one of the oldest and most dynamic branches of biological sciences, focusing on the study of animal life, their structure, function, behavior, and interactions with the environment. Traditionally, zoological studies relied heavily on morphological observations and field-based investigations. However, the rapid advancement of science and technology has transformed zoology into a highly interdisciplinary field, incorporating tools from molecular biology, biotechnology, computational sciences, and environmental engineering (Wilson, 2016; Futuyma, 2013).

In recent years, the growing demand for sustainable resource management, biodiversity conservation, and improved animal health has driven the integration of innovative technologies into zoological research. These advancements have enabled scientists to explore complex biological systems at molecular, cellular, and ecosystem levels. The application of genomics, proteomics, and bioinformatics has provided unprecedented insights into genetic diversity, evolutionary relationships, and species adaptation (Lewin *et al.* , 2018).

Furthermore, technological innovations such as artificial intelligence (AI), remote sensing, and geographic information systems (GIS) have revolutionized wildlife monitoring and ecological studies. These tools allow researchers to analyze large datasets, predict ecological changes, and develop effective conservation strategies (Allan *et al.* , 2020). The incorporation of biotechnology has also enhanced areas such as aquaculture, animal breeding, and disease management, contributing significantly to food security and economic development.

This chapter aims to explore progressive pathways in science and technology that are shaping modern zoology, emphasizing their applications, benefits, and future potential.

2. Role of Biotechnology in Zoological Research

2.1 Genetic Engineering and Molecular Biology

Genetic engineering has revolutionized zoology by enabling precise manipulation of genes to study their functions and improve desirable traits. Techniques such as CRISPR-Cas9 allow targeted gene editing, facilitating research in developmental biology, disease resistance, and evolutionary studies (Doudna & Charpentier, 2014). Molecular biology tools, including PCR and DNA sequencing, are widely used for species identification, genetic diversity analysis, and phylogenetic studies.

2.2 Applications in Animal Health and Aquaculture

Biotechnology plays a crucial role in improving animal health through vaccine development, disease diagnostics, and immunological studies. In aquaculture, probiotics, prebiotics, and plant-based bioactive compounds are used to enhance growth performance and disease resistance, reducing dependency on antibiotics (Nayak, 2010).

3. Genomics, Proteomics, and Bioinformatics

The advent of omics technologies has opened new avenues in zoological research. Genomics helps in decoding entire genomes, while proteomics and metabolomics provide insights into protein expression and metabolic pathways. Bioinformatics tools enable the analysis of large datasets, facilitating gene annotation, evolutionary studies, and functional predictions (Lesk, 2019).

These technologies are particularly useful in conservation biology, where genetic information is used to assess population structure, identify endangered species, and design conservation strategies.

4. Artificial Intelligence and Computational Zoology

Artificial intelligence and machine learning are increasingly being used in zoology for data analysis, behavioral studies, and ecological modeling. AI-based image recognition systems help in species identification and wildlife monitoring, while predictive models assist in understanding migration patterns and climate change impacts (Allan *et al.* , 2020).

Computational tools also support drug discovery, disease prediction, and simulation of biological processes, enhancing research efficiency and accuracy.

5. Environmental and Conservation Technologies

Technological advancements have significantly improved conservation efforts. Remote sensing and GIS are used to monitor habitat changes, deforestation, and biodiversity loss. Environmental DNA (eDNA) techniques allow non-invasive detection of species in aquatic and terrestrial ecosystems, aiding in biodiversity assessment (Thomsen & Willerslev, 2015).

Additionally, biotechnological approaches such as cryopreservation and cloning are being explored for the conservation of endangered species.

6. Emerging Trends in Zoological Research

To clearly present the major advancements shaping modern zoology, the following table summarizes key emerging trends, their tools, applications, and significance:

Table 1: Emerging Trends in Zoological Research

Trend	**Key Tools / Techniques**	**Applications in Zoology**	**Significance**
Nanotechnology	Nanoparticles, Nano-biosensors, Drug delivery systems	Targeted drug delivery, disease diagnostics, toxin detection	Enhances treatment efficiency and precision in animal health
Synthetic Biology	Gene circuit design, DNA synthesis, CRISPR tools	Development of disease-resistant species, metabolic engineering	Enables creation of customized biological systems
Artificial Intelligence (AI)	Machine learning, Deep learning, Image recognition	Wildlife monitoring, species identification, behavioral analysis	Improves data analysis accuracy and predictive modeling
Bioinformatics	Genome databases, Sequence analysis software	Gene annotation, evolutionary studies, protein modeling	Facilitates handling of large biological datasets
Environmental DNA (eDNA)	DNA barcoding, PCR, Metagenomics	Non-invasive species detection, biodiversity assessment	Supports conservation without disturbing habitats
CRISPR and Genome Editing	CRISPR-Cas9, TALENs	Gene editing for growth, immunity, and disease resistance	Revolutionizes genetic improvement in animals
Remote Sensing & GIS	Satellite imaging, Geographic Information Systems	Habitat mapping, migration tracking, climate impact analysis	Aids large-scale ecological monitoring

6.1 Nanotechnology

Nanotechnology is being applied in drug delivery, diagnostics, and environmental monitoring. Nanoparticles can be used to deliver targeted treatments in animals, improving therapeutic efficiency.

6.2 Synthetic Biology

Synthetic biology involves designing and constructing new biological systems. It has potential applications in developing disease-resistant species and improving metabolic pathways.

6.3 Integrative and Interdisciplinary Approaches

Modern zoology increasingly relies on integrating multiple disciplines, including ecology, genetics, computer science, and environmental science, to address complex biological problems.

7. Challenges and Ethical Considerations

Despite technological advancements, several challenges remain, including high research costs, technical limitations, and ethical concerns related to genetic modification and animal welfare. Regulatory frameworks and public acceptance also play crucial roles in the adoption of new technologies.

8. Future Perspectives

The future of zoology lies in the integration of advanced technologies such as AI, big data analytics, and precision biotechnology. These innovations will enable more efficient research, better conservation strategies, and sustainable utilization of animal resources. Collaborative and interdisciplinary research will be essential for addressing global challenges such as climate change, biodiversity loss, and food security.

Conclusion

Progressive pathways in science and technology have transformed zoology into a dynamic and interdisciplinary field. From molecular biology to artificial intelligence, these advancements have enhanced our understanding of animal systems and their interactions with the environment. The integration of these technologies offers promising solutions for sustainable development, conservation, and improved animal health. Continued innovation and responsible application of these tools will be key to shaping the future of zoological research.

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MATHEMATICAL MODELING AND ANALYSIS OF THE FACILITATION FACTOR IN CARRIER-MEDIATED TRANSPORT THROUGH LIQUID MEMBRANES

P. Jeyabarathi and L. Rajendran
Department of Mathematics, AMET, deemed to be University, Chennai, India
Corresponding author E-mail: bsc.jeya@yahoo.com, raj_sms@rediffmail.com

Abstract

This paper presents a modified Adomian Decomposition Method (MADM) for obtaining approximate analytical solutions to nonlinear boundary layer–type reaction–diffusion equations arising in carrier-mediated transport through liquid membranes. The proposed modification enhances the convergence and computational efficiency of the standard Adomian method, enabling accurate treatment of coupled nonlinear terms without linearization. The governing equations, incorporating reversible reaction kinetics between solute and carrier species, are transformed into a dimensionless form and solved analytically. The resulting expressions are used to evaluate concentration profiles and the facilitation factor, which quantifies the enhancement of solute transport due to carrier interaction.

Keywords: Carrier-Mediated Transport, Liquid Membrane Systems, Facilitation Factor, Nonlinear Reaction–Diffusion Modelling, Modified Adomian Decomposition Method (MADM).

1. Introduction

Carrier-mediated transport in liquid membranes is an important mechanism for enhancing mass transfer in separation processes, particularly when simple diffusion is insufficient to achieve the desired flux. In such systems, a solute S reversibly reacts with a mobile carrier L to form a complex LS, which diffuses across the membrane and subsequently releases the solute at the permeate side. This coupled reaction–diffusion mechanism significantly improves transport efficiency and selectivity.

The mathematical formulation of this process leads to a system of nonlinear second-order differential equations, where diffusion of each species is coupled through reversible reaction kinetics. The governing equations account for spatial variations in the concentrations of S, L, and LS, as well as the forward and backward reaction rates. Due to the inherent nonlinearity arising from the interaction term $C_S C_L$, obtaining exact analytical solutions is generally difficult.

To overcome this limitation, approximate analytical techniques are employed. In this work, a modified Adomian Decomposition Method (MADM) is utilized to solve the resulting boundary value problem efficiently. The model is further expressed in dimensionless form to generalize the analysis and reduce the number of governing parameters. Particular attention is given to the evaluation of the facilitation factor, which quantifies the enhancement of solute transport due to carrier interaction. This study provides a systematic analytical framework for understanding the influence of reaction–diffusion coupling in liquid membrane systems.

Facilitated diffusion [1] is a carrier-mediated transport process in which a solute (S) diffuses through a membrane and undergoes a reversible homogeneous reaction with a ligand (L) present within the membrane, forming a complex (LS). This mechanism extends classical passive transport by incorporating chemical interactions that enhance mass transfer. Consequently, facilitated diffusion has attracted considerable attention across multiple scientific disciplines. In membrane biophysics, the transport of oxygen is known to occur through facilitation by carrier molecules such as hemoglobin and myoglobin [2–5], significantly improving transport efficiency compared to simple diffusion. In chemical engineering, carrier-mediated diffusion has emerged as a promising separation technique, offering high selectivity due to specific carrier–solute interactions, along with substantial facilitation factors [6–9]. Furthermore, in applied mathematics, facilitated diffusion represents an important area of study because it is governed by nonlinear reaction–diffusion equations, which present significant analytical and computational challenges [10,11].

Barbero *et al.* [12] obtained the solution of reaction–diffusion equations of facilitated diffusion using the boundary element method. However, to the best of our knowledge, there was no rigorous analytical expression corresponding to the concentration profiles for all values of parameters reported. The purpose of this communication is to arrive at an analytical expression for concentration species at a carrier-mediated transport process using the Adomian decomposition method

2. Mathematical Formulation of the Problem

In carrier-mediated transport, a solute Sreacts reversibly with a mobile carrier $L$to form a solute–carrier complex LS, which facilitates transport across the membrane. The mechanism involves three sequential steps: (i) complex formation at the feed side, (ii) diffusion of the complex through the membrane phase, and (iii) dissociation at the permeate side, releasing the solute and regenerating the carrier.

The reversible reaction can be represented as:

$$L + S \underset{k_{-1}}{\overset{k_1}{\leftrightarrows}} LS \ (1)$$

where $k_1$and $k_{-1}$are the forward and backward reaction rate constants, respectively.

This reaction–diffusion coupling governs the spatial distribution of species within the membrane and significantly enhances mass transfer compared to simple diffusion, particularly when the carrier exhibits strong affinity for the solute.[12]

Governing Equations in General Geometry

Using this operator, your system becomes:

$$D_S\left(\frac{1}{\chi^n}\frac{d}{d\chi}\left(\chi^n\frac{dC_S}{d\chi}\right)\right)=k_1C_SC_L-k_{-1}C_{LS}\ (2)$$

$$D_L\left(\frac{1}{\chi^n}\frac{d}{d\chi}\left(\chi^n\frac{dC_L}{d\chi}\right)\right)=k_1C_SC_L-k_{-1}C_{LS}\ (3)$$

$$D_{LS}\left(\frac{1}{\chi^n}\frac{d}{d\chi}\left(\chi^n\frac{dC_{LS}}{d\chi}\right)\right)=k_{-1}C_{LS}-k_1C_SC_L\ (4)$$

The dimensionless boundary conditions

$$\text{At } \chi=0, C_S(0)=C_\tau, C_L(0)=0, C_{LS}(0)=C_\tau\ (5)$$

$$\text{At } \chi=1, C_S(1)=0, C_L(1)=C_\tau, C_{LS}(1)=0\ (6)$$

To convert Eqs. (2)–(4) into a dimensionless form, introduce appropriate scaling for space and concentrations.

$$u=\frac{C_S}{C_\tau}, v=\frac{C_L}{C_\tau}, w=\frac{C_{LS}}{C_\tau}, y=\frac{x}{d}, \alpha=\frac{k_1C_\tau d^2}{D}, \beta=\frac{k_{-1}d^2}{D}\ (7)$$

The dimensionless form are nonlinear differential equations (2–4) using (7)

The reaction–diffusion system governing the carrier-mediated transport process in a liquid membrane can be extended from planar geometry to a unified geometrical framework by introducing the generalized Laplacian operator.

$$u''(y)+\frac{N}{y}u(y)=\alpha\, u(y)v(y)-\beta\, w(y) \quad (8)$$

$$v''(y)+\frac{N}{y}v(y)=\alpha\, u(y)v(y)-\beta\, w(y) \quad (9)$$

$$w''(y)+\frac{N}{y}w(y)=-\alpha\, u(y)v(y)+\beta\, w(y) \qquad (10)$$

The boundary conditions are

$$u(0)=1, v(0)=0, w(0)=1\ (11)$$

$$u(1)=0, v(1)=1, w(1)=0\ (12)$$

The approximate analytical expressions of concentrations of species using Modified Adomian decomposition method.

$$u(y,\alpha,\beta,N)=(1-y)+\frac{(1-\alpha)(y^4-y)}{4N+12}+\frac{\alpha(y^3-y)}{3N+6}+\frac{\beta(y-y^2)}{2N+2}\ (13)$$

$$v(y,\alpha,\beta,N)=y+\frac{(1-\alpha)(y^4-y)}{4N+12}+\frac{\alpha(y^3-y)}{3N+6}+\frac{\beta(y-y^2)}{2N+2}\ (14)$$

$$w(y,\alpha,\beta,N)=(1-y)+\frac{(1-\alpha)(y-y^4)}{4N+12}+\frac{\alpha(y-y^3)}{3N+6}+\frac{\beta(y^2-y)}{2N+2}\ (15)$$

where u, v and w are dimensionless concentration species and α and β are dimensionless reaction parameters.

The facilitation factor becomes

$$F=\frac{\left(\frac{du}{dy}\right)_{y=1 \text{ for given } \alpha,\beta}}{\left(\frac{du}{dy}\right)_{y=1 \text{ for } \alpha=0 \text{ and } \beta=0}}=\frac{(-1)+\frac{3(1-\alpha)}{4N+12}+\frac{2\alpha}{3N+6}-\frac{\beta}{2N+2}}{-1+\frac{3}{4N+12}}\ (16)$$

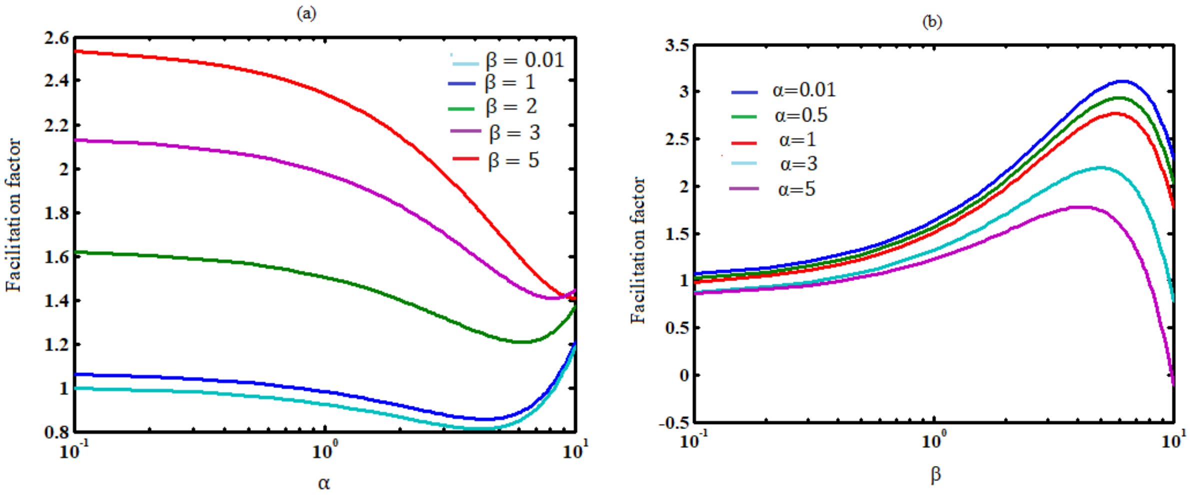

Figure 1: The facilitation factor versus of the α and β for the liquid membrane using the Eq. (16)

The figures illustrate the influence of parameters α and β on the facilitation factor. In Fig. (a), as α increases, the facilitation factor generally decreases for all β values, indicating that higher reaction resistance suppresses transport efficiency. Larger β values yield higher facilitation factors, reflecting stronger carrier interaction, although a slight decline is observed at high α. In Fig. (b), increasing β initially enhances the facilitation factor due to improved complex formation, reaching a maximum before declining at large β. Additionally, higher α reduces the peak magnitude, demonstrating the competing effects of reaction kinetics and diffusion limitations in the transport process.

Conclusion

In this study, a modified Adomian Decomposition Method (MADM) has been successfully applied to analyze a nonlinear reaction–diffusion model describing carrier-mediated transport in a liquid membrane. The proposed method provides an efficient analytical framework for solving coupled boundary layer equations without requiring linearization or numerical discretization. Approximate analytical expressions for the concentration profiles of all species were obtained, enabling a detailed evaluation of the facilitation factor. The results demonstrate that the facilitation factor is strongly influenced by reaction kinetics and transport parameters, reflecting the interplay between diffusion and reversible complex formation. Overall, the present approach offers a reliable and accurate tool for investigating carrier-mediated membrane systems and can be extended to more complex geometries and reaction mechanisms.

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FOOD SAFETY AND HAZARD MANAGEMENT IN A GROWING WORLD: CHALLENGES IN SUPPLY CHAINS AND PUBLIC HEALTH

Sayed Rizwan A.
Department of Microbiology,
Sir Sayyed College of Arts, Commerce and Science, Aurangabad (Maharashtra)
Corresponding author E-mail: sayedra31@gmail.com

World population increasing, so does the demand for safe food and healthy food. Globally different statutory requirements are followed by the food sector in accordance with the quality and safety aspects. Increasing cases of food borne illness, food poisoning and food allergen, it has become more important than ever to ensure that food is free from harmful contaminants. In India, 65% of the population resides in the village where major occupation of the inhabitants is agriculture. India ranks leading position in the production of many principal crops, fruits and vegetables, milk, etc. But irreparable agricultural losses occur due to post harvest management practices, lack of timely processing, storage and transport especially of perishable foods.

Food Safety: Safe food is one of the three absolute essentials of life and since time immemorial human beings, conscionably or unconsciously, has been concerned about the safety of his food, as for as possible, poisonous species.

In global food market now consumer safety is the top most priority. Almost 70% of the illnesses now prevailing in the society are due to food, water, air borne microbial infections and intoxications, heavy metal, pesticide residues, veterinary drug and other chemical residues toxicities. We still remember severe pandemic in Europe by swine flu / influenza, which killed more than 50, million people during 1918-20 and in 2009-10 WHO has declared swine flu as pandemic disease affecting peoples of around 203 countries.

Currently around 85,000 chemical agents are produced and used in industrialized countries out of this less than 45% have undergone basic toxicological tests and many of them are causing severe toxicities and casualties leading to gastroenteritis, congenital malformations, asthma, cancer and neurological and behavioral disorders. Majority of these chemicals are found in essential commodities such as water, air, soil, and foods without which we can't survive.

Hazards in Supply Chain: The food industry world over is based on foundation of consumer's safety. Safe food or food safety is defined as freedom from danger, injury or damage or hazard to population consuming it. Hazards can be defined as the probability that injury or danger or damage to human health after use of the food. Danger can be encountered only if there exist some hazardous substance in food.

There are many opportunities for food to be contaminated between production and consumption. Food can be contaminated at the farm, during handling, processing, storage or in the sea in case of sea foods. The hazard is linked with toxicity. Hazards can be divided into following groups.

- Microbiological/biological hazards
- Chemical hazards, Physical hazards and
- Nutritional hazards

Food Contamination and Spoilage: Growing plants as well as animals bears typical flora on their surfaces and may become contaminated from outside sources. The number of organisms will depend on type of the plant, animal and environment and may range from a few hundred or thousands per square centimeter of surface to millions. One of the major causes of spoilage of food is growth and activity of microorganisms. The soil, water, sewage, air, animals, persons and processing equipment act as sources of contamination.

The food spoilage occurs due to growth and activity of micro-organisms, insects and native enzymes of plant.

Deleterious effects of these hazards include deterioration of food materials, unacceptable degradation of environment, production of allergies, infections, toxic metabolites and food poisoning out breaks. Public health concerns are associated with contamination of foods, ingredients, water, beverage and other consumables. Losses to the economy due to this in terms of spoilage are very heavy. In USA, annual post harvest losses are estimated at $ 7,750 million and in India the figure is around Rs. 60 thousand crores.

Biological Hazards: It includes fungi, bacteria, viruses, parasites, insects and pests. These are responsible for food borne hazards in any type of food establishment. The microorganisms can cause food borne infections, intoxications, and toxin-mediated infections.

When a living, disease-causing microorganism is ingested along with a food, it can cause a *food borne infection.* This can lead to the common symptoms of food borne illness such as diarrhoea. Bacteria, virus and parasites are examples of microorganisms that can cause infection. *Intoxication* is caused when a living organism multiplies in or on a food and produces a chemical waste or toxin. If the food containing the toxin is ingested the toxin causes an illness. The common examples of food intoxications are *Clostridium botulinum* and *Staphylococcus aureus.* Intoxication may also occur when an individual consumes food that contains manmade chemicals such as cleaning agents or pesticides.

A toxin-mediated infection is caused when a living organism is consumed with food (as in the case of an infection). Once the organism is inside the human body it produces a toxin that causes the illness. Toxin-mediated infection is different from intoxication because the toxin is produced inside the human body.

The risks and dangers associated with food borne illness are much greater for certain members of the population such as infants and young children, the elderly, pregnant women, and those with suppressed immune systems as occurs with AIDS.

In America public health efforts to promote a "heart healthy" diet have helped to boost the consumption of fresh fruit and vegetables. These items were the leading vehicle associated with food borne disease outbreaks.

Cost of microbial risks to human health is as high as nutritional imbalance and is assessed nearly 10,000 times of total risks due to environmental pollutants and 1 million times those of pesticides and food additives. To the processor, products, associated with defects due to microbial growth or public health causes adverse publicity and losses in sales and profits.

The hazardous microbes are categorized degree of severity which is based upon pathogenicity, number of consumers affected, infective dose, case fatality ratio, pathological effects on the host, persistence in the body of the host, duration of illness, cross-infection, etc.

Table 1: Hazardous Microorganisms and Parasites

Severe Hazards	**Moderate Hazards: Potentially Extensive Spread**	**Moderate Hazards: Limited Spread**
Clostridium botulinum types A, B, E, and F *Shigella dysenteriae* *Salmonella Typhi*; paratyphi A, B *Hepatitis* A and E *Brucella abortus; B. suis* *Vibrio cholerae* 01 *Vibrio vulnificus* *Taenia solium* *Trichinella spiralis*	*Listeria monocytogenes* *Salmonella spp.* *Shigella spp.* *Enterovirulent Escherichia coli (EEC)* *Streptococcus pyogenes* *Rotavirus* *Norwalk virus group* *Entamoeba histolytica* *Diphyllobothrium latum* *Ascaris lumbricoides* *Cryptosporidium parvum*	*Bacillus cereus* *Campylobacter jejuni* *Clostridium perfringens* *Staphylococcus aureus* *Vibrio cholerae,* non-01 *Vibrio parahaemolyticus* *Yersinia enterocolitica* *Giardia lamblia* *Taenia saginata*

Viruses: Viral infections make up perhaps one third of cases of food poisoning in developed countries. In the US, more than 50% of cases are viral and noroviruses are the most common food borne illness, causing 57% of outbreaks in 2004. Foodborne viral infection is usually of intermediate (1–3 days) incubation period, causing illnesses which are self-limited in otherwise healthy individuals, and are similar to the bacterial forms described above.

Parasites: Most food borne parasites are zoonoses.

Nematode: *Anisakisspp., Ascaris lumbricoides, Eustrongylides spp, Trichinella spiralis, Trichuris trichiura*

***Protozoa:** Acanthamoeba and other free-living amoebae, Cryptosporidium parvum, Cyclospora cayetanensis, Entamoeba histolytica, Giardia lamblia, Sarcocystis hominis, Sarcocystis suihominis, Toxoplasma gondii.*

Foods contaminated by infected food handlers and untreated water contaminated by human faeces contais parasites like *Cryptosporidium, Giardia lamblia, Entamoeba histolytica*

Parasitic Infections (Kingdom Animalia): Fresh water contaminated with certain types of snails that carry schistosomes and causes schistosomiasis. Drinking water contaminated with feces (usually canid) containing eggs causes ascariasis due to *Ascaris lumbricoides.*

Trends Contributing Food Poisoning

Five major trends contribute to the possible increase in food borne diseases.

i. Change in diet - In the earlier 7000 food items were available now >30,000 food items
ii. The increased use of commercial food services.
iii. New methods of producing and distributing food.
iv. New or re-emerging infectious food borne agents.
v. Growing member of people at high risk for severe or fatal food borne agents.

Chemical hazards

- Naturally occurring toxicants (e.g. marine biotoxins, mycotoxins)
- Environmental or industrial contaminants (e.g. mercury, lead, PCBs, dioxin, radionucleides)
- Residues of agricultural chemicals such as pesticides, of veterinary drugs and of surface sanitizers
- Toxic substances migrant from packaging or other materials in contact with food
- New issues in toxicology (e.g. allergenicity, endocrine disruption from pesticide residues).

Non-infective agents: heavy metal poisoning, including, cadmium, copper, lead, tin and zinc fish toxins that are present in some shellfish or fish like paralytic shellfish poisoning or ciguatera plant toxins which occur naturally in some foods such as toxic fungi and green potato skins toxic cyanobacteria (blue green algae) overgrowth in water.

There are number of chemical compounds, concentration of which are toxic to human health but the incidences of acute chemical intoxication are very low. However, long-term low-level exposure to some chemical contaminants may be associated with serious diseases such as neurological damage, birth defects & cancer.

Table 2: Types of Chemical Hazards and Examples

Naturally Occurring Chemicals	Added Chemicals
Mycotoxins (e.g., aflatoxin) from mold Scombrotoxin (histamine) from protein decomposition Ciguatoxin from marine dinoflagellates Toxic mushroom species Shellfish toxins (from marine dinoflagellates) Paralytic shellfish poisoning (PSP) Diarrhetic shellfish poisoning (DSP) Neurotoxic shellfish poisoning (NSP) Amnesic shellfish poisoning (ASP) Plant toxins Pyrrolizidine alkaloids Phytohemagglutinin	**Agricultural chemicals** Pesticides, fungicides, fertilizers, insecticides, antibiotics and growth hormones Polychlorinated biphenyls (PCBs) **Industrial chemicals** Prohibited substances (21 CFR 189) Toxic elements and compounds: Lead, zinc, arsenic, mercury, and cyanide **Food additives:** Direct - allowable limits under GMPs Preservatives (nitrite and sulfiting agents) Flavor enhancers (monosodium glutamate) Nutritional additives (niacin) Color additives Secondary direct and indirect Chemicals used in establishments (e.g., lubricants, cleaners, sanitizers, cleaning compounds, coatings, and paints) Poisonous or toxic chemicals intentionally added (sabotage)

Natural Toxicants and Human Disease: Acquired Toxins

- Microbial toxins-toxigenic food borne bacteria and intoxication due to toxin produced in the food such as *B. cereus, S. aureus* and *C. botulinum.*
- Mycotoxins (e.g. aflatoxin)
- Mushrooms (mold)

Growth of commonly occurring filamentous fungi in foods may result in production of toxins known as mycotoxins, which can cause a variety of ill effects in humans, from allergic responses to immuno suppression and cancer. The most important mycotoxins are aflatoxins, ochratoxin A, fumonisins, tnchothecenes and zearalenone.

Aflatoxins are a type of mycotoxin produced by *Aspergillus* species of fungi, such as *A. flavus* and *A. parasiticus.* The umbrella term aflatoxin refers to four different types of mycotoxins produced, which are B_1, B_2, G_1, and G_2. Aflatoxin B_1, the most toxic, is a potent carcinogen and has been directly correlated to adverse health effects, such as liver cancer, in many animal species. Aflatoxins are largely associated with commodities produced in the tropics and subtropics, such as cotton, peanuts, spices, and maize.

Ochratoxin is a mycotoxin that comes in three secondary metabolite forms, A, B, and C. All are produced by *Penicillium* and *Aspergillus* species. The three forms differ in that Ochratoxin B (OTB) is a nonchlorinated form of Ochratoxin A (OTA) and that Ochratoxin C (OTC) is an ethyl ester form Ochratoxin A. *Aspergillus ochraceus* is found as a contaminant of a wide range of commodities including beverages such as beer and wine. *Aspergillus carbonarius* is the main species found on vine fruit, which releases its toxin during the juice making process. OTA has been labeled as a carcinogen and a nephrotoxin, and has been linked to tumors in the human urinary tract, although research in humans is limited by confounding factors.

Ergot Alkaloids are compounds produced as a toxic mixture of alkaloids in the sclerotia of species of *Claviceps,* which are common pathogens of various grass species. The ingestion of ergot sclerotia from infected cereals, commonly in the form of bread produced from contaminated flour, cause ergotism the human disease historically known as St. Anthony's Fire. Modern methods of grain cleaning have significantly reduced ergotism as a human disease, however it is still an important veterinary problem.

Fumonisins toxins are produced by over 50 species of *Fusarium* and have a history of infecting the grain of developing cereals such as wheat and maize. They include a range of mycotoxins, such as: the fumonisins, which affect the nervous systems of horses and may cause cancer in rodents; the trichothecenes, which are most strongly associated with chronic and fatal toxic effects in animals and humans; and **zearalenone,** which is not correlated to any fatal toxic effects in animals or humans. Some of the other major types of Fusarium toxins include: beauvercin and enniatins, butenolide, equisetin, and fusarins.

Trichothecene Toxins: Deoxynivalenol (vomitoxin) and nivalenol are among the many trichothecene mycotoxins produced by Fusanum species. DON causes vomiting and feed refusal in pigs at levels near 8 mg/kg of feed42. It was responsible for a large-scale human toxicosis in India in 1988, and human toxicoses have also been reported from China, Japan and Korea. Symptoms m humans include anorexia, nausea, vomiting, headache, abdominal pain, diarrhoea, chills, giddiness and convulsions.

Zearalenone: Zearalenone is an oestrogenic toxin, also produced by *F. graminearum* and closely related species. The effect of zearalenone in animals is a well- defined syndrome. Maize, barley and wheat grains infected with *F. graminearwn* and containing zearalenone cause genital problems in domestic animals, especially pigs. Symptoms include hyperaemia and oedematous swelling of the vulva in prepubertal gilts, or, in more severe cases, prolapse of the vagina and rectum. Reproductive disorders in sows include infertility, fetal resorption or mummification, abortions, reduced litter size and small piglets. Zearalenone has been implicated in several incidents of precocious pubertal changes in children.

T-2 Toxin: T-2 Toxin is a tricothecene produced by species of Fusarium and is one of the more deadly toxins. If ingested in sufficient quantity, T-2 toxin can severely damage the entire digestive tract and cause rapid death due to internal hemorrhage. T-2 has been implicated in the human diseases alimentary toxic aleukia and pulmonary hemosiderosis. Damage caused by T-2 toxin is often permanent.

Vomitoxinor Deoxynivalenol (DON): Vomitoxin, chemically known as Deoxynivalenol, a tricothecene mycotoxin, is produced by several species of Fusarium. Vomitoxin has been associated with outbreaks of acute gastrointestinal illness in humans. The FDA advisory level for vomitoxin for human consumption is 1ppm.

Citrinin: Citrinin is a nephrotoxin produced by Penicillium and Aspergillus species. Renal damage, vasodilatation, and bronchial constriction are some of the health effects associated with this toxin.

Gliotoxin: Gliotoxin is an immunosuppressive toxin produced by species of Alternaria, Penicillium and Aspergillus.

Sterigmatocystin: Sterigmatocystin is a nephrotoxin and a hepatotoxin produced by Aspergillus versicolor. This toxin is also considered to be carcinogenic. Other mycotoxins include - Penicillic acid, roquefortine, cyclopiazonic acid, verrucosidin.

Hence, there are many mycotoxins that can cause adverse health effects and even death in humans. The synergistic effect of exposure to multiple mycotoxins simultaneously is very poorly understood. Even more poorly understood are the by-products of mycotoxin degradation. More research is required in this field for better understanding.

Endotoxins: Endotoxin is the name given to a group of heat stabile lipopolysaccharide molecules present in the cell walls of gram-negative bacteria that have a certain characteristic toxic effect. The lipid portion of each molecule is responsible for its toxicity and can vary between bacterial species and even from cell to cell. When inhaled, endotoxin creates an inflammatory response in humans that may result in fever, malaise, alterations in white blood cell counts, headache, respiratory distress and even death. It is common to the environment due to the ubiquitous nature of Gram-negative bacteria. Exposure to elevated levels of endotoxin primarily occurs through exposure to aerosols from specific reservoirs such as cotton mills, wastewater treatment facilities, air washers, humidifiers and any other occupational settings where Gram-negative bacteria can flourish.

Alkaloids

- Ciguatera poisoning
- Grayanotoxin (honey intoxication)
- Mushroom toxins
- Phytohaemagglutinin (red kidney bean poisoning; destroyed by boiling)

- Pyrrolizidine alkaloids
- Scombrotoxin
- Tetrodotoxin (fugu fish poisoning)

Allergens

Cereals (rice, wheat, barley, etc.), peanuts, peas, lentils, soya beans, strawberries, bananas, mangoes, pineapples, sesame, poppy and caraway seeds, tea, chocolate, coffee, yeasts, alcoholic beverages, honey and other foods likely to contain pollen. **Caffeine:** Tea, coffee, cola- type soft drinks. **Cyanide:** Apricot kernels, peach kernels, apple seeds, cassava, young bamboo shoots, bitter almonds, coloured varieties of lima beans. Favism Broad beans. **Goitrogens:** Cabbage, Brussels sprouts, broccoli, kale, turnips, swedes, mustard seeds, horseradish. **Haemagglutinins:** Uncooked legumes (castor beans, kidney beans, lima beans, soya beans, lentils, peas). **Lathyrogens:** Chickpeas. Oxalic acid: Spinach, rhubarb. **Nitrates and nitrites**: Celery, lettuce, spinach, cabbage, cured meats. **Pyrrolizidine alkaloids:** Comfrey, some 'herbal' teas. **Solanine:** Sprouted and 'greening' potatoes.

Mushroom Toxins

There are a number of recognized mushroom toxins listed below with specific, and sometimes deadly, effects:

- Alpha-amanitin (deadly: causes liver damage 1-3 days after ingestion) - principal toxin in genus Amanita
- Phallotoxin (causes gastrointestinal upset) - also found in poisonous Amanitas
- Orellanine (deadly: causes kidney failure 3 weeks after ingestion) - principal toxin in genus Cortinarius
- Muscarine (sometimes deadly: can cause respiratory failure) - found in genus Omphalotus
- Gyromitrin (deadly: causes neurotoxicity, gastrointestinal upset, and destruction of blood cells) - principal toxin in genus Gyromitra
- Coprine (causes illness when consumed with alcohol) - principal toxin in genus Coprinus
- Ibotenic acid and muscimol (hallucinogenic) - principal toxin in A. muscaria, A. pantherina, and A. gemmata
- Psilocybin and psilocin (hallucinogenic) - principal toxin in genus Psilocybe
- Arabitol (causes gastrointestinal irritation in some people)
- Bolesatine a toxin found in Boletus satanas
- Ergotamine (deadly: affects the vascular system and can lead to loss of limbs and death): An alkaloid found in genus Claviceps.

Mad Cow Disease (Prions)

Mad cow disease is one of the most lethal and shocking illness in the world today. This dreadful malady is scientifically known as Bovine Spongiform Encephalopathy. Bovine Spongiform Encephalopathy is transmissible neurodegenerative fatal brain disease of cattle. When it occurs in human is called as variant Creutzfelt Jakob disease.

Bovine spongiform encephelopathy (BSE) first diagnosed in Great Britain in 1986 and in Canada 2003. Humans can contract a related illness, variant Creulzfeldt Jackob disease (VCJD) by eating infected beef. The agent responsible for BSE is generally believed to be a malformed protein called a prion. Prions cause normal proteins in the brain to become deformed, which lead to sponge like helps in the brain called spongiform. The contaminated feed ingredients are the source of the illness in cattle.

Mad cow disease caused by prion an abnormal protein which is highly stable, resistant to freezing, heating at cooking temperature, pasteurization drying, UV light. Nature of agent is still matter of debate i.e. prion or virus particle.

Heavy Metal Contamination, Sources and Toxicity

Heavy Metal Contamination is a general term given to describe a condition in people who have abnormally high levels of toxic metals in the body. Common examples are mercury, lead, cadmium and arsenic. This contamination can be very real, detrimental to health and deadly.

Heavy metals are subtle, silent, stalking killers. They enter the body with our food, water, air we breathe and by skin contact. They slowly accumulate in the kidneys, liver, pancreas, bones, central nervous system and brain where they degrade health without being noticed or diagnosed. Heavy metals can and do cause cancer without ever being implicated in the diagnosis. Heavy metals cause sodium retention leading to high blood pressure. Heavy metals can and do cause heart disease and mental retardation. Everyone is contaminated with heavy metals, some seriously, without ever knowing it.

Heavy metals can enter the body from a wide variety of sources including foods, drinks, contaminated air, and contact with the skin, vaccines, injections and implants within the body.

Symptoms of toxic heavy metal poisoning can be mental retardation in children, dementia in adults, central nervous system (CNS) disorders, kidney (renal) diseases, liver (hepatic) diseases, insomnia, personality changes, emotional instability, depression, panic attacks, memory loss, headaches, vision disturbances including peripheral neuropathy, excess salivation, excess sweating and lack of coordination (ataxia). Death is often caused by encephalopathy (diseases of the brain) or cardiovascular diseases (CVD). Heavy metal toxicity can cause the blood pH to become acidic. The body buffers this acidity by extracting calcium from the bones. The calcium (not a heavy metal) tends to accumulate in the soft tissue of the arteries causing hardening of the arteries. Removing calcium from soft tissue is extremely difficult, although the protocol present here may be helpful in reducing hardening of the arteries as well as the removing the toxic heavy metals.

Table 3: Tolerances and critical limits in fish and fish products

Sr. No.	Substance	Maximum levels	
		US (ppm)	Eu mg/kg wet wet
1.	Arsemic	75-56	--
2.	Cadmium	3-4	0.05-1.0
3.	Lead	1.5-1.7	0.2-1.0
4.	Methyl mercury	1.0	1.0
5.	Diedrin	0.0	--

Organic Compounds

Polychlorinated compound formed when organic compounds are burn in presence biphenyls, dioxins (compounds formed when organic compounds are burnt in presence of chlorine), and insecticides. The chemicals stability of all these compounds to accumulate and persist in the environment.

Dioxins are mainly by products of industrial processes but can also result from natural processes, such as volcanic eruptions and forest fires. Dioxins are unwanted by products of a wide range of manufacturing processes including smelting, chlorine bleaching of paper pulp and the manufacturing of some herbicides and pesticides. In terms of dioxin release into the environment, waste incinerators (solid waste and hospital waste) are often the worst culprits, due to incomplete burning.

The chemical name for dioxin is: 2, 3, 7, 8- tetrachlorodibenzo para dioxin (TCDD). The name 'dioxins' is often used for the family of structurally and chemically related polychlorinated dibenzo para dioxins (PCDDs) and polychlorinated dibenzofurans (PCDFs). Certain dioxin-like polychlorinated biphenyls (PCBs) with similar toxic properties are also included under the term "dioxins". Some 419 types of dioxin-related compounds have been identified but only about 30 of these are considered to have significant toxicity, with TCDD being the most toxic.

Table 4: Dioxin amounts in common foods

Sr. No.	Food commodity	Picogram toxic equivalent /g fat	
		Minimum	Maximum
1.	Milk products	0.5	3.8
2.	Meat and meat products	0.1	16.7
3.	Poultry	0.7	2.2
4.	Fish	2.4	214.3
5.	Eggs	1.2	4.6
6.	Fat and Oils	0.2	2.6
7.	Bread & cereals	0.1	2.4

Antibiotics Residues

With the increased use of veterinary drugs in food productions, there is global concern about the consumption of low levels of antimicrobial residues in aquatic food and the effects of these residues on human health. The potential hazards due to these chemicals drugs or allergies, toxic effects changes in the colonization pattern of human gut flora and acquisition of drug resistance in pathogens in the human body.

Pesticide

A pesticide is any substance, preparation or organism prepared or used for destroying any pest. Pesticides help in maximizing the food production, protect seeds and prolong the life of produce. However, they also leave toxic residues on treated commodities. If the residue found in any particular food is above certain level it may affect human health or the environment. Therefore, the manufacture, sale and use of pesticides are regulated by a process called 'registration'. To safeguard the consumer health from unreasonable health risk posed by pesticide residues, the international tolerances are set by WHO-FAO. The basic rules set by WHO-FAO for safety standards are obligatory for member counties of WTO. These rules apply to domestic and imported food products. The monitoring of pesticide residues in food is being carried out by almost all nations regularly.

The SPS Agreement of the WTO entered in to force on 1st January, 1995 addresses the challenges of food safety, animal and plant. The Codex Alimentarius Commission (one of the three bodies) is the international food safety standards setting body within FAO-WHO. Codex Committee on Pesticide Residues (CCPR) recommends to Codex Alimentarius Commission to establish maximum residue limits for pesticides.

Insecticides Pesticides Toxicity

Some pesticides are so highly toxic that very small quantities can kill a person, while exposure to a sufficient amount of almost any pesticide can make a person ill. Since even fairly safe pesticides can irritate the skin, eyes, nose, or mouth, it is a good idea to understand how pesticides can be toxic so you can follow practices designed to reduce or eliminate your exposure and the exposure of others to them. The commonly used pesticides are carbaryl, diazynon, dicofol, dimithioate, endosulphan, lindane, malathion, pyrethrins etc.

Residues of Veterinary Drugs: It include the parent compounds and / or their metabolites in dry edible portion of the animal product. A veterinary drug is defined as any substance applied or administrated to a food producing animal, such as meat or dairy animals, poultry, fish and beef for therapeutic, prophylactic or diagnostic purposes or for the modification of physiological function or behavior. The MRL VD limits are defined by CAC.

Additives and Chemicals Developed During Processing: High temperature heating (roasting) of the foods develops brown colours. The roasted foods are reported to be containing a chemical known as acrylamide formed by reaction between protein & carbohydrate. It is present in various fried & baked foods in the range of 10 to 4000 ppb. It is known to involved in carcinogenesis, causes neurological damage, genetic mutation and impaired fertility. The carbohydrate rich foods even after boiling, steaming or prepared at low temperature also found to contain acrylamide in detectable amount. The recently FDA of USA highlighted this as a protein hazard that acrylamide might pose in future. The fried samples in USA & Canada reported 1265 to 3700 ppb of acryl amide. The present daily intake of acryl amide in US, Europe and other industrialized countries could be as high as 18 ug./ Kg. of body weight while current safe level for this toxic chemical in water is fixed at 0.2 mg/Kg. of body weight. Asparagine, one of the consistent amino acids present in all proteins, has been found to react with glucose when heated forming the acrylamide. The Nestle Lab. reported that carbohydrate (dicarbonyls) also can react with amino acids like glycine, methionine & cysteine beside asparagine, to produce acrylamide under simulated conditions.

Common Adulterants/Contaminants

Adulteration in food is normally present in its most crude form; prohibited substances are either added or partly or wholly substituted.

Genetically Modified Foods

Soybean was tried to improve its nutritional quality by inserted gene from Brazil nut. However, in their testing, they found that the protein produced was the one responsible for the allergencity of Brazil nuts i.e. allegenicity was also transferred to the soybeans. This soybean has never been marketed.

Some people worry that live GMF's could transfer antibiotic resistant genes to people and it could limit the number of antibiotics in medical treatment. To counter act this, regulatory authorities advise that, wherever GMF's are to be consumed live, eg. Yoghurt made using modified starter cultures, the marker genes should be eliminated from the final product. This is only a problem with recent products as a DNA including antibiotic resistant gene, is altered by the cooking process.

Physical Hazards in the Agri-Food Chain

Numbers of physical hazards like stones, metal pieces, hairs, pieces of plastics etc. are involved in food which causes harm to health.

Illness and injury can result from hard foreign objects in food. These physical hazards can result from contamination and/or poor procedures at many points in the food chain from harvest to consumer, including those within the food establishment.

Determining Level of Risk

The potential significance or risk of each hazard should be assessed by considering its likelihood of occurrence and severity. The estimate of risk for a hazard occurring is based upon a combination of experience, epidemiological data, and information in the technical literature. Severity is the degree of seriousness of the consequences of a hazard if it were to become an actuality. Hazard identification in conjunction with risk estimation provides a rational basis for determining which hazards are significant and must be addressed in the HACCP plan. To determine risk during the hazard analysis, safety concerns must be differentiated from quality concerns. There may be differences of opinion, even among experts, as to the risk of a hazard. The food establishment must rely upon the expert opinion published in peer reviewed literature or experts who actively assist in the development of the HACCP plan. The hazards must at least include those that are commonly associated with a specific product. If a hazard that is commonly associated is dismissed from the plan, the basis for rejecting it must be clearly stated in the hazard analysis so that it is understood and agreed to by the regulatory authority reviewing the HACCP plan.

Table 5: Main Materials as Physical Hazards and Common Sources

Material	Injury Potential	Sources
Glass fixtures	Cuts, bleeding; may require surgery to find or remove	Bottles, jars, light, utensils, gauge covers
Wood	Cuts, infection, choking; may require surgery to remove	Fields, pallets, boxes, buildings
Stones, metal fragments	Choking, broken teeth Cuts, infection; may require surgery to remove	Fields, buildings, machinery, fields, wire, employees
Insulation	Choking; long-term if asbestos	Fields, improper plant processing
Bone	Choking, trauma	Building materials
Plastic	Choking, cuts, infection; may require surgery to remove	Fields, plant packaging materials, pallets, employees
Personal effects	Choking, cuts, broken teeth; may require surgery to remove	Employees

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FUTURE TRENDS IN SCIENCE AND TECHNOLOGY RESEARCH

K. Prabhu* and C. Amirthakumar
Department of Physics, AMET University, Kanathur, Tamilnadu - 603112
*Corresponding author E-mail: k.prabhuresearch@gmail.com

Abstract

The rapid advancement of science and technology is reshaping research paradigms, enabling unprecedented innovation across disciplines. Emerging domains such as artificial intelligence, quantum computing, biotechnology, and sustainable engineering are transforming the global research landscape. This chapter critically examines future trends in science and technology research, emphasizing digital transformation, interdisciplinary convergence, sustainability, and ethical considerations. The study integrates insights from recent literature and bibliometric analyses to identify emerging research directions. Findings suggest that data-driven research, automation, and collaborative innovation ecosystems will dominate future scientific advancements. This paper also highlights key challenges, including ethical concerns, resource limitations, and knowledge fragmentation. Finally, future directions are proposed to guide researchers and policymakers toward sustainable and impactful research development.

Keywords: Artificial Intelligence, Emerging Technologies, Sustainability, Interdisciplinary Research, Innovation.

1. Introduction

The field of science and technology research has evolved significantly over the past century, transitioning from isolated disciplinary studies to highly integrated and interdisciplinary frameworks. The rapid growth of digital technologies, globalization, and increased investment in research and development (R&D) has accelerated innovation across multiple sectors [1], [2]. In recent years, the emergence of advanced computational tools, artificial intelligence, and big data analytics has further transformed research methodologies, enabling more efficient data processing and predictive modeling [3]. Forecasting future trends in science and technology research has become essential for strategic planning, funding allocation, and policy formulation. Bibliometric studies and trend analysis techniques are increasingly used to identify emerging research domains and predict future developments [1], [4]. These approaches allow researchers to analyze citation networks, publication patterns, and technological advancements to anticipate future innovations.

Furthermore, science and technology research is increasingly influenced by global challenges such as climate change, energy demand, healthcare accessibility, and sustainable development. Addressing these complex issues requires interdisciplinary collaboration and the integration of multiple technologies [5], [6]. As a result, modern research emphasizes convergence between disciplines such as engineering, biology, computer science, and environmental science. This chapter aims to provide a comprehensive analysis of future trends in science and technology research by examining key emerging technologies, interdisciplinary approaches, and societal impacts. The paper also identifies challenges and proposes future research directions to guide researchers and policymakers in navigating the evolving research landscape.

2. Artificial Intelligence and Machine Learning

Artificial Intelligence (AI) and Machine Learning (ML) are among the most transformative technologies shaping the future of scientific research. These technologies enable automation, predictive analytics, and intelligent decision-making, significantly enhancing research efficiency and accuracy [7], [8]. AI has revolutionized data analysis by enabling researchers to process large datasets and extract meaningful insights. Machine learning algorithms can identify patterns and trends that are not easily detectable through traditional analytical methods. This capability is particularly valuable in fields such as healthcare, climate science, and engineering, where complex datasets are common [9].

In healthcare, AI is used for disease diagnosis, drug discovery, and personalized medicine. For example, deep learning models can analyze medical images to detect diseases such as cancer with high accuracy [10]. Similarly, AI-driven drug discovery platforms can significantly reduce the time and cost required to develop new medications [11]. In environmental science, AI is used for climate modeling, weather prediction, and resource management. Machine learning algorithms can analyze historical climate data to predict future trends and assess the impact of climate change [12]. These insights are crucial for developing effective mitigation and adaptation strategies.

AI is also transforming engineering and manufacturing through automation and smart systems. Industry 4.0 technologies, such as robotics and IoT, rely heavily on AI to optimize production processes and improve efficiency [13]. Predictive maintenance, powered by machine learning, allows industries to anticipate equipment failures and reduce downtime. Despite its advantages, AI also presents several challenges, including ethical concerns, data privacy issues, and algorithmic bias [14]. Ensuring transparency, fairness, and accountability in AI systems is essential for their widespread adoption. Looking ahead, AI is expected to play an even more significant role in scientific research, enabling autonomous experimentation, real-time data analysis, and advanced simulations. The integration of AI with other emerging technologies will further enhance its impact, making it a cornerstone of future scientific innovation.

3. Big Data and Data-Driven Research

The exponential growth of data has led to the emergence of data-driven research paradigms, where scientific discoveries are increasingly based on large-scale data analysis [1], [15]. Big data technologies enable researchers to collect, store, and analyze vast amounts of structured and unstructured data, providing valuable insights into complex systems. One of the key advantages of big data is its ability to support predictive analytics. By analyzing historical data, researchers can identify trends and make informed predictions about future events. This capability is widely used in fields such as healthcare, finance, and environmental science [16]. In scientific research, big data facilitates the integration of diverse datasets from multiple sources. For example, in genomics, researchers can analyze large-scale genetic data to identify disease markers and develop personalized treatments [17]. Similarly, in climate science, big data is used to analyze environmental data and model climate change scenarios [12]. Another important aspect of data-driven research is real-time data analysis. With the help of advanced analytics tools, researchers can process data in real time, enabling faster decision-making and more efficient research processes [18]. This is particularly useful in applications such as disaster management, where timely information is critical.

Big data also plays a crucial role in trend forecasting. Bibliometric analysis and machine learning techniques can be used to analyze publication data and identify emerging research topics [1], [4]. This helps researchers and policymakers prioritize research areas and allocate resources effectively. However, the use of big data also presents challenges, including data privacy, security, and management issues [19]. Ensuring data quality and integrity is essential for obtaining reliable results. In the future, big data is expected to become even more integral to scientific research, with advancements in data storage, processing, and analytics technologies. The integration of big data with AI and IoT will further enhance its capabilities, enabling more sophisticated and data-driven research approaches.

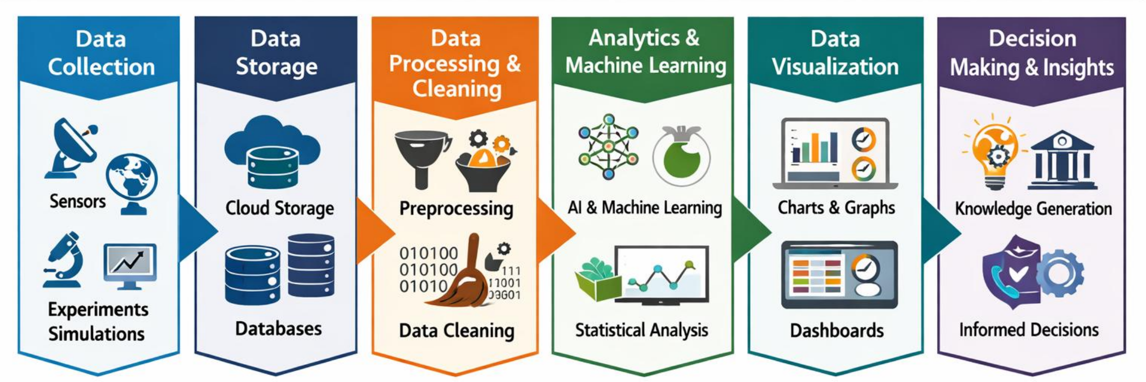

Figure 1: Big Data and Data-Driven Research Framework

Big data and data-driven research framework illustrating the transformation of raw data into actionable knowledge. Fig. 1 depicts the workflow of data-driven research, beginning with data collection from sources such as sensors, experiments, and digital platforms. The collected data is stored in scalable systems like cloud storage and databases. It then undergoes preprocessing and cleaning to ensure quality and consistency. In the analytics stage, machine learning and statistical methods are applied to extract patterns and insights. The results are presented through data visualization tools such as charts and dashboards for better interpretation. Finally, the insights support decision-making and knowledge generation, highlighting the role of big data in enabling efficient, accurate, and innovation-driven scientific research.

4. Internet of Things (IoT) and Smart Systems

The Internet of Things (IoT) is a transformative technology that enables the interconnection of devices, sensors, and systems, facilitating real-time data exchange and automation [13], [20]. IoT plays a crucial role in the development of smart systems, which are increasingly being used in various domains, including healthcare, agriculture, and urban planning. In smart cities, IoT technologies are used to monitor and manage infrastructure, traffic, energy consumption, and waste management. Sensors and connected devices provide real-time data, enabling efficient resource management and improved quality of life [21]. For example, smart traffic systems can reduce congestion and improve transportation efficiency.

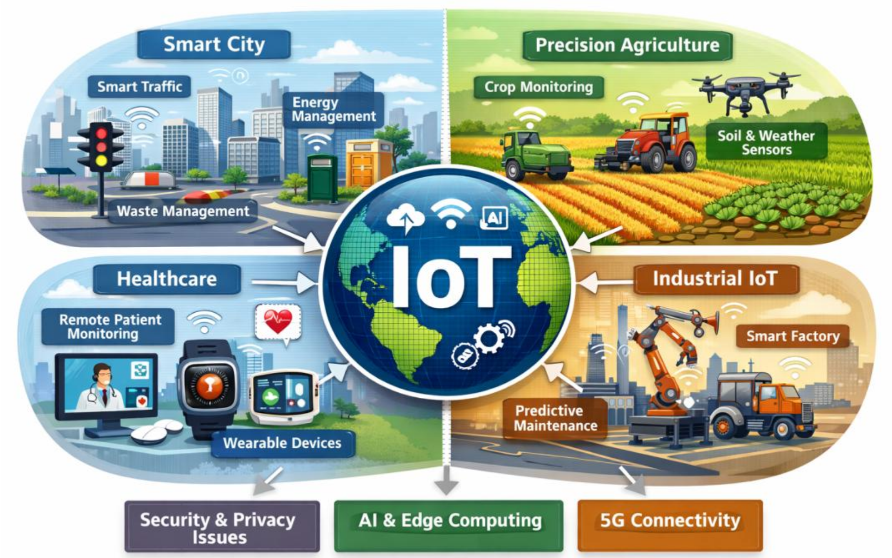

Figure 2: Applications and Future Trends of the Internet of Things (IoT)

In agriculture, IoT enables precision farming, where sensors monitor soil conditions, weather patterns, and crop health. This allows farmers to optimize resource usage, improve crop yields, and reduce environmental impact [22]. IoT is also widely used in healthcare for remote patient monitoring and telemedicine. Wearable devices can track vital signs and provide real-time health data to healthcare providers, enabling early diagnosis and timely intervention [23]. Industrial IoT (IIoT) is transforming manufacturing processes by enabling automation, predictive maintenance, and efficient resource utilization. Smart factories use IoT technologies to monitor equipment performance and optimize production processes [13]. Despite its benefits, IoT faces challenges related to security, privacy, and interoperability [24]. Ensuring secure communication and data protection is critical for the successful implementation of IoT systems. Future trends in IoT include the integration of AI, edge computing, and 5G technologies, which will enhance connectivity, reduce latency, and improve system performance. These advancements will further expand the applications of IoT and drive innovation across various sectors.

The fig. 2 illustrates the Internet of Things (IoT) connecting smart city infrastructure, precision agriculture, healthcare, and industrial systems. It shows how sensors and devices enable real-time data exchange, improving efficiency and automation. The diagram also highlights challenges like security and future trends such as AI, edge computing, and 5G connectivity integration.

5. Renewable Energy and Sustainability

Sustainability has become a central focus of science and technology research, driven by the need to address environmental challenges such as climate change, resource depletion, and pollution [5], [25]. Renewable energy technologies, including solar, wind, and hydropower, are playing a key role in reducing greenhouse gas emissions and promoting sustainable development. Advancements in solar energy technologies, such as photovoltaic cells and concentrated solar power systems, have significantly improved energy efficiency and reduced costs [26]. Similarly, wind energy technologies have become more efficient and cost-effective, making them a viable alternative to fossil fuels [27]. Energy storage technologies, such as batteries and super-capacitors, are also critical for the integration of renewable energy into power systems. These technologies enable the storage of excess energy and ensure a stable energy supply [28]. Fig. 3 shows renewable energy generation, energy storage, circular economy, water management, and smart grid integration for sustainable development and reduced environmental impact.

Figure 3: Sustainable Energy and Resource Systems

In addition to energy generation, sustainability research focuses on resource management, waste reduction, and environmental protection. Circular economy approaches aim to minimize waste and promote the reuse and recycling of materials [29]. Water resource management is another important area of sustainability research. Advanced technologies, such as desalination and wastewater treatment, are being developed to address water scarcity and improve water quality [30]. Despite significant progress, challenges remain in the adoption of renewable energy and sustainable technologies, including high initial costs, infrastructure limitations, and policy barriers [31]. Future research will focus on improving energy efficiency, developing advanced materials, and integrating renewable energy systems with smart grids. The adoption of sustainable technologies will be essential for achieving global environmental goals and ensuring long-term economic and social development.

6. Interdisciplinary Research and Convergence

Interdisciplinary research is increasingly recognized as a key driver of innovation in science and technology. By integrating knowledge and methodologies from multiple disciplines, researchers can address complex problems that cannot be solved within a single field [6], [32]. One of the most prominent examples of interdisciplinary research is the integration of AI and healthcare. AI technologies are used to analyze medical data, develop diagnostic tools, and improve patient care [10]. Similarly, the convergence of nanotechnology and medicine has led to the development of advanced drug delivery systems and targeted therapies [33]. In environmental science, interdisciplinary approaches are used to study climate change, biodiversity, and ecosystem dynamics. Researchers from different fields collaborate to develop comprehensive solutions for environmental challenges [5].

Interdisciplinary research also plays a crucial role in the development of smart cities, where technologies such as IoT, AI, and data analytics are integrated to improve urban living conditions [21]. Despite its benefits, interdisciplinary research faces challenges related to communication, collaboration, and knowledge integration [34]. Researchers must overcome disciplinary boundaries and develop a common understanding to work effectively together. Future trends in interdisciplinary research include the development of collaborative platforms, open science initiatives, and cross-disciplinary education programs. These efforts will facilitate knowledge sharing and promote innovation.

Conclusion

The future of science and technology research is characterized by rapid advancements, interdisciplinary collaboration, and digital transformation. Emerging technologies such as AI, big data, IoT, and renewable energy are reshaping research paradigms and creating new opportunities for innovation. To fully realize the potential of these technologies, it is essential to address challenges related to ethics, data privacy, and resource allocation. Collaboration between researchers, policymakers, and industries will be crucial for driving sustainable and impactful research. This chapter provides a comprehensive overview of future trends in science and technology research and serves as a valuable resource for researchers and decision-makers.

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DEEP LEARNING FOR PROTEIN STRUCTURE PREDICTION AND DESIGN

Ranjana
Department of Zoology,
Patna Science College, Patna University, Patna, Bihar, 800005, India.
Corresponding author E-mail: ranjana.prakash81@gmail.com, ranjanazoolpsc@pup.ac.in

Abstract

The prediction and rational design of protein structures represent one of the most consequential challenges in modern biology. Deep learning has fundamentally transformed this field, transitioning from decades of incremental progress to near-experimental accuracy within a few years. This chapter provides a comprehensive review of deep learning architectures and methodologies applied to protein structure prediction and computational design. We discuss the evolution from early convolutional neural network approaches through attention-based transformers, equivariant neural networks, diffusion models, and protein language models. The landmark achievements of AlphaFold2 [1] and RoseTTAFold [2] are examined in detail, alongside emerging tools for de novo protein design. We address critical challenges including multi-chain complex prediction, membrane proteins, and intrinsically disordered regions. Applications spanning drug discovery, vaccine development, and synthetic biology are surveyed. Finally, we identify open problems and outline future directions for the integration of deep learning with experimental structural biology. This chapter aims to serve as a foundational reference for researchers entering this rapidly evolving field and for practitioners seeking to leverage computational tools in protein science.

Keywords: Protein Structure Prediction, Deep Learning, Alphafold, Protein Design, Evoformer, Diffusion Models, Protein Language Models, CASP, Inverse Folding, De Novo Design.

1. Introduction

Proteins are the molecular machines of life, performing virtually every biological function — catalyzing chemical reactions, transmitting signals, providing structural support, and defending against pathogens. Their function is inextricably linked to their three-dimensional structure, yet the relationship between amino acid sequence and folded conformation — the protein folding problem — evaded solution for over half a century [3]. The experimental determination of protein structures through X-ray crystallography, nuclear magnetic resonance (NMR) spectroscopy, and cryo-electron microscopy (cryo-EM) has yielded over 220,000 entries in the Protein Data Bank (PDB) [4], yet this represents only a minute fraction of the hundreds of millions of known protein sequences.

The advent of deep learning has catalyzed unprecedented progress in computational structural biology. The Critical Assessment of Protein Structure Prediction (CASP) experiment, which benchmarks computational methods against experimentally determined structures, has documented this transformation with striking clarity. At CASP13 in 2018, DeepMind's AlphaFold achieved top performance using novel deep learning approaches [5]. At CASP14 in 2020, AlphaFold2 produced predictions with median GDT-TS scores exceeding 90, effectively solving the backbone structure prediction problem for single-chain globular proteins under many conditions [1]. This achievement, described by many researchers as one of the most significant scientific breakthroughs of the decade, opened new horizons not only for structure prediction but also for the computational design of proteins with novel functions.

This chapter is organized as follows. Section 2 provides background on protein structure and the biological problem. Section 3 traces the historical development of computational methods. Section 4 details the architecture of AlphaFold2 and related systems. Section 5 covers protein language models. Section 6 discusses de novo protein design with generative models. Section 7 surveys benchmark datasets. Section 8 outlines applications, and Section 9 discusses future challenges.

2. Protein Structure: Biological Background

2.1 Hierarchical Organization

Protein structure is conventionally described at four hierarchical levels [6]. The *primary structure* is the linear amino acid sequence encoded by the gene. The *secondary structure* comprises local regular patterns — predominantly alpha-helices and beta-sheets — stabilized by hydrogen bonds between backbone atoms. The *tertiary structure* is the complete three-dimensional arrangement of all atoms in a single polypeptide chain. The *quaternary structure* describes the arrangement of multiple polypeptide subunits in oligomeric complexes. Deep learning methods have been developed to predict all levels of this hierarchy, with the most dramatic recent advances in tertiary structure prediction.

2.2 The Sequence–Structure–Function Paradigm

The central paradigm of protein biophysics holds that a protein's amino acid sequence uniquely determines its three-dimensional structure under physiological conditions, which in turn determines its biological function — the so-called sequence–structure–function relationship [7]. This paradigm underpins the biological motivation for computational structure prediction: if we can accurately predict structure from sequence, we can infer function for the vast number of uncharacterized proteins and design novel proteins with desired functions.

However, this paradigm involves important caveats. Intrinsically disordered proteins (IDPs) and intrinsically disordered regions (IDRs) lack a stable folded structure yet perform crucial biological roles [8]. Membrane proteins adopt different folding principles due to the lipid bilayer environment. Protein–protein and protein–ligand interactions may induce conformational changes. These complexities represent ongoing challenges for deep learning approaches.

3. Historical Development of Computational Methods

3.1 Early Physics-Based and Statistical Approaches

The history of computational protein structure prediction spans more than 50 years. Early methods were grounded in physical chemistry — energy minimization using molecular mechanics force fields (AMBER, CHARMM, GROMOS) and Monte Carlo sampling sought to identify the lowest free-energy conformation [6]. These approaches, while physically principled, suffered from incomplete energy functions and an astronomical conformational search space.

Fragment-based assembly methods, exemplified by Rosetta, made significant progress by leveraging structural fragments from the PDB as building blocks for de novo folding simulations [7]. Homology modeling — building structural models based on evolutionarily related proteins of known structure — proved effective when suitable templates existed, achieving accuracies within 1–2 Å backbone RMSD for closely related sequences. Comparative modeling tools such as MODELLER and SWISS-MODEL became widely used in structural biology practice.

3.2 The Role of Evolutionary Information

A pivotal conceptual advance came with the recognition that evolutionarily correlated mutations in multiple sequence alignments (MSAs) contain information about residue–residue contacts in the folded structure [3]. If two residues are spatially proximate, mutation of one tends to be compensated by mutation of the other to maintain the structural and functional integrity of the protein. Statistical models to extract this co-evolutionary signal — direct coupling analysis (DCA) and its variants — emerged as powerful tools for contact prediction and subsequently drove neural network approaches.

3.3 The Deep Learning Revolution

The application of deep learning to protein structure prediction began in earnest around 2017–2018. Convolutional neural networks trained on PDB-derived features were found to predict inter-residue distances and orientations with dramatically better accuracy than previous statistical approaches [5]. The first AlphaFold system demonstrated this capability at CASP13. Subsequent years saw rapid architectural innovation culminating in AlphaFold2, which introduced the Evoformer attention architecture and structure module based on invariant point attention [1], achieving a qualitative leap in prediction accuracy.

4. AlphaFold2 and Modern Structure Prediction Architectures

4.1 Overview of AlphaFold2

AlphaFold2 represents the most consequential advance in structural bioinformatics since the development of X-ray crystallography [1]. Its architecture addresses protein structure prediction as an end-to-end machine learning problem, taking as input a query sequence and a multiple sequence alignment (MSA) and producing as output atomic-level coordinates for all heavy atoms of the protein backbone and sidechains.

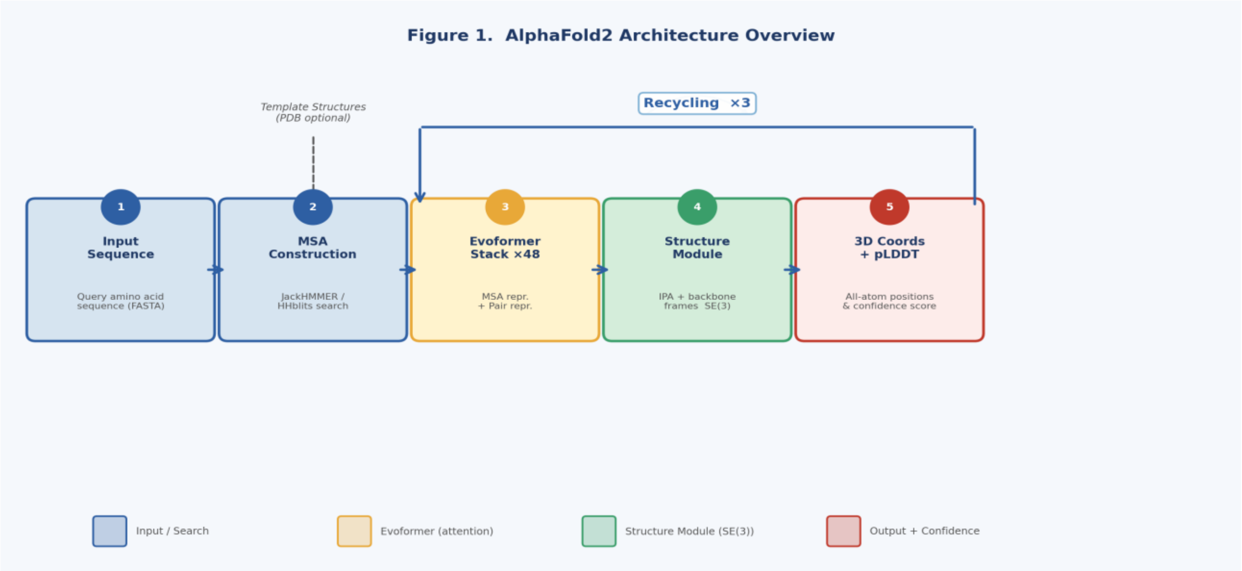

Figure 1. Schematic overview of the AlphaFold2 architecture, illustrating data flow from sequence input through the Evoformer stack and structure module to final atomic coordinate output. The recycling mechanism iteratively refines representations across three passes [1]

4.2 The Evoformer Architecture

The Evoformer is a novel transformer-based architecture that jointly processes two types of representations: an MSA representation of shape ($N_{seq} \times L \times c$) capturing evolutionary information across aligned sequences, and a pair representation of shape ($L \times L \times c$) encoding pairwise relationships between all residue pairs [1]. Evoformer blocks interleave row-wise and column-wise attention over the MSA representation with triangle multiplicative updates and triangle attention over the pair representation, enabling complex long-range communication across the protein sequence.

The triangle multiplicative updates implement a soft enforcement of the triangle inequality over inter-residue distances, reflecting the geometric constraint that the distance between residues i and k must be compatible with distances to intermediate residues j. This inductive bias, derived from the geometry of 3D space, proves crucial for accurate tertiary structure modeling.

4.3 The Structure Module

Given the pair representation from the Evoformer, the structure module generates 3D backbone frames using invariant point attention (IPA) [1]. IPA operates on local reference frames defined by backbone N–Cα–C atoms, making it equivariant to global rigid-body transformations. The structure module iteratively updates backbone frames and torsion angles, followed by a recycling step in which updated 3D coordinates are projected back into the pair representation. Side-chain conformations are predicted separately using torsion angle regression.

4.4 RoseTTAFold

Developed concurrently with AlphaFold2, RoseTTAFold introduced a three-track neural network architecture [2] processing sequence, distance, and coordinate information in parallel with cross-track communication. While somewhat less accurate than AlphaFold2 for single-chain prediction, RoseTTAFold excels in multimer prediction and was the first system extended to protein–nucleic acid complexes (RoseTTAFold2NA). Its open-source release accelerated community adoption and independent research.

4.5 Comparison of Current Methods

Table 1: Comparative overview of major deep learning methods for protein structure prediction

Model	Year	Method	GDT-TS	Key Advance
AlphaFold1	2018	CNN + MSA	~60%	First DL entry in CASP13
AlphaFold2	2021	Evoformer + SE(3)	~92%	Near-experimental accuracy
RoseTTAFold	2021	3-track network	~79%	Open-source; speed
ESMFold	2022	Language model	~74%	Single sequence; fast
OmegaFold	2022	Geom. transformer	~75%	No MSA required
HelixFold	2022	End-to-end DL	~80%	Industry deployment
UniFold	2023	AlphaFold2 variant	~91%	Multi-chain assembly

GDT-TS: Global Distance Test Total Score; MSA: Multiple Sequence Alignment; CNN: Convolutional Neural Network; SE(3): Special Euclidean group in 3D. Performance figures represent published benchmarks on CASP14/CAMEO datasets.

5. Protein Language Models

5.1 From NLP to Biology

The success of large language models (LLMs) such as BERT and GPT in natural language processing inspired analogous approaches for protein sequences, where amino acids are treated as tokens and proteins as 'sentences' in an evolutionary 'language' [15]. Protein language models (PLMs) are pre-trained on hundreds of millions of sequences from databases such as UniRef90, learning distributed representations that capture evolutionary, structural, and functional properties without any structure supervision during training.

5.2 ESM Model Family

The Evolutionary Scale Modeling (ESM) family from Meta AI represents the most extensively characterized series of protein language models [16]. ESM-1b (650M parameters) demonstrated that PLM embeddings encode structural information, with attention patterns correlating with residue–residue contacts. ESM-2 (scaling from 8M to 15B parameters) showed that larger models encode increasingly accurate structural information. ESMFold extends ESM-2 with a lightweight structure prediction head, enabling single-sequence structure prediction at speeds 60× faster than AlphaFold2, facilitating proteome-scale structure prediction [16].

5.3 ProtTrans and Other PLMs

The ProtTrans family [17] trained transformer architectures including BERT-like (ProtBERT, ProtAlbert) and autoregressive (ProtGPT2, ProtT5) models on up to 216M protein sequences. ProtT5-XL (3B parameters) yields state-of-the-art sequence embeddings for downstream tasks including secondary structure prediction, subcellular localization, and variant effect prediction. Importantly, PLM embeddings trained on sequences alone capture sufficient information for many tasks traditionally requiring explicit structural information.

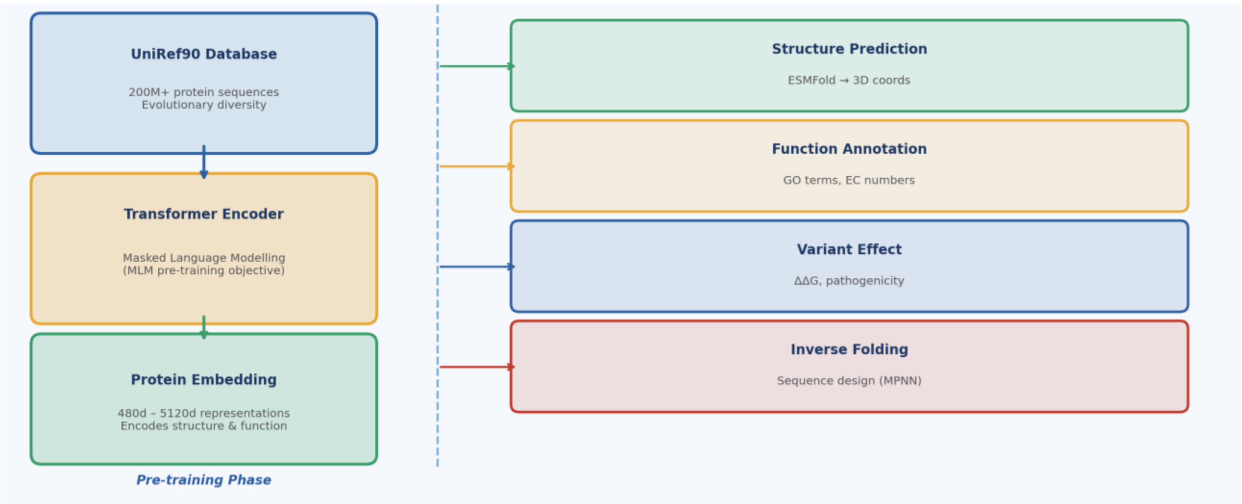

Figure 2: Schematic of protein language model (PLM) pre-training and transfer learning paradigm. The base transformer is pre-trained by masked token prediction on large sequence databases and subsequently adapted to diverse downstream tasks [15,16]

6. Deep Learning for Protein Design

6.1 The Inverse Folding Problem

Whereas structure prediction asks 'given a sequence, what is the structure?', the inverse folding problem asks 'given a desired structure (or function), what sequences will fold into it?' [9]. Classical approaches to inverse folding (e.g., Rosetta's fixed-backbone design) relied on energy-based scoring functions. Deep learning methods dramatically improve upon these through learned sequence–structure relationships.

6.2 ProteinMPNN

ProteinMPNN [9] is a message-passing graph neural network for protein sequence design trained on PDB structures. The protein backbone is represented as a graph with nodes at Cα positions and edges connecting residues within a distance threshold, augmented with backbone dihedral angles and inter-residue distances as edge features. ProteinMPNN achieves 52.4% native sequence recovery on test proteins — substantially above the ~32% baseline of Rosetta — and designed sequences show high experimental success rates in cell-free expression and structural validation.

6.3 Diffusion Models for De Novo Design

Generative diffusion models have emerged as the leading paradigm for de novo protein backbone design [10][11]. These models learn to reverse a stochastic noise process applied to protein structures, enabling sampling of novel protein backbones conditioned on diverse functional specifications. RFdiffusion [10], built on RoseTTAFold, has demonstrated remarkable versatility: generating binders to therapeutic targets, designing symmetric oligomers, constructing enzyme active site scaffolds, and producing protein cages for drug delivery. Experimental validation of RFdiffusion designs using SPR, cryo-EM, and cellular assays has confirmed that computationally designed proteins can achieve binding affinities and structural accuracy matching natural proteins.

6.4 Summary of Design Tools

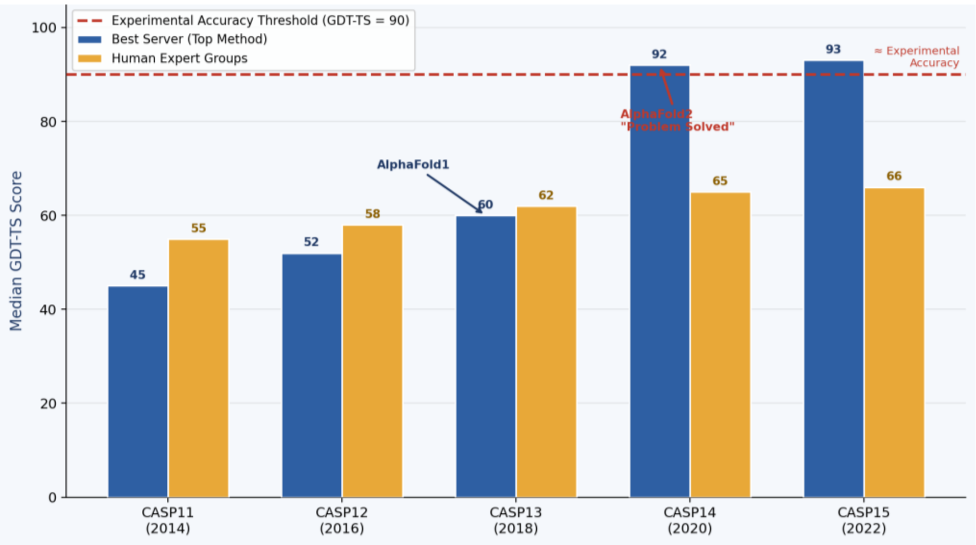

Figure 3: Progression of protein structure prediction accuracy as measured by median GDT-TS score in CASP competitions from 2014 to 2022. AlphaFold2's performance at CASP14 represents a discontinuous improvement surpassing all prior methods and approaching experimental accuracy [1,5]

Table 2: Deep learning tools for protein sequence and structure design

Tool	Architecture	Task	Performance	Ref
ProteinMPNN	Message-passing GNN	Inverse folding	52.4% seq recovery	[9]
RFdiffusion	SE(3) diffusion	De novo design	High success rate	[10]
Chroma	Graph diffusion	Conditional design	Programmable	[11]
LigandMPNN	GNN + ligand context	Binding site design	>70% activity	[12]
FrameDiff	SE(3) diffusion	Backbone gen.	TM-score >0.7	[13]
PiFold	Inverse folding	Sequence design	51.9% recovery	[14]

GNN: Graph Neural Network; SE(3): Special Euclidean group; SPR: Surface Plasmon Resonance. Performance metrics from published benchmarks.

7. Benchmarks, Datasets, and Evaluation Metrics

7.1 Key Datasets

Training and evaluating deep learning models for protein structure requires large, high-quality datasets [4]. The Protein Data Bank (PDB), founded in 1971, remains the primary repository for experimentally determined protein structures, currently containing over 220,000 entries. Structural data are complemented by sequence databases — UniProtKB/Swiss-Prot (manually curated), TrEMBL (computationally annotated), and UniRef (clustered at various sequence identities) — providing the evolutionary diversity essential for MSA construction and PLM pre-training.

Table 3: Key datasets and benchmarks in protein structure prediction and design

Dataset / Benchmark	Size	Task	Notes
PDB (Protein Data Bank)	~220,000 structures	Training / validation	Gold standard experimental
UniProt / UniRef90	>200M sequences	Pre-training	Evolutionary diversity
CASP14 targets	87 domains	Structure prediction	Near-atomic accuracy era
CATH / SCOP	~500K domains	Classification	Structural hierarchy
AlphaFold DB	~200M structures	Predicted structures	Proteome-scale coverage
CAMEO (weekly)	~50 chains/week	Continuous benchmark	Blind prediction

PDB: Protein Data Bank; CASP: Critical Assessment of Protein Structure Prediction; CATH: Class, Architecture, Topology, Homology; CAMEO: Continuous Automated Model EvaluatiOn.

7.2 Evaluation Metrics

Several metrics are employed to assess prediction quality [18]. The *Global Distance Test Total Score (GDT-TS)* measures the fraction of Cα atoms within distance thresholds of 1, 2, 4, and 8 Å from their experimental positions, averaged across thresholds. GDT-TS ≥ 90 is widely considered 'near-experimental accuracy'. The *Template Modeling Score (TM-score)* is length-normalized and ranges from 0 to 1 (TM ≥ 0.5 indicates the same SCOP fold). The *predicted Local Distance Difference Test (pLDDT)* is a per-residue confidence metric output by AlphaFold2, calibrated to the lDDT-Cα score, and serves as a reliable indicator of model quality and region-level disorder.

8. Applications in Biomedicine and Biotechnology

8.1 Drug Discovery and Target Identification

Accurate structural models of disease-relevant proteins enable structure-based drug discovery even in the absence of experimental crystal structures [19]. AlphaFold2 structures have been used for virtual screening campaigns against previously intractable targets, including proteins that resist crystallization or are present at low copy numbers in cells. The AlphaFold Protein Structure Database, launched by EMBL-EBI in collaboration with DeepMind, provides predicted structures for virtually the entire human proteome and over 1 million other species, constituting an unprecedented resource for target identification and hit-to-lead optimization.

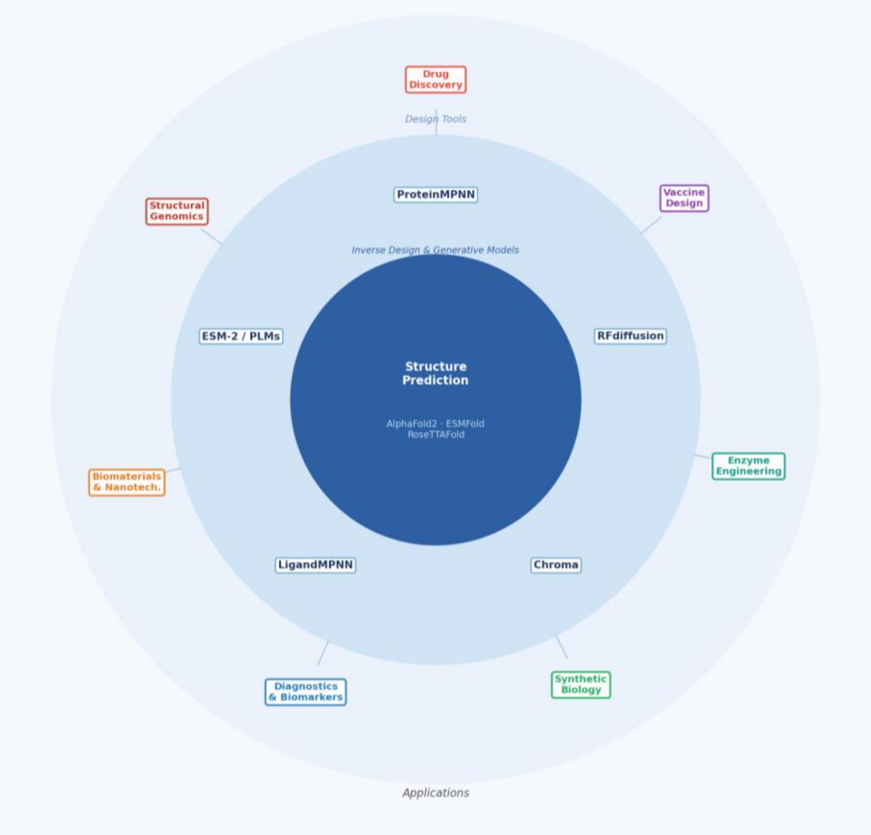

Figure 4: Landscape of deep learning applications in protein science, organized from core structure prediction capabilities through computational design tools to translational biomedical and biotechnological applications [1,9,10,19,20].

8.2 Vaccine and Therapeutic Protein Design

Computational protein design tools are accelerating the development of next-generation vaccines and biologics [20]. Designed protein nanoparticles displaying viral antigens in immunogenically favorable geometries have entered clinical trials for influenza, RSV, and SARS-CoV-2. Computationally designed miniprotein binders to cytokines and checkpoint receptors offer a new modality for immunotherapy. The integration of deep learning design tools with high-throughput experimental screening platforms (yeast display, cell-free expression, deep mutational scanning) has created a powerful closed-loop discovery engine.

8.3 Enzyme Engineering

Enzyme engineering represents a transformative application of computational protein design [9][12]. Deep learning methods can design enzyme active sites with specified catalytic geometries for reactions not found in nature, scaffold these active sites in stable protein folds, and optimize existing enzymes for improved thermostability, altered substrate specificity, or reduced immunogenicity. Industrial biotechnology applications include the design of enzymes for plastic degradation, biofuel production, and synthesis of pharmaceutical intermediates.

9. Challenges and Future Directions

9.1 Persistent Challenges

Despite remarkable progress, significant challenges remain. Multimeric protein complexes — particularly large assemblies with more than 10 chains — remain difficult to model with high accuracy [1]. AlphaFold-Multimer achieves lower accuracy than single-chain AlphaFold2 for complexes with limited co-evolutionary information. Intrinsically disordered proteins and regions (IDPs/IDRs), which constitute a substantial fraction of eukaryotic proteomes, lack stable secondary and tertiary structure and are not amenable to static structure prediction — requiring instead the characterization of conformational ensembles [8].

Membrane proteins, which constitute approximately 25–30% of human genes and >60% of drug targets, adopt structures highly dependent on lipid bilayer composition and are underrepresented in the PDB training data [6]. Current models show reduced accuracy for transmembrane regions relative to soluble proteins. Furthermore, predicting protein conformational dynamics — the transitions between active and inactive states, allosteric mechanisms, and ligand-induced conformational changes — remains a largely unsolved problem that is critical for understanding protein function and designing allosteric drugs.

9.2 Emerging Methodological Directions

Several methodological frontiers hold particular promise. The integration of cryo-EM density maps as experimental constraints in model building is being accelerated by machine learning-driven map interpretation and flexible fitting [18]. Flow matching and consistency models are emerging as computationally efficient alternatives to score-based diffusion for protein generation [13]. Foundation models unifying structure, sequence, function, and dynamics — analogous to multimodal LLMs in NLP — represent an ambitious but potentially transformative direction. The development of interpretable AI methods that relate model internal representations to known biological mechanisms will be essential for scientific insight rather than mere prediction.

9.3 Integration with Experiment

The most productive path forward will involve tight integration of computational prediction and design with high-throughput experimental validation [20]. Active learning frameworks that use model uncertainty to guide experimental exploration, combined with automated laboratory platforms and robotic protein expression systems, promise to dramatically accelerate the design-build-test-learn cycle. The development of standardized benchmarks and community challenges

— extending CASP to cover protein complexes, IDPs, and designed proteins — will be essential for rigorous evaluation of emerging methods.

Conclusion

Deep learning has precipitated a paradigm shift in structural biology, transitioning protein structure prediction from an aspirational computational challenge to a practical, high-accuracy tool available to the entire scientific community. The Evoformer architecture of AlphaFold2 [1] and the three-track network of RoseTTAFold [2] established new accuracy benchmarks, while protein language models [15][16] and generative diffusion models [10] are extending computational capabilities to protein design. The AlphaFold Protein Structure Database has democratized access to structural information at proteome scale, providing an invaluable resource for the entire life science community [19].

As these technologies mature and are integrated with experimental platforms, we anticipate transformative impacts on drug discovery, synthetic biology, and our fundamental understanding of the molecular mechanisms of life. The convergence of unprecedented model accuracy, open-source tools, and large-scale experimental validation pipelines positions the next decade as a golden era for protein science — with deep learning as its central enabler.

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LEAP AND CAPTURE: INSIDE THE HUNTING WORLD OF JUMPING SPIDERS

Rakhesh S[1], Chinna Babu Naik V*[1], Sujay Hurali*[2],
B Vishwanath[3], Akhilesh Kokkula[1] and Sureskumar K[1]
[1]Division of Crop Protection,
ICAR-Indian Institute of Rice Research, Hyderabad – 500030, Telangana
[2]Department of Entomology, Agricultural Research Station, Gangavathi,
University of Agricultural Sciences, Raichur– 574104, Karnataka
[3]Department of Entomology,
University of Agricultural Sciences, Dharwad– 580005, Karnataka
*Corresponding author E-mail: chinnaenton@gmail.com, morphosis77@gmail.com

Abstract

Jumping spiders (Family: Salticidae) represent one of the most diverse and behaviourally sophisticated groups within the order Araneae, exhibiting remarkable adaptations that make them highly efficient predators in terrestrial ecosystems. This paper explores the unique hunting strategies, ecological significance, and adaptive traits of jumping spiders, emphasizing their visually guided predation and behavioural flexibility. Unlike web-building spiders, salticids rely on exceptional vision, hydraulic limb extension, and precise motor coordination to stalk and capture prey, often leaping distances up to 50 times their body length. Advanced predatory strategies such as detouring, aggressive mimicry, trial-and-error learning, and "smoke-screen" tactics highlight their cognitive complexity, particularly in species like *Portia fimbriata*. In addition to their predatory efficiency, jumping spiders play a vital role in agroecosystems as natural biocontrol agents, preying on a wide range of insect pests. Their ecological importance is further complemented by their economic potential, as spider venoms provide bioactive peptides with applications in medicine and bioinsecticide development, while spider silk offers exceptional material properties for industrial and biomedical uses. Behavioural traits such as araneophagic, myrmecophagy, mimicry, and diverse courtship and maternal strategies underscore their evolutionary success. Overall, jumping spiders exemplify a unique convergence of morphological innovation, sensory specialization, and behavioural adaptability. Their role in pest regulation, combined with their scientific and economic relevance, highlights their importance as both ecological regulators and valuable models for studying complex predatory behaviour and evolutionary biology.

Keywords: Jumping Spiders, Salticidae, Visual Predation, Behavioural Adaptability, Biological Control, Bioactive Compounds.

1. Introduction

In the kingdom Animalia, dominant groups include the insect orders Coleoptera, Hymenoptera, Lepidoptera, Diptera, and Hemiptera, along with mites and spiders. Spiders, belonging to the order Araneae, represent the largest order of arachnids and rank seventh in overall species diversity, with 51,624 species described across 4,352 genera and 135 families. They are air-breathing arthropods characterized by eight legs and chelicerae bearing venom-injecting fangs. Their effectiveness as predators is attributed to traits such as high prey consumption rates, strong searching ability (particularly in hunting spiders), broad host range, adaptability to food-limited conditions, low metabolic rate, energy conservation mechanisms, and polyphagous feeding behaviour.

Jumping spiders (Salticidae: Araneae) form the largest spider family, comprising 6,616 described species (World Spider Catalog, 2023). They are among the most abundant insect predators in terrestrial ecosystems, consuming large numbers of prey without causing plant damage. These spiders are diurnal hunters with exceptional vision. While most spiders lack the structural complexity for acute vision, salticids possess uniquely advanced eyes with remarkable resolution, unmatched among animals of similar size. They represent an evolutionary outcome in which a small, silk-producing organism with a simple nervous system has developed highly refined visual capabilities, enabling diverse and complex predatory strategies.

Unlike hexapods, jumping spiders lack wings and do not possess powerful extensor muscles in their legs like grasshoppers, planthoppers, or sand flies. Instead, they depend on an internal hydraulic mechanism for movement. When preparing to jump, they increase haemocoel pressure by pumping fluid into their legs, allowing rapid extension and propulsion. This mechanism enables them to leap distances up to 50 times their body length.

2. Economic Importance of Spiders

Spiders have evolved highly complex and diverse venom peptides with wide-ranging pharmacological activities over more than 300 million years. These venoms are used for both prey capture and defense, and therefore contain peptides that target prey (primarily arthropods) as well as predators (other arthropods or vertebrates). Many of these peptides selectively modulate key biological targets such as ion channels, receptors, and signaling pathways involved in physiological processes. Because these targets are often implicated in disease pathophysiology, spider venoms are considered a valuable source of bioactive peptides with significant therapeutic potential.

Since the first description of the peptide Lycosin-I and its reported anticancer activity in 2012, research on this compound from the venom of *Lycosa singoriensis* has advanced rapidly. Lycosin-I has been shown to suppress tumour growth *in vivo* through a dual mechanism: activation of the mitochondrial apoptosis pathway and inhibition of cancer cell proliferation.

Spider venom peptides have also demonstrated strong potential as bioinsecticides. In 2014, a spider venom-derived peptide was registered with the US Environmental Protection Agency. The active ingredient in the commercial product *Spear T*®, GS-ω/κ-HXTX-Hv1a, is a neurotoxin that targets insect BKCa and CaV channels. This product is primarily used against greenhouse pests and is effective against a wide range of insect orders including Lepidoptera, Coleoptera, Diptera, Orthoptera, Thysanoptera, and Hemiptera, while remaining safe for mammals and honeybees. The success of GS-ω/κ-HXTX-Hv1a demonstrates that spider venom peptides can be successfully developed into commercial bioinsecticides.

Spider silk possesses remarkable properties such as high strength-to-weight ratio, toughness, elasticity, vibration damping, and electrical conductivity. It is also hypoallergenic, making it highly biocompatible and suitable for applications in both medical and textile industries. As a raw protein, spider silk can rival high-strength materials like Kevlar, carbon fibre, stainless steel, aluminium, and polypropylene. The major ampullate spider silk (MaSp) protein can be dissolved in water and processed into a variety of products, including films, gels, coatings, fibres, and adhesives.

Although spiders (order Araneae) represent a highly diverse group of arachnids, they are all obligate predators, with many species feeding on herbivorous pest insects. Orb-web weavers (Araneidae and Tetragnathidae) commonly prey on homopterans such as leafhoppers, as well as Diptera and Orthoptera, particularly grasshoppers. Smaller sheet-web weavers (Linyphiidae, Dictynidae, and Theridiidae) capture Diptera, Hemiptera, and Homoptera (notably aphids and leafhoppers), along with beetles from the family Curculionidae. Funnel-web weavers (Agelenidae, Atypidae, Ctenizidae, and Eresidae) prey on Orthoptera, Coleoptera, and Lepidoptera. Hunting spiders (Lycosidae, Oxyopidae, Thomisidae, and Salticidae) frequently capture Orthoptera, Homoptera, Hemiptera, Lepidoptera, Thysanoptera, Diptera, and some Coleoptera and Hymenoptera.

Many plants produce nectar from extrafloral nectaries (EFNs), specialized structures that typically attract ants, which serve as plant defenders. However, EFNs can also attract other arthropod predators. For instance, jumping spiders (*Eris* sp. and *Metaphidippus* sp.) associated with *Chamaecrista nictitans* (Caesalpineaceae) have been observed feeding on nectar in addition to preying on herbivores, ants, bees, and other spiders. This indicates that plants with EFNs can form beneficial interactions not only with nectar-feeding ants but also with other predatory arthropods.

3. How Jumping Spiders Differ from Other Group of Spiders

Predatory Strategy: Detouring

Jumping spiders (Family: Salticidae) are known for their ability to take indirect routes to reach prey, a behaviour termed “detouring.” This capability is considered rare among invertebrates and is thought to have evolved in relation to the salticids’ uniquely complex eyes and highly developed vision. Salticids are typically active, insectivorous hunters that do not rely on webs. For most species, observing complete predatory sequences in natural conditions is often unpredictable. However, the genus *Portia* is an exception; these spiders frequently invade webs and employ aggressive mimicry to deceive and capture other spiders. Such extended predatory sequences, centered around the web, are comparatively easier to observe. *Portia fimbriata* is especially noted for its tendency to take detours while approaching prey. This behaviour is likely adaptive, as it often needs to enter a web cautiously to avoid alerting the resident spider and to ensure its own safety. In some cases, the predator–prey relationship may reverse, and *Portia* itself can become prey. In this context, the present study provides field-based observations of apparent detouring behaviour in *P. fimbriata*, highlighting the complexity of its predatory strategies in natural conditions.

Case Study I: Detouring Behaviour of *Portia fimbriata* (Jackson and Wilcox, 1993)

This study was conducted at an established field site near Cairns, North Queensland, Australia, to investigate detouring behaviour in *Portia fimbriata*, a web-invading jumping spider. Adult females were collected and maintained in captivity for 1–7 days before being tested under natural conditions. Five species of web-building spiders were used as prey: *Argiope appensa*, *Nephilengys malabarensis*, *Achaearanea krausi*, *Inola subtilis*, and *Psilochorus sphaeroides*. These species commonly occur in the study area and construct webs on tree trunks or rock ledges, allowing controlled placement of *P. fimbriata* at fixed distances (100–200 mm below the web).

The prey species represented diverse web types: orb webs (*A. appensa*, *N. malabarensis*), space webs (*A. krausi*), sheet webs (*I. subtilis*), and dome webs (*P. sphaeroides*). Experiments were conducted between 8:00 AM and 10:00 AM, aligning with the natural hunting period of *P. fimbriata*. Observations continued until 1:00 PM or until predation occurred, the prey left the web, or the predator moved away.

A "clear-cut detour" was defined as an indirect route to the web during which the spider temporarily lost visual contact with it. Such detours were recorded in 18 cases with *A. appensa*, 2 with *N. malabarensis*, 5 with *A. krausi*, 2 with *I. subtilis*, and 1 with *P. sphaeroides*. Trials where *P. fimbriata* failed to scan (n = 30) or entered the web directly were excluded from analysis.

During hunting, *P. fimbriata* exhibited scanning behaviour by slowly pivoting and fixating on objects using its principal eyes. A representative observation involved an *A. appensa* web positioned on a tree trunk with an overhanging limb. Initially, *P. fimbriata* scanned and intermittently moved while fixating on the prey. After about 20 minutes, it moved laterally away from the web, circled the tree to a position where the web was no longer visible, and ascended the trunk over approximately 15 minutes.

Despite losing sight of the web, the spider progressed steadily, pausing frequently. Upon re-emerging on the side of the tree near the web, it remained temporarily obstructed by the limb. It then navigated onto the limb, gradually repositioning until the web came back into view. After further scanning and adjustments, *P. fimbriata* positioned itself beneath the limb and descended via a dragline, ultimately capturing the prey with a precise attack.

These observations highlight the complexity and planning involved in detouring behaviour, demonstrating advanced predatory strategies in *P. fimbriata* under natural conditions.

Predatory Strategy: Trial and Error Behaviour

In *Portia*, aggressive mimicry involves remarkable behavioural complexity, supported by a highly diverse repertoire of vibratory signals. The spider generates these signals by manipulating, plucking, or striking the web using its eight legs and two palps, often in various combinations. It can also produce signals by flicking its abdomen, either independently or coordinated with appendage movements. Many of these behaviours are thought to have evolved from ancestral grooming actions.

Web-building spiders possess a strong ability to detect and discriminate among vibrations transmitted through their webs, and their responses vary depending on species, sex, age, experience, and feeding condition. Despite this variability, *Portia* successfully preys on a wide range of web-building spiders, typically those ranging from one-tenth to twice its own body size.

Research at the University of Canterbury, Christchurch, New Zealand, in collaboration with Stimson Wilcox of the State University of New York, investigated how *Portia* selects appropriate signals from its extensive repertoire. Using a computer-based system to record and playback web vibrations—effectively enabling interaction in the spiders' "language"—the studies revealed that *Portia* relies on two key strategies: (i) the use of specific preprogrammed signals when encountering familiar prey cues, and (ii) flexible adjustment of signals based on real-time feedback from the prey.

Predatory Strategy: Smoke Screen Behaviour

Another example of the flexibility in *Portia*'s predatory strategy is the "smoke-screen" tactic. Field observations have shown that when wind causes the web to vibrate, these background movements mask other signals transmitted through the silk. During such conditions, *Portia* increases its movement and approaches the prey more rapidly. Laboratory experiments using artificial airflow confirmed that *Portia* deliberately exploits these vibrations as a form of camouflage to conceal its approach.

In the absence of wind, *Portia* can generate its own vibratory "smoke screen." While moving across the web, it produces larger, deliberate vibrations that mimic those caused by a breeze, effectively masking the subtle signals generated by its footsteps. Notably, this behaviour is selective. *Portia* employs both opportunistic (wind-assisted) and self-generated masking primarily when hunting other spiders, but not when attacking trapped insects or feeding on egg sacs, where such camouflage is unnecessary.

Predatory Strategy: Courtship

Courtship in jumping spiders (Salticidae) is highly complex, largely driven by intersexual selection, where males must overcome female resistance through elaborate displays and striking ornamentation. All salticids rely on visual courtship signals, which is expected given their acute vision. However, communication is not limited to visual cues; instead, salticids commonly use multichannel communication, adding to the overall complexity of their behaviour.

Displays in individual species are often intricate and species-specific. For instance, *Habronattus hallani* (Richman) males move sideways and leap while displaying iridescent femora, whereas *Habronattus coecatus* (Hentz) males' approach slowly with raised front legs and periodically lift their third pair of legs. *Hentzia palmarum* (Hentz) males exhibit a zigzag approach, tilting the abdomen and spreading chelicerae. Display repertoires can be extensive; *Corythalia canosa* possesses around 30 distinct display elements that can be combined in various ways, while *Platycryptus undatus* (DeGeer) appears to have a smaller repertoire. Such interspecific variation further contributes to behavioural diversity.

In addition to visual signals, tactile communication often occurs when males and females come into contact prior to mating. Some species also use stridulation, while pheromonal communication—both volatile (olfactory) and silk-associated (contact chemoreception)—plays an important role. Another key mode of communication is vibratory signalling transmitted through silk. Although salticids are primarily hunting spiders, they still produce silk for nests used in resting, moulting, and reproduction. Males of many species perform vibratory courtship on the female's nest silk and may enter the nest to mate, even in low-light conditions where vision is limited.

Courtship strategies vary depending on context. Males use vibratory displays for females inside nests, visual displays for females outside, and may cohabit with subadult females after constructing a secondary chamber on the nest until mating becomes possible. This flexibility reflects conditional strategies, where behaviour changes based on circumstances.

A notable parallel exists between predatory and courtship behaviour in salticids. In both contexts, individuals employ conditional strategies, adjusting tactics based on prey type or the female's location, maturity, and receptivity. This adaptability highlights salticids as an important model for studying behavioural complexity and conditional strategies in zoology.

Predatory Strategy: Maternal Behaviour

In Salticidae, courtship and mating are followed by oviposition, and maternal care of eggs and newly hatched juveniles is widespread, if not universal. Females spin silken egg sacs and typically remain with them, presumably for protection, although the exact nature of defense against predators and parasitoids is not fully understood. The most common egg sac consists of a roughly spherical cluster of eggs enclosed in dense silk within a cocoon-like nest.

However, considerable variation exists in egg sac design and placement. Lyssomanine salticids deposit loosely covered, widely spaced eggs on leaves and guard them in the open. The European species *Marpissa rumpfi* (Scopoli) constructs multiple flat egg sacs, stacking three to five layers within a nest. *Holcolaetis* guards a flat, papery egg sac exposed on tree trunks. *Euryattus* selects dead, rolled leaves as oviposition sites and suspends them using strong silk lines, while *Pellenes nigrociliatus* (L. Koch) exhibits similar behaviour but utilizes snail shells instead of leaves. In contrast, *Thiania* seals two green leaves together with silk and lays eggs within the enclosed space.

Predatory Strategy: Silk Utilization

Salticids use silk not only for nest and egg sac construction but also as a dragline during movement. This safety line allows them to recover if they lose footing in vegetation. Some species rest at night suspended from draglines and may also drop on silk lines while feeding. They also disperse through a behaviour known as ballooning, where individuals release silk strands from their spinnerets and are carried by air currents while positioned at vegetation edges or hanging from a dragline. Although Salticidae are widely recognized as active, visually oriented hunting spiders, web-building behaviour does occur and is considered a possible evolutionary remnant from web-building ancestors.

Certain salticids construct functional prey-capturing webs. *Pellenes arcigerus* (Walckenaer) and *Spartaeus* build sheet webs, with *Spartaeus* known to capture moths, while the predatory behaviour of *P. arcigerus* remains less studied. *Portia*, in addition to invading other spiders' webs, constructs a distinctive funnel-shaped aerial web to capture prey. *Euryattus* spins a delicate space web, primarily in juvenile stages, and also uses dead leaves as oviposition sites. *Simaetha* builds dense space webs, often incorporating a cocoon-like nest, and sometimes nests independently. Interestingly, *Simaetha* may construct its web within communal webs of *Badumna candida* (L. Koch), a social amaurobiid spider in Australia, where it exploits trapped insects from the host web.

Predatory Strategy: Mimicry

In addition to aggressive mimicry in which a predator tricks its prey by making deceptive signals on a web. Batesian mimics are prey species that deceive their predators and this type of mimicry may be common in salticids. Ant mimicry is the best known. Many salticids are remarkably similar to ants in morphology and in locomotory behaviour. Ants are avoided by many predators of spiders, suggesting that the ant-like salticids are Batesian mimics. Data are scarce to support this supposition, but showed that birds fail to distinguish between ants and an ant-like salticid, *Synageles venator* (Lucas).

Besides ant-like salticids, there are also wasp-like and beetle-like species. *Phidippus apacheanus* Chamberlin & Gertsch, for example, is remarkably similar to velvet ants (mutillid wasps) in both general appearance and locomotory behaviour. *Agassa cyanea* (Hentz) resembles flea beetles and has been collected in the company of flea beetles. Numerous salticids, including species in at least four genera (*Agassa, Sassacus, Cylistella and Coccorchestes*) resemble chrysomelid beetles.

Batesian mimicry is a reasonable hypothesis to account for the wasp mimicry because wasps have potent stings. The advantage of beetle mimicry is not as clear, but the hard exoskeleton and the prevalence of noxious tastes in some beetle species lends credence to the notion that Batesian mimicry has been important in the evolution of beetle-like Salticidae.

Orsima formica (Peckham & Peckham) from Borneo is apparently a "generalized, reverse insect mimic". This salticid waves its abdomen and spinnerets in a fashion to resemble the head of an ant or beetle. That is, this salticid uses its rear end to mimic the front end of an insect.

There is another way the tables can be turned; sometimes the insect tricks the salticid. Certain fruit flies have markings on their wings that resemble a salticid performing a threat display. A salticid that sees the fly's wing displays back, as if it had seen a rival, giving itself away to the fly. An even more remarkable mimic of this type is a recently discovered fulgorid planthopper nymph that bears a close resemblance to a jumping spider when viewed from the rear. These are unusual instances in which prey species mimic a predator to gain protection from the same predator mimicked.

4. Morphological and Behavioural Adaptations of Jumping Spider

4.1 Visual Hunting Behaviour

jumping spiders in catching prey. The responses consist of 3 primary patterns, each of which is subdivided into discrete motor elements, as follows: Orientation—Alert, Swivel, and Alignment; Pursuit—Follow, Run, and Stalk; and Capture—Pre-crouch, Crouch, and Jump. The units of behaviour selected are characteristic of the hunting sequence, and as such are of potential systematic and physiological importance. The distance separating the spider from its prey is shown to be a determining factor in the establishment of a particular response pattern.

Salticid Eye

Salticids possess four pairs of eyes, with the large anterior median (principal) eyes being the most prominent. Surrounding them are three pairs of smaller secondary eyes that function mainly as motion detectors. The anterior lateral eyes assist in forward vision and depth perception, while the posterior lateral eyes provide a wide field of view. Together, these eyes enable nearly 360° vision. In some primitive groups, the posterior median eyes are well developed, though they are reduced in most salticids.

The principal eyes provide exceptional visual acuity, allowing jumping spiders to detect and identify prey, mates, and rivals from distances of up to 30 body lengths. During hunting, the spider orients its principal eyes toward the prey, stalks carefully, and finally performs a precise, visually guided jump after attaching a dragline. Vision also plays a key role in other behaviours, including mate recognition and responses to visual cues, even from stationary objects.

Structurally, salticid eyes differ markedly from those of vertebrates and insects. The principal eyes have a tiered retina with four layers, including a specialized central region (fovea) where photoreceptors are densely packed for sharp image resolution and shape recognition. The layered and staircase-like arrangement helps compensate for optical limitations such as chromatic aberration.

Each principal eye contains a long, movable eye tube controlled by muscles, allowing complex movements such as scanning and tracking, though it cannot adjust focus by changing length. This design functions like a telephoto system, enhanced by an additional lens that increases magnification. The eyes likely support dichromatic color vision and achieve optimal resolution based on receptor spacing.

Despite their small size, salticid eyes are highly specialized and efficient. Their ability to perceive shapes and distinguish prey relies on active eye movements, particularly scanning.

Understanding these mechanisms remains a key area for future research, as their visual processing differs fundamentally from that of larger, more complex eyes.

4.2. Araneophagy

Jumping spiders are active predators that typically hunt a wide range of small arthropods, mainly insects, though they may also capture other spiders. While they are generally considered generalist feeders, instances of cannibalism and spider predation have been reported. Such araneophagic behaviour usually occurs opportunistically, particularly when smaller or weaker spiders are within reach. However, feeding on other spiders is not a regular habit in most salticids and tends to arise under specific conditions, such as limited availability of preferred prey.

Case Study II: Prey-Specific Attack Tactics in Araneophagic Jumping Spiders (Harland and Jackson, 2005)

Most jumping spiders (Salticidae) are visually guided insectivorous hunters, but species of the genus Portia are exceptional. In addition to stalking prey, they build capture webs and invade the webs of other spiders, which are often their preferred prey. Entering another spider's web exposes Portia to high risk, as even minor mistakes can trigger a fatal counterattack. To overcome this, Portia uses aggressive mimicry, generating web signals through precise movements of its legs, palps, and abdomen. These signals either lure the resident spider within striking distance or keep it calm during approach. Portia may also synchronize its movements with moments when the prey is distracted or when environmental factors, such as wind, reduce the prey's ability to detect vibrations.

The study compared Portia's attack strategies against dangerous prey (spiders) and safer prey (flies). Three Portia species—P. *fimbriata, P. labiata,* and *P. africana*—were tested using two spider prey species, *Badumna longinquus* and *Pholcus phalangioides*, along with flies (Musca domestica and Drosophila immigrans). Hunger levels were standardized, and prey size was maintained at approximately 75% of the predator's body length. Experiments were conducted in controlled enclosures, including modified "reduced webs" to minimize structural variability.

During trials, Portia typically began by scanning its surroundings, then fixating on prey before initiating a stalking sequence. The sector from which stalking began varied, but Portia often adjusted its position before attacking. Two mechanisms enabled this: maneuvering around stationary prey or waiting for prey to change orientation.

Results showed that Portia altered its attack position significantly more often when facing spider prey than when attacking flies. Sector changes occurred in about 50% of trials with *P. phalangioides* and 66% with *B. longinquus*, compared to only 13% with flies. However, the nature of these adjustments differed depending on prey type.

When attacking *B. longinquus*, a robust spider that lunges forward with powerful chelicerae, Portia frequently shifted from anterior to posterior sectors, avoiding the dangerous front region. Most attacks were launched from behind, targeting safer areas. In contrast, *P. phalangioides*, which uses long legs to wrap prey in silk, required a different strategy. Instead of targeting a specific body region, Portia exploited gaps between the spider's legs, avoiding contact that could trigger a defensive response.

Regardless of prey type, Portia consistently aimed for the cephalothorax. This region houses the central nervous system and represents a critical vulnerability. Attacks directed here quickly immobilized prey, usually within seconds. In contrast, when Portia accidentally targeted the abdomen, prey struggled for longer periods. By grasping the cephalothorax, Portia also limited the prey's ability to retaliate using its legs or fangs.

Overall, the study demonstrates that Portia does not rely on a fixed hunting strategy but instead adjusts its attack tactics based on the specific risks posed by different prey. This prey-specific behavioural flexibility highlights the advanced predatory intelligence of araneophagic jumping spiders.

4.3 Myrmecophagy

Myrmecophagy refers to the feeding behaviour in which animals consume ants (family Formicidae). Although jumping spiders are generally insectivorous, some species include ants as part of their diet. These spiders exhibit specialized adaptations and behaviours that enable them to prey on ants effectively. They may rely on stealth and patience to approach ant colonies or actively target foraging ants, capturing them opportunistically. However, myrmecophagy is not common to all jumping spiders; dietary preferences vary among species depending on factors such as body size, habitat, and availability of prey.

Case Study III: Ant-Eating Jumping Spiders (Jackson *et al.* , 1998)

This study examined prey-capture behaviour and prey preferences of nine ant-eating jumping spider species from the Philippines, including *Siler*, *Euophrys*, and *Chalcotropis*. These spiders inhabit varied microhabitats such as leaf litter, tree trunks, vegetation, and building walls. Although they consume a wide range of arthropods, they show a strong tendency to prey on ants.

Experiments were conducted using petri dishes and specialized testing boxes under three conditions: well-fed, starved (15 days), and extra-starved (21 days). Prey preference was assessed using three methods: alternate-day tests, simultaneous presentation of ant and non-ant prey, and alternative-prey tests during feeding. In all trials, prey size was standardized relative to the spider.

Results showed that these salticids consistently preferred ants over other insects, confirming their classification as myrmecophagic or ant-specialists. However, they are not strictly dependent on ants and also feed on diverse prey in both laboratory and natural conditions.

Behaviourally, these spiders exhibit specialized ant-specific capture strategies. For example, *Myrmarachne* species approach prey by running, tapping with forelegs (mimicking ant antennae), and then lunging instead of jumping. This behaviour supports Batesian mimicry, allowing them to maintain an ant-like appearance while hunting and reducing detection by predators.

Table 1: Ant Workers (Hymenoptera: Formicidae) used in laboratory as living prey and motionless lures

Subfamily	Tribe	Species	Body length (mm)	Origin
Dolichoderinae	Dolichoderini	*Dolichoderus bituberculatus* Mayr	4	Philippines
	Tapinomini	*Iridomyrmex darwinanus* (Forel)	2	New Zealand
		Iridomyrmex sp.	3–5	Philippines
		Tapinoma melanocephala (Fabricius)	1–3	Philippines
Formicinae	Camponotini	*Camponotus* sp.	3–7	Philippines
		Polyrhachis dives Smith	5–6	Philippines
		Polyrhachis sp.	6	Philippines
	Lasiini	*Lasius crypticus* Wilson	2	USA
	Melophorini	*Prolasius advena* (Smith)	3	New Zealand
	Oecophyllini	*Oecophylla smaragdina* (Fabricius)	7–8	Philippines
	Phagiolipidini	*Anoplolepis longipes* (Jerdon)	7	Philippines
Myrmicinae		*Crematogaster* sp.	2–3	Philippines
		Huberia striata (Smith)	4	New Zealand
		Monomorium (Chelaner) antarcticum (White)	3–4	New Zealand
		Pheidologeton sp.	4–5	Philippines
		Solenopsis geminata (Fabricius)	4	Philippines
Ponerinae	Odontomachini	*Odontomachus* sp.	5	Philippines
	Ponerini	*Diacamma vagans* (Fabricius)	12	Philippines
Pseudomyrmecinae		Unknown species	4–5	Philippines

4.4. Web Invasion and Aggressive Mimicry

Spider webs exhibit remarkable diversity, ranging from loosely structured three-dimensional webs to highly organized two-dimensional orb webs and dense sheet webs. In many species, web stickiness is enhanced by specialized secretions. Cribellate spiders produce extremely fine, wool-like sticky threads, whereas ecribellate spiders deposit droplets of fluid glue along the silk at regular intervals. Typically, cursorial spiders and those building non-sticky webs avoid adhesive webs, and spiders with cribellate silk tend to adhere to similar web types. However, *Portia* is an exception: although it spins non-sticky webs, it can traverse and hunt effectively on almost all web types, including both cribellate and ecribellate sticky webs.

When *Portia* enters another spider's web, it effectively enters the prey's sensory domain, as the web functions as an extension of the resident spider's sensory system. This makes the interaction highly risky, since detection by the web owner can trigger defensive or predatory responses, potentially reversing roles and placing *Portia* in danger. Rather than directly chasing prey, *Portia* employs a more strategic approach by generating vibratory signals on the web. These signals mimic those produced by trapped insects, deceiving the resident spider into approaching. Once the prey is within range, *Portia* launches a rapid attack. This strategy, where a predator deceives its prey by imitating another stimulus (such as trapped prey), is known as aggressive mimicry.

4.5 Ambush Predation

Jumping spiders are efficient ambush predators that rely on their excellent vision to detect and stalk prey. They often remain motionless, waiting patiently for the right moment to attack unsuspecting targets.

4.6 Jumping and Pouncing

As their name suggests, jumping spiders possess remarkable leaping ability, enabling them to cover several times their body length. This agility allows them to rapidly pounce on prey or evade threats, subduing prey with a venomous bite.

4.7 Silk Lasso Technique

Some jumping spider species use a specialized hunting method known as the "silk lasso." They produce a silk thread and hold it with their front legs while approaching prey. At close range, they launch themselves, using the silk as a सुरक्षा line, which can be retracted if necessary. This strategy helps capture prey that may be beyond direct jumping range.

4.8 Wasteful Killing

Spiders can influence prey populations by killing more prey than they consume. Studies have shown that wolf spiders and jumping spiders may kill significantly more prey—sometimes up to 50 times more—than required for feeding, even when satiated. This behaviour has also been observed in other lycosids. Similarly, web-building spiders may trap more insects than they can utilize. For instance, the golden orb-weaver *Nephila clavipes* (Linnaeus) produces yellow silk that acts as a super-stimulus, attracting herbivorous insects that are typically drawn to flowers or young leaves. A related phenomenon is intraguild predation or cannibalism, where spiders prey on one another. Although not extensively studied, this behaviour may indirectly influence pest populations by altering predator dynamics.

Case Study IV: Spider Predation in Agroecosystems

Spiders (Order Araneae) are obligate predators and play an important role in suppressing herbivorous pest insects in agroecosystems. For effective biological control, predators must reduce pest populations below economic thresholds and maintain them at stable levels—roles that spiders are well suited to perform.

Table 2: Common spider (Araneae) families, genera, and species found in agroecosystems

Family	Common Name	Genus / Species
Hunting Spiders		
Clubionidae	Sac Spiders	*Cheiracanthium inclusum* (Hentz)
		Cheiracanthium mildei Koch
		Clubiona spp.
Lycosidae	Wolf Spiders	*Rabidosa rabida* (Walckenaer)
		Lycosa antelucana Montgomery
		Pardosa pseudoannulata (Bösenberg & Strand)
		Hogna spp.
		Pardosa spp.
Oxyopidae	Lynx Spiders	*Oxyopes salticus* Hentz
		Peucetia viridans (Hentz)
Salticidae	Jumping Spiders	*Phidippus audax* (Hentz)
		Pelegrina galathea (Walckenaer)
Thomisidae	Crab Spiders	*Misumenops* spp.

Different spider groups target different pest types. Orb-web weavers (Araneidae, Tetragnathidae) mainly capture leafhoppers, flies, and grasshoppers, while sheet-web weavers (Linyphiidae, Dictynidae, Theridiidae) feed on aphids, leafhoppers, and small beetles. Funnel-web weavers prey on orthopterans, beetles, and caterpillars. Hunting spiders (Lycosidae, Oxyopidae, Thomisidae, Salticidae) actively capture a wide range of pests including orthopterans, hemipterans, lepidopterans, thrips, flies, beetles, and hymenopterans. Salticids, in particular, are known to prey on major agricultural pests such as aphids, leafhoppers, caterpillars, thrips, and beetles.

Spiders occupy different microhabitats within crop systems—from ground level to the canopy—allowing them to exploit diverse prey communities. Their varied hunting strategies and activity periods (diurnal or nocturnal) further enhance their effectiveness, as they capture prey encountered during their active phases.

Overall, the diversity in prey range, habitat use, and hunting behaviour enables spiders to contribute significantly to both pest reduction and population stabilization in agricultural ecosystems.

Case Study V: Biocontrol Potential of *Phidippus clarus* (Hoefler *et al.* , 2006)

Spiders are important generalist predators in agroecosystems and can suppress key pest populations. This study evaluated the jumping spider *Phidippus clarus* as a biological control agent against the fourlined plant bug, *Poecilocapsus lineatus*, a serious pest of many crops including sweet basil (*Ocimum basilicum*).

P. clarus, a visually oriented, active hunter, preys on a wide range of economically important pests. It is considered a promising biocontrol agent due to traits such as wide distribution, broad diet, ability to detect prey visually, flexible foraging strategies (sit-and-wait and active hunting), learning ability, and ease of laboratory rearing.

The experiment was conducted in greenhouse enclosures using basil plants under three treatments: (1) bugs only, (2) bugs + spiders, and (3) control (plants only). After plant establishment, 65 plant bugs were introduced into each relevant enclosure, followed by the addition of 10 female *P. clarus* per enclosure in the spider treatment.

Results showed significantly higher bug mortality in the bug + spider treatment compared to the bug-only treatment, indicating effective predation by *P. clarus*. Plant growth was also impacted: plants exposed only to bugs were significantly shorter than those in the spider treatment and control. Notably, plant height in the spider treatment was comparable to the control, suggesting that spider predation reduced pest damage. However, chlorophyll content did not differ significantly among treatments.

Overall, the study demonstrates that *Phidippus clarus* can effectively reduce pest populations and mitigate plant damage, highlighting its potential as a valuable biocontrol agent in agroecosystems.

Case Study VI: Natural Prey of *Salticus tricinctus* (Guseinov, 2005)

This study examined the natural diet of the jumping spider *Salticus tricinctus*, a medium-sized, zebra-striped species distributed across regions such as Azerbaijan, Israel, and Central Asia. In Azerbaijan, it inhabits arid environments like semi-deserts and steppes, where it is commonly found on shrub bark. Field surveys were conducted over four years (1996–1999) on the Absheron Peninsula near Ganly-Gyol Lake. Observations (45 surveys, ~49 hours) focused on spiders found on shrubs, and prey items were collected directly from individuals holding prey.

Out of 40 observed feeding instances, 37 prey items were analyzed. These belonged to six arthropod orders, mainly insects. Diptera dominated the diet (70.3%), especially chironomid midges (nematocerans). The second most common prey were homopterans (aphids). Other prey included a moth, psocopteran, ant (*Messor denticulatus* queen), and a spider.

The results indicate that *S. tricinctus* is a generalist predator but shows a preference for soft-bodied and relatively safe prey. Winged insects comprised about 91.9% of its diet, likely reflecting its arboreal habitat. Unlike some specialized salticids, it avoids dangerous prey such as worker ants and web-building spiders.

Table 3: Prey composition of *Salticus tricinctus*

Prey Group	Category	N	%
Insect			
Diptera	Total	26	70.3
	Brachycera		
	Calliphoridae	1	2.7
	Tachinidae	1	2.7
	Others	2	5.4
	Nematocera		
	Chironomidae	21	56.8
	Limoniidae	1	2.7
Homoptera	Aphidina	7	18.9
Hymenoptera	Formicoidea (*Messor denticulatus*)	1	2.7
Lepidoptera		1	2.7
Psocoptera		1	2.7
Arachnida			
Araneae		1	2.7
Total		37	100

Case Study VII: Feeding Behaviour and Prey Preference of *Menemerus bivittatus* (Chaubey, 2019)

This study evaluated the habitat, feeding capacity, and prey preference of the gray wall jumping spider, *Menemerus bivittatus*, a common predator found on walls and tree trunks in India. As an active hunter, it relies on keen vision to stalk and capture prey rather than using webs.

Experiments were conducted under laboratory conditions using common prey such as house flies, rice moths, mosquitoes (adults and larvae), and small insects. Spiders were starved for 24 hours before testing. In prey preference trials, multiple prey types were offered simultaneously, while in feeding capacity trials, individual prey types were provided separately. Observations were recorded after 12 hours.

Results showed that both juvenile and adult spiders preferred small flies, which are commonly encountered on walls. The spiders exhibited typical salticid hunting behaviour—stalking followed by a rapid leap to subdue prey. They demonstrated high predation efficiency and were capable of capturing insects up to twice their body size, including moth pests.

Overall, *M. bivittatus* is an effective generalist predator with strong potential for controlling household and agricultural insect pests due to its high feeding capacity, visual acuity, and active hunting strategy.

Table 4: Feeding potential / prey preference of *Menemerus bivittatus*

S. No.	Lepidoptera	Diptera	Homoptera	Orthoptera	Coleoptera	Total
1	12	12	8	8	0	41
2	14	11	7	7	1	40
3	13	14	8	6	0	41
4	15	11	5	7	1	39
5	13	10	7	5	0	35
6	11	12	6	4	1	34
7	13	10	8	7	0	37
8	10	11	5	5	1	32
9	13	12	8	6	0	39
10	14	9	6	5	1	35
Mean ± S.D.	12.80 ± 1.48	11.20 ± 1.40	6.80 ± 1.23	6.00 ± 1.25	0.50 ± 0.52	37.30 ± 3.16

Conclusion

The predatory behaviour of jumping spiders represents a highly refined set of hunting strategies that make them efficient and successful predators. Their actions are driven purely by the need for food and survival, and they pose no significant threat to humans or other non-prey organisms. On the contrary, they play a beneficial role by helping to regulate populations of insects and other pests. Overall, their hunting behaviour highlights the diversity and complexity of natural systems, and their unique combination of keen vision, agility, and behavioural flexibility makes them a fascinating subject for scientific study and an excellent example of evolutionary adaptation.

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GREEN CHEMISTRY APPROACHES IN PLASTIC RECYCLING: TOWARDS A CIRCULAR ECONOMY

Radhika Prakash Karad

Department of Chemistry,

Shri. Kumarswami Mahavidyalaya, Ausa, Latur (413512), Maharashtra, India

Corresponding author E-mail: radhikakarad2000@gmail.com

Abstract

The increase of worldwide plastic pollution has required a move from linear "take-make-dispose" models to a circular economy. As the time passes quality of material is decreased which is “downcycling”, often caused by conventional mechanical recycling methods. This article is about current advancements in green chemistry which aimed at plastic waste management, particularly on catalytic depolymerization, enzymatic recycling and the usage of safe solvents for recycling. By sticking to the 12 Principles of green chemistry like waste prevention, the use of renewable feedstocks and the atom economy, researchers are evolving closed-loop systems which change plastics to their original monomeric forms without the use of high energy or toxic byproducts of traditional methods.

Keywords: Circular Economy, Downcycling, Green Chemistry, Enzymatic Recycling, Closed-Loop Systems.

Introduction

It is estimated that plastic production shall increase tremendously by 2050, still only few fractions of plastic waste is recently recycled. Green chemistry provides a way to reconstruct both the material design and processes that is used to recover them. The aim is to go beyond the reshaping (mechanical recycling) and melting towards modern biological and chemical routes that is used to conserve the innate value of the polymer [1]. Current studies highlight that for a transformation to be successful, the intensity of energy for these processes must be dramatically lowered through innovative catalysis [2]. Moreover, the incorporation of lifecycle assessments (LCA) guranteed that " green " solutions do not fortuitously transfer environmental pressure elsewhere [3].

1. Chemical Recycling and Catalytic Depolymerization

Process of chemical recycling contains converting polymer chains into smaller elements, such as monomers, dimers or trimers etc. This process maintains the backbone of carbon for further use, which is not possible after incineration [4].

- **Hydrolysis and Solvolysis:** Methodologies like neutral hydrolysis are gaining momentum as they work at lower temperatures and help to prevent excessive pH conditions, improving safety [5]. Acid hydrolysis is solid technique for post-consumer PET, however it needs cautious handling of corrosive agents [6].

- **Catalytic Pathways:** Enhancing the selectivity of PET and polyurethane (PU) depolymerization is possible due to the advancements of catalysts such as organocatalysts and metal oxide catatlysts (e.g., TiO_2 , ZnO) [7]. Features like high recyclability, reducing waste production during the process of recycling itself is achievable by designing new aged diversified catalysts [8].
- **Microwave-Assisted Recycling:** To accomplish rapid, volumetric heating, considerably decreasing the time of reaction for polyester depolymerization have been possible by current inventions like microwave irradiation [9].
- **Green Solvents:** Particular retrieval of pristine polymers from mixed waste streams using clean bio-solvents is acheived by solvent based dissolution using Hansen Solubility Parameters (HSP) [10].

2. Biocatalytic and Enzymatic Approaches

Usage of designed enzymes that work under moderate and aqueous conditions is one of the most helpful " Green " frontiers.

- **Enzymatic Recycling:** Selective deterioration of Polyethylene Terephthalate (PET) can be made by specialized enzymes like PETase and MHETase [11]. These biological catalysts help in the retrieval of refined terephthalic acid (TPA) and ethylene glycol (EG) from complex textile waste [12].
- **AI-Driven Design:** Current research emphasizes the usage of Artificial Intelligence in the designing of de novo hydrolases that surpasses naturally evolved enzymes in both catalytic rate and thermal stability [13].
- **Microbial Upcycling:** Incorporation of microbial associations to "upcycle" plastic waste into high- performance biological plastics like Polyhydroxyalkanoates (PHA) depicts a true circular bio-economy [14]. Conversion of waste into high performance materials is done by this bio "upcycling" [15].

3. Photocatalytic Degradation: Harnessing Solar Energy

Growing green chemistry approach includes the usage of photo-activated catalysts to disintegrate bulk polymers and microplastics at ambient temperatures.

- **Heterogeneous Photocatalysis:** Use of TiO_2 or carbon nitrides for the conversion of polyethylene into liquid fuels using only sunlight as the power source has successfully discovered by the researchers [16].
- **Waste-to-Hydrogen:** New photolytic systems are being evolved that deteriorate plastic waste while producing green hydrogen at a time, depicting a "two fold success" for sustainability [17].

4. Design for Recyclability and Policy

Green chemistry also highlights the " leading end" of the lifecycle. Preparing plastics that are "recyclable by design " is vital for prolonged sustainability [18].

- **Covalent Adaptable Networks (CANs):** Preparing polymers with reconstructible chemical bonds is easy to disintegrate and re-process without loss of mechanical integrity of the polymer [19].
- **Bio-based Alternatives:** Replacing fossil-fuel plastics with bio-PET or polylactic acid (PLA) decreases the footprint of carbon and assures that the material can assimilate into existing green recycling streams [20].
- **Standardization:** To attain a closed loop economy, universal norms for plastic purity and additive disclosure are necessary to inhibit the accumulation of " persistent chemicals" in recycled products [21].

Conclusion

The move toward Green Chemistry or environment benign chemistry in plastic recycling is no longer hypothetical. With the processes like hydrolysis, solvolysis, microwave assisted recycling, use of green solvents for recycling, the integration of AI in enzyme engineering, microbial upcycling, photocatalytic degradation, designing the plastics in such a way that it,s design is recyclable and the commercialization of large-scale plants, the industry is moving toward a model where plastic is treated as a high-performance carbon feedstock rather than waste.

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SMART AGRIBOT: AN IoT-BASED PRECISION FARMING ROBOT WITH AI-DRIVEN IRRIGATION AND SEED SOWING

Mamatha Sure*[1] and Nikitha Jajala[2]

[1]Department of Computer Science & Engineering,
Hyderabad Institute of Technology and Management, Hyderabad, Telangana, India
[2]Department of Computer Science & Engineering (Data Science),
Malla Reddy College of Engineering & Technology (MRCET), Hyderabad, Telangana, India
*Corresponding author E-mail: sure.mamatha@gmail.com

Abstract

Agriculture plays a critical role in global food security, but traditional farming methods face numerous challenges. Amid rising labor costs, water scarcity, and inefficiencies in traditional farming methods, the current article introduces a Smart Agribot, an IoT-based precision farming robot powered by renewable energy and artificial intelligence. The Agribot integrates sensors, machine learning models, and automated systems to optimize agricultural tasks such as irrigation, seed sowing, and field monitoring. Key features of the Agribot include optimal watering schedules, which leverage soil moisture, temperature, humidity, and weather forecast data to ensure precise irrigation using decision tree and random forest algorithms. Equipped with a soil moisture sensor, DHT sensor, and sonar sensor, the robot navigates autonomously, avoids obstacles, and adapts to the environmental conditions. Further, powered by a solar panel and controlled by an Arduino Uno, the Agribot utilizes a submersible pump for efficient irrigation, and a Bluetooth module for remote operation. This sustainable and cost-effective solution not only reduces human labor; it also enhances productivity, offering a transformative approach to precision agriculture.

Keywords: Precision Farming, Renewable Energy, Artificial Intelligence, Agribot.

Introduction

Agriculture is the foundation of global food security, directly supporting millions of livelihoods. Yet, it is increasingly strained by rising labor costs, water scarcity, and inefficient resource management. These challenges demand innovative approaches to sustain productivity and meet the growing food demands. Precision farming, which utilizes advanced technologies such as IoT and artificial intelligence, has emerged as a transformative solution to optimize agricultural practices. By integrating these technologies, traditional farming can evolve into a smarter and more efficient system that addresses resource constraints to ensure sustainability. Agriculture remains at the core of human existence; however, farmers face many challenges such as increasing labor costs, water shortages, and inefficient practices that waste resources. Such increasing pressures to provide more food to the growing populations cannot rely on outdated methods; instead, practical and affordable methods must be used to modernize agricultural practices. With Smart Agribot, farmers' efforts and reliance on manual labor will be reduced. Simultaneously, water usage will be optimized and precision on farmlands can be maintained. This initiative incorporates technology into agriculture for simplicity, sustainability, and resource conservation.

The most recent advancements in IoT-driven agriculture show progress in precision farming, resource optimization, and sustainability. An IoT-based solar Agribot can accurately predict soil moisture with a 98.63% success rate using SVM and Sparse Linear Regression. IoT and solar-powered seed distribution systems can dispense and manage power efficiently. ESP32 sensors improve real-time monitoring of water management and crop yields but are prone to system failures. Machine learning algorithms like SVM, KNN, and decision trees have been implemented on Agribots for optimized irrigation and crop management by improving power consumption and scalability. CNNs have en- hanced the automation of agricultural tasks, like wind speed measurement and disease detection, though adaptability to varying conditions is limited. Real-time data integration with weather forecasting optimizes irrigation but faces adoption and calibration challenges. Hybrid models combining IoT with predictive analytics improve water efficiency and productivity, though connectivity and reliability issues persist. Threshold-based pump control algorithms further enhance automated irrigation and resource management, but challenges such as limited scalability, sensor calibration, and dependency on cloud connectivity remain significant.

Few significant challenges faced by state-of-the-art systems in IoT-driven agriculture include the problem of scalability, particularly for systems that integrate additional variables in agriculture. High costs, environmental dependency, and diffi- culties in calibrating sensors prevent large-scale implementa- tion. In addition, real-world applications suffer from inconsis- tent performance due to weather variability and dependence on solar power. Connectivity challenges include Wi-Fi limitations and sensor reliability issues, preventing widespread large- scale deployments and the need for real-time data accuracy. Furthermore, the lower adaptability to different environmental conditions and the particular needs of crops decrease the robustness of some models. Hybrid solutions integrating pre- dictive analytics and IoT are still facing reliability issues, inefficiencies in power management, and problems in scaling. Such weaknesses emphasize the need for even more adaptable, cost-effective, and scalable IoT solutions in agriculture.

- **P5**: Challenges of the problem space.
- **P6**: Explain your approach to solve the problem here.
- **P7**: Point-wise contributions of your paper.
- **P8**: Organization of the rest of the paper.

Literature Survey

Dr. Gulbir Singh *et al.* [1] proposed a solar-powered IoT- based Agribot for efficient irrigation and farm monitoring. The Agribot uses sensors to collect data on soil moisture, temperature, humidity, and atmospheric pressure to optimize water usage. It employs Sparse Linear Regression (SLR) and Support Vector Machine (SVM) algorithms for predicting soil moisture. The proposed system allows users to make irrigations through the web-based or mobile application interface in real-time. SLR outperformed SVM by achieving a prediction accuracy of 98.63 percentage. The advantage of this system is that it reduces water wastage and energy dependency due to the use of solar power and precision irrigation. However, the system faces challenges like limited scalability in its current prototype form and dependence on weather predictions, which may affect its accuracy in dynamic environments.

Vakiti *et al.* [2] designed an IoT-based solar-powered automatic seed dispenser for efficient agricultural applications. The system combines the features of solar energy with that of IoT by utilizing an ESP32 microcontroller and soil moisture, temperature, and humidity sensors for real-time monitoring. The system helps automate the soil ploughing, seed dispensing, and irrigation processes for sustainable and precise farming. The system was able to deliver reliable performance through optimal conditions for seed germination, reduction of manual labor and operational costs. Its advantages include sustainability through solar energy, real-time monitoring, and automation. However, it has its drawbacks, such as reliance on consistent sunlight and the need for technical expertise for maintenance.

Boralkar. [3] proposed an IoT-based smart agriculture system using the ESP32 microcontroller to automate field monitoring and irrigation. The system integrates sensors like soil moisture, pH, sunlight, rain, and temperature sensors to collect real-time environmental data, which is transmitted wirelessly to a cloud platform. A mobile application allows farmers to monitor and control the system remotely, including features like automatic water pump operation based on tank level and soil moisture. Advantages include efficient resource utilization, less water wastage, and increased crop productivity. The system is dependent on internet connectivity and has a relatively high setup cost, which is one of the major drawbacks. It may improve in the future to be less costly and offer offline functions to increase accessibility.

Srivastava *et al.* [4] proposed an IoT-based Agribot to revolutionize smart farming and farm monitoring by integrating sensors, UAVs, and robotics. The system automates key agricultural tasks like soil sampling, irrigation, fertilization, crop monitoring, and harvesting while enabling real-time data collection and analysis. This technology allows farmers to make precise decisions, optimizing resource usage and improving crop productivity. The benefits are lower labor costs, improved efficiency, and sustainability through judicious use of water and fertilizers. However, the high energy requirements and initial investment are significant drawbacks to widespread adoption. Improving these factors with renewable energy solutions and cost-effective designs may make it more accessible to smaller farms.

Ismaili *et al.* [5] proposed an IoT-based irrigation system for smart agriculture to optimize water usage and enhance crop productivity. The system uses an Arduino Uno R4 Wi-Fi microcontroller and sensors to monitor Total Dissolved Solids (TDS), pH, and soil moisture, with data transmitted to the Arduino Cloud for real-time analysis and alerts. Initial results demonstrated efficient irrigation management and potential scalability to larger agricultural fields using long-range communication protocols like LoRa. The advantages of this system include the minimization of wastage of water, real-time monitoring, and easy decision-making for farmers towards sustainability in farming. It lacks short-range Wi-Fi connectivity and reliance on external power sources besides other costs incurred in scaling up to a larger application. These challenges indicate areas that could be improved in the future, including incorporating solar power and advanced wireless technologies.

Sneha *et al.* [6] developed an Agricultural Robot called Agri-Bot and a Wind Sensor system for smart farming. Agri-Bot performs automated irrigation, plowing, and leaf disease detection using the Raspberry Pi Pico, ESP32 camera, and algorithms using the machine learning approach and controls through the Blynk app. The Wind Sensor system has an anemometer of 4 cups with IR sensors and uses the ESP32 microcontroller for displaying the wind speed and direction, displaying results on the LCD. The Agri-Bot achieved accurate disease classification and efficient task automation, while the Wind Sensor provided precise environmental data for optimized farming decisions. The system reduces manual effort, improves crop health, and supports remote monitoring. However, the Agri-Bot's outdoor use requires additional protection, and the Wind Sensor may need recalibration for non-standard setups.

Ghilan *et al.* [7] proposed an IoT-based precision irrigation system for smart farming that integrates various environmental sensors, such as soil moisture, temperature, humidity, water level, and light, with weather data. Using an ESP32 microcontroller, the system sends data to the ThingSpeak platform, allowing farmers to monitor and analyze conditions in real time. The system adjusts irrigation schedules based on weather forecasts, improving water efficiency and crop yields. The proposed system has shown to be very scalable and gives accurate, actionable insights to farmers. Its drawbacks include high initial cost, reliance on internet connectivity, and possible inaccuracies in data due to errors in sensors or weather forecasts.

Togneri *et al.* [8]. developed a hybrid and data-driven model for Water Need Estimation (WNE) in IoT-based smart irrigation systems using supervised machine learning techniques like deep learning. Their model uses data from IoT sensors and weather stations to estimate soil moisture and optimize irrigation. The approach demonstrates good scalability and adaptability to diverse geographic and climatic conditions, with transfer learning addressing the cold-start problem. The advantages include flexibility over various environments, improved water use efficiency, and increased reduction in environmental impact. The drawbacks include sensitivity to the quality of data, reliance on a robust IoT infrastructure, and difficulties in managing large volumes of sensor data.

Saha *et al.* [9] developed a precision agriculture system that integrates IoT and WSN to improve the efficiency of farming. The system applies IoT-enabled sensors to collect real-time data on soil moisture, temperature, and nutrient levels, which is analyzed for optimizing irrigation, pest control, and fertilizer application. It helps farmers cut down waste, reduce costs, and increase crop yields by automating data collection and analysis. The advantages of the system include real-time monitoring, improved resource management, and sustainability. However, the challenges are high initial costs, limited connectivity in rural areas, and data security concerns, which need to be addressed for widespread adoption.

Kakelli *et al.* [10] proposed an IoT-based Agribot for precision agriculture and farm monitoring to overcome the problems in resource management and water wastage. The system integrates sensors such as soil moisture, temperature, and humidity, using an Arduino Uno R3 microcontroller to collect and send data to the cloud via ESP8266 Wi-Fi module. The Agribot automates irrigation based on soil moisture levels, thereby optimizing water use and reducing manual labor. This will operate on solar power; the collected data will display and analyze on cloud-based platforms for real-time monitoring. While the system hugely reduces water wastage, makes irrigation efficiency better, these have some challenges to consider also: the system is totally dependent on consistent internet connection and has the potential inaccuracy of sensors.

Table I: Literature Survey

Author	Year	Objectives	Methodology	Result	Limitations
Dr. Gulbir Singh, Sreelatha Reddy	2024	Develop an IoT-powered solar Agribot for efficient irrigation, real-time monitoring, and optimized water management.	Support Vector Machine (SVM), Sparse Linear Regression (SLR).	Achieved 98.63% soil moisture prediction accuracy, efficient irrigation scheduling, and energy-efficient solar-powered operations.	Scalability issues, weather variability, high costs, data dependency, and limited integration with additional agricultural variables.
Vakiti *et al.*	2024	Automate seed distribution using solar power and IoT for efficient, sustainable, and data-driven agriculture.	IoT, decision algorithm, solar power management, Bluetooth control, real-time monitoring.	Efficient seed dispensing, real-time monitoring, optimal power usage, and reliable performance.	Scalability, weather dependency for solar power, sensor calibration, and system durability in harsh conditions.

Radhika R. Boralkar	2024	Automate farming using IoT for efficient resource management.	Sensors integrated with ESP32.	Improved water management, increased crop yield, reduced costs.	System failure risks, sensor calibration, manual override needed.
Dr. Vivek Srivastava	2024	Improve farming efficiency with IoT-based Agribots for precision.	Support Vector Machine (SVM), K-Nearest Neighbor (KNN).	Increased efficiency, reduced resource waste, better crop management.	Power consumption, sensor calibration, environmental factors, scalability issues.
Shpend Ismaili	2024	Optimize irrigation and monitor soil health for agriculture.	Decision tree, machine learning for environmental data analysis.	Real-time data monitoring, improved irrigation decisions, optimized crop growth.	Wi-Fi limitations, power management for large-scale deployment, sensor accuracy.
Sneha M	2024	Automate agricultural tasks with sensors and IoT technology.	Classification algorithms and Convolutional Neural Networks.	Accurate wind speed, disease detection, and task performance.	Limited environmental data and system adaptability in diverse fields.
Akram Ghilan	2024	Optimize irrigation through real-time data and weather forecasts.	Data analysis with ThingSpeak, MATLAB, weather integration.	Real-time data visualization, efficient irrigation, improved crop yield.	Data accuracy, cost, adoption by farmers, system calibration.
Rodrigo Togneri	2023	Enhance smart irrigation using IoT-based water need estimation.	Supervised ML, hybrid models for soil moisture and WNE.	Improved water efficiency, reduced energy costs, higher crop productivity.	Data quality, sensor reliability, climate/geography limitations in models.
Pallabi Saha	2023	Improve crop yields with sensors for soil moisture and irrigation.	IoT, WSN, predictive analytics, decision trees.	Optimized irrigation, better crop management, water and cost savings.	Connectivity, data accuracy, high costs, environmental impact.

Kakelli Anil	2020	Automate irrigation, monitor soil, and optimize crop care.	Threshold-based pump control algorithms.	Real-time data updates, automated irrigation, enhanced resource management.	Limited scalability, sensor calibration issues, dependency on cloud connectivity.

Problem Statement and Background

Problem Statement

In modern agriculture, maintaining optimal soil moisture and ensuring effective irrigation can be quite a challenge. This is especially true in areas where water resources are limited and traditional irrigation methods are inefficient. Imagine a farm where crops are either over-watered or under-watered because the farmer cannot continuously monitor the soil moisture content. This leads to water wastage, increased operational costs, and potentially lower crop yield.

To address this issue, we develop an IoT-based automated system for agricultural irrigation. This system will monitor soil moisture levels and other environmental factors, such as temperature and humidity, using sensors. Based on sensor data, the system will trigger an irrigation process, when necessary.

Objectives

- **Design and Develop an Autonomous Agriculture Robot**: Create a robot for autonomous seed sowing and drip irrigation with high efficiency and precision.
- **Revolutionize Agricultural Practices**: Automate labor-intensive tasks to enhance productivity and optimize farming processes.
- **Implement Autonomous Navigation and Obstacle Avoidance**: Integrate sensors and algorithms for autonomous navigation and obstacle detection.
- **Achieve Precision in Seed Sowing and Drip Irrigation**: Ensure accurate seed placement and efficient water usage to promote optimal plant growth.
- **Ensure Environmental Resilience and Sustainability**: Design the robot to withstand harsh conditions and operate efficiently for long-term sustainability.
- **Reduce Labor Requirements and Improve Crop Yield**: Reduce labor by 50%, increase seed germination by 10%, and save water.
- **Transform Agriculture Through Automation**: Automate key farming processes to optimize resource use and boost crop yields.
- **Utilize Sensor Data and Machine Learning for Optimized Irrigation**: Collect and analyze data from sensors (soil moisture, environmental conditions) to apply machine learning models that predict and optimize irrigation schedules, ensuring efficient water usage and improved crop health.

Background

In modern agriculture, the integration of robotics, IoT, and renewable energy is transforming traditional practices into efficient, sustainable systems. Autonomous robots equipped with sensors, such as DHT11 for temperature and humidity and soil moisture sensors, enable precise seed sowing and irrigation. Solar-powered battery systems further enhance operational efficiency, ensuring eco-friendly and uninterrupted functionality in remote areas. These advancements aim to address challenges like labor shortages, resource wastage, and the demand for sustainable farming solutions.

System Model/Architecture

The proposed system integrates IoT technology, sensors, robotics, and solar energy to create an autonomous agriculture robot capable of performing essential farming tasks such as seed sowing and drip irrigation. The architecture consists of several interconnected modules, each designed to handle specific responsibilities, ensuring that the system operates efficiently and sustainably under diverse agricultural conditions.

A. System Modules

The system is built around multiple key modules that work together seamlessly:

- **Power Management Module**: The robot is powered by a solar panel, which charges its battery cells during the day. This ensures a sustainable energy source for uninterrupted operations, even in remote areas.
- **Sensor Module**: The robot is equipped with various sensors to gather environmental data:
    - ➢ **DHT11 Sensor** is used to measure temperature and humidity, providing insights into weather conditions.
    - ➢ **Soil Moisture Sensor** monitors the water content in the soil, helping the system make accurate decisions about when and how much to irrigate.
    - ➢ **Sonar Sensor** enables the robot to detect and avoid obstacles.
- **Control Module**: At the heart of the system lies a micro-controller (Arduino Uno), which acts as the robot's brain. It processes data from the Bluetooth module and sensors and executes decisions such as starting the wheels, activating the irrigation pump, dispensing seeds, or stopping the bot when an obstacle is detected.
- **Communication Module**: The robot features an HC-05 Bluetooth module for remote control and navigation monitoring. Farmers can use a mobile application to control and track the robot's operations. The NodeMCU ESP8266 is responsible for transferring sensor data to a Google Sheet for real-time monitoring and historical analysis.
- **Actuation Module**: The robot's actions are carried out by its actuators:
    - ➢ The **submersible pump** irrigates the field based on real-time soil moisture data.

  - A **precision seed dispenser** ensures that seeds are planted at the correct spacing, promoting optimal growth conditions.
- **Navigation Module**: The robot moves around the field using four DC geared motors, providing smooth and precise movement. It uses a sonar sensor to detect obstacles in its path, and when an obstacle is detected, the robot automatically stops to avoid a collision.
- **Energy Management Module**: The robot is powered by a solar panel, which continuously charges the battery during daytime, ensuring the robot stays operational throughout its tasks.

Implementations and Performance Analysis

A. Experiment Setup

- **Project Implementation**: The robot is designed to perform essential farming tasks like seed sowing and irrigation. It uses sensors such as soil moisture, temperature, and humidity to automate these tasks and optimize resource usage.
- **Programming Languages and Libraries**: The project utilizes:
  - C++ with the Arduino IDE for hardware control, including motor and Bluetooth management.
  - Python for data analysis and machine learning, with libraries such as scikit-learn, pandas, and matplotlib.
- **Machine Specifications**: Experiments were conducted on a system with the following specifications:
  - Intel Core i5 Processor (12th Gen), 16GB RAM, Windows 10, Arduino IDE.
- **Assumptions**: The system was tested under the assumption that it operates in stable environmental conditions, with reliable sensor data and minimal external interference.
- **Experiment Parameters**: The following parameters were used:
  - **Network Setup**: HC-05 Bluetooth module for remote control, and NodeMCU ESP8266 for sending sensor data to Google Sheets for real-time monitoring.
  - **Machine Learning**: A **Random** Forest classifier was used to predict the optimal irrigation timing based on sensor data, including soil moisture, temperature, and humidity. The model was trained using historical data to make predictions about when irrigation should be triggered.

Sensor data, including soil moisture, temperature, and humidity, were processed to fill missing values using mean imputation: $Xfilled = \frac{\sum_{i=1}^{n} Xi}{n}$ (1)
where $Xfilled$ represents the filled value, Xi is each sensor reading, and n is the total number of non-missing values. Evaluation and Predicted Results The model was able to predict irrigation times with notable patterns that occur during high- temperature or low-moisture

conditions. The best-predicted irrigation time, based on historical and real-time data, was identified as thresholds were defined for decision-making:

- Soil Moisture (M): 1500 units
- Temperature (T): 26°C
- Humidity (H): 55

The binary target variable I (Irrigation Needed) was calculated using the following equation: $I = 1, \text{if } M < 1500 \text{ or } T > 26 \text{ or } H < 55$
$I = 0, \text{otherwise}$

Best Predicted Time = 01: 21 PM

This timing was derived by sorting and filtering predicted timestamps using the equation: $\text{Irrigation Timings} = \{t \in \text{Timestamp} : \text{Predicted Irrigation} = 1\}$

The optimized irrigation schedule minimized water usage as it was able to identify dry conditions. Real-time predictions were validated using a historical dataset, which resulted in consistent results. The solar-powered source of energy ensured that the experiments ran sustainably. Water Use Efficiency Formula To calculate Water Use Efficiency (WUE), the following formula was applied: $WUE = \frac{\text{Yield (kg)}}{\text{Water Used (m^3)}}$

This measures the amount of water the system saves from being wasted and the amount it produces in return.

The system's reliance on sensor accuracy and robust IoT infrastructure highlights its sensitivity to environmental and network conditions. However, its ability to integrate machine learning for autonomous decision making demonstrates significant advancements in precision agriculture.

Figure 1: Seed Sowing

Time-based features (hour, minute, day, month) were extracted from the timestamps to enhance model interpretability.

Results

The proposed IoT-based agriculture robot successfully optimized agricultural practices by integrating predictive irrigation and seed sowing. Using real-time sensor data, including soil moisture, temperature, and humidity, the system, powered by a solar energy source, used a random forest classifier to predict optimal irrigation times with high precision and identified the best irrigation schedule at 1:21 PM. This automation reduced water usage, improved water use efficiency, reduced labor, and increased seed germination rates. The uniform distribution of seeds was achieved by the robot's seed sowing mechanism Figure 1, thereby ensuring optimal crop growth. Sensor calibration ensured reliable data, with missing values addressed through mean imputation. The machine learning model, which attained a precision of 92 percentages, demonstrated robust predictions under changing environmental conditions. Challenges such as internet dependency and outdoor durability were mitigated through local data caching and enhanced protection. The results highlighted the potential of the system to revolutionize agriculture by improving resource management, reducing operational costs, and supporting sustainable, data-driven farming practices. The results indicated a reduction in water, a reduction in manual labor, and an increase in seed germination rates; the machine learning model accurately predicted irrigation schedules at a rate of 92 percentage. The proposed solution offers an integrated, cost-effective and scalable solution relative to the state-of-the-art system due to autonomous navigation, predictive analytics, and renewable energy, hence avoiding problems with sensor inaccuracy and reliance on internet connectivity. Future directions include the addition of nutrient and pH sensors for optimized fertilizer use, AI- driven dynamic irrigation, and improved system durability and offline operation capabilities for a wider application in remote agricultural areas.

Conclusion

An IoT-based autonomous agriculture robot that will help reduce the inefficiencies and resource wastage associated with traditional agricultural practices, particularly in irrigation and seed sowing. The system will integrate sensors, robotics and machine learning to monitor environmental factors, predict future irrigation needs, and automate seed sowing with high precision.

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About Editors

Dr. Archana Mahavir Ramteke is an Assistant Professor in the Department of Chemistry at K. D. K. Engineering College, Nagpur. She holds an M.Sc. and Ph.D. degree and has over 20 years of teaching experience at undergraduate and postgraduate levels. She completed her Ph.D. in 2016 and has published research papers in reputed national and international journals. Her scholarly contributions have received 36 citations, with an h-index of 3 and an i10-index of 2. She is a recognized Ph.D. supervisor at Rashtrasant Tukadoji Maharaj Nagpur University. Dr. Ramteke is actively involved in guiding research scholars and mentoring students. Her academic journey reflects a strong commitment to teaching, research, and scientific advancement, contributing meaningfully to the development of chemical sciences and fostering academic excellence through dedicated educational and research initiatives in her institution.

Dr. Pradip Duryodhan Satav is an Assistant Professor in the Department of Botany, Microbiology and Biotechnology at Science College, Nanded, with over 13 years of undergraduate teaching experience. He holds a Ph.D. in Microbiology from SGBAU Amravati and qualified CSIR NET-JRF in Life Sciences. His research specialization includes Industrial, Food, and Medical Microbiology. He has a strong publication record in reputed journals and actively participates in conferences and academic activities. His doctoral work focused on banana wine production, optimization, and chemical analysis. He is proficient in ICT-enabled teaching using Google Classroom and digital platforms. He has completed professional training programs and refresher courses. He has contributed to institutional responsibilities, including NCC activities, examination duties, and organizing academic and community outreach programs.

Dr. Ashwini V. Yankati is a dedicated Lecturer in the Department of Home Science at BVVS Akkamahadevi Women's Arts, Science and Commerce College, Bagalkot. She has made notable contributions to academia through teaching and research. She has published 10 research papers, authored 8 book chapters, and written 2 books in her field. Her research interests include Gerontology and Early Childhood Care and Education, with a focus on improving quality of life and child development outcomes. She has received the Young Budding Scientist Award and Young Researcher Award in recognition of her academic excellence. Dr. Yankati continues to inspire students and contributes actively to the advancement of Home Science education, research, and community-oriented developmental initiatives.

Dr. Verma is an Assistant Professor in the Department of Personalized and Molecular Medicine at Era University, Lucknow, India. His expertise includes molecular biology, infectious diseases, genome analysis, and pharmacogenomics, with a focus on personalized medicine. With over five years of research experience, he has published 52 works, including research papers, reviews, books, and book chapters in reputed journals. He has received Young Scientist and Best Researcher Awards from various scientific societies. He is a life member of several professional organizations and serves as Assistant Editor and advisory board member for reputed journals. His current research focuses on translational approaches, particularly integrating pharmacogenomics into clinical practice, with emphasis on improving healthcare outcomes in the Indian population through precision medicine and evidence-based research strategies.

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