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INSIGHT, DISCOVERY, LEARNING, INNOVATION, AND IMPACT

NATURE'S HIDDEN TRAP!

When Beauty become survival

By

Rosalind Franklin

Council of Scientific Research

(RFCSR)

September 15, 2026



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LETTER *From the* EDITOR

Dear Readers,

The most interesting advances in science often arise not from finding simple answers, but from learning to ask better questions. The September 2026 issue of Science Factors reflects this spirit, bringing together discoveries that challenge familiar assumptions and reveal unexpected connections across biology, medicine, technology and the natural world.

We begin with nature itself. A seemingly ordinary mountain flower turns out to obtain nutrients from captured insects, inviting us to reconsider the boundary between ordinary plants and carnivory. In the underground societies of naked mole-rats, chemistry becomes a language through which a queen influences reproduction and social order. Elsewhere, engineered probiotic bacteria demonstrate the possibility of sensing changes in blood glucose and responding with a therapeutic signal.

The issue takes us across remarkable scales of scientific enquiry: from the genomes of communities in the Thar Desert, where ancestry, environment and culture have left intertwined signatures, to towering tropical trees adapting their internal architecture. We also look outward to the turbulent plasma of the Sun and the remnants of dying stars.

Medicine and biotechnology provide another important thread. Our contributors examine emerging approaches to cancer, neurodegenerative disease, chronic wounds, drug-resistant infections and precision therapeutics. Across these fields, one theme is increasingly clear: the boundaries betw-

 **Dr. Animesha Rath**
The Editor-in-Chief

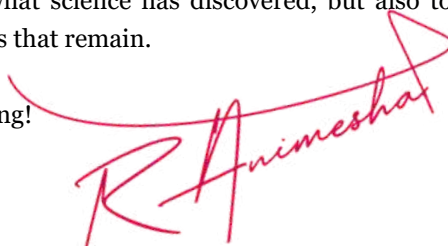
een disciplines are becoming less distinct. Chemistry meets biology, engineering meets medicine, and computation meets genomics.

This movement from understanding to application is equally evident in developments spanning biotechnology, artificial intelligence, cleaner transport, aquaculture, environmental protection, space science and intelligent engineering. Together, they remind us that innovation is most valuable when scientific imagination is accompanied by evidence, responsibility and a clear understanding of the problem being addressed.

No single issue can capture the breadth of contemporary science. It can, however, reflect the qualities that sustain scientific progress: curiosity, scepticism, careful observation and the willingness to revise what we thought we knew.

It is in that spirit that we present the September 2026 issue of Science Factors. I hope these pages encourage you not only to appreciate what science has discovered, but also to consider the questions that remain.

Happy reading!



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SCIENTIFIC RESEARCH EMPOWERS SOCIAL PROGRESS !

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FEATURED RESEARCH

Behind every discovery lies a story of curiosity, perseverance, and wonder. Science unfolds through relentless research and bold explorations into the unknown. These are the journeys that shape our understanding of the world—and beyond.

 | By **Dr. Manas Prusty**

A PREDATOR AMONG THE MOUNTAIN FLOWERS

FEATURED

High in the mountains of Shangri-La in Yunnan, China, imagine a young field botanist named Mei walking across a rocky alpine slope. Plants grow from narrow cracks between stones, where soil and nutrients are scarce. Among them, Mei notices an unusual flowering plant, *Saxifraga candelabrum*. At first, there seems to be nothing threatening about it: a cluster of leaves close to the ground and tall flowering branches reaching toward the mountain sun. But when Mei bends down for a closer look, she notices something strange. Tiny insects are stuck along the plant. Its stems and branches are covered with reddish, sticky glandular hairs, and small flies have become trapped on them. Some are still struggling; others have been there much longer. Could this ordinary-looking alpine flower actually be hunting insects?

The question would have sounded familiar to Charles Darwin. In 1875, while studying carnivorous plants, Darwin wondered whether some members of the genus *Saxifraga* might also be carnivorous because of their glandular hairs. He tried feeding experiments, but the evi-

dence was not enough to settle the question. More than a century later, *S. candelabrum* offered scientists another opportunity to investigate Darwin's idea using modern tools. Mei's fictional journey represents the real scientific investigation described in the study. The researchers first asked what should be required before calling a plant truly carnivorous. Simply finding dead insects stuck to a plant is not enough.

A genuine carnivorous plant should be able to attract prey, capture it, digest it and obtain nutrients from it. The team therefore set out to test each part of this sequence. Back on the mountain, Mei begins counting. The insects are not isolated accidents. The researchers found an average of about 71 trapped insects on mature plants. When they examined old herbarium collections, they discovered trapped insects on 43 of 45 flowering specimens, showing that insect capture was a regular occurrence. Experiments provided another clue: scent appeared to help attract insects. When floral odour was blocked, insect visitation decreased, while chemical analysis revealed floral compounds that could potentially attract them. Yet the plant faces a delicate problem. It needs insects for pollination as well as for food. Killing every visitor would be disastrous. Intriguingly, *S. candelabrum* mostly trapped small insects such as chironomid gnats that were poor pollinators, while larger, effective pollinators were rarely caught. The plant therefore



 | By **Dr. Manas Prusty**

appears to perform an extraordinary balancing act feeding on some insect visitors while allowing useful pollinators to escape.

But Mei still cannot call the mountain plant a predator. A sticky surface could simply be a defence mechanism that accidentally kills insects. The crucial question is what happens after capture. In the laboratory, researchers tested the glandular hairs for phosphatase, an enzyme associated with digestion in carnivorous plants. The hairs of *S. candelabrum* showed enzyme activity, whereas a related non-carnivorous *Saxifraga* did not. The researchers then performed their most convincing experiment. They raised fruit flies containing a special stable form of nitrogen, ^{15}N , and placed these labelled insects on the plant. If the plant was merely trapping insects, this labelled nitrogen should not become incorporated into its tissues. But it did. The ^{15}N signal increased significantly inside *S. candelabrum*, while non-carnivorous control plants did not show the same enrichment. The researchers also checked the surrounding soil to rule out nitrogen entering indirectly through the roots. The evidence pointed toward one conclusion: the plant was obtaining nitrogen from its prey.

There was one more chapter to the mystery. The scientists wanted to know whether the story of this newly recognized carnivore was also written into its genome. They assembled a chromosome-scale genome of *S. candelabrum* and compared it with other carnivorous and non-carnivorous plants. The comparisons revealed signs of convergent evolution: distantly related carnivorous plants had independently developed similar genetic changes associated with functions needed for carnivory. Among sticky-trap plants, these included processes related to prey attraction, digestion and nutrient absorption. Across a wider range of carnivorous plants, researchers found additional similarities involving digestive enzymes, nutrient processing and amino-acid metabolism. Evolution had not followed exactly the same genetic route in every carnivorous plant, but it repeatedly arrived at similar biological solutions. Faced with nutrient-poor environments, very different plants had independently evolved ways to supplement what their roots could obtain from the soil with animals.

As Mei leaves the rocky slopes of Shangri-La, the small flowering plant no longer seems ordinary. *Saxifraga candelabrum* grows where nutrients are difficult to obtain, and researchers suggest that glandular hairs that may once have defended the plant against herbivores evolved into stru-

ctures capable of capturing small insects. These insects became an additional source of nutrients, while larger pollinators continued visiting its flowers. More than a century after Darwin wondered whether *Saxifraga* could cross the boundary between ordinary flowering plants and carnivores, modern field experiments, enzyme tests, isotope tracing and genomics have provided compelling evidence that at least one member of the genus has done exactly that. The discovery leaves an even larger mystery. Sticky glandular hairs occur in other *Saxifraga* species and many other flowering plants. If a carnivore could remain overlooked in a familiar plant lineage for so long, how many other quiet predators might be hiding among the world's flowers?

QUIZ TIME!

TEST YOUR SCIENCE KNOWLEDGE

 While exploring the rocky mountains of Shangri-La, a botanist notices that *Saxifraga candelabrum* regularly traps small insects on its sticky glandular hairs.

However, simply finding trapped insects is not enough to prove that the plant is carnivorous.



Q. Which finding would provide the strongest evidence that the plant actually uses insects as a source of nutrition?

A The plant grows mainly in nutrient-poor rocky habitats.



B Many small insects are found stuck to its stems.



C Nitrogen labelled with ^{15}N from insects is detected inside the plant's tissues.



D The flowers produce scents that attract visiting insects.



REFERENCE

Zhang, XJ., Deng, T., Lin, N. et al. Identification of carnivory in the flowering plant *Saxifraga* via multidisciplinary evidence. *Nat Commun* 17, 7557 (2026). <https://doi.org/10.1038/s41467-026-75288-y>

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 | By Dr. Avijit Das

A QUEEN'S SCENT AND THE SECRET OF SOCIAL ORDER

FEATURED

Deep beneath the dry landscape of East Africa, a young naked mole-rat named Nia lived in a maze of dark underground tunnels. Nia shared her home with dozens of relatives. Some searched for roots and tubers, others dug tunnels, and stronger animals guarded the colony. Yet one animal was different the queen. She was larger, powerful and almost the only female that had babies. Nia and the other females were physically capable of reproduction, but while the queen remained in the colony, their reproductive systems stayed strangely quiet. Nia often passed the queen in the narrow tunnels, where smell was far more useful than sight. Scientists had wondered about this unusual society for decades. How could one female prevent so many others from reproducing? Was it simply because they feared her, or was the queen sending an invisible chemical message throughout the colony?

One day, imagine a researcher named Amani deciding to search for that invisible message. Amani collected odours from queens, males and non-breeding females and analysed their chemical contents. Among hundreds of compounds, one molecule stood out: isopropyl myristate, or IPM. It was abundant in queens but nearly absent from ordinary non-breeding females and males. IPM was found in secretions from several parts of the queen's body and became particularly abundant around ovulation. It also has low volatility, meaning it does not disappear into the air very quickly. Amani imagined the queen moving through the underground tunnels, brushing against surfaces and leaving traces of this chemical behind. Whenever Nia encountered the queen or travelled through places she had recently visited, she could potentially encounter IPM. The researchers now had a strong candidate for the mysterious signal that might announce the queen's presence throughout the colony.

But finding IPM on the queen was not enough. Amani needed to discover whether Nia could actually detect it. Experiments showed that IPM activated sensory neurons in the naked mole-rat's nose as well as smell-related regio-



 | By Dr. Avijit Das

ns of the brain. Behaviour provided another clue. When animals were offered normal bedding and bedding containing IPM, high-ranking naked mole-rats tended to avoid the IPM. These animals were particularly important because high-ranking females were the most likely to compete for the queen's position. When researchers disrupted the animals' sense of smell, this avoidance disappeared. IPM was also linked to changes in prolactin, a hormone involved in reproductive suppression. The researchers proposed that when Nia smelled IPM, the information travelled from her nose towards brain pathways controlling reproductive hormones. Higher prolactin helped keep her reproductive system inactive. The queen therefore might not need to constantly threaten other females. Her chemical presence could silently communicate a powerful message: "The queen is here; remain a non-breeder."

Then came the most dramatic experiment. Imagine that one morning Nia searched the tunnels, but the queen was gone. Normally, this would transform the colony. High-ranking females could become reproductively active and begin fighting to become the next queen. But Amani and the research team did something remarkable. Although the queen had been removed, they added IPM to the colony bedding every day. For 12 weeks, the queenless colony remained surprisingly stable. The expected dominance battles did not begin, prolactin remained high and progesterone stayed low, showing that reproduction remained suppressed. Then the researchers stopped adding IPM. The peaceful situation quickly changed. Prolactin decreased, progesterone increased and females began showing sexual behaviour. High-ranking individuals became aggressive, and competition became so intense that one female was killed. Eventually, one dominant female gained weight, became reproductively active, became pregnant and later gave birth. IPM therefore appeared capable of doing much more than simply creating a recognizable smell. It helped maintain both reproductive suppression and social stability even when the queen herself was absent.

Nia's underground world revealed something extraordinary about mammalian society. The queen appears to produce a chemical message connecting smell, the brain, hormones, reproduction and social behaviour. When the queen is present, she produces IPM, which other colony members detect through smell. Prolactin remains high, reproductive activity stays suppressed and the colony remains relatively stable. When the queen dis-

appears, IPM declines, prolactin falls and progesterone rises. Reproductive activity returns, competition begins and eventually another female can become queen. This system resembles what scientists have observed in bees, ants and other social insects, where queen pheromones help prevent workers from reproducing. The researchers therefore suggest that IPM behaves somewhat like a mammalian queen pheromone or "social hormone." IPM may not act alone, because behaviour and other sensory signals could also help maintain the colony hierarchy. Nevertheless, Nia's story captures the remarkable central discovery: deep inside a dark underground colony, the queen does not need words to announce her authority; her chemistry can speak for her.



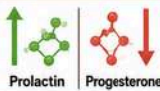
A queen naked mole-rat is removed from her colony. Normally, high-ranking females soon become reproductively active and begin competing to become the new queen.

Researchers want to test whether the queen's chemical signal isopropyl myristate (IPM) can maintain reproductive suppression even without the queen.

 **What would provide the strongest evidence that IPM is maintaining reproductive suppression?**

A  **The females spend more time exploring the tunnels.**

B  **The females eat more food after the queen is removed.**

C  **Females exposed to IPM maintain high prolactin, low progesterone, and do not become reproductively active.**

D  **The females begin producing more sounds after IPM exposure.**

REFERENCE

Khallaf, M.A., Hart, D.W., Luo, W. et al. A queen odour mediates reproductive suppression in a eusocial mammal. *Nature* 656, 390–398 (2026). <https://doi.org/10.1038/s41586-026-10772-5>.

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 | By Dr. Preeti Sharma

WHEN BACTERIA SENSE SUGAR TO CONTROL BLOOD GLUCOSE

FEATURED

In the busy city of Shanghai, China, a young researcher named Mei was thinking about a problem faced by millions of people with type 2 diabetes. Blood sugar does not remain at the same level throughout the day. It may rise sharply after a meal and fall again several hours later, yet medicines are often taken at fixed times and doses. Some diabetes medicines work through GLP-1, a hormone that helps control blood sugar by encouraging insulin release. Mei wondered whether a medicine could instead respond automatically to the body's changing needs. What if something inside the intestine could detect when glucose became too high, release treatment, and stop when glucose returned toward normal? Researchers in Shanghai explored this possibility by engineering the probiotic bacterium *Escherichia coli* Nissle 1917. They created a living system called GIFT, designed to sense glucose and

produce a therapeutic molecule only when needed.

Mei imagined each engineered bacterium as a tiny guard carrying its own sugar detector. At the heart of this detector was a protein called HexR. When glucose was low, HexR helped keep the therapeutic gene switched off. When glucose increased, however, bacterial metabolism produced a molecule called KDPG, which changed HexR's behaviour and allowed the genetic switch to turn on. The researchers connected this system to the production of GLP-1, meaning high glucose could trigger the bacteria to produce a molecule that helps lower blood sugar. When glucose fell again, production decreased. The scientists first tested whether this glucose switch really worked. They found that GIFT responded much more strongly to high glucose than to low glucose. Importantly, the response was reversible: when glucose increased, the system switched on; when it decreased, the system switched off; and when glucose rose again, it could reactivate. To Mei, it was like an automatic light controlled by a sensor, except glucose was the signal and medicine was the output. The researchers next gave the engineered probiotics orally to diabetic mice. After reaching the intestine, the bacteria sta-



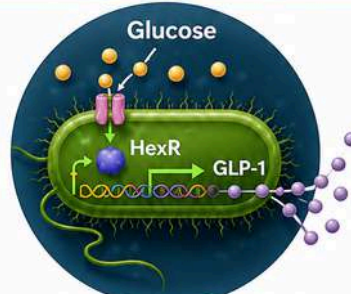
 | By Dr. Preeti Sharma

yed temporarily rather than permanently colonizing the animals. When glucose was high, GIFT became active and produced GLP-1. Insulin increased and blood glucose decreased. The researchers then continued treatment for around 30 days. The diabetic mice showed better fasting glucose control, improved glucose tolerance and insulin sensitivity, and lower HbA1c, an important measure of long-term glucose control. Several experiments also showed improvements in body weight, fat accumulation, triglycerides and cholesterol. One experiment particularly interested Mei. The scientists gave the animals foods containing different amounts of sugar. High-sugar foods such as cola and chocolate caused glucose to rise and activated the bacterial sensor, whereas low-sugar foods produced much smaller responses. This showed that the engineered bacteria could respond dynamically to glucose changes associated with food rather than simply producing GLP-1 continuously.

Mei's team also wanted to know whether better glucose control could reduce some longer-term effects of diabetes. In diabetic mice, GIFT treatment was associated with reduced inflammation and oxidative stress and improvements in measurements of liver and kidney damage. Changes were also observed in the gut microbiome, including increases in some beneficial bacteria. The researchers compared GIFT with semaglutide, an established GLP-1 receptor agonist. Although GIFT produced much less GLP-1 than the pharmacological exposure achieved with semaglutide, it still produced therapeutic effects. Another experiment examined the danger of blood sugar falling too low when treatments were combined with insulin. In these mouse experiments, adding semaglutide to insulin increased hypoglycaemic events, whereas adding GIFT did not increase them. This suggested a possible advantage of glucose-responsive treatment: as glucose falls, therapeutic production can also decrease. Longer-term testing also found GIFT generally well tolerated in mice, without a detectable adaptive immune response during the study.

But Mei knew that success in mice was only an early step. The researchers therefore tested GIFT in cynomolgus monkeys that had spontaneously developed type 2 diabetes. A single oral dose increased GLP-1 and insulin and significantly lowered blood glucose, with the effect lasting for up to three days. The scientists then gave GIFT every three days for five weeks. The five diabetic monkeys showed improved glucose control, better glucose tolerance and reduced insulin resistance, while tests did not indicate important deterioration in liver or kidney function. Looki-

ng at the results, Mei imagined a different kind of future medicine: not simply a fixed-dose drug, but a living medicine capable of sensing a problem and responding to it. Still, GIFT has not yet been demonstrated as a diabetes treatment in humans. Larger and longer studies will be needed to establish its safety, stability, dosing and control. For now, the study offers an exciting possibility: engineered probiotics might someday remain quietly in the intestine, become active when glucose rises, deliver a therapeutic signal, and quiet down again when their job is done



Engineered probiotic bacteria (GIFT) sense high glucose in the intestine and produce GLP-1. They are given orally and stay temporarily in the intestine.

Which statement best explains the main advantage of GIFT over a conventional fixed-dose GLP-1 drug?

- A** GIFT produces much higher amounts of GLP-1 than conventional drugs, leading to stronger and faster glucose control.
- B** GIFT releases GLP-1 only when glucose is high and reduces production when glucose returns to normal, providing on-demand therapy and potentially fewer side effects.
- C** GIFT permanently colonizes the intestines and continuously produces GLP-1 regardless of glucose levels.
- D** GIFT works only in mice but not in non-human primates or humans.

REFERENCE

Guan, N., Kong, D., Gao, X. et al. Glucose-responsive probiotics for glycaemic modulation in mice and monkeys. *Nature* (2026). <https://doi.org/10.1038/s41586-026-10909-6>.

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Threads in the Sand: What the Genomes of the Thar Desert Tell Us About India

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Areas of Expertise: Genomics | Human molecular genetics | functional genomics of Alu repeats | Ayurgenomics | genetics of rare diseases.

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Areas of Expertise: Population Genomics | Human Genetics

While monuments crumble and written histories fade, human DNA preserves stories that stretch to millennia. India, home to nearly 1.48 billion people has one of the richest archives of migration, adaptation, and social life in its genomes. Thar is the world's most densely populated hot deserts, where extreme heat, aridity, intense UV radiation and scarce vegetation test the limits of survival. It is home to communities whose traditions in pottery, weaving, embroidery, leatherwork, metalworking, woodcraft, pastoralism, and trade have endured for centuries- occupations that are cultural identities as much as livelihoods, passed down through generations. About 85% of the Thar lies within India, across Rajasthan, Gujarat, Punjab, and Haryana, with the rest extending into Pakistan's Sindh and Cholistan regions. Far from isolated, it has for millennia been one of South Asia's great migration corridors, sitting at the eastern edge of the ancient Indus Valley Civilisation. Archaeology has long shown the Indus Valley's connections with North-West India, Central Asia, and beyond.

Despite a geographical and documented history, the genetic diversity of the Thar's own inhabitants has remained surprisingly understudied. This gap sits inside a story that population genomics in India has been piecing together for over decades. A comprehensive study from the early 2000s from the Indian Genome Variation Consortium (IGVc) had provided the first comprehensive genetic landscape encompassing diverse populations of India at a national scale. Further substantiated by the recent large-scale Genome India initiative. Building on IGV, we have traced migration histories across the subcontinent, identified disease-risk variants specific to Indian populations, characterised adaptations to high-altitude living, studied populations shaped by long exposure to malaria, examined how non-native groups admixed into India over time, and uncovered founder mutations behind rare genetic disorders in India's endogamous communities. Ancient DNA studies elsewhere reconstructed the timeline, Ancestral North Indian and Ancestral South Indian ancestry framework, the arrival of Steppe pastoralist and Iranian-related ancestries, and genomic evidence from sites connected to the Indus Civilisation. However, these had not looked closely at the desert - an extreme environm-

What we already knew

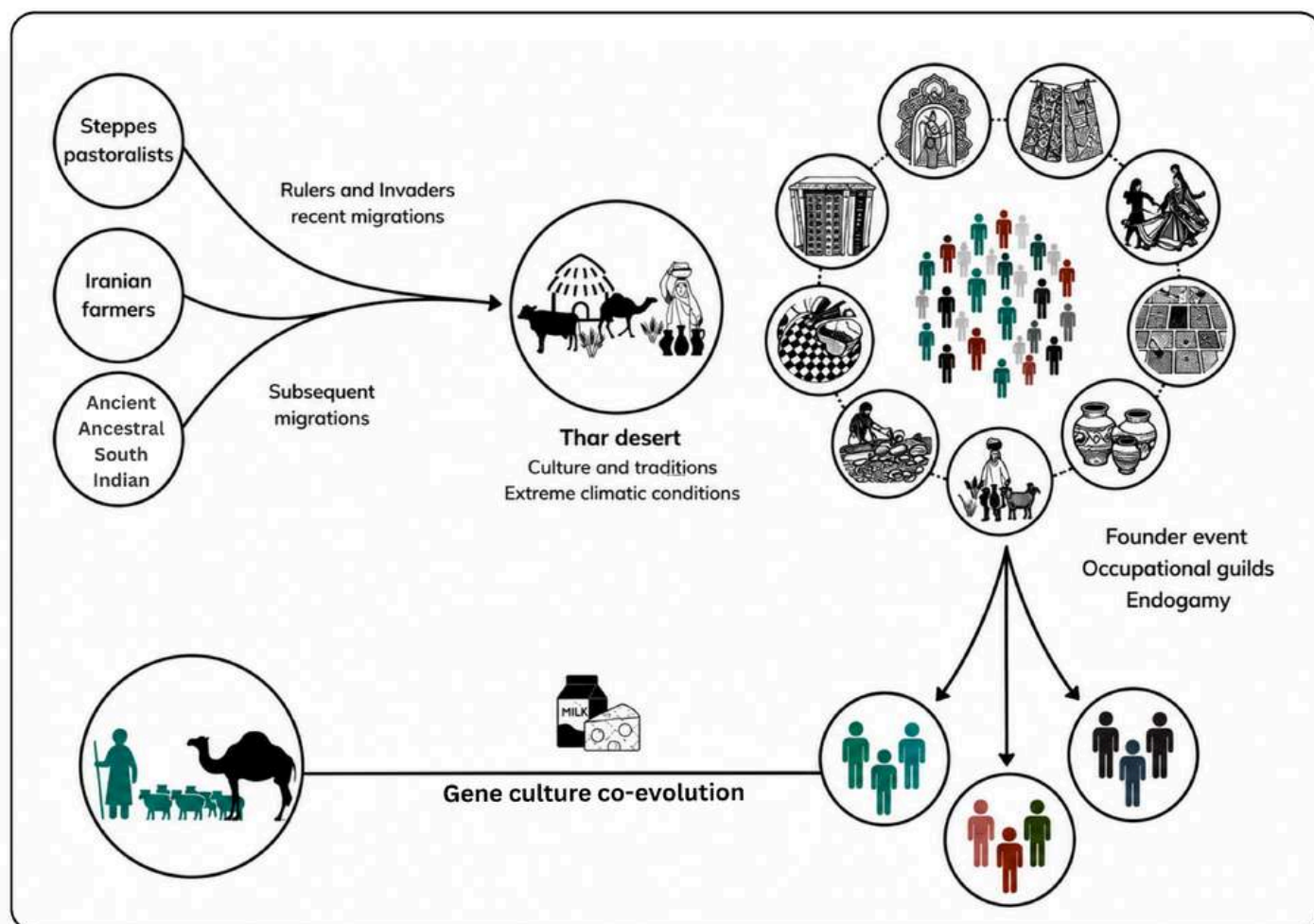


Figure 1: Demographic history, occupational specialization, founder events, endogamy, and gene-culture co-evolution shaping the genomic diversity of Thar Desert populations.

ment is a place where natural selection would be most evident and in these genomes one is likely to find stories of such struggles, this is the gap the present study set out to fill. Under the initiative project of Thar DESIGNS at IIT Jodhpur where a group of investigators set out to understand Desert Ecosystem Innovations Guided by Nature and Selection in the microbes, plants, animals, humans and ecosystem as a whole.

We analysed genome-wide SNP data from 176 individuals across eight traditional occupational communities in the Thar — seven artisan groups and one pastoral community in conjunction with genome-wide data available from global populations as well as ancient DNA. With the question of who are the people of the Thar? When did their ancestors arrive, and how far have they travelled both in ancient times and in the recent past? How is that history written into their genomes today? And how has culture shaped their survival in this landscape? Answering these is also a first step towards a pressing question: what happens to people adapted to an extreme/ancestral environment w-

hen they are displaced into a very different one, a concern that matters to all transitioning populations worldwide.

What the genome reveal

Despite close geographic proximity, artisan and pastoral communities such as potters, metalworkers, leatherworkers, woodworkers, weavers, Persian gold-embossers, embroidery artisans, and pastoralists form distinct genetic clusters rather than one uniform population, the study found heterogeneity each carrying its own demographic history. Their genomes carry South Asian ancestry alongside varying West Eurasian-related contributions, forming part of a broader north-south genetic cline. Pastoralists and groups such as woodcarvers and gold-embossers cluster closer to West Eurasian lineages, while potters and performers align more with southern clines. Present-day communities also show genetic continuity with the ancient Indus Periphery populations, echoing archaeological evidence that crafts such as pottery, wood art, gold embossing, tie and dye, we-

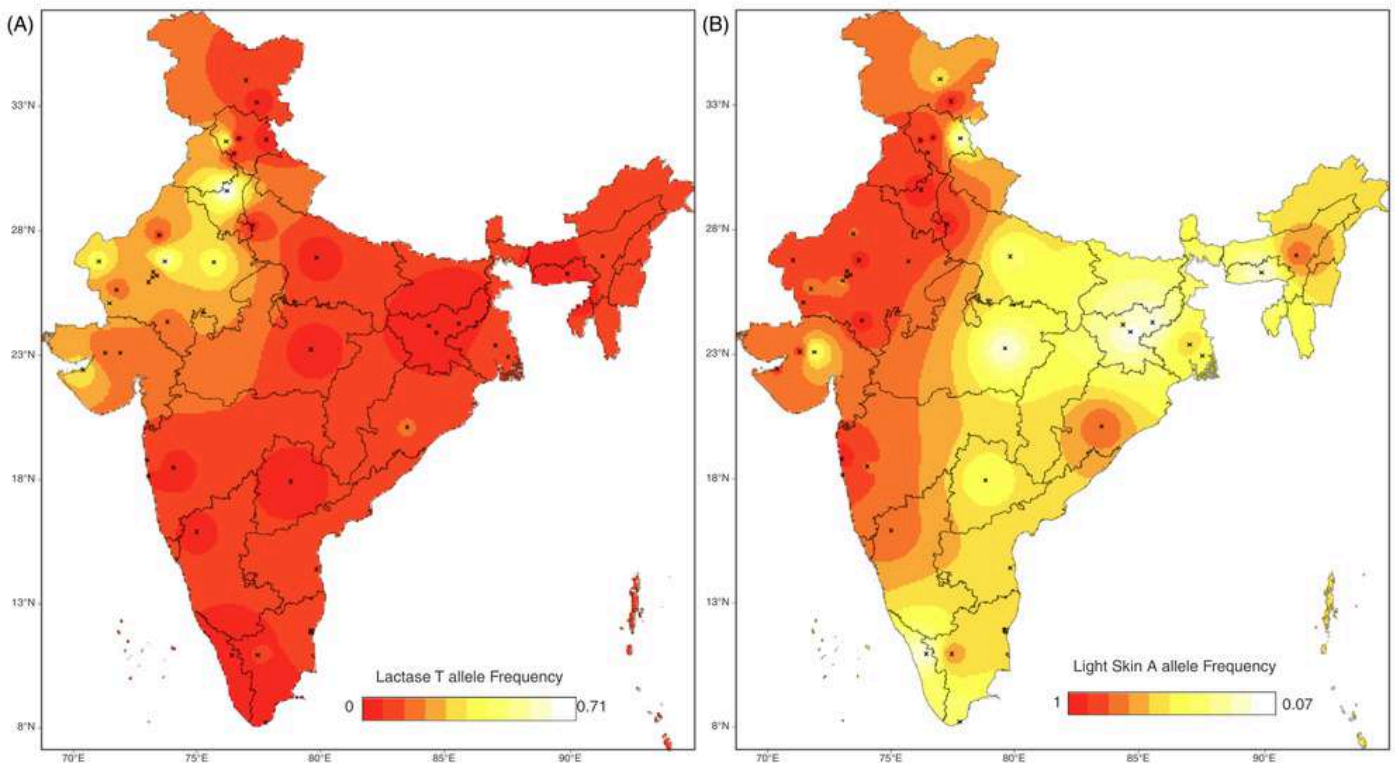


Figure 1: A) *LCT* rs4988235 (T allele) and (B) *SLC24A5* rs1426654 (A allele) across Indian populations. The color gradient represents the observed allele frequency range of the T allele of *LCT* and the A allele of *SLC24A5* in North and Northwest Indian populations.

aving-embroidery, leatherworking, and animal husbandry trace back to the Indus (Harappan) civilisation. These genomes also have varying signatures of later migration, including Neolithic Iranian-related and Eurasian Steppe-related ancestries. Genetic modelling suggests West Eurasian-related admixture at approximately 60-80 generations ago, with more recent founder events around 500-600 years ago, coinciding with medieval trade expansion and documented migrations, including of Persian-descended and tie-dye artisans. Some Thar communities showed stronger founder effects, along with elevated runs of homozygosity and identity by descent. These patterns suggest that the communities have remained relatively small and genetically isolated and shared ancestry within the communities over the generations. Role of Ancestry as well as adoption of cultural practices appears to have left detectable imprints in a few populations. The clearest example is seen in MCM6/*LCT* region, which is known for lactase persistence - ability to digest lactose into adulthood. with the strongest signal among pastoral groups due to dairy dependency and

“

The story of the Thar is not written only in archaeological ruins, it is written within the DNA of the people who continue to call the desert home.

”

cultural centrality of livestock appears as gene-culture co-evolution. The desert also receives some of the highest sunlight exposure in South Asia, which might suggest selection toward genes associated with darker pigmentation as seen in other deserts. Instead, the Thar population retains the lighter skin pigmentation gene associated with SLC24A5, a relic of European ancestry highlighting possibilities in different routes to UV adaptations. This emphasizes the need for contextualising ancestry and culture for understanding phenotypic and genotypic variations in geographically dispersed populations.

What we don't yet know

This study is a first step, not a final answer- Extreme-environment populations remain underrepresented in the reference panels much of human genomics relies on, and ancient DNA study is limited and challenging in South Asia's climate, leaving many gaps. Small, endogamous communities are statistically demanding to study and carry real ethical sensitivity, given how closely genetic findings *can map onto occupation and community identity*. A genetic signature of selection or founder risk is only a starting point: connecting it to actual disease burden requires functional and clinical follow-up studies. The open question is the one that motivated this work is what happens, biologically and medically, when populations adapted over centuries to a specific environment move away from it? As rapid urbanisation, changing diets, and the erosion of traditional lifestyles reshape health across the globe, this question is a live concern for displaced and transitioning populations everywhere. The throughline across our work is that India's genetic diversity cannot be understood through geography or ancestry alone. The Thar communities not only carry imprints of ancestral migrations but having settled in an extreme environment show distinct gene-culture coevolution and founder signatures shaped as much by occupation and marriage practice as by landscape. This has relevance for rare disease risk, and ascribing community-specific disease risks when natives transition to new environments with ancestral genomes - a classic example of Genome-Environment mismatch. Insights from these studies are important for setting baselines for precision medicine for stratified and more effective public health interventions. We are at present integrating these insights, with multi-omics in Thar populations that are transitioning from rural-to-urban environment for improved public health solutions for resident as well as non-resident communities.

ABOUT THE AUTHORS

Dr. Mitali Mukerji has been the convenor of the Indian Genome Variation Consortium project that provided the first comprehensive genetic landscape of India. She also led the Indian team in a PanAsia Consortium project that was a collaboration of 10 countries to study peopling of Asia. Her research has traced subcontinental migration histories, disease-risk variants, high-altitude and malaria-linked adaptations, non-native admixture, and founder mutations underlying rare disorders in India's endogamous communities. The Thar Desert study extends this program into an unexplored extreme environment, revealing how occupation, culture, and ancestry jointly shaped genetic diversity among its craft and pastoral communities. Mr. Rishabh Jain, PhD scholar in Bioscience and Bioengineering at IIT Jodhpur. He conducted the population genomics analyses of Thar Desert artisan and pastoral communities, examining population structure, ancient admixture, and natural selection to reveal how occupation, culture, and ancestry shaped their genetic diversity.

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The molecular machinery that helps plants survive heat



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Areas of Expertise: Protein homeostasis and proteostasis | Molecular chaperones | HSP70/J-domain protein systems | Heat-stress response | Plant stress biology



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Areas of Expertise: Protein homeostasis and proteostasis | Molecular chaperones | HSP70/J-domain protein systems | Heat-stress response | Plant stress biology

When we think about the impact of climate change on agriculture, our minds often turn to parched soils and empty reservoirs. However, beneath the visible wilt of a stressed crop, a complex molecular struggle unfolds. Unlike animals, plants cannot escape to cooler environments. Rooted firmly in the soil, they must survive wherever they grow, relying exclusively on their internal defence systems.

But what actually happens inside a plant during extreme heat?

The answer lies deep within the cell. Heat affects one of life's most fundamental building blocks, proteins. These microscopic molecules perform nearly every task inside a plant, from capturing sunlight to producing energy and regulating growth. For proteins to function, they must maintain a precise three-dimensional shape. High temperatures disturb this delicate structure, causing proteins to unfold and stick together into harmful aggregates. If this damage spreads unchecked, cells lose their ability to function, and the plant may not survive.

Fortunately, plants have evolved an extraordinary molecu-

lar quality-control system that constantly monitors, repairs, and protects proteins during stressful conditions. Understanding this hidden rescue machinery has been the focus of our laboratory for many years.

The cell's molecular rescue team

Fortunately, plant cells are equipped with a sophisticated protein quality-control system that continuously monitors and repairs damaged proteins. At the heart of this system are molecular chaperones, specialized proteins that help other proteins maintain or regain their correct shape. Among these, the HSP70 (Heat Shock Protein 70) family serves as one of the cell's primary repair systems. Hsp70 recognizes proteins that have begun to unfold, prevents them from forming irreversible clumps, and gives them another opportunity to fold correctly.

However, HSP70 cannot accomplish this task alone. It relies on a group of helper proteins known as J-domain proteins (JDPs). These proteins act as coordinators, identifying where damage has occurred and guiding HSP70 to the proteins that need immediate attention. Plants possess an unusually large and diverse collection of JDPs, reflecting the wide variety of environmental stresses they



Figure 1: AtDJB3 helps plants recover from prolonged heat stress. Plants lacking AtDJB3 (atdjb3) showed poor recovery after heat stress, whereas plants producing higher levels of AtDJB3 (AtDJB3-OE) recovered more effectively than the wild type (WT). Seedlings were exposed to 37°C for 48 h and photographed after recovery under normal growth conditions.

encounter throughout their lives. Over the past several years, our laboratory has been interested in understanding how individual JDPs contribute to the protection of plants from environmental stress. Although many members of this family have been identified, the specific functions of most remain largely unexplored.

A new piece of the puzzle: AtDJB3

Our recent work focused on one such protein, AtDJB3, in the model plant *Arabidopsis thaliana*. We found that AtDJB3 responds remarkably quickly when plants are exposed to high temperatures. As heat stress begins, AtDJB3 accumulates rapidly and relocates to areas within the cell where damaged proteins gather. Our earlier work showed that AtDJB3 helps clear these protein aggregates, enabling damaged proteins to recover their normal function. This behaviour suggested that AtDJB3 is actively involved in the plant's response to heat rather than simply being produced as a consequence of stress. To understand its importance, we examined plants in which AtDJB3 was absent. Under normal conditions, these plants grew just like healthy plants. However, when exposed to prolonged heat stress, they showed a dramatic reduction in their ability to recover. In contrast, plants producing higher levels of AtDJB3 survived heat stress much more successfully. Our work further revealed that AtDJB3 functions together with HSC70-1, one of the major members of the HSP70 family involved in protecting plant cells during heat stress. AtDJB3 helps ensure that HSC70-1 reaches damaged proteins efficiently, allowing the cell to restore protein quality before irreversible damage occurs.

But is repairing damaged proteins only part of the story?

Heat survival also depends on the rapid activation of hundreds of protective genes. These genes produce additional molecular chaperones and other stress-response proteins that prepare the plant to cope with prolonged high temperatures. Our research showed that AtDJB3 is also essential for activating many of these protective genes. In plants lacking AtDJB3, this genetic response was significantly weakened, leaving the plants less capable of surviving extended heat stress. Together, these findings reveal that AtDJB3 performs two closely connected functions. It helps maintain protein quality by supporting the HSP70 chaperone system, while also enabling the plant to activate its broader heat-response programme.

From basic discovery to climate-resilient crops

Our work on AtDJB3 was carried out in *Arabidopsis thaliana*, a small flowering plant widely used as a model in plant biology. Although it is not a crop, many of the cellular mechanisms that protect *Arabidopsis* from heat are remarkably similar to those found in important food crops such as rice, wheat, maize, and tomato. This means that understanding how AtDJB3 helps maintain protein quality and activate the heat response provides valuable clues for improving crop resilience. As tools such as genome editing, molecular breeding, and precision biotechnology continue to advance, discoveries like these could help scientists strengthen the plant's own natural defence systems. The goal is not to create plants that tolerate higher temperatures, but crops that continue to grow, flower, and produce stable yields even under increasingly unpredictable climates. Perhaps the most important lesson is that solutions to future agricultural challenges often begin with fundamental research. By understanding how

individual proteins cooperate inside a single plant cell, we build the knowledge needed to develop the climate-resilient crops of tomorrow.

Conclusion

Rising global temperatures are placing increasing pressure on plants, making it more important than ever to understand how they naturally cope with heat stress. Our work shows that AtDJB3, one out of more than a hundred JDPs found in Arabidopsis, can play a surprisingly important role by helping cells both repair damaged proteins and activate protective responses during heat stress. By uncovering the molecular machinery that protects plant cells, we move one step closer to understanding the remarkable resilience of plants and to finding new ways to safeguard agriculture in a changing climate.

ABOUT THE AUTHORS

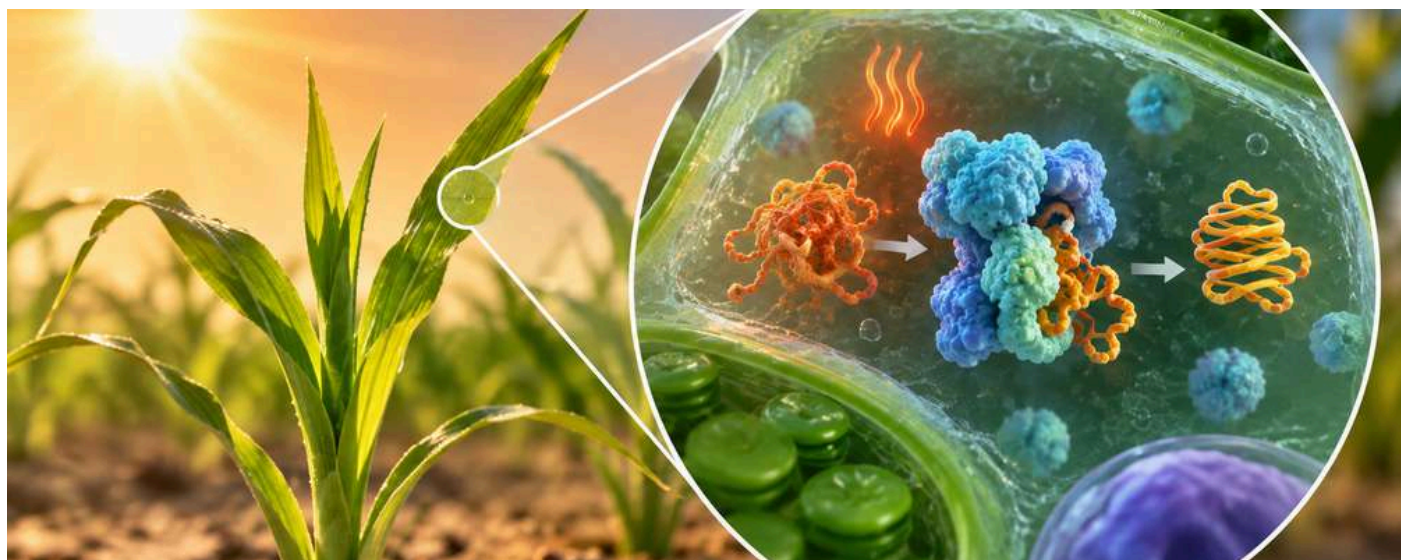
Dr. Chandan Sahi and his team at IISER Bhopal study how plants and other living cells protect their proteins and cope with stressful conditions. Their research focuses on special proteins called molecular chaperones, which help other proteins fold correctly, remain stable and function properly. Their work helps explain how these cellular protection systems support healthy plant growth and survival under environmental stress.

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Every discovery
about how
plants respond
to heat brings
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equipped for a
changing
climate.”

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From Fruit Peels to Future Technologies: Transforming Biomass Waste into High-Value Materials



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Areas of Expertise: Waste Valorization | Environmental Remediation | Circular Bioeconomy | Electrochemistry | Food Packaging



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Areas of Expertise: Waste Valorization | Nanocomposites | Activated Carbon | Energy Storage

The increasing generation of agricultural and food-processing waste has created a major environmental challenge, but it also represents an important opportunity for developing

sustainable technologies. Fruit peels, seeds, shells, and other plant residues are commonly discarded despite containing valuable carbonaceous materials and diverse bioactive compounds. The research field of biomass waste valorization aims to transform these underutilized resources into high-value products through chemical, thermal, biological, and materials-engineering approaches. This field is particularly important because it connects waste management with resource recovery, clean energy, sustainable food preservation, and the circular bioeconomy. Fruit residues such as orange and pomegranate peels contain cellulose, hemicellulose, lignin, pectin, polyphenols, flavonoids, essential oils, and other functional constituents, making them versatile feedstocks for producing activated carbon, energy-storage materials, natural preservatives, nutraceutical ingredients, and other

value-added products. The central concept is to move beyond conventional waste disposal and instead extract maximum value from biomass while minimizing environmental impact.

From Fruit Waste to Energy and Food Applications

One of the important advances in this field is the development of biomass-derived activated carbon as a functional material for energy and environmental applications. Through controlled carbonization and activation, biomass can be transformed into porous carbon with suitable surface functionality, making it useful for supercapacitors, batteries, adsorption, catalysis, sensors, and environmental remediation. Our research has demonstrated the potential of orange peel as a precursor for activated carbon and its integration with iron phosphate through an in situ hydrothermal process to develop an electrode material for supercapacitor applications. The porous carbon provides an accessible framework for electrolyte interaction and charge transport,

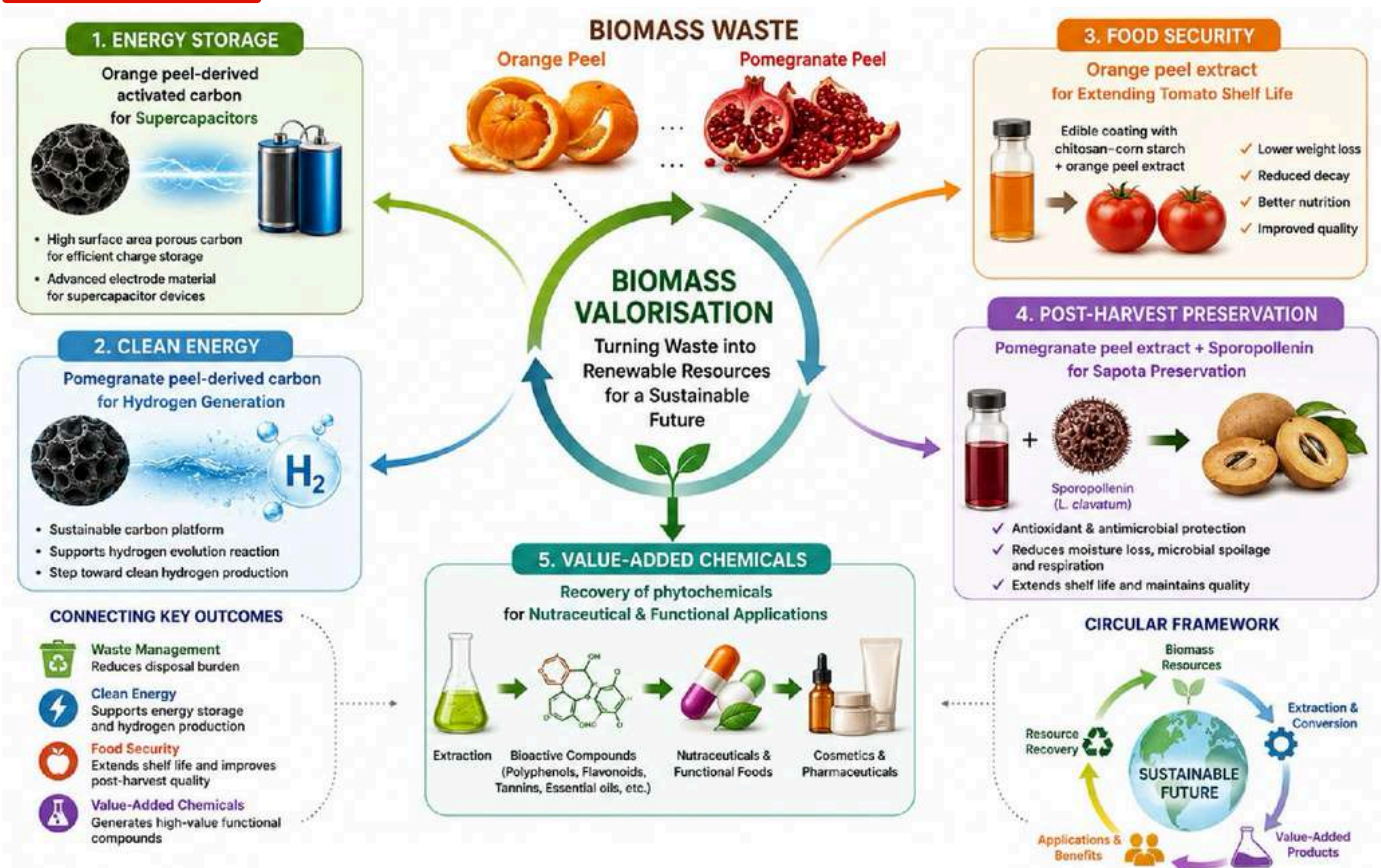


Figure 1: Biomass waste valorization into activated carbon, clean hydrogen, bioactive compounds, food-preservation systems, and nutraceuticals, supporting waste reduction and a sustainable circular bioeconomy.

while iron phosphate contributes additional electrochemical activity. The resulting composite was further utilized in a prototype symmetric solid-state supercapacitor, demonstrating how a discarded fruit-processing residue can be converted into a functional material for energy-storage technology.

The application of biomass-derived carbon is also being extended towards hydrogen generation, an important area in the transition towards cleaner energy systems. Pomegranate peel-derived activated carbon provides a renewable carbon platform with suitable surface characteristics for hydrogen-evolution processes. Our work explored the use of pomegranate peel-derived activated carbon prepared under acidic activation conditions, where the functionalized carbon surface and reaction environment contributed to hydrogen generation. These developments demonstrate that biomass-derived materials can participate in both energy storage and energy conversion, broadening the role of agricultural waste beyond conventional low-value utilization. Although improvements in catalytic efficiency, stability, reaction optimization, and scalability remain necessary, biomass-derived carbon represents a promising platform for future

clean-energy technologies.

Another important advance is the development of natural and active food-packaging systems using bioactive compounds recovered from fruit residues. Orange peel extract contains compounds such as limonene, linalool, phenolics, and flavonoids that provide antioxidant and antimicrobial functionality.

In our study, orange peel extract was incorporated into a chitosan–corn starch edible coating for tomatoes. The extract complemented the physical barrier provided by the coating, helping to reduce oxidative deterioration and microbial spoilage, while the semipermeable coating reduced moisture loss and helped regulate respiration. Consequently, coated tomatoes demonstrated lower weight loss and decay and better retention of nutritional and sensory characteristics during storage. This work demonstrates that a fruit-processing residue can be converted into a functional ingredient for extending the post-harvest shelf life of fresh produce. The same principle has been explored for sapota preservation through the combination of pomegranate peel extract and *Lycopodium clavatum*-derived sporopollenin.

Pomegranate peel provides antioxidant and antimicrobial compounds, while sporopollenin can act as a natural carrier and protective matrix for bioactive molecules. When incorporated with chitosan and corn starch, the resulting coating provides a multifunctional preservation system capable of addressing moisture loss, microbial deterioration, respiration, and ripening. These developments demonstrate the increasing importance of combining naturally derived polymers, biomass-derived bioactive compounds, and functional biological materials to develop sustainable post-harvest technologies.

A further advancement is the recovery of high-value phytochemicals and nutraceutical compounds from biomass waste. Fruit peels are rich sources of polyphenols, flavonoids, tannins, essential oils, pigments, and other functional molecules. Instead of losing these compounds through disposal, appropriate extraction and purification strategies can recover them for potential applications in functional foods, nutraceuticals, food packaging, pharmaceutical formulations, cosmetics, and other value-added products. Molecularly imprinted materials provide an additional opportunity for selective recognition and recovery of specific target molecules (Quercetin, 4-Hydroxybenzoic acid etc. in the peels), potentially improving the efficiency of extraction, separation, and detection processes. Such developments are moving biomass utilization towards a biorefinery model in which different components of a single waste stream can be converted into multiple useful products.

Towards a Zero-Waste Biorefinery Approach

This multidisciplinary approach also supports the concept of zero-waste production. Rather than assigning a single application to an entire biomass residue, different fractions can be directed towards their most appropriate uses. Bioactive compounds can be extracted for food, nutraceutical, or preservation applications, while the remaining carbon-rich fraction can be converted into activated carbon for energy or environmental applications. Suitable residual fractions may also be explored for animal feed, composting, bioenergy, or other resource-recovery pathways, subject to appropriate safety and technical evaluation. Such sequential utilization increases the value obtained from the original biomass and reduces the quantity ultimately entering the waste stream.

Challenges in Scaling Biomass Technologies

Despite significant progress, several challenges continue to

limit the large-scale implementation of biomass-derived technologies. The first is the inherent variability of biomass. Its chemical composition depends on plant species, geographical origin, cultivation conditions, maturity, and processing history. This variability can influence the properties of activated carbon and the concentration and activity of extracted bioactive compounds. Standardized feedstock characterization and reproducible processing are therefore essential.

A second challenge is the scale-up of laboratory processes. Materials that demonstrate excellent performance under controlled laboratory conditions may not necessarily be economically or environmentally viable at industrial scale. Activation processes may require significant energy or chemical inputs, while bioactive-compound extraction can involve solvents and multiple purification steps. Future research should therefore place greater emphasis on green extraction methods, energy-efficient processing, solvent recovery, techno-economic assessment, and life-cycle analysis.

For energy applications, further improvements are required in electrode performance, long-term cycling stability, device-level energy density, manufacturing consistency, and scalability. For food-preservation systems, regulatory safety, coating uniformity, sensory acceptance, storage stability, and real-world supply-chain performance require further investigation. In the field of bioactive extraction, the identification, purification, stability, bioavailability, and safety of recovered compounds remain important areas for further research. Addressing these knowledge gaps will be essential for translating promising laboratory findings into practical technologies.

Connecting Waste, Energy and Food through a Circular Bioeconomy

The most important message from the current state of biomass research is that biomass waste should no longer be viewed simply as a disposal problem; it should be considered a renewable resource and a potential source for multiple value-added products. Our research illustrates this transition through distinct applications: orange peel-derived activated carbon for energy storage, pomegranate peel-derived carbon for hydrogen-generation studies, orange peel extract for extending tomato shelf life, pomegranate peel extract and sporopollenin for sapota preservation, and recovery of phytochemicals for nutraceutical and functional applications. These examples

demonstrate how biomass valorization can connect waste management, clean energy, food security, and value-added chemical production within a circular framework.

The Future of Biomass Valorization

The future of the field should therefore move from simple biomass conversion towards integrated biomass-refinery and zero-waste strategies, in which each component of the feedstock is directed towards its highest-value application. Success will depend not only on developing materials with excellent laboratory performance but also on demonstrating reproducibility, safety, economic feasibility, environmental benefits, and scalability. The key scientific challenge is consequently to transform biomass waste into products that are not only technically effective but also genuinely sustainable throughout their life cycle. This shift, from treating waste as an end product to using it as a starting material for innovation, represents the central opportunity for biomass research in the emerging circular bioeconomy framework.

ABOUT THE AUTHORS

Prof. Anupama Kumar is a Professor of Chemistry at VNIT Nagpur whose research focuses on turning agricultural and food-processing waste into useful and sustainable products. Her work uses biorefinery and circular-bioeconomy approaches to recover valuable compounds from fruit and vegetable waste and develop applications in clean energy, nutraceuticals, food preservation and sustainable materials. Her research has also led to patented technologies and industry-linked work, helping move biomass valorisation from laboratory research towards practical applications.

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Waste is not the
end of a
resource, it is
the beginning of
a new
opportunity for
human
innovation.”

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Who Decides What Is Beautiful? The Changing Science and Culture of Female Beauty



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Areas of expertise: Dermato-Venereology | Dermatosurgery | Aesthetic Medicine

Beauty has fascinated philosophers, artists, physicians, and scientists for millennia. It should be understood as dynamic shaped by both biological features and cultural evolution rather than as universal or immutable standards. Michel Foucault (1926–1984) stated that the human body is not ‘naturally’ given, but a historical, social and cultural construct in which power and knowledge inscribe themselves, and so is female beauty. Beauty standards are norms, values, and expectations established by culture and society that define what it means to be considered beautiful. In recent times the social media have an immense impact on what is recognized as beautiful, attractive and desirable.

Key message:

The female beauty ideal refers to societal standards and perceptions regarding the appearance of women, which vary significantly across different cultures, ethnicities, and historical periods.

Looking back to antiquity, beauty was not limited to appearance or attractiveness. It always contained a symbolic importance a-

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*Female beauty’s
always seen to
improve about the
age of puberty; but,
if we should
attempt to define in
what this beauty
consists or what
constitutes its
perfection, we
should find nothing
more difficult to
determine*
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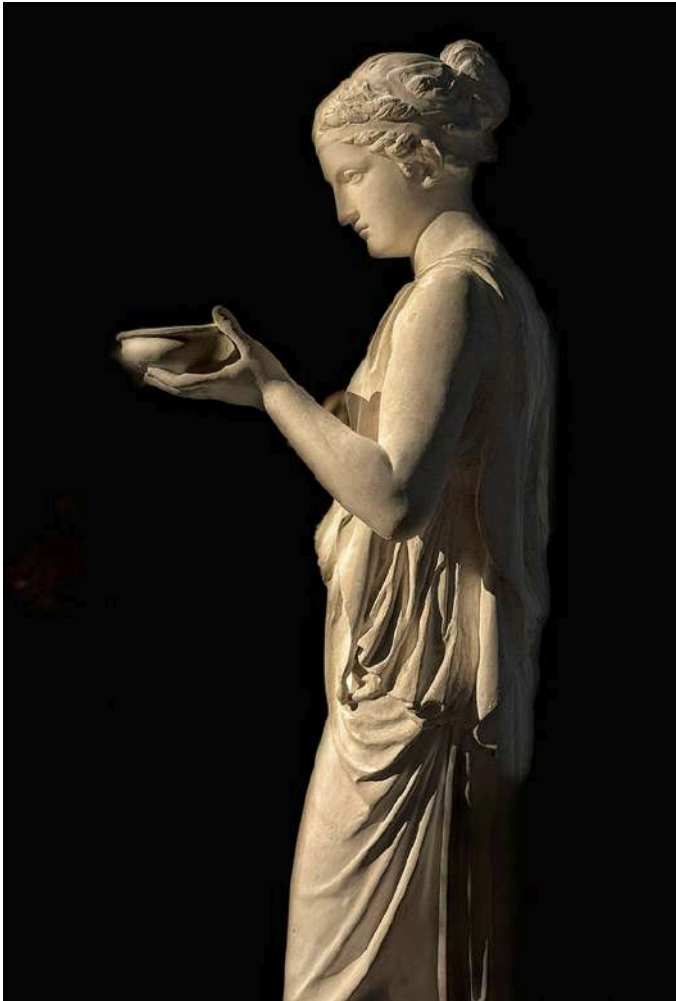
Oliver Goldsmith ‘An History of the Earth, and Animated Nature’. Vol. 2. London: J. Nourse, 1774, p. 76

nd a philosophical background in ancient Egyptian, Greek or Chinese culture. The Greek philosopher Plato (428-348 BC) claimed that all human bodies share the quality of beauty. He believed in the distinction between the noble beauty of the soul and the wickedly tempting beauty of the body.

In ancient Imperial Rome elite women were expected to have fair skin and long hair, with a preference for fuller, more curvaceous figures. Beauty reflected the status of women of the imperial court and Vestal Virgins which went far beyond the claim to please the spouse.

It is worth mentioning that the concepts of beauty multifaceted. For instance, roundness was perceived as an autonomous aesthetic model of female beauty in Africa while in ancient Egypt slender arms and legs and a faint female breast had been admired.

The European Middle Ages (5th–15th centuries) changed the view on female beauty dramatically. Under the influence of Christian theology physical beauty became secondary to spiritual virtue, modesty, and moral purity. Indeed, artificial or enhanced beauty was considered sinful and inspiring lust. Pale fair skin, a high and exposed forehead, finely plucked eyebrows, and long



blonde or sandy hair became standards of Gothic art. The ideal female beauty was closely linked to sanctity rather than sensuality.

During Renaissance (15th–16th centuries) beauty was viewed as an outward reflection of inner virtue. The standard of female beauty prized fair skin, rosy cheeks, thin or plucked eyebrows, and long hair. Women used epilation or shaving of the hairline to gain a high polished forehead. Thinness was considered a sign of illness. The ideal body was full and curvaceous, featuring wide hips and a rounded belly, symbolizing health, prosperity, and fertility.

In the Baroque period (17th century) beauty was defined by opulence and intense emotion. Characterized by dynamic curves, the prevailing standard of beauty viewed the human form as a reflection of divine drama and earthly prosperity. The female ideal was celebrated through a lush, voluptuous physique with generous proportions; rounded bellies, wide hips, abundant soft tissues and skin with a soft glow were prized.

During Enlightenment (18th century) philosophical aesthetics was founded by Alexander Gottlieb Baumgarten (1714–1762), who defined beauty (*pulcritudo*) intellectually as the ‘perfection of sensory cognition’ (*perfectio cognitionis sensitivae*). In France the Enlightenment debates linked beauty and aesthetic qualities to political, philosophical and spiritual values as reflected exemplarily by Madame de Pompadour (1721–1764). This example nicely demonstrates that physical beauty presented an element of risk and unpredictability into the world of social hierarchy.

The nineteenth century combined Romantic ideals of emotional beauty with Victorian concepts of modesty and domestic virtue. Women took control of their bodies, manipulating their shapes through diet, fashion, and exercise. Rosy cheeks, full lips, and a tiny waist were considered hallmarks of beauty. Clothing, like the corsets, played a significant role in body shaping.

The 20th century broke with established beauty standards. From the Roaring Twenties with slender women with long limbs and a relatively flat chest reflecting women's emancipation and shifting social roles to the mammary madness with an obsessive focus on women's breasts and its symbolic and erotic import in Post-World War II US America. Social media (press, film and TV) discovered female beauty as a well selling subject. A whole industry of cosmetics and pharmacy participated from the desire of beauty with partly questionable products such as whitening or breast creams. The popularity of the British model Twiggy (born 1949) testified to the influence of youth culture in the late 1960s. By the 1980s and 1990s, physical fitness, toned musculature, and athleticism became increasingly valued, reflecting broader cultural emphasis on exercise and health.

Key message:

The female beauty ideal often represents unachievable standards. This unattainable increasingly standardized ideal is often influenced by social media and virtual digitalized images while diversity of beauty is still largely missing.

In the 21st-century traditional, rigid moulds and standards are being broken, replaced by an era of radical self-expression. Body modifications with tattoos and piercing have become increasingly popular. Rather than pursuing a classical ideal, modern beauty is highly fluid and influenced by globalization, digital image editing, and advances in aesthetic medicine.



Since antiquity, female beauty has been considered a product of art and only artistic intervention can carry to perfection. Art is now replaced by arbitrary virtual images in social media. Selfies are all the rage. Aesthetic standards prevalent in the virtual realm are prized —characterized by full lips (often bordering on the exaggerated), sculpted cheekbones, and flawless, filter-like skin („Instagram faces“). In people with skin of colour skin whitening still plays an important role. Digital platforms can amplify highly curated or manipulated images, contributing to unrealistic expectations regarding skin quality, body proportions, and everlasting youthful appearance. Unfortunately, there is abundant misinformation on procedures and outcome. Body dissatisfaction is rising posing serious health risks. In a recent investigation on beauty standards of the fashion industry revealed that physique ideals remain stable, despite diversification of media and fashion representation. It seems that beauty has become a consumer product dictated by brands. But this is not beau-

ty, it's appearance only. Inclusion of a diversity of beauty concepts is still a challenge.

ABOUT THE AUTHORS

Prof. Dr. Uwe Wollina is a distinguished dermatologist and former Head of the Department of Dermatology and Allergology at Städtisches Klinikum Dresden, Germany. His work spans clinical dermatology, dermato-oncology, dermatosurgery, wound healing and aesthetic dermatology. Through extensive clinical and scientific research, he has contributed to improving the understanding and treatment of skin diseases and skin cancers, while also exploring the medical, cultural and historical dimensions of beauty and aesthetics.

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The Sperm Selection Puzzle: How Microfluidics Could Recreate Nature

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Areas of Expertise: Bio-microfluidics | Fluid Mechanics | Microfluidics

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Areas of Expertise: Microfluidics | Fluid Mechanics | Cell Separation

From an extraordinary journey inside the female reproductive tract to tiny engineered channels, scientists are exploring whether the principles of natural sperm selection can be recreated on a chip.

Imagine a race where millions of runners participate; the track changes along the way, narrow passageways act as gates, some sections are almost syrup-like, and reaching the finish line first doesn't necessarily mean you are the best runner. In many ways, this describes the journey of a sperm cell.

A human sperm is only about 50–60 micrometres long, yet it must navigate a reproductive tract millions of times larger than itself. Along the way, it encounters changing fluids, confined spaces, fluid flow, temperature differences and chemical signals. Millions of sperm may begin the journey, but only a small fraction reach the vicinity of the egg. More importantly, the sperm that arrives is not necessarily simply the fastest. Motility matters, but so do shape, structural integrity and overall cellular health. Nature, therefore, performs a remarkable process of selection long before fertilization occurs. The race is not si-

mply about speed; it is about competence. Infertility turns this biological puzzle into an important global health challenge. The World Health Organization estimates that about one in six couples of reproductive age experience infertility during their lifetime. The causes can involve the male partner, the female partner, both, or remain unexplained. In men, problems with sperm number, movement and shape are common contributors, while female infertility may involve the ovaries, uterus, fallopian tubes or reproductive hormones.

Assisted reproductive technologies have created new possibilities for people facing infertility. In intrauterine insemination (IUI), prepared sperm are introduced directly into the uterus, bringing the selected sperm closer to the site of fertilization. In in vitro fertilization (IVF), eggs and sperm are brought together in the laboratory, whereas in intracytoplasmic sperm injection (ICSI), an embryologist selects an individual sperm and injects it directly into a mature egg. As the treatment becomes more technically selective, from IUI to IVF and particularly ICSI, the quality of the sperm available for selection becomes increasingly important.

Fertility centers commonly use swim-up, in which motile sperm migrate into fresh culture medium, and density-gradient centrifugation, in which sperm are separated according to their physical properties using centrifugation. Both are established and useful methods. However, these methods involve sample handling and, particularly with centrifugation, mechanical forces that can place additional stress on sperm. Processing can contribute to cellular and oxidative stress and may affect delicate structures, including sperm DNA. More fundamentally, conventional methods cannot reproduce the changing flow, confined spaces, fluid properties and chemical signals that sperm encounter inside the female reproductive tract. This difference between how nature selects sperm and how we select them in the laboratory has become an important motivation for microfluidic research.

Microfluidics is a branch of science and engineering concerned with controlling very small volumes of fluids, often inside channels comparable in size to individual cells. At this scale, researchers can control fluid movement, confinement, surfaces and gradients around living cells. For sperm, this creates an opportunity to build a miniature environment that reproduces selected features of their natural journey.

From Understanding Sperm Behaviour to Engineering Selection

Recent research indicates that sperm actively respond to their physical environment. Our research has followed this idea from understanding sperm behaviour to using that knowledge for selection. We first examined sperm motion in environments designed to resemble aspects of the female reproductive tract. This work showed how sperm can adapt their flagellar waveform, the pattern of movement produced by the tail, to maintain propulsion as surrounding fluid conditions change.

We then investigated rheotaxis, the tendency

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*Natural sperm
selection is not
simply a race
for speed; it is
a complex
journey that
favours
functional
competence.*”

of sperm to orient and swim against fluid flow, as an important long-distance navigation mechanism. We observed that many sperm preferentially adopted rheotactic behaviour and tended to migrate along channel boundaries. This suggested that a natural navigation behaviour could also guide sperm inside a microfluidic environment.

These observations led to the development of our Microfluidic-Assisted Sperm Sorter (MASS). The device uses engineered microchannels to exploit sperm responses to fluid flow and nearby boundaries, aiming to provide a controlled route for obtaining sperm suitable for downstream IVF and ICSI applications. The important point is not simply that the device is small. The physics inside it is deliberately designed around sperm biology. This is the essence of biomimetic engineering: rather than forcing biology to fit the machine, we ask the machine to learn from biology.

Why Has Translation Been Slow?

Despite rapid progress, relatively few microfluidic sperm-selection technologies have moved from laboratory research into routine fertility practice. The challenge is not simply to separate sperm efficiently. A clinically useful system must work reliably with real patient samples, accommodate differences in sperm quality, provide reproducible results and fit naturally into an embryology laboratory workflow.

Patient samples can vary enormously. Some contain millions of highly motile sperm, while others contain very few. In severe male infertility, sperm may need to be recovered from testicular tissue. In non-obstructive azoospermia, where sperm production is severely impaired and sperm may be absent from the semen, viable sperm can be exceptionally rare.

A device designed around an “average” sample may therefore struggle precisely where the clinical need is greatest. Future systems will need to accommodate differenc-

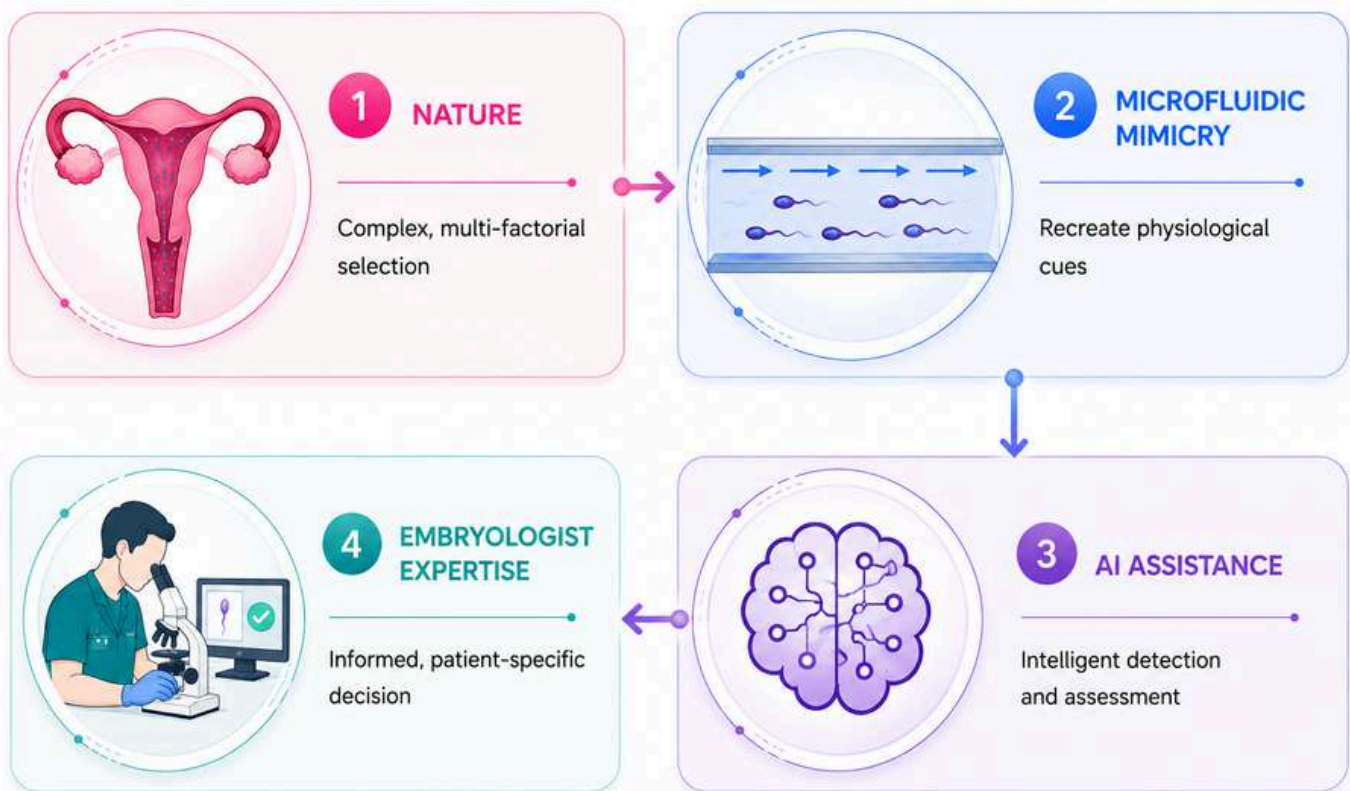


Figure 1: A Potential workflow for next generation sperm selection: biomimetic microfluidics recreates selected features of the reproductive environment, AI assists sperm detection and assessment, and the embryologist integrates this information for final clinical selection.

es in sperm number, movement and sample type rather than applying a single strategy to every patient.

Artificial intelligence could provide another important layer. Finding a rare sperm can be like searching for a moving needle in a microscopic haystack. AI can rapidly analyse images, identify potential sperm and track their movement. Combining automated imaging with microfluidic handling could reduce prolonged manual searching and help identify sperm that might otherwise be difficult to find.

The goal, however, should not be to replace embryologists. A more realistic future is a partnership: microfluidics provides the physical environment, AI provides rapid analysis, and the embryologist provides clinical judgement. Microfluidics can shape where sperm go. AI can help identify which sperm deserve attention.

From Sperm Separation to Precision Selection

For decades, sperm preparation has largely asked: How can we obtain enough motile sperm?

The next generation may ask a harder question: How can

we identify sperm with greater biological competence while preserving their function?

Motility matters, but so do morphology, DNA integrity, cellular energy systems and other aspects of sperm health. Microfluidic selection is showing promise in improving several laboratory measures of sperm quality, although the connection between these improvements and successful reproductive outcomes is still being established.

The future may therefore not belong to one universal sperm sorter. It may belong to adaptive systems. A highly motile semen sample may require one approach, while a sample with very few sperm, elevated DNA damage or testicular sperm may require another.

Nature has already been doing something remarkably similar for millions of years. The female reproductive tract uses fluid flow, geometry, changing fluid properties, temperature and chemical signals to progressively narrow a huge sperm population to a small group of candidates. The challenge for engineers is to understand these process-



Members of our research group, from left to right: Mr. Dhiraj Puri, Prof. Gautam Biswas, Prof. Siddhartha Tripathi, and Prof. Vadiraj Hemadri.

es well enough to reproduce the parts that matter. The opportunity for microfluidics is therefore not to compete with nature, but to learn from it. By recreating selected features of the reproductive environment and eventually combining them with real-time imaging and artificial intelligence, future systems could move sperm preparation beyond simple enrichment toward more intelligent and biologically informed selection. The future of infertility treatment may not be a machine that chooses the “perfect” sperm. It may be a system that helps embryologists make a better-informed choice. And that is where a tiny microfluidic chip may have a surprisingly large role to play.

ABOUT THE AUTHORS

Prof. Siddhartha Tripathi and Dhiraj B. Puri at BITS Pilani, Goa Campus, study how sperm cells move through fluids and narrow spaces. Their research looks at how sperm respond to fluid flow, thickness of the fluid, and surrounding channel walls, including their natural tendency to swim against a flow, known as rheotaxis. Using this knowledge, they developed the Microfluidic-Assisted Sperm Sorter (MASS), a device that uses natural sperm behaviour to help select healthy and actively moving sperm cells more efficiently.

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Building Brain-Inspired Electronics with Organic Molecules



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Areas of Expertise: Energy materials | Optoelectronics | Higher Education Research
| Memristors | Condensed matter physics

Can non-living materials “remember”? Not like a human brain, but perhaps in a way that could transform future technology. Today’s computers largely keep memory and processing separate, constantly shuttling data between different components, a process that consumes both time and energy. Our brain operates very differently: its neurons and synapses can sense, store information, learn from experience, and process new signals together, using remarkably little energy. Inspired by nature, scientists are developing neuromorphic electronics, a new generation of smart electronic materials and devices designed to mimic the basic functions of biological neural systems. By using materials that can adapt their physical state in response to past activity, these devices can potentially provide a unified framework for storing and processing information. The result could be faster, more adaptive and energy-efficient hardware, bringing computing a step closer to the remarkable efficiency of biological systems.

Our research interest lies at an emerging intersection of organic molecular materials, optoelectronics and neuromorphic electronics, with a central question: Can we design a molecule whose electronic response behaves like a synapse? The answer is increasingly yes. Organic molecules are particularly attractive because their electronic, optical and structural properties can be modified through molecular design. Unlike conventional inorganic semiconductors, where properties are often strongly constrained by composition and crystal structure, organic materials offer an enormous chemical design space. Their donor and acceptor groups, molecular conjugation, symmetry, packing, intermolecular interactions and even the precise position of a functional group can be

deliberately manipulated. This molecular freedom is important because an artificial synapse does not merely need to conduct electricity. It must possess a controllable history. The response to a second stimulus should depend on what happened during the first; repeated stimulation should strengthen or modify the response; and information may need to persist after the stimulus has disappeared. Organic semiconductors can exhibit such behaviour through photoinduced charge generation, charge trapping and detrapping, molecular charge transfer, and structural disorder. These mechanisms can generate phenomena analogous to paired-pulse facilitation, short- and long-term plasticity, excitatory postsynaptic currents and spike-number-dependent learning.

From electronic devices to artificial synapses

The development of artificial synapses has advanced rapidly using metal oxides, two-dimensional materials, perovskites and other emerging semiconductors, demonstrating impressive memory and synaptic plasticity. Organic materials offer a complementary advantage: they can often be synthesized by simple chemistry, solution-processed, fabricated under mild conditions and chemically tailored, making them attractive for flexible, low-cost and large-area neuromorphic electronics. An especially exciting development is optoelectronic synapses. Biological vision does not simply record light intensity; the brain interprets its temporal and spatial patterns. Similarly, an artificial photosynapse can use light as both an input signal and a trigger for memory. This behaviour can arise from photoinduced charge trapping, photoactive electrets and defect-related processes. The key advance is that the material itself can perform part of the information processing, rather than merely transmitting signals to an

external processor.

The molecule matters and so does its geometry

Our recent collaborative work shows how molecular engineering can be a powerful strategy for neuromorphic materials. We studied a family of donor–acceptor–donor (DAD) organic luminophores with nearly identical chemical compositions but different positions of methoxy donor groups. This provided a clean test of how molecular arrangement alone can influence electronic and synaptic behaviour. The differences were substantial. The regioisomers showed distinct molecular conformations, crystal packing, optical properties, charge-transfer characteristics and memory responses. The 2,6-isomer became strongly twisted due to steric crowding, while the 2,4- and 3,5-isomers remained more planar, enabling stronger electronic communication. Their different packing and intermolecular interactions further influenced charge transport and trapping. This highlights a key principle of organic electronics: molecular structure goes beyond chemical composition. Molecules with the same elemental composition can behave very differently because their three-dimensional arrangement determines how electrons move, where they are trapped and how molecules interact. The device results reinforced this structure-property relationship. The 3,5-isomer achieved a photoresponsivity of 41.25 A W^{-1} and detectivity of $4.57 \times 10^{11} \text{ Jones}$, while also showing persistent photocurrent after illumination was removed. The 2,4-isomer exhibited particularly strong

synaptic behaviour: repeated light pulses produced enhanced postsynaptic currents, with a PPF index of $\sim 196\%$ under a 10-second UV pulse followed by a 2-second interval. At the microscopic level, these memory effects arise from charge generation, molecular charge transfer and charge trapping within the crystalline environment. The 2,4-isomer, which has the largest calculated void space ($\sim 24.4\%$ of the unit-cell volume), may provide favourable sites for charge trapping, while stronger intermolecular interactions can help stabilize the stored charge. Thus, the macroscopic phenomenon of “memory” can emerge directly from molecular packing and nanoscale charge dynamics.

From mimicry to molecular computing

The most exciting possibility is that neuromorphic functionality can be encoded directly into molecular architecture. Instead of optimizing a material only after synthesis, we could design molecules for a desired computing function from the outset. This marks a conceptual shift from materials for electronics to molecules for computation. However, the field remains far from mature. Demonstrating PPF or long-term potentiation in a laboratory device is not enough to build practical neuromorphic systems. Key challenges include understanding and controlling charge traps, achieving reproducible molecular packing over large areas, improving environmental and operational stability, lowering operating voltages, broadening optical response

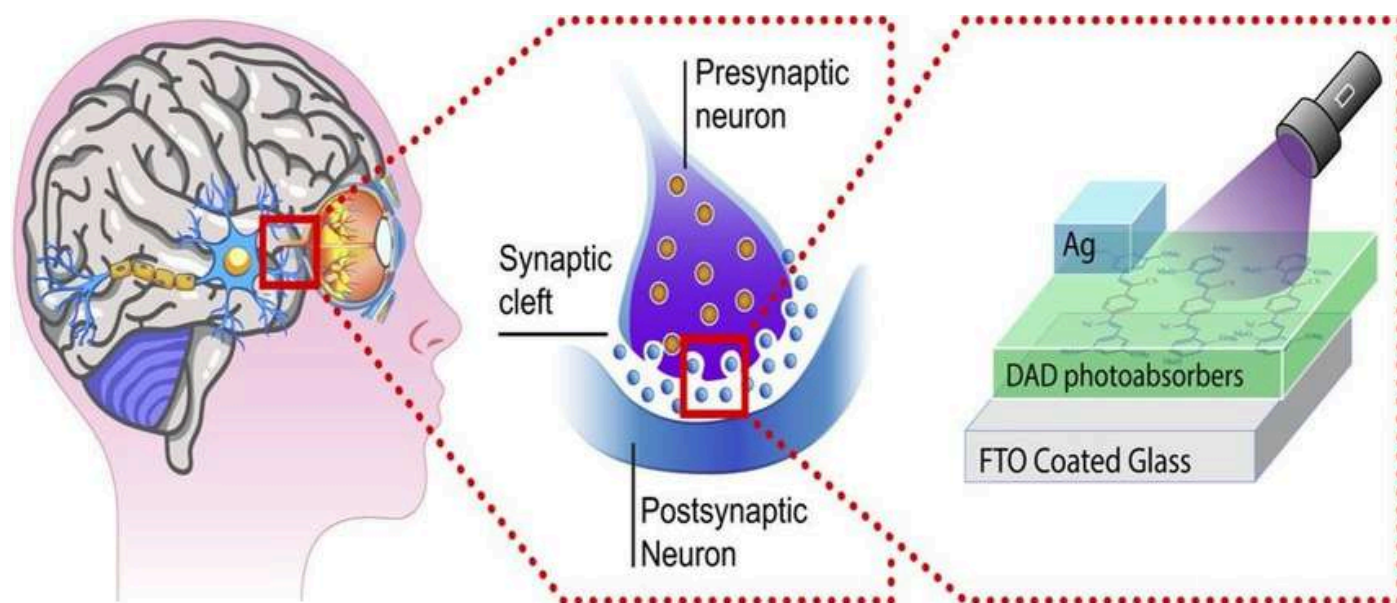


Figure 1: Schematic representation of the functioning of a biological synapse and an artificial synaptic device.

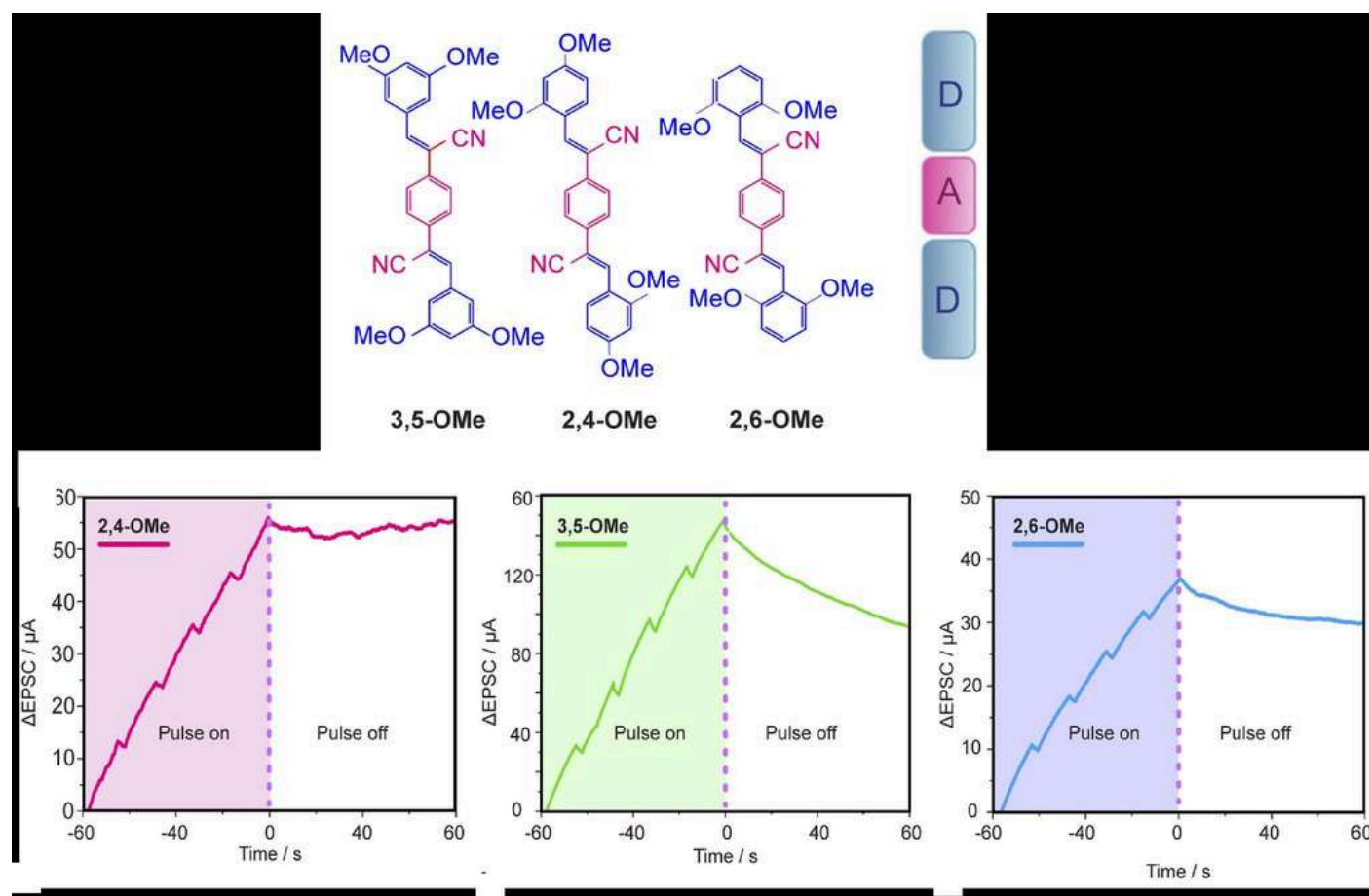


Figure 2: Structures of the DAD molecules and changes in EPSC in response to 365 nm light pulses (10 s duration, 2 s interval) at a +100 mV bias.

and integrating individual synapses into dense arrays. A fundamental challenge is balancing charge mobility and memory. Fast electronics favour efficient charge transport, while memory requires controlled trapping and delayed release. Too few traps give weak memory; too many immobilize carriers and slow the device. The goal is therefore to engineer the appropriate distribution of electronic states and relaxation times. Ultimately, the field must move beyond isolated demonstrations toward reproducible multilevel states, low-energy operation, long endurance, device uniformity and integration with sensing and computing architectures. Organic materials offer exceptional chemical tunability; the challenge is to translate that molecular freedom into predictable, reliable device behaviour.

From materials for electronics to molecules for computation

The current state of the field can be captured in one idea: the molecule itself can become part of the computational architecture. Learning-like behaviour in organic electronics

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*The future of
neuromorphic
electronics may lie not
only in smarter
devices, but in
molecules designed to
learn.*

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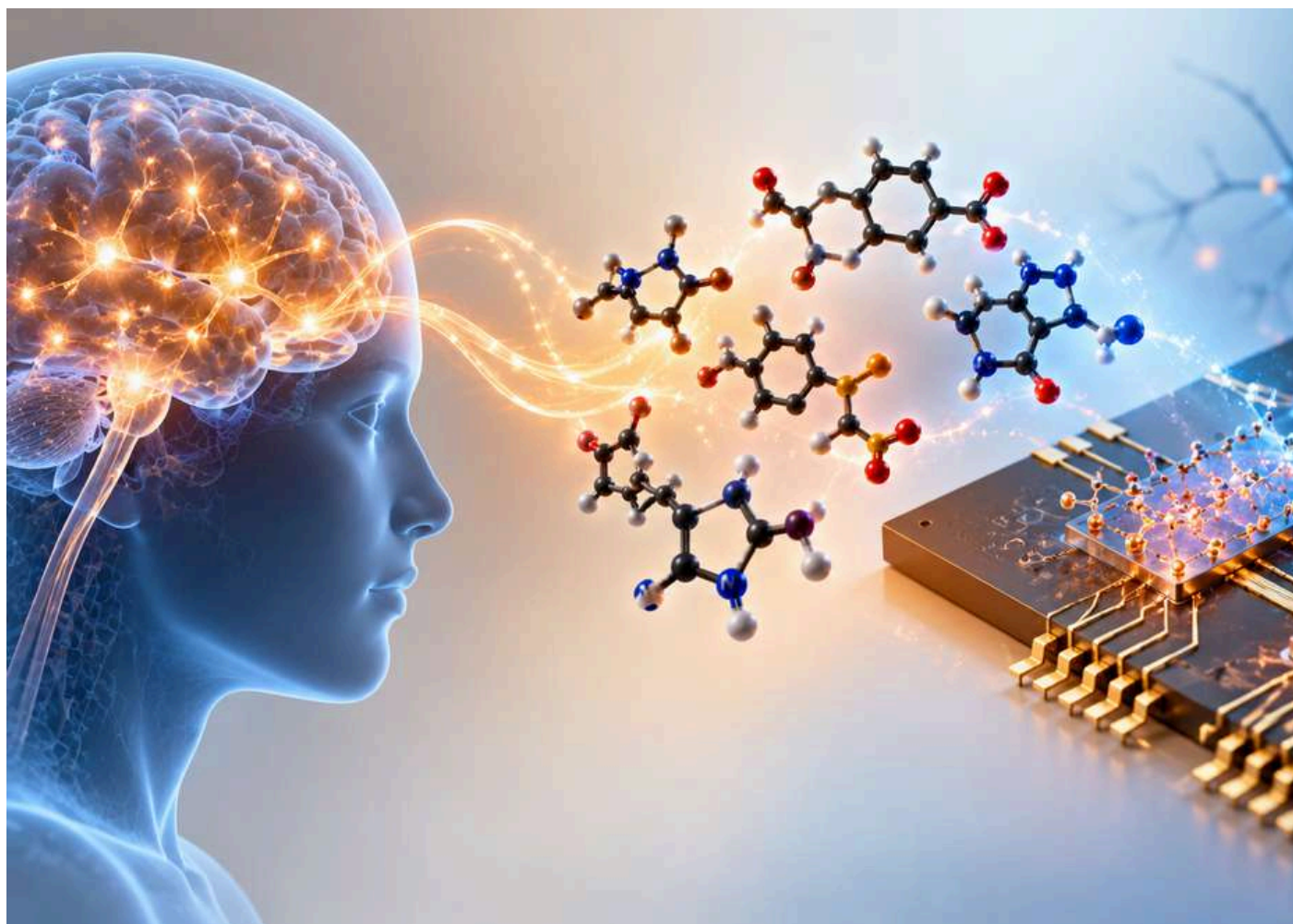
can emerge from the interplay of molecular conjugation, donor-acceptor charge transfer, crystal packing, intermolecular interactions, defects, voids and carrier trapping, without requiring complex circuits. Our recent study shows that even regioisomerism, the position of a functional group within an otherwise similar molecule, can tune optoelectronic synaptic behaviour. This points to an exciting future in which neuromorphic materials are designed not simply to imitate a transistor or synapse, but to sense, remember and process information intrinsically. Organic molecules are particularly promising because chemistry offers extraordinary control over molecular structure. Establishing reliable links between molecular architecture, charge dynamics and learning behaviour could increasingly blur the boundaries between chemistry, materials science and computing. The ultimate goal is not merely to build machines that look like brains, but to create materials that embody some of the brain's fundamental principles: adaptation, memory and information processing so that matter itself becomes an active participant in computation.

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Dr. Rabindra Nath Gayen is an Associate Professor of Physics at Jadavpur University, whose research focuses on optoelectronic materials, semiconductor thin films, nanomaterials, solar cells and advanced electronic devices. His work explores how specially designed materials can improve light sensing, energy conversion and information storage. His recent collaborative research demonstrated organic devices capable of showing synaptic memory behaviour, contributing to the development of brain-inspired electronics and smart memory devices.

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Unlocking Lifelong Health: How Physical Literacy Inspires Lasting Activity and supports Healthy ageing



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Areas of Expertise: Physical education | sports science | Wellness and Yoga

A wellness-oriented lifestyle is a key determinant of functional health. Various lifestyle factors, such as physical activity, nutrition, emotional balance, and environmental conditions, collectively influence physiological functioning and overall health. Physical and nutritional wellness, which are closely linked, play particularly significant roles in shaping functional health. Sustaining optimal physical wellness throughout the lifespan is critical for promoting healthy ageing. Since physical wellness cannot be stored for future use, it must be maintained consistently throughout life. Establishing regular physical exercise habits from childhood is therefore essential for lifelong healthy ageing. The World Health Organisation (WHO) reports that global physical inactivity is increasing, which is expected to contribute to a substantial rise in non-communicable diseases (NCDs) worldwide. According to a major study cited in the WHO's fact sheet on physical inactivity trends, 31% of adults currently do not meet the recommended 150 minutes of moderate or 75 minutes of

vigorous physical activity per week. This proportion is projected to increase to 35% by 2030 if current trends continue. Furthermore, 80% of adolescents are physically inactive. The anticipated rise in NCDs due to insufficient physical activity may result in a significant increase in premature mortality and disability, as well as a financial burden potentially exceeding \$300 billion by 2030.

Traditional Physical Education and sports on Physical activity behaviours

Traditional Physical Education programs in educational institutions, often characterised by student-centred and activity-based approaches, have not demonstrated effectiveness in achieving sustained behavioural change at the population level. Although participation in physical activities in educational settings may provide temporary motivation, it often does not lead to a lifelong commitment to physical activity. With the exception of a few European countries, rates of physical inactivity are generally rising, including in nations renowned for sporting success such as

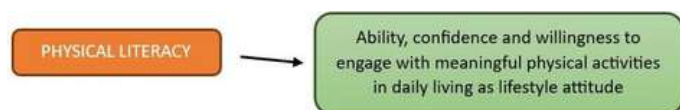


Figure 1: Physical Literacy

the United States and China. As a result, the dominant sports culture in these countries has not effectively promoted positive physical activity behaviours among the general population. Promoting intrinsic, self-motivated engagement in regular, evidence-based physical activity is essential for supporting lifelong adherence to physical activity behaviours even under difficult and adverse conditions. Within this context, the concept of Physical Literacy may play a pivotal role.

Physical Literacy-meaning and key aspects

Physical literacy refers to the comprehensive set of attributes required to motivate individuals to engage in regular, scientifically informed physical activity, thereby optimising functional health. True physical literacy enables consistent participation in appropriate physical activities. The primary driving force in this process is intrinsic motivation, which encourages voluntary participation regardless of prevailing conditions, as individuals adapt and remain active. This intrinsic motivation arises from interconnected factors, including knowledge of exercise science, understanding the effects of physical activity on

immunity and functional health, appreciation for aesthetics, and confidence to participate in various physical activities both individually and in groups. Such confidence is often developed through early engagement in physical activities and recognition of possessing adequate fitness. Additionally, competence in group settings for mutual benefit further enhances confidence, particularly as urban populations increasingly participate in recreational group activities such as marathon running and cycling. Therefore, intrinsic motivation and confidence significantly promote participation in both individual and group physical activities, shaping individuals' physical activity behaviours and choices.

Mechanism of Physical Literacy

Physical literacy comprises three primary competencies that interact to promote physical literacy in individuals. Psychological competency can be categorised into four domains: cognitive, emotional, affective, and behavioural. These domains are mutually interdependent and are also linked with physical and social competencies. Cognitive competency in physical literacy requires individuals to understand the science of physical exercise, including the rationale for exercise, the selection of appropriate exercises based on individual needs and circumstances, safe exercise practices, and the significance of body aesthetics and posture management.

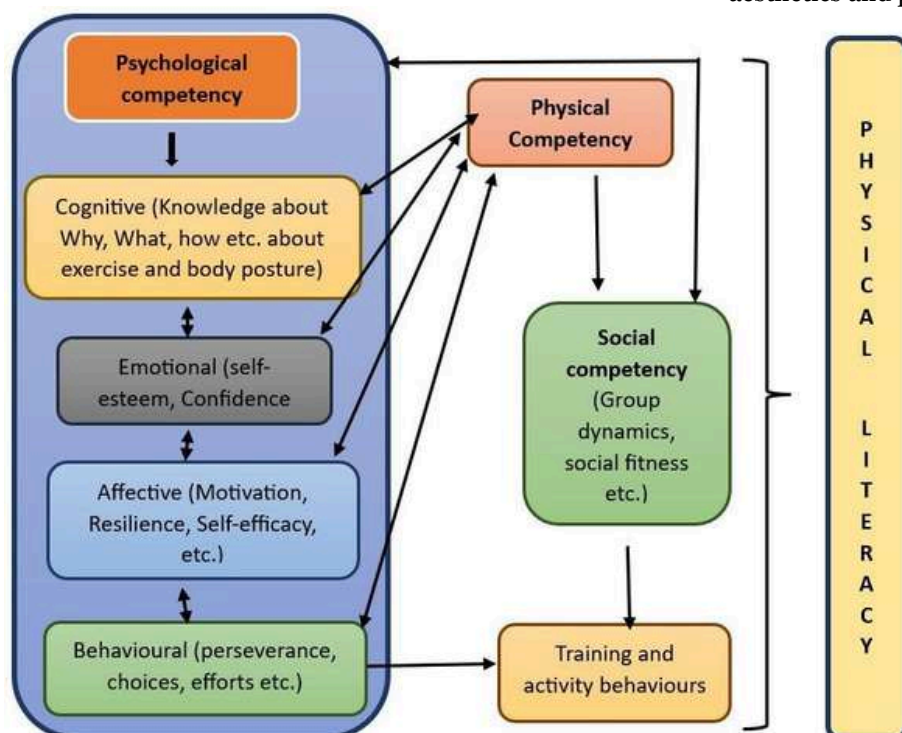


Figure 2: Mechanism of Physical Literacy

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Physical literacy has the potential to substantially enhance intrinsic motivation, a factor that is essential for sustaining long-term physical activity within the population.
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This scientific understanding should also include interdisciplinary elements such as the role of nutrition in exercise. The rationale for regular exercise is informed by the concept of exerkines. Exercise science has demonstrated that physical activity stimulates nearly all organs and tissues to produce hormone-like substances known as exerkines, which circulate throughout the body and facilitate communication among organs to optimise and maintain physiological function, thereby enhancing immunity and overall health. A strong desire to achieve and maintain an aesthetically pleasing physique can also serve as a significant intrinsic motivator for exercise. Physical competence refers to possessing an optimal level of skill in executing physical tasks and maintaining physical fitness. Developing such competence typically requires consistent participation and practice from childhood, often facilitated by formal physical education and sports programs. Mastery of various physical skills can motivate individuals to engage in physical activities by fostering confidence and self-efficacy. When combined with knowledge of exercise science, which emphasizes the importance of physical activity for health, intrinsic motivation for physical activity is further enhanced. Additionally, social competence the ability to understand and adapt to social environments enables individuals to interact effectively within groups and communities, promoting both personal and collective physical activity interests. Physical literacy education should encompass physical, psychological, and social competence to continuously enhance overall physical literacy from childhood onward. A comprehensive understanding of these interrelated components helps individuals become more confident, self-motivated, and resilient, thereby increasing adherence to physically active lifestyles even under challenging circumstances. Ongoing physical literacy education from childhood through higher education fosters a sustained commitment to healthy physical activity and behaviours, ultimately supporting healthy ageing.

How to raise a healthier generation through Physical Literacy

National governments should enact new legislation and actively promote physical literacy education for all individuals. Achieving this objective requires a dual strategy: addressing both those within mainstream educational institutions and those outside formal education. For students in schools and universities, updating curricula and implementing changes is often more

straightforward. However, reaching individuals beyond the classroom remains a significant challenge. Traditional physical education, which incorporates a variety of activities and sports, should continue for young children through middle school to foster skill development, fitness, and confidence. Equally important is the integration of scientific knowledge about exercise and body posture, introduced progressively from middle school through university as a compulsory, credit-based, and examinable component of education. The curriculum should systematically address all three pillars of physical literacy. For individuals outside formal education, governments should establish dedicated ministries and departments to implement digital and other outreach initiatives, thereby increasing accessibility to physical literacy. Collaboration with social organisations is also essential for disseminating these messages. In the current digital era, sharing information about physical literacy is more feasible than ever before. Although it may not be realistic to expect universal attainment of the highest level of physical literacy, it is imperative to ensure that all individuals acquire a solid foundation that enables them to remain active and healthy throughout their lives.

ABOUT THE AUTHORS

Dr. Venkata Rajasekhar Kali and Dr. Sandhya Sree Meda work in the fields of physical education, sports science, wellness and yoga. Dr. Kali's expertise also includes sports physiology and sports nutrition, while Meda brings experience in physical education and wellness. Together, their work promotes physical literacy and active lifestyles, encouraging people to develop the knowledge, confidence and motivation needed to participate in physical activity.

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Evolving Landscape and Clinical Potential of Robotic Telesurgery

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Areas of Expertise: Robotic Surgery | Colorectal Surgery | Proctology

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Areas of Expertise: Robotic Surgery | Colorectal Surgery | Proctology

In the last 4 decades surgery has evolved from open techniques to minimally invasive robotic assisted approaches with progressive improvements in precision, visualisation and ergonomics. The critical barrier was the geographical dependency, with need for the surgeons to operate in the same room as the patient. This leaves underserved regions, military environments and space missions vulnerable. The telesurgery or remote surgery decouples the surgeon from operating room and serves as a transformative solution. The escalation of telemedicine during the COVID-19 pandemic, has increased public acceptance of remote surgery.

Lancet Commission on Global Surgery, estimates that 4.8 billion people are unable to access essential surgical services. High-quality referral centres for training and treatment remain concentrated in metropolitan cities, leaving remote or low-resource hospitals underserved. In this context, telesurgery emerges as a potential equalizer, bridging geographic barriers and expanding opportunities for both patient care and professional development. Robotic Surgery is a type of minimally invasive surgery wh-

ere a surgeon uses a computer console to control the robotic arms. After more than 2 decades of experience with robotic surgery, the safety and benefits are well established, particularly while working in narrow and confined spaces such as the pelvis and the chest. The concept of telemedicine was explored by the NASA in 1970s with particular interest in treating astronauts in space. The advancements in Robotic Surgery have made the Robotic Telesurgery (or remote surgery) possible, wherein the robotic technology and wireless networking are used to connect patients and surgeons who are geographically distant. Significant advances in telecommunications and robotic surgery led to the idea that telerobotic surgery being considered a viable option. The Lindbergh operation was the worlds first telesurgery performed in 2001 between Strasbourg (France) and New York (US) using a remotely controlled robotic system connected by a dedicated high speed fibre-optic network. Widespread adoption subsequently slowed due to infrastructure costs, limited bandwidth, and unresolved ethical and legal issues. Over the next two decades, telesurgery has progressed slowly, which may have been due to the limitations of robotic systems and the lack of advanced and stable telecommuni-

ations. High infrastructure costs and unresolved ethical and legal issues also hindered the progress. The advent of 5G wireless networks has been a game changer. In recent years the advancement of robotic expertise and technology coupled with stable telecommunication has led to faster development of telesurgery. The capability of robotic telesurgery has been adequately tested recently using multiple newer platforms. Current worldwide experiences demonstrate that remote robotic surgery can be performed safely when critical requirements are fulfilled, namely with a fast, stable, and low-latency connection, properly trained personnel on both ends using advanced platforms. Robotic telesurgery is rapidly reshaping the way surgical care is delivered across the globe. By combining advanced robotics with high-speed communication networks, surgeons can now operate on patients remotely, breaking down geographical barriers and expanding access to specialized medical expertise. Mobile telesurgery units have been developed using a portable surgical robot which could be deployed near a frontline or disaster area, and expert surgeons may operate it from a safe zone.

Challenges and Benefits of Telesurgery

Wider practical implementation of robotic telesurgery will need to address the challenges of communication reliability, cybersecurity, data privacy and work within ethical, legal and regulatory frameworks. Another important challenge that hinders its adoption is latency period which is primarily a delay that exists in data trans-

mission between the surgeon's input and the robotic system's response. Latency period greatly impacts telesurgery performance with an ideal value being less than 200 milliseconds. Having a backup surgical team onsite is essential for safe robotic telesurgery. This ensures that if a connectivity issue arises, a capable team can take over immediately, minimizing risk. A special consent form for telesurgery should illustrate the technical set-up, potential network-related risks, backup plans in case of technical failure, and the credentials of the remote surgeon.

Robotic telesurgery has the potential to reduce disparities in medical expertise, enable real-time surgical training through tele-proctoring and improve patient outcomes worldwide. Patients in rural or remote areas, who previously had limited access to specialists, can now benefit from procedures performed by leading surgeons located hundreds or even thousands of kilometres away. It can also facilitate the collaboration between specialist surgical teams by providing real-time interaction among surgeons from various specialties and geographical locations. Telerobotic surgery eliminates the expenses required to travel to specialized medical centres, facilitates early interventions and reduces patient stress and discomfort.

India's First Robotic Telesurgery for Rectal Cancer: The APCC Experience

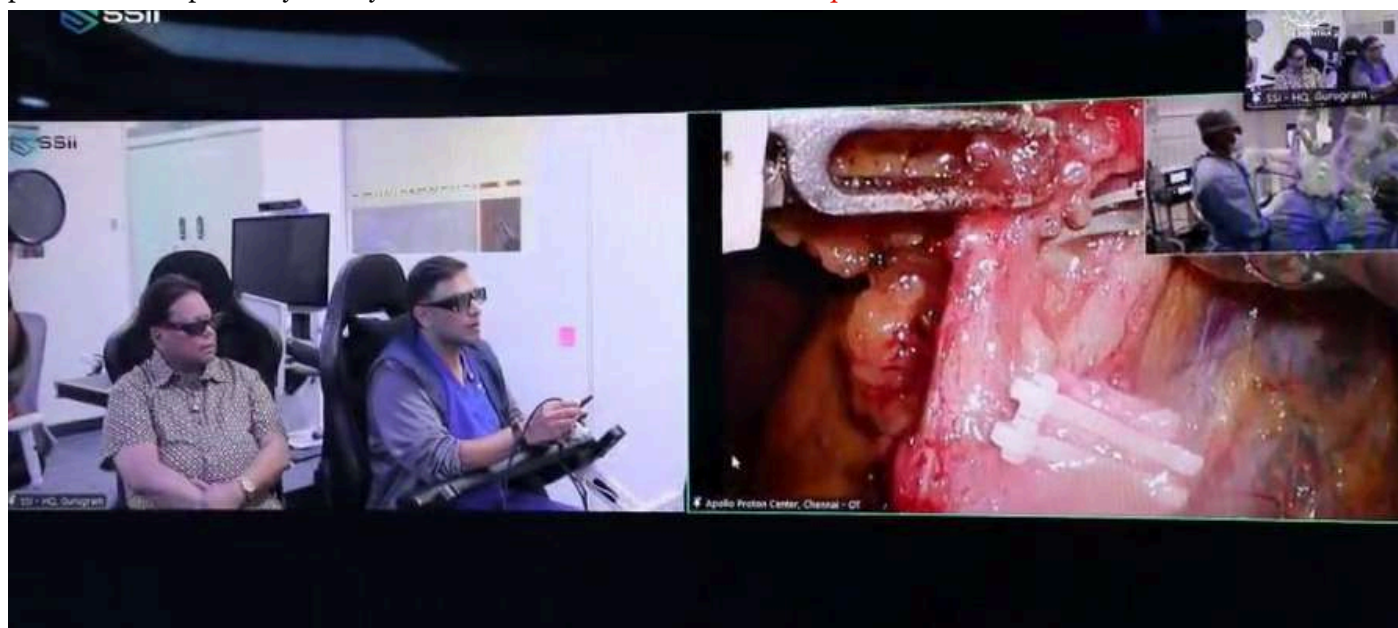


Figure 1: India's first ever robotic telesurgery for Rectal cancer performed between Chennai and SS Innovations headquarters in Gurugram.

Apollo Proton Cancer Center, Chennai in collaboration with SS Innovations successfully deployed India's indigenously developed SSI Mantra Surgical Robotic System to deliver advanced minimally invasive care with a series of Robotic Colorectal procedures.

A secure dedicated wired 5G network was used with average latency of 45 ms. Collaboration achieved a major milestone with India's first ever robotic telesurgery for Rectal cancer performed over a distance of 2200 km between Chennai and SS Innovations headquarters in Gurugram. The seamless execution demonstrated the safety, precision and reliability of the SSI Mantra systems telesurgery capabilities by integrating cutting edge made in India technology with clinical expertise. This initiative demonstrates the potential of scalable, accessible and affordable robotic surgical care for the patients across India and globally. The collaboration can be extended between multiple hospitals at multiple other cities and towns so that even surgeons with less experience in robotic colorectal surgery can be mentored and at the same time their patients can also get access to the best skill sets available.

The Future of Robotic Telesurgery

Robotic telesurgery, combined with advances in AI, high-speed communication, and supercomputing, will revolutionize current surgical practice. Artificial intelligence can overcome human visual limitations in identifying microscopic tissue boundaries particularly during cancer clearance operations.

It can also provide real time navigation in identifying critical vascular and neural structures with microscopic precision thereby reducing unintentional injury to these tissues. One of the major drawbacks of robotic assisted surgery is the lack of tactile feedback. In addition to the raw visual feedback, AI has the potential to sense tissue tension more precisely and guide the surgeon in preventing unintentional tearing of tissues and overcome the absence of tactile feedback. The renewed enthusiasm for the development of telesurgery is both humanitarian and practical.

Even though the world's first robotic telesurgery happened in 2001, subsequent progress had been slow due to the limitations of robotic systems and the lack of advanced and stable telecommunications. Recent few years have seen faster development with the capability of robotic telesurger-

y being adequately tested using multiple newer platforms. Our team at Apollo Proton Cancer Center in collaboration with SS Innovations performed India's first ever robotic telesurgery for Rectal cancer over a distance of 2200 km. Wider practical implementation of robotic telesurgery will need to address the technical and ethical challenges and work within legal and regulatory frameworks. Telesurgery is likely to progress from novelty to a more routine option in surgical care in the near future.



Figure 2: Robotic Telesurgery bedside team

ABOUT THE AUTHORS

Prof. Senthil Kumar Ganapathi and Prof. Venkatesh Munikrishnan are specialists in colorectal and robotic surgery at Apollo Proton Cancer Centre, Chennai. Their work explores how robotic telesurgery can allow expert surgeons to operate on patients from distant locations. Their experience helps demonstrate the safety and practical potential of telesurgery, with the goal of making advanced surgical care more accessible to patients.

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The New Face of Water Pollution: Beyond Microplastics



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Areas of Expertise: Environmental monitoring and assessment

Twenty years ago, water pollution was something we could usually see. Oil slicks floating on rivers, untreated sewage entering streams, plastic bottles washed onto beaches and industrial discharge, these were clear indications that an ecosystem was in distress. Scientists measured nutrients, heavy metals and microbial contamination, assuming that these indicators captured most of the story. Today, we know that they do not. Some of the most important pollutants are now invisible. Tiny fragments of plastic, residues of medicines we consume, industrial chemicals designed to resist degradation, personal care products and hundreds of other synthetic compounds are quietly moving through rivers, estuaries, wastewater, groundwater and even drinking water. Some are present in extremely low concentrations, parts per billion or even parts per trillion, but are highly persistent, bioavailable and are now a significant problem for ecosystem and human health.

The Rise of Contaminants of Emerging Concern

One of the biggest misconceptions about Contaminants of Emerging Concern (CECs) is that they are “new” pollutants.

In reality, many of these chemicals have been part of our daily lives for decades. What is new is our ability to detect them and understand their potential impacts. CECs include a diverse group of substances such as pharmaceuticals, antibiotics, endocrine-disrupting compounds, PFAS, personal care products, flame retardants and plastic additives. The sources of these contaminants in the environment include domestic wastewater, industrial activities, hospitals, agriculture and urban runoff. Many are biologically active, persistent and can build up in aquatic environments, although they can be present at very low concentrations. Their high abundance has challenged the conventional notion of water pollution and created a need for more comprehensive monitoring, improved wastewater treatment and science-based environmental policy. Our research findings over several years have mirrored this transformation in scientific thinking. The investigation added to a much more complicated picture of microplastic pollution in tropical aquatic environments. From studying the estuaries of Kerala to coastal ecosystems, wastewater treatment plants and indoor environments, the issue of microplastics was not always standalone, but rather came in clusters. They were often found alongside pharmaceutic-

cals, per- and polyfluoroalkyl substances (PFAS), plastic additives, personal care products, flame retardants and other contaminants of emerging concern, suggesting that today's aquatic environments are primarily impacted by multifaceted mixtures of contaminants.

Microplastics: More Than Plastic Debris

Microplastics first attracted global attention because they were visible reminders of plastic pollution. But what we know about them has changed in leaps and bounds in the last 10 years. Today, we know that microplastics rarely travel alone. The most surprising finding was that microplastics were not simply passive debris floating through rivers and estuaries. They acted more like tiny environmental carriers, providing surfaces onto which other contaminants could attach and travel. They can carry pharmaceuticals, pesticides, heavy metals, PFAS, microorganisms and other pollutants in aquatic environments. It was this realization that shifted the way we understood pollution. We stopped questioning only the number of microplastics and started asking what they were carrying, how they reacted with other contaminants and what those interactions meant for ecosystem health. Microplastics, in many ways, are the tip of the iceberg for a much bigger story about the environment, beyond plastic.



Figure 1: Field sampling of river water for the assessment of emerging contaminants and microplastic pollution in a tropical aquatic ecosystem.

The effects of microplastics and emerging contaminants have been studied in different aquatic systems in the tropical region of Southern India. Research conducted in the estuaries of Kerala showed that pollution is not homogeneous and that the degree of pollution varied between sites depending on human activities and environmental conditions. Furthermore, we discovered that elevated levels of microplastics were correlated with a larger number of emerging contaminants, highlighting the need to investigate mixtures of contaminants as opposed to contaminants alone. Our study along the Kerala coast has also produced useful baseline data for long-term monitoring and ecological risk assessment in tropical marine environments.

Why Conventional Wastewater Treatment Is Not Enough

Wastewater treatment plants were also identified as a key aspect of this problem in our investigations. While treatment facilities are very effective at removing suspended solids, nutrients, organic matter and disease-causing microorganisms, they were never designed to remove many of the synthetic chemicals found in modern medicines, consumer products and industrial activity. As a result, pharmaceuticals, PFAS, personal care products and other emerging contaminants can be observed in treated effluents and enter rivers, estuaries and coastal waters. These contaminants are continuously added to the environment through domestic and industrial uses. Protecting water quality today therefore requires not only better wastewater treatment but technologies that can provide solutions to these newly recognized pollutants. Monitoring programmes must also be developed, together with a greater understanding of the behaviour of emerging contaminants in the environment. Understanding these challenges has shaped the direction of our research.

In addition to environmental monitoring, we have explored advanced treatment technologies capable of removing contaminants that resist conventional treatment processes. Hybrid photocatalytic-electrocatalytic oxidation systems have been found to be useful for degradation of persistent organic pollutants, while microbial fuel cells demonstrate the possibility of combining wastewater treatment with the generation of renewable energy. These strategies will work together to shift towards a more sustainable water management practice that involves addressing pollution and resource recovery as complementary functions.

New Technologies for Detecting Invisible Pollution

Detection of contaminants has increased greatly in the last decade. Scientists can now detect hundreds of compounds at extremely low concentrations that were previously unknown, using more sophisticated analytical methods such as high-resolution mass spectrometry. Meanwhile, technologies such as biosensors, artificial intelligence, machine learning and wastewater-based epidemiology are transforming the way we look at environmental health. These tools are enabling scientists to go beyond basic water quality measurements towards more advanced smart water-quality tools that can detect pollution sources sooner and help inform evidence-based environmental stewardship.

The Future of Water Pollution Research

The greatest lesson from our research is that water pollution can no longer be understood by studying one contaminant at a time. Complex mixtures of plastics, chemicals and other emerging pollutants are present together in rivers, estuaries and coastal ecosystems, and the interactions of such mixtures are only partially understood. The next generation of research is about understanding the invisible pollutants that cannot be routinely monitored. The

extent to which certain contaminants, such as nanoplastics, PFAS, pharmaceuticals and antimicrobial resistance, are understood is still limited, especially when they are found in combination as “cocktail” mixtures. Future research will increasingly combine environmental chemistry, toxicology, microbiology, engineering and data science to gain a deeper understanding of their behaviour and devise effective solutions. As critical as this will be is the ability of treatment technology to be sustainable and capable of removing persistent contaminants while generating useful resources. The ability to identify these contaminants, understand their interactions and create more intelligent and sustainable solutions will all be important for protecting our water resources. Innovation, teamwork and a new approach to pollution prevention will be needed to protect our water resources. This version is much better structurally because the Q&A information is no longer separated from the main story. I have preserved the author's language as much as possible, while removing places where essentially the same statement occurred twice and making only minor grammatical adjustments for continuity.



Figure 2: Collection of wastewater samples from a sewage treatment plant to investigate the occurrence and fate of emerging contaminants.

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*The real challenge is not
simply detecting
pollutants, but
understanding their
journey through the
environment.*

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ABOUT THE AUTHORS

Dr. Muthukumar and her research team work across environmental monitoring, microplastics, emerging contaminants, water and wastewater quality, and sustainable remediation. Their research provides important insights into the occurrence, fate, and ecological impacts of contaminants in aquatic ecosystems, while advancing innovative treatment approaches, including catalytic ozonation and electro- and photo-electrocatalytic oxidation. Their interdisciplinary work highlights the need for integrated and sustainable solutions to emerging water pollution challenges. By connecting environmental assessment with advanced treatment technologies, their work supports the development of cleaner water systems and more resilient aquatic environments.

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Hidden Chemistry Above the Oceans: How Reactive Molecules Shape Climate and Aerosol Formation



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Areas of Expertise: Atmospheric chemistry | Interstellar Chemistry | Microwave Spectroscopy | Gas-phase kinetics

Aerosols, the tiny solid particles or liquid droplets suspended in air, affect the Earth's climate in various ways and span a diverse size range from a few nanometers to several micrometers. About a quarter of the solar radiation reaching the Earth's atmosphere is reflected by aerosol, exerting a direct effect on the Earth's radiation field and thus affecting its surface temperature. Beside this direct effect, aerosols also exert an indirect effect on climate by modifying cloud albedo through the formation of cloud condensation nuclei (CCN). Beside their climatic effects, aerosols and particulate matter also exert adverse effects on human health. According to the United Nations report, air pollution is the second highest cause of mortality around the world causing millions of deaths every year. Given the immense importance of aerosols on environment and human health, it is imperative to ask what are their sources and how are they formed. As the oceans cover two-thirds of the Earth's surface, chemistry in marine boundary layer (MBL) plays a pivotal role in shaping the climate, particularly in remote regions where continental influence is minimal. Sulfur species such as Dimethyl sulfide (DMS) emitted from oceanic phytoplankton is known to be the primary source of CCN in MBL. The second-generation oxidation products derived from marine emission can modify the clouds and droplets properties either by participating in new particle formation or by undergoing direct partitioning from gas to aerosol phase. Recently, a new atmospheric emission methane sulfonamide (MSAM) was detected during Air Quality and Climate Change in the Arabian Basin (AQABA) campaign in the Somalia upwelling region of the Arabian Sea, the fifth largest upwel-

ling region in the world. Data collected during the campaign strongly indicated a source linked to phytoplankton blooms. MSAM is a multifunctional molecule having both sulfur and nitrogen atoms-that are traditionally linked to aerosol formation. The physical and chemical processes undergone by the molecule near its emission source determine how far the molecule can be transported and how its local chemistry can influence marine sulfur cycling, and its downstream climate effects. Hence, knowledge of the processes that can remove MSAM from the atmosphere is important for the evaluation of its effects on the climate. Although the field measurements indicated that both DMS and MSAM have similar atmospheric lifetime, the reaction of MSAM with OH radical i.e. 'the detergent of the atmosphere,' was found to be much slower than that of DMS. Various studies also found the reactivity of MSAM toward other major atmospheric oxidants to be rather limited. Considering the slow reaction of MSAM with the major oxidants, previous studies concluded that the dry deposition to the ocean surface is the dominant and effectively-only significant removal pathway.

A New Pathway for Removing MSAM from the Atmosphere

Challenging this notion, we recently published (Syed Ibrahim J., Surabhi Gupta, Goutam Chowdhury, and Mausumi Goswami, Environmental Science & Technology, 2026) the findings of a new chemical reaction pathway that can remove MSAM from the atmosphere at rates comparable to its dry deposition process. We argued that before accepting dry deposition as the sole significant sink

for MSAM, it is necessary to assess its reaction inventory against oxidants that had not yet been considered. Interestingly, alkenes, are emitted in substantial quantities from biologically productive marine regions such as the Arabian Sea. Alkenes, when they come into contact with atmospheric ozone (in a process known as ‘ozonolysis’), can produce highly reactive species called ‘Criegee intermediates’ (CI). We hypothesized that CIs should be present in marine environments and could constitute an important sink for MSAM that had not previously been examined.

How Criegee Intermediates React with MSAM

With the help of Density Functional Theory (DFT) calculations, we showed that the reaction of CIs with MSAM generated, with substantial rate, a unique class of hydroperoxides. The hydroperoxides once formed are unlikely to revert to reactants under atmospheric conditions. Especially, the smallest CI formaldehyde oxide (CH₂OO) and anti-CH₃CHOO (generated from the ozonolysis of *cis*-/trans- 2-butene) react with MSAM at rates fast enough to surpass the reaction with OH radical.

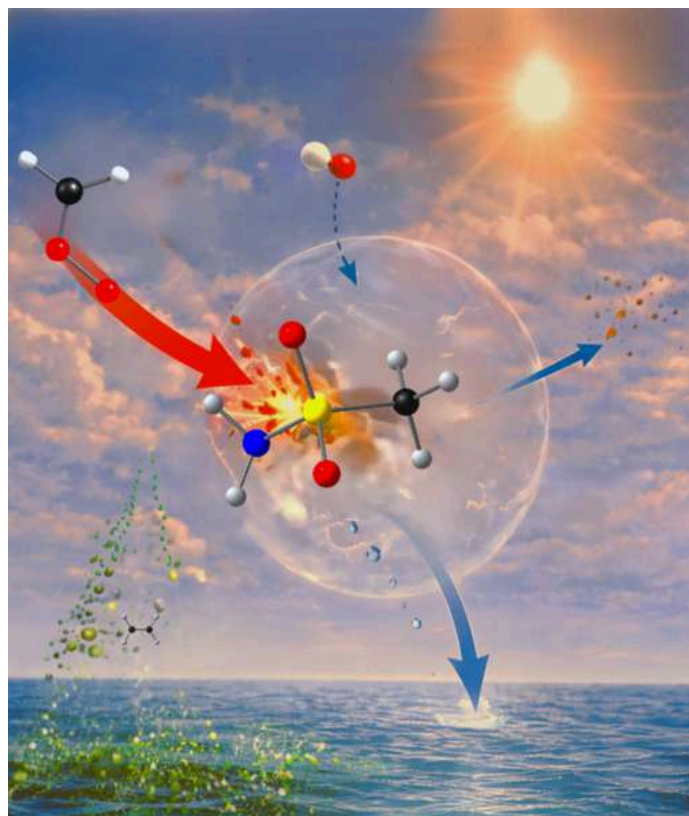


Figure 1: An artistic representation of different transformation paths of methanesulfonamide in the marine environment leading to aerosol formation. A fast reaction with Criegee intermediate is depicted by the solid red arrow.

Other highly substituted CIs reacted at slower rates, but even their reactions were found to be competitive with the OH removal pathway. Notably, our studies indicated that the removal rate of MSAM by CIs increased at colder tropospheric temperatures; at 200 K, the ratio of rate constants for CI versus OH reactions approached ~100 specifically for anti-methacrolein oxide (anti-MACRO; produced via the ozonolysis of isoprene), corresponding to a lifetime roughly ten times shorter than that from the OH reaction alone. Overall, accounting for the inventory of CIs considered in our study, reactions with CIs with MSAM can surpass the OH-radical reaction rate for several CIs across the tropospheric temperature range. Particularly for the CIs such as CH₂OO and anti-CH₃CHOO, the reaction can rival the dry deposition rate. In addition, the reaction of MSAM with certain CIs can be as fast as OH + DMS under atmospheric conditions.

What This Chemistry Could Mean for Marine Aerosols

We also estimated the relative branching ratios of the products and found that the product distribution varied with the nature and substituents on CI backbone. While the reactions of MSAM with CIs such as CH₂OO, *syn*-CH₃CHOO, (CH₃)₂COO, and *syn*-methyl vinyl ketone oxide (*syn*-MVKO) were found to proceed exclusively via a single mechanism, the reactions with *anti*-CH₃CHOO and *anti*-MACRO proceeded via two distinct pathways forming different functionalized hydroperoxides. Detailed mechanistic study indicated that under atmospheric conditions, the generated hydroperoxides are resistant to internal dissociation. Importantly, these functionalized hydroperoxides, which retain both the nitrogen and sulfur of the parent MSAM molecule would potentially be low volatile with decent solubility in aqueous medium. Thus, the hydroperoxide products generated in the reaction of MSAM and CIs can partition into the condensed phase. Such aqueous-phase partitioning will affect the properties of particulate matter and aerosols, in a manner comparable to other sulfur-containing hydroperoxides, such as hydroperoxymethyl thioformate, that are already known to affect cloud uptake and the marine sulfur-dioxide budget. However, we do realize that any conclusion regarding the ultimate fate of these hydroperoxides remains conjectural at this stage and will require further investigation. Taken together, the findings establish that Criegee intermediate chemistry is a previously unrecognized major atmospheric sink for MSAM. Our studies indicate that in marine regions with high biological activity, chemical processes such as the reactions with CIs

can become an important removal route for MSAM and dry deposition alone will not govern its atmospheric removal rate. Given that the simplest CI formaldehyde oxide (CH_2OO) is generated from the ozonolysis of essentially all biogenic alkenes, including isoprene, we concluded that CI-mediated removal of MSAM is likely to be particularly significant in biologically active marine regions such as the Somalia upwelling zone, where it may result in an atmospheric lifetime for MSAM close to that of DMS. More broadly, the study opens a new line of inquiry into sulfur-nitrogen cycling in the marine environment, and establishes the need for further experimental work that may provide important insight into aerosol formation process in the biologically active region of the Earth's ocean.

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As the oceans cover two-thirds of the Earth's surface, chemistry in marine boundary layer (MBL) plays a pivotal role in shaping the climate.

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ABOUT THE AUTHOR

Dr. Mausumi Goswami leads the Laboratory of Atmospheric and Interstellar Chemistry at Vellore Institute of Technology (VIT), Vellore, where her research focuses on understanding molecular processes in the atmosphere and interstellar environment using spectroscopic and computational approaches. Her recent work has particularly advanced the understanding of Criegee intermediates and atmospheric sulfur chemistry, including the discovery of a previously unrecognized pathway for the removal of methane sulfonamide from the atmosphere.

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Electrochemical Divergent Synthesis of Bioactive Heterocycles by Regulating the Applied Electricity



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Areas of Expertise: Electrochemical Organic Synthesis | Visible-Light Photocatalysis | Iodine Catalysis | Green Chemistry | Synthesis of New and Novel Drug Molecules



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Areas of Expertise: Fluorine Chemistry and Fluoroalkylation | Electrochemical Organic Synthesis | Visible-Light Photocatalysis | Synthesis of New and Novel Drug Molecules

Nitrogen-containing heterocycles (N-heterocycles) serve as the structural backbone for the majority of modern pharmaceuticals. Recent data indicate that N-heterocycles are present in approximately 82% of small-molecule drugs approved by the FDA since 2013. Among these, pyrazole and its derivatives, such as pyrazolines and pyrazolones, are particularly prominent. The incorporation of the trifluoromethyl (CF₃) group into these heterocyclic cores is a strategic design choice in drug discovery. The CF₃ moiety enhances metabolic stability, increases lipophilicity, and improves binding affinity and bioavailability. Consequently, developing efficient methods for synthesizing CF₃-tethered N-heterocycles is of paramount importance to the pharmaceutical industry. Traditional synthetic routes to these molecules often involve stoichiometric amounts of toxic oxidants and expensive metal catalysts. Organic electrochemistry offers a compelling green alternative by using electricity as the primary redox reagent. By replacing hazardous chemical reagents with electrons derived from renewable energy, th-

ese methods enable transformations under mild conditions, often producing hydrogen gas as the sole byproduct.

Advancing Organic Synthesis through Electrochemistry Harnessing Radicals with Electricity

A central advancement in this field is the electrochemical generation of reactive radical intermediates. The ability to access C-, O-, and N-centred radicals via direct electrolysis has significantly expanded synthetic capabilities. These radical species are instrumental in triggering cascade reactions, leading to the efficient formation of new C-C and C-heteroatom bonds. Such radical-based strategies enable the construction of highly functionalized molecules that were previously challenging to access through conventional polar pathways.

Metal-Free Routes to Greener Synthesis

A significant trend in recent research is the development of metal-free and external-oxidant-free protocols. These methods align with the core principles of green chemistry

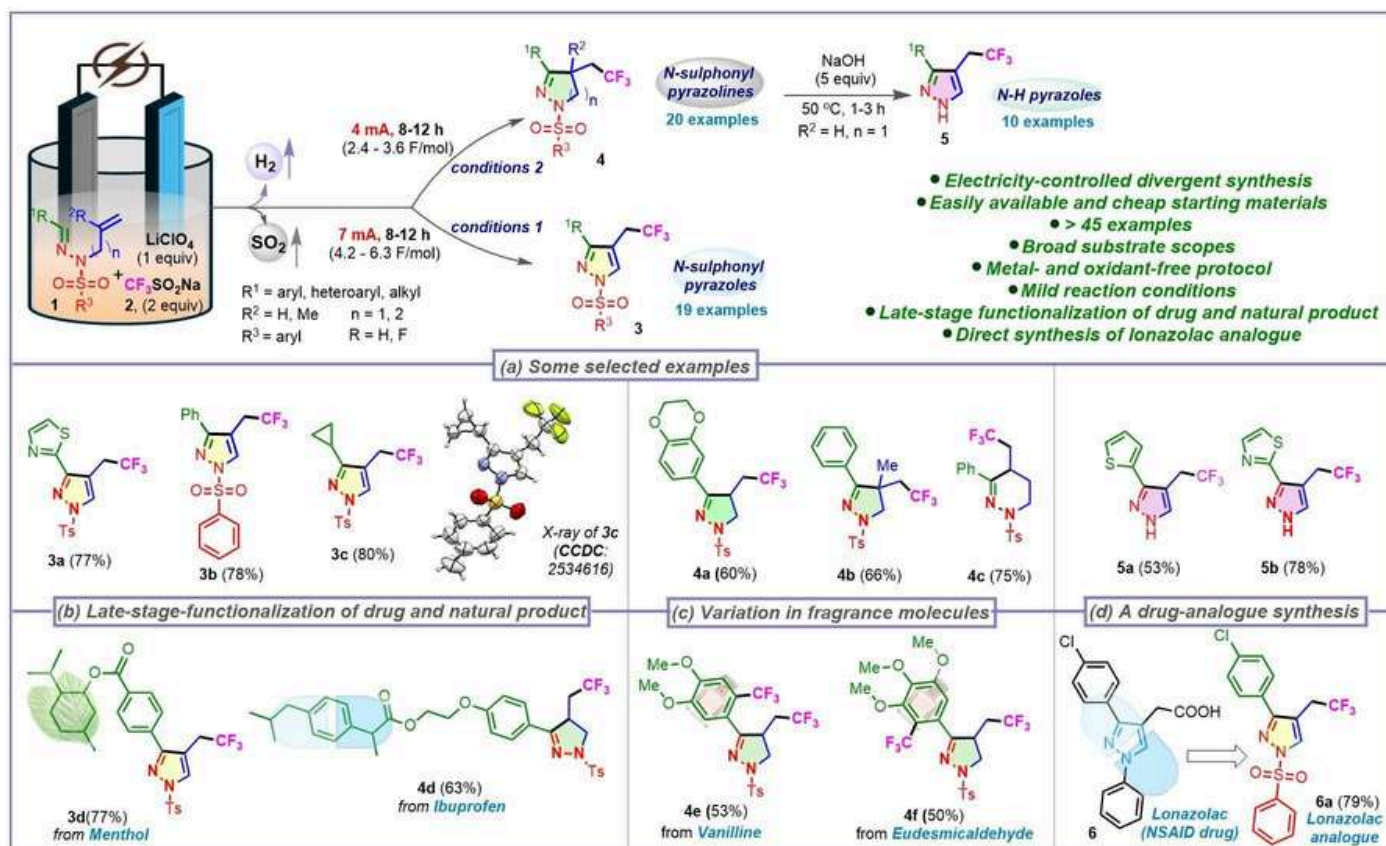


Figure 1: Electricity-controlled, divergent synthesis: (a) Some selected examples of 4-fluoroalkyl-substituted N-sulfonylpyrazolines, N-sulfonylpyrazoles and N-H pyrazoles, (b) late-stage functionalization of drug and natural product, (c) Lonazoloc drug analog

by eliminating the need for transition-metal catalysts and hazardous oxidants. These processes typically employ inexpensive electrodes and operate at ambient temperatures, further improving their sustainability profile.

Precision Functionalization of Indoles

Indoles represent a versatile class of building blocks in organic synthesis. Recent electrochemical advances have enabled regioselective functionalization of indoles at various positions (C2, C3, and N1). These strategies utilize electrons to facilitate cross-coupling and cyclization reactions without the need for pre-functionalized starting materials. The ability to target specific sites within the indole ring enables the synthesis of diverse derivatives with potential bioactivity, thereby stimulating further research into indole-based therapeutics.

Combining Light and Electricity for Chemical Synthesis

The integration of photochemistry and electrochemistry, known as electrophotocatalysis, represents an emerging frontier. This hybrid approach leverages the benefits of photons as reagents while using an electric potential to tune

the redox state of catalysts. Electrophotocatalysis is particularly effective for transformations such as C-H functionalization and reductive cross-coupling, enabling reaction modes that are inaccessible via single-modality methods.

Controlling Molecular Synthesis with Electricity Electricity as a Switch for Divergent Synthesis

A landmark contribution to the field is the development of electricity-controlled divergent synthesis of biologically active N-heterocycles. Our recent studies have demonstrated that product selectivity can be precisely modulated by adjusting the applied current during constant-current electrolysis. For example, the transformation of N-allyl-N'-benzylidenesulfonohydrazides **1** with CF₃SO₂Na **2** can yield β-trifluoroethyl-substituted N-sulfonylpyrazoles **3**, N-sulfonylpyrazolines **4**, or N-H pyrazoles **5** depending solely on the electrical parameters employed. When a mixture of **1** and **2** was electrolyzed with a constant current of 7 mA for 8-12 h (4.2–6.3 F/mol, conditions 1), 4-trifluoroethyl N-sulfonylpyrazoles **3** were formed, howe-

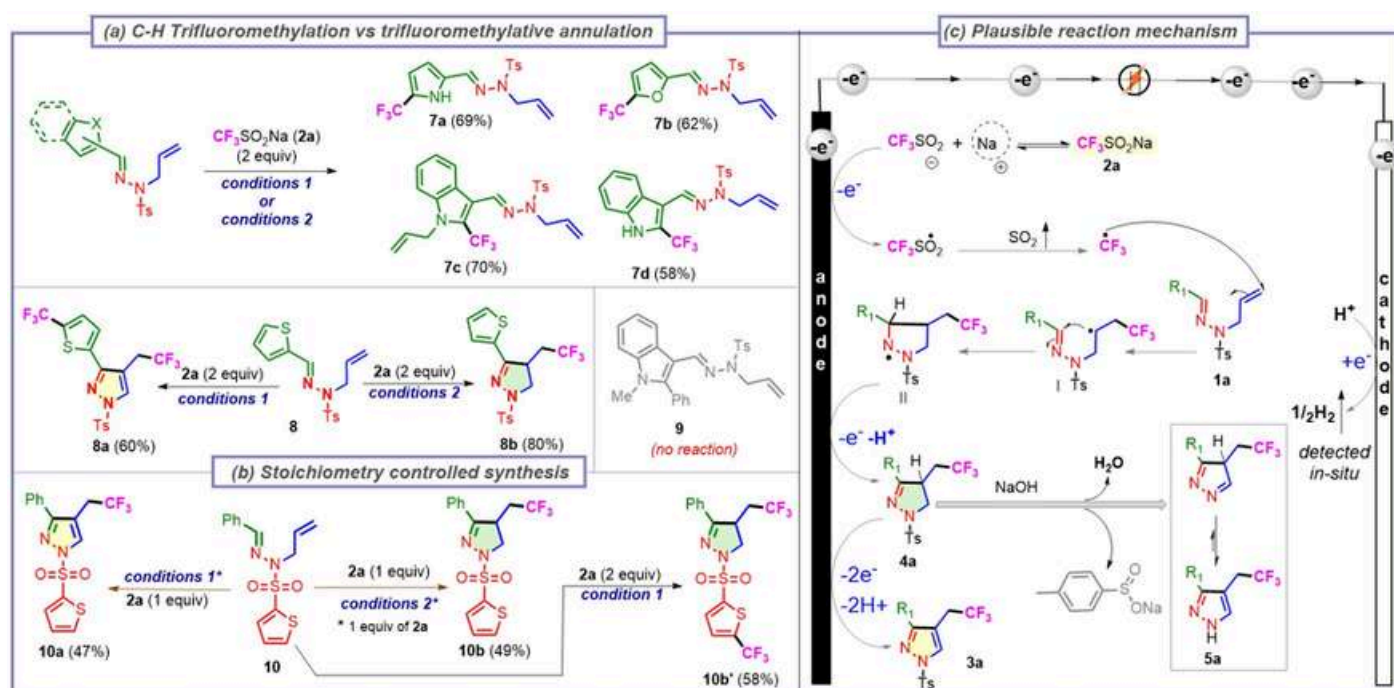


Figure 2: (a) C-H trifluoromethylation vs trifluoromethylative annulation, (b) stoichiometry-controlled trifluoromethylative annulation, and (c) plausible reaction mechanism.

ver, a constant-current-electrolysis (CCE) with 4 mA current for 8–12 h (2.4–3.6 F/mol, conditions 2) furnished 4-trifluoroethyl N-sulfonylpyrazolines 4, which after the treatment with NaOH afforded the corresponding N-H pyrazoles 5 (Figure 1).

Thus, by simply tuning the applied electric current during constant-current electrolysis, one can selectively synthesise three different classes of bioactive N-heterocycles.

The method exhibits broad substrate applicability and tolerance toward various functional groups, encompassing derivatives from fragrances, pharmaceuticals, and natural products (Figure 1a–1c). Electricity serves as the sole reagent, producing H_2 as a harmless byproduct, highlighting the protocol's significant sustainability. The authors' 2026 JACS Au paper confirms this electricity-controlled, metal- and external-oxidant-free strategy and its broad functional-group tolerance.

Controlling Trifluoromethylation with Radical Chemistry

The synthesis of CF_3 -tethered heterocycles often proceeds through a tandem sequence of regioselective radical trifluoromethylation, annulation, and oxidation. Controlling the reactivity of the $\bullet\text{CF}_3$ radical generated by sources such as Langlois' reagent is a major challenge beca-

use the radical can attack multiple sites on the substrate.

The development of selective radical trifluoromethylative annulation protocols represents a significant advance in overcoming these competitive pathways.

Interestingly, electron-rich heteroaryl such as indole, pyrrole, and furan-substituted substrates underwent chemoselective C–H trifluoromethylation of the heteroaryl component over annulation (Figure 2a). Notably, when the second position of indole was blocked (9), it still did not undergo trifluoromethylative annulation.

These findings underscore the distinct reactivity of the $\bullet\text{CF}_3$ radical in relation to (hetero) aryl-substituted N-allylsulfonylhydrazides.

Moreover, thiophene-substituted substrates underwent Langlois' reagent stoichiometry-controlled trifluoromethylative annulation and C–H trifluoromethylation (Figure 2b).

Extending the Strategy to Drugs and Natural Products

The robustness of this electrochemical protocol is demonstrated by its use in the late-stage functionalization (LSF) of existing drugs and natural products (3d, 4d – 4f), such as ibuprofen and menthol (Figure 1b–1c). Successful

CF₃ incorporation and heterocyclic construction have been achieved on molecules such as ibuprofen and menthol. Furthermore, this method has enabled the direct synthesis of an analogue of the marketed drug Lonazolac 6, i.e., 6a (Figure 1d), thereby demonstrating its potential utility in pharmaceutical manufacturing.

Understanding How Electricity Controls the Reaction

Several control experiments and mechanistic studies have been conducted to elucidate the origin of the electricity-controlled, chemoselective synthesis of 4-trifluoroethyl N-sulfonylpyrazoles 3, N-sulfonylpyrazolines 4, and N-H pyrazoles 5 from 1 and 2.

These studies revealed that •CF₃ radical was generated via a preferential single-electron-oxidation (SET) CF₃SO₂Na 2 at the anode, followed by the elimination of SO₂ gas and subsequent reduction of the sodium ion at the cathode to form a major deposition of sodium metal on the cathode (Figure 2c). The electrophilic •CF₃ radical was then added to the terminal position of the allyl functional group of the substrate 1, regioselectively to form the nucleophilic alkyl (2o) radical (I), which, after radical annulation, SET at anode, and deprotonation furnished the 4-trifluoroethyl N-sulfonylpyrazolines 4 under conditions 2 (CCE at 4 mA).

However, under condition 1 (CCE at 7 mA), the in situ-generated 4-trifluoroethyl N-sulfonylpyrazolines underwent two-electron oxidation and two-proton elimination to directly afford 4-trifluoroethyl N-sulfonylpyrazoles 3. When the in situ-generated 4-trifluoroethyl N-sulfonylpyrazolines were treated with NaOH (5 equiv) at 50 °C, 4-trifluoroethyl N-H pyrazoles 5 were formed.

Challenges in Electrochemical Synthesis

Despite significant progress, several challenges remain. Achieving high regioselectivity in multi-site substrates is a persistent hurdle, as the high reactivity of radical intermediates can lead to undesired side reactions. Furthermore, the physical organic principles governing electrochemical transformations are highly complex, with outcomes that are sensitive to electrode materials, electrolytes, and applied electric fields.

A deeper mechanistic understanding, supported by computational modelling and spectroscopic monitoring, is necessary to optimise these reactions for broader application. Moreover, while many protocols are successful at the laboratory scale, transitioning to industrial-scale production requires further development in flow electrochemistry to ensure efficient mass and heat transfer.

Towards a More Sustainable Future for Drug Synthesis

Electrochemical synthesis of CF₃-tethered N-heterocycles has transitioned from a niche methodology to a central pillar of sustainable organic chemistry. By harnessing radical reactivity and electricity-controlled selectivity, researchers have developed efficient, metal-free protocols that address long-standing limitations in the controlled, divergent synthesis of biologically active molecules and in drug discovery. As the field continues to integrate, enabling technologies like electrophotocatalysis and flow chemistry, the precise and sustainable use of electrons will undoubtedly play a vital role in the synthesis of next-generation pharmaceuticals.

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Our research demonstrates how precise control of applied current during constant-current electrolysis can achieve selectivity in product formation, leading to the divergent synthesis of potential molecules.

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ABOUT THE AUTHORS

Prof. Tanmay Chatterjee and his team at BITS Pilani, Hyderabad Campus work on green organic synthesis, electrochemistry, fluoroalkylation, iodine catalysis and visible-light photocatalysis. Their research develops sustainable methods for synthesising medicinally important molecules using safer reagents and fewer metal catalysts. A key contribution is their electricity-controlled synthesis of CF₃-containing pyrazolines and pyrazoles, demonstrating how electrical current can selectively direct the formation of different bioactive molecules and advance greener drug synthesis. Their work highlights how combining electrochemistry with modern organic synthesis can reduce chemical waste, improve reaction selectivity.

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SCIENCE STORIES RESEARCH & EXPLORATIONS

Behind every discovery lies a story of curiosity, perseverance, and wonder. Science unfolds through relentless research and bold explorations into the unknown. These are the journeys that shape our understanding of the world—and beyond.

 | By Dr. Ipsita Mohanty

THE SNAKE'S SECRET DEFENSE: TURNING NATURAL PROTEINS INTO ANTIVENOM

In a laboratory in the United States, a young researcher named Ethan was fascinated by a strange question: How can a venomous snake carry such dangerous chemicals without being harmed by them? Snakebite is a serious global health problem, killing many people and leaving others with permanent injuries. Ethan knew that conventional antivenom saves lives, but producing it is complicated. Venom is usually injected into animals such as horses or sheep, which then produce antibodies. These antibodies are collected and purified to make antivenom. Although effective, such treatments may work differently against different snake species, require large doses, and sometimes cause unwanted immune reactions. One afternoon, Ethan discussed this with his colleague Maya. She asked, "What if the snake has already solved this problem?" Vipers are naturally resistant to many effects of their own venom because their blood contains molecules that can block imp-

ortant toxins. Perhaps evolution had already created a natural form of antivenom.

Ethan and Maya became interested in the Western Diamondback rattlesnake, *Crotalus atrox*. Its venom contains several toxins, including dangerous enzymes called metalloproteinases, or MPs. These enzymes damage tissues and blood vessels, causing severe bleeding and problems with blood clotting. Yet rattlesnake blood contains protective proteins capable of interfering with them. One important family is called FETUA proteins, which evolved from a blood protein called Fetuin-A. Ethan imagined them as a security team circulating through the snake's bloodstream. The researchers studied several FETUA proteins to see how well each could stop venom damage. They discovered that the proteins behaved differently. FETUA-2 completely prevented hemorrhage in one experiment, while FETUA-5 strongly reduced it. FETUA-3 could block certain metalloproteinase activities in laboratory tests, but when used alone, it could not prevent serious bleeding or protect animals from lethal venom. Clearly, there was no single perfect protective protein.



 | By Dr. Ipsita Mohanty

Maya wondered whether the proteins might be designed to work together. When FETUA-2 was tested alone against a lethal dose of Western Diamondback venom, it provided only partial protection. FETUA-3 alone also failed to save the mice. Then the researchers combined FETUA-2 and FETUA-3, and something remarkable happened: all the treated mice survived without obvious symptoms of envenomation. Ethan realized that the proteins complemented each other. FETUA-2 appeared to block metalloproteinases strongly associated with hemorrhage, while FETUA-3 targeted other metalloproteinase activities. It was like having two different keys locking two doors through which venom could cause damage. A mixture containing FETUA-2, FETUA-3 and FETUA-5 also completely protected the mice. Interestingly, these proteins did not block other important venom toxins, such as phospholipase A2 or serine proteases. This suggested that stopping the right combination of metalloproteinases could be enough to prevent death from this particular hemorrhagic rattlesnake venom.

But Ethan wondered whether the same natural defense could work against other venomous snakes. The researchers next tested venom from the Eastern Diamondback rattlesnake, *Crotalus adamanteus*. Here, FETUA-2 and FETUA-3 together were not enough. Complete protection required FETUA-2, FETUA-3 and FETUA-5, showing that different venoms may require different combinations. The results became even more impressive when the FETUA mixture was compared with conventional antivenom. Against Western Diamondback venom, the combination had a median effective dose of about 5.6 mg/kg and was approximately ten times more potent by weight than CroFab in this experimental comparison. The researchers then tested venoms from more distant pit vipers. The FETUA proteins completely protected mice against lethal Malayan pit viper venom and provided significant protection against the hundred-pace viper, even though these snakes are separated from rattlesnakes by millions of years of evolution.

At the end of the study, Ethan and Maya realized that they had discovered more than another venom-blocking molecule. They had uncovered a defensive strategy shaped by millions of years of evolution. Vipers have evolved proteins in their blood that protect them from some of their own dangerous toxins, and scientists may be able to use this natural system to design new treatments. FETUA proteins could potentially be produced as recombinant pr-

oteins and combined into carefully selected mixtures capable of targeting venoms from several species. However, much more research is needed. Most of these experiments were performed in mice, different snakes may require different combinations, and FETUA proteins target metalloproteinases rather than every venom toxin.

They therefore cannot yet replace conventional antivenom. Still, Maya's original question remained powerful.



A researcher tests natural FETUA proteins from rattlesnake blood. FETUA-2 alone reduces venom damage but does not fully protect. FETUA-3 alone also fails. But FETUA-2 and FETUA-3 together allow the animals to survive a lethal dose without symptoms.



What is the best explanation for this result?

A

FETUA-2 and FETUA-3 turn the venom into a harmless substance.

B

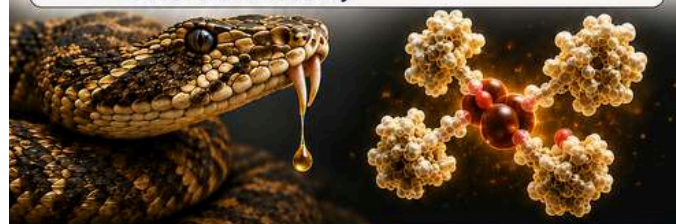
The two FETUA proteins complement each other by blocking different metalloproteinase activities in the venom.

C

FETUA-3 prevents the snake from producing venom.

D

Combining the proteins causes the animals to produce conventional antivenom antibodies immediately.



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 | By Dr. Sivan Friedman

THE OCEAN'S IRON CHOICE

In a research centre in Irvine, California, a young ocean scientist named Maya studied a glowing map of the world's oceans. Beside her was Daniel, an ecosystem modeller from California, while their colleague Freja, working with marine researchers in Denmark, joined them online. They were discussing an unusual idea for fighting climate change: adding tiny amounts of iron to the ocean. Iron is an important nutrient for phytoplankton, microscopic organisms that use sunlight and carbon dioxide to grow. In some ocean regions, iron is naturally scarce, limiting phytoplankton growth. Adding iron can therefore trigger large blooms. As phytoplankton absorb CO₂ and some eventually sink, they can carry carbon into deeper water. "It sounds simple," Maya said. "Add iron and let plankton capture carbon." Daniel disagreed. "Ocean currents connect everything. We need to know what happens far beyond the place where the iron is added." That became the central question of their research.

The team built a detailed computer model of the ocean, including currents, nutrients and different plankton groups. They selected ten ocean regions and simulated adding iron for 60 years. In many places, phytoplankton responded strongly and removed more carbon from the atmosphere. But adding more iron did not always produce proportionally greater benefits. At high amounts, each additional dose became less effective. More importantly, the effects did not remain inside the fertilized region. Ocean currents carried iron and nutrients far away. Sometimes this helped because iron reached other iron-poor waters and stimulated additional phytoplankton growth. In other cases, the first bloom consumed so many nutrients that water leaving the fertilized area contained less food for plankton elsewhere. The researchers described this as "nutrient robbing." Maya realized that fertilizing one patch could influence ecosystems hundreds or thousands of kilometres away. The ocean behaved not as separate regions, but as one enormous connected system.

Two regions became especially interesting: the Southern



 | By Dr. Sivan Friedman

Ocean around Antarctica and the equatorial Pacific. Both could support substantial carbon removal, but their ecological consequences were very different. In the Southern Ocean, currents carried some added iron into other iron-limited waters, where it encouraged further phytoplankton growth. This extended the carbon-removal benefit beyond the original fertilized area, while harmful effects on the nitrogen cycle remained relatively limited. The equatorial Pacific was different. Iron also stimulated strong plankton growth there, but these organisms consumed large amounts of other nutrients. As the water moved away, neighbouring regions could become nutrient-poor. The plankton community also shifted toward smaller organisms, potentially changing the marine food web. “We might remove carbon here,” Freja explained, “but create problems somewhere else.” The researchers therefore considered the Southern Ocean a high-benefit, lower-risk region, while the equatorial Pacific offered high carbon-removal potential but carried considerably greater ecological risks.

The team then asked what these changes could mean for marine ecosystems. Smaller phytoplankton in the equatorial Pacific could provide less energy to larger zooplankton and eventually affect fish that depend on them. Fertilization could also expand oxygen-minimum zones, where oxygen levels are already very low, potentially reducing suitable habitat for marine animals. Maya then asked another important question: “What happens when we stop adding iron?” The researchers extended their simulations beyond the fertilization period. Recovery differed greatly between locations. The Southern Ocean recovered relatively well, with its ecosystem moving closer to its original state. The equatorial Pacific recovered more slowly because some added iron remained within ocean circulation and continued influencing nutrients and plankton communities. Ecological effects could therefore continue for decades after fertilization stopped. “Stopping the treatment doesn’t necessarily stop the consequences,” Freja said. This showed that any climate intervention must be judged not only by what happens while it is operating, but also by how easily the ecosystem can recover afterward.

Looking at the final results, Maya understood why ocean iron fertilization could not be judged simply as good or bad. The simulations suggested that it could produce meaningful carbon removal, with the strongest scenarios achieving roughly 0.14–0.70 gigatonnes of CO₂ per year. Yet ecological changes could spread far beyond the fertilized region, and some benefits might not remain per-

oteins and combined into carefully selected mixtures capable of targeting venoms from several species. However, much more research is needed. Most of these experiments were permanent. Measuring the true carbon removal would also be difficult because ocean currents transport nutrients, iron and biological effects across enormous distances. A local increase in phytoplankton would not necessarily reveal the intervention’s total global benefit. The key question was therefore not simply, “Can adding iron help the ocean capture carbon?” The study suggested that it can.

A research team plans to add iron to an iron-poor ocean region to boost phytoplankton growth and remove CO₂ from the atmosphere.

Location A removes more CO₂, but causes nutrient loss nearby, reduces larger zooplankton, and expands low-oxygen zones.

Location B also removes substantial CO₂, but causes less ecological disturbance and the ecosystem recovers better after fertilization stops.

Which location should the team choose to balance effective carbon removal with protection of the marine ecosystem?

- A** Location A, because only the amount of CO₂ removed matters.
- B** Location A, because reducing zooplankton improves carbon storage.
- C** Location B, because it combines substantial carbon removal with lower ecological risk and better recovery.
- D** Either location, because iron fertilization has the same ecological effects everywhere.



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 | By Dr. Priyangana Deb

THE GIANTS THAT LEARNED TO CARRY WATER

Deep in the tropical rainforest of Sabah, Malaysian Borneo, a young forest researcher named Sabah stood beneath a tree so tall that its crown seemed to disappear into the sky. Around her grew giant dipterocarp trees, some towering more than 60 metres above the forest floor. Beside her, Kinabalu prepared ropes and climbing equipment. They wanted to answer an important question: Does becoming extremely tall make a tree more vulnerable to drought? Water absorbed by roots must travel all the way to the highest leaves, sometimes more than 70 metres upward. Gravity makes this journey even harder. Scientists had therefore suspected that very tall trees might struggle to supply their crowns with enough water, especially during drought. This mattered because giant trees store enormous amounts of forest carbon. “If height makes these trees weaker,” Sabah wondered, “what will happen as droughts become more severe?”

Sabah and Kinabalu studied 38 dipterocarp trees from five species, ranging from about 7 to 71 metres tall. Collecting samples was challenging because climbers had to reach branches at different levels of the canopy. The resea-

rchers measured 25 characteristics related to water transport, examining leaves, wood and water-conducting vessels. They also monitored tree growth. Sabah imagined the xylem vessels as microscopic drinking straws carrying water upward. Traditionally, scientists expected that a longer pathway would create greater resistance, making water transport increasingly difficult in taller trees. If this idea was correct, the tallest trees should experience poorer water supply and greater risk of hydraulic failure. Then nature provided a valuable test. A powerful El Niño drought struck Borneo during 2023–2024, allowing the researchers to see whether the tallest trees really suffered more when water became scarce.

When the measurements were examined, Kinabalu noticed something remarkable. The giants did not simply use the same plumbing system as smaller trees—their plumbing changed as they grew taller. Water-conducting vessels became wider toward the base of larger trees, reducing resistance to water movement. At the base of a 70-metre tree, vessels were about 2.2 times wider than those of a 10-metre tree. “The tree is solving its own engineering problem,” Kinabalu said. By widening its vessels, the tree could compensate for the much longer journey from roots to leaves. Gravity still caused leaves high in the canopy to have lower water potential. However, once the researchers accounted for gravity, the relationship between tree height



 | By Dr. Priyanga Deb

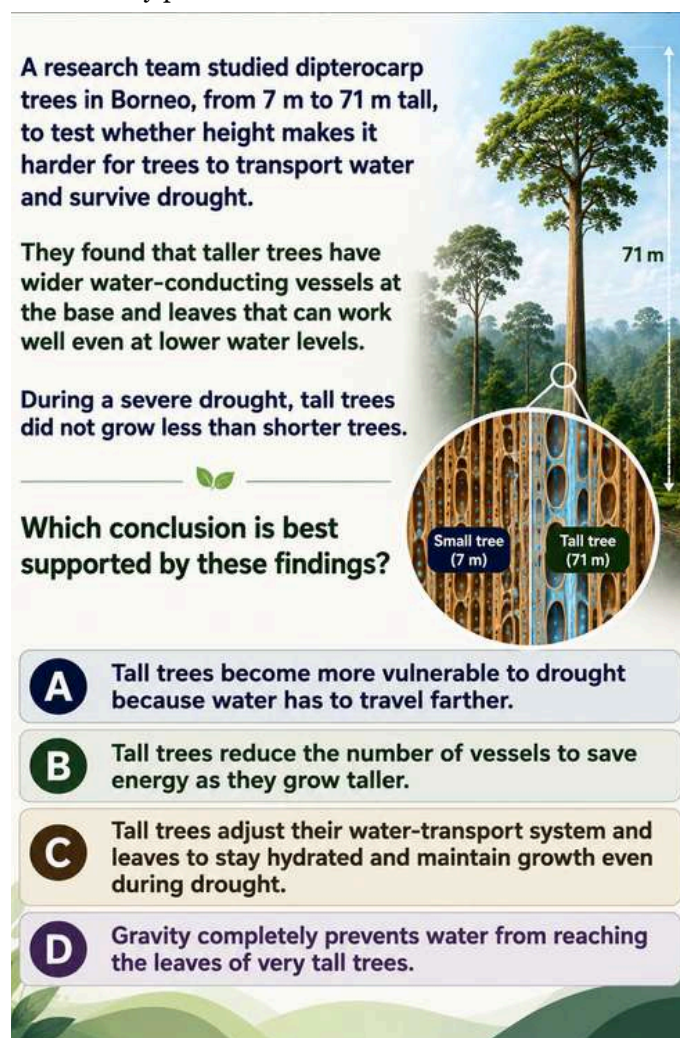
height and leaf water potential disappeared. In other words, becoming taller did not automatically make the tree's water-transport system less effective. Its internal structure adjusted as the tree grew.

Sabah then examined the leaves. Those at the top of giant trees experienced stronger sunlight, warmer air and greater water demand than leaves growing in shade below. Yet they also adjusted their physiology to tolerate these challenging conditions. Their turgor loss point changed, helping cells continue functioning at lower water potentials. The researchers also investigated embolism, which occurs when gas bubbles form inside xylem vessels and block water movement, rather like air blocking a drinking straw. Scientists had expected the tallest trees to be particularly vulnerable to this problem. Surprisingly, resistance to embolism did not consistently decrease with tree height. Instead, differences between upper and lower parts of the canopy appeared important. Exposed branches experienced very different conditions from shaded ones. "Perhaps height alone isn't the main issue," Sabah said. "Maybe the environment surrounding each branch matters just as much." The findings suggested that canopy position and local conditions could strongly influence how trees manage water.

Then came the strongest test: the 2023–2024 El Niño drought. Rainfall dropped about 35% below the long-term average, temperatures increased by around 1.6°C, and the forest became unusually dry. If height made trees hydraulically vulnerable, the tallest giants should have suffered the greatest reductions in growth. But that did not happen. Of 42 trees monitored for growth, 18 grew less during the drought, and they were not specifically the tallest individuals. Growth during recovery was also unrelated to height. Standing beneath the dipterocarps again, Sabah saw the giants differently. Their height was not simply a weakness. As they grew, their vessels widened and their leaves adjusted to difficult conditions. The study does not mean that every giant tree is protected from drought; even taller trees and other forests still need investigation. But it challenges a major assumption: being taller does not automatically mean having a weaker water system. For Sabah and Kinabalu, these forest giants revealed an extraordinary ability to change their internal design as they reach toward the sky.

This adaptation could have consequences far beyond the individual trees. Giant dipterocarps form the backbone of Borneo's rainforests, storing carbon and shaping the enviro-

onment for countless other species. Understanding how they move water and respond to drought may therefore help scientists predict how tropical forests will cope with a warmer, drier future. For Sabah and Kinabalu, the lesson was clear: these giants survive not simply by enduring their height, but by continuously adapting to it. Their success also reminds us that forests are dynamic systems, capable of remarkable biological adjustment. Discovering the limits of this flexibility will be essential for protecting tropical forests and the vital climate, biodiversity and ecological services they provide.



A research team studied dipterocarp trees in Borneo, from 7 m to 71 m tall, to test whether height makes it harder for trees to transport water and survive drought.

They found that taller trees have wider water-conducting vessels at the base and leaves that can work well even at lower water levels.

During a severe drought, tall trees did not grow less than shorter trees.

Which conclusion is best supported by these findings?

- A** Tall trees become more vulnerable to drought because water has to travel farther.
- B** Tall trees reduce the number of vessels to save energy as they grow taller.
- C** Tall trees adjust their water-transport system and leaves to stay hydrated and maintain growth even during drought.
- D** Gravity completely prevents water from reaching the leaves of very tall trees.

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 | By Dr. Priyanka

THE LAST JOURNEY OF A DYING STAR

At the El Sauce Observatory in Chile, a young astronomer named Elena stared at a strange glowing object on her computer screen. She and her colleague Sauce were studying the Helix Nebula, the beautiful remains of a dying star located about 650 light-years from Earth. At its centre was a white dwarf—the hot leftover core of a star that had once been much larger. Before reaching this stage, the star had thrown enormous amounts of gas, dust and other material into space. Elena knew that such material was important because stars produce and redistribute elements that can later become part of new stars and planets. But there was a mystery. Scientists knew that this expelled material must eventually mix with the thin gas between stars, called the interstellar medium, yet they rarely had the chance to watch this final mixing process directly. “We know where the material begins its journey,” Elena told Sauce, “and we know it eventually becomes part of interstellar space. But what happens in between?” The Helix Nebula was about to provide an extraordinary answer.

Elena and Sauce examined the nebula using MOTHRA, a

new telescope system at the Chilean observatory. Instead of relying on one enormous mirror, MOTHRA uses many high-quality telephoto lenses equipped with special filters. When completed, the system will contain 1,140 lenses, allowing astronomers to detect extremely faint structures in space. One evening, Elena carefully studied an image made using light from glowing hydrogen, known as H α emission. The familiar bright centre of the Helix was beautiful, but something much fainter caught her attention. On the eastern outskirts were many delicate curved structures. Some looked like tiny crescents, while others appeared like broken arcs. The team eventually identified at least 22 of them. “It looks like a forest of cosmic bows,” Sauce said. These were bow shocks. A bow shock can form when an object moves rapidly through surrounding material, rather like the curved wave that develops in front of a boat travelling through water. Here, however, the “boats” were pieces of material thrown out by a dying star, and the “water” was the thin gas filling interstellar space.

The team investigated how quickly these pieces were moving. The Helix Nebula itself travels relative to the surrounding interstellar gas at about 45 kilometres per second. On its eastern side, the old stellar material is expanding in a direction that creates particularly strong co-



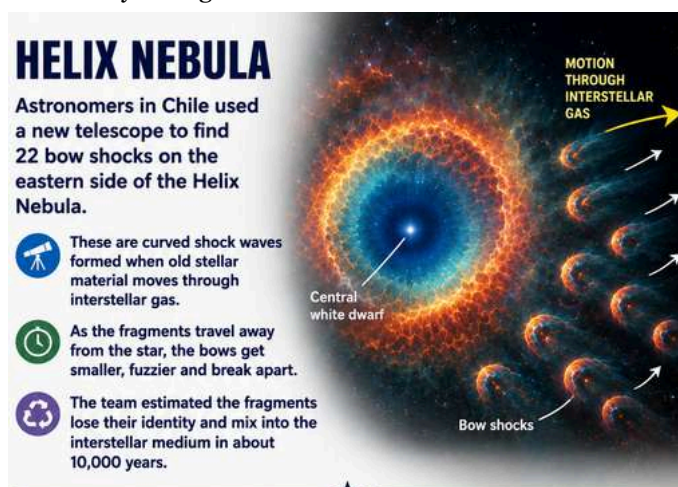
 | By Dr. Priyanka

llisions with the surrounding gas. By examining the light produced by these shocks, the researchers estimated shock speeds of roughly 80–90 kilometres per second. The stellar fragments themselves appeared to be expanding outward at around 35–45 kilometres per second. Even more interesting was their age. Their speed and distance from the centre suggested that they had been travelling for approximately 20,000–30,000 years. That meant the material was probably expelled before the main planetary nebula appeared. It likely came from an earlier period when the dying star was an asymptotic giant branch, or AGB, star, losing its outer layers through powerful winds and outflows. “So these arcs are telling us a story from before the Helix looked the way it does today,” Elena said. They were seeing ancient stellar material still completing its journey into interstellar space.

Then Sauce noticed an even more fascinating pattern. The bow shocks did not all look alike. Those closer to the central white dwarf were large, thin and clearly defined. Farther away, however, they became smaller, broader, fuzzier and more broken apart. Across the region studied, their characteristic size decreased by roughly 100 times. It was almost as though the researchers were looking at different stages in the lifetime of the same type of object. A dense fragment begins its outward journey relatively intact. As it races through interstellar gas, a bow shock forms in front of it. Repeated interaction with the surrounding medium gradually strips material away. The fragment becomes smaller and less organized, while some of its gas mixes into its surroundings. Eventually, the once-coherent piece loses its identity completely. Elena realized that the beautiful arcs were therefore not simply decorations around the Helix Nebula. They were signs of destruction and recycling happening at the same time. The shocks showed where the fragments were, while also revealing how interaction with the surrounding gas was gradually tearing those fragments apart.

Using the way the bows changed with distance, the researchers estimated that these coherent fragments are disrupted on a timescale of roughly 10,000 years. Elena looked again at the glowing Helix and thought about what that number meant. A star may live for billions of years, but once pieces of its expelled material are exposed to the surrounding interstellar medium, they can lose their separate identity relatively quickly on astronomical timescales. Gas, dust and elements once held inside a star are gradually returned to the galaxy. One day, some of that recycled material may become incorporated into another cloud of gas and contribute to a new generation of stars or

planets. The 22 bow shocks had therefore revealed much more than a collection of unusual arcs. They provided a rare view of one of nature's great recycling processes. Sauce smiled at Elena. “We began by looking at the death of a star,” he said, “but what we are really seeing is material preparing for another beginning.” Around the fading Helix, ancient pieces of a dying star were slowly disappearing into interstellar space, returning their material to the galaxy from which future worlds could eventually emerge.



HELIX NEBULA

Astronomers in Chile used a new telescope to find 22 bow shocks on the eastern side of the Helix Nebula.

- These are curved shock waves formed when old stellar material moves through interstellar gas.
- As the fragments travel away from the star, the bows get smaller, fuzzier and break apart.
- The team estimated the fragments lose their identity and mix into the interstellar medium in about 10,000 years.

WHAT DO THE BOW SHOCKS IN THE HELIX NEBULA MOST DIRECTLY REVEAL ABOUT THE FATE OF MATERIAL EJECTED BY DYING STARS?

- A** The fragments speed up as they move away from the star due to gravitational slingshot effects.
- B** The fragments remain stable for millions of years before mixing into the interstellar medium.
- C** The fragments interact with interstellar gas, are gradually stripped apart, and mix into it within about 10,000 years.
- D** The bow shocks are caused by new stars forming inside the Helix Nebula.

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 | By Dr. Dhanashree Mundhe

THE VIRUSES WITHIN: WHAT COVID-19 CAN AWAKEN

When Emily arrived at a hospital in the United States with COVID-19, everyone naturally focused on SARS-CoV-2. She had fever, difficulty breathing and extreme tiredness. But SARS-CoV-2 was not necessarily the only virus inside her body. Like most people, Emily had encountered several viruses during her lifetime. Some, including Epstein–Barr virus (EBV) and cytomegalovirus (CMV), can remain quietly inside cells for years. Others carry herpes simplex virus or members of the Anelloviridae family. Usually, the immune system keeps these viruses under control, and people may never know they are there. But serious illness can disturb this balance. Scientists therefore wondered whether COVID-19 could allow these sleeping viruses to reactivate. More importantly, could this hidden viral activity be associated with severe COVID-19 or health problems that continue long after the original infection? Understanding this could reveal that COVID-19 affects not just one virus, but an entire hidden viral community within us.

To investigate, imagine Daniel, a scientist working with a large American medical team. Daniel and his colleagues st-

udied 1,154 people hospitalized with COVID-19 across 20 hospitals in the United States. Some recovered relatively quickly, while others, like Michael, became critically ill. Researchers collected samples during hospitalization and followed participants for as long as a year. They examined blood immune cells, nasal samples and respiratory samples from some ventilated patients. Rather than simply determining whether patients had encountered other viruses previously, the scientists searched for viral transcripts, which provided evidence that viruses were transcriptionally active. They combined these findings with measurements of immune cells, inflammatory molecules, proteins and metabolites. This allowed them to examine several processes together: SARS-CoV-2 infection, immune responses, the activity of other viruses and changes in each patient's health. By following patients over time, they could also see whether different viruses became active at particular stages of illness and recovery.

What Daniel's team discovered was striking. Nearly half of the participants showed evidence of at least one reactivated virus during acute COVID-19. But different viruses became active at different times. EBV was commonly detected around hospital admission and then became less frequent. HSV1 and CMV tended to appear later, while Anelloviridae followed another pattern. Viral reactivation was also associated with disease severity. EBV, CMV, HSV1



 | By **Dr. Dhanashree Mundhe**

and Anelloviridae were linked with more serious COVID-19. Traditionally, viral reactivation is often associated with people whose immune systems are strongly suppressed. However, these events also occurred in patients who were not chronically immunosuppressed. Severe illness, inflammation and disruption of normal immune control might therefore create conditions that allow previously controlled viruses to awaken. The findings suggested that severe COVID-19 can involve a much more complicated viral environment than SARS-CoV-2 alone. The timing of these awakenings also suggested that each virus may respond differently to the changing conditions inside a sick patient's body.

Another patient, Sarah, helped Daniel think about what might be happening inside the immune system. Different reactivated viruses were associated with different immune changes. EBV was linked with changes involving B cells, while CMV was associated with changes in several T-cell populations. Researchers also found relationships with inflammatory signalling molecules, metabolism and gene activity. But this created an important question: were the awakened viruses making COVID-19 worse, or was severe COVID-19 waking the viruses? The study could not prove which came first. Severe SARS-CoV-2 infection might create enough inflammation and physiological stress to reactivate dormant viruses. Alternatively, once active, these viruses might add further immune stimulation. Both processes could potentially occur together. Therefore, the researchers did not conclude that EBV, CMV or another virus directly causes severe COVID-19. Instead, the findings revealed an important relationship between SARS-CoV-2, resident viruses and the body's immune response. Future experiments will be needed to determine whether controlling particular reactivated viruses could actually improve patient outcomes.

Months later, another patient, Olivia, had recovered from her initial infection but still experienced persistent physical problems. Her experience raised the final question: could viral reactivation also be connected with long COVID? During follow-up, researchers continued detecting some viral activity. Particularly interesting was Anelloviridae, a widespread group of viruses carried by many healthy people. Anelloviridae transcripts were more common in a group experiencing persistent physical difficulties, even after researchers considered factors such as age, immunosuppressive medication and initial COVID-19 severity. This does not prove that Anelloviridae causes long COVID. Its activity could instead be a sign that the immune system remains distur-

bed after infection. Interestingly, acute EBV activity was not higher among people who later developed long COVID. The study therefore ends with an important mystery. COVID-19 may involve more than fighting one new virus; severe infection can disturb viruses already living quietly within us. Understanding when these viruses awaken, why they reactivate and whether they influence recovery could eventually help scientists identify people at greater risk and develop better ways to understand both severe COVID-19 and long COVID.

In this quiet transformation, destruction becomes creation. The Helix Nebula reminds us that stellar death is not truly an ending, but part of the galaxy's continuing cycle of renewal.

A 58-year-old man is hospitalized with severe COVID-19. He does not take immunosuppressive medicines and has no known immune disorder.

During hospitalization, tests detect transcripts of Epstein-Barr virus (EBV) in his blood. Later, cytomegalovirus (CMV) transcripts appear, and both are associated with high inflammatory markers and severe disease.

Which explanation best matches the findings from large studies on virus reactivation in COVID-19?

- A** Viral reactivation in COVID-19 occurs only in people with weakened immune systems.
- B** Reactivated viruses like EBV and CMV can be detected during acute COVID-19 even in immunocompetent individuals.
- C** Severe COVID-19 can be accompanied by reactivation of multiple chronic viruses, and this reactivation is associated with disease severity and inflammation.
- D** Reactivated viruses are always the direct cause of severe COVID-19.

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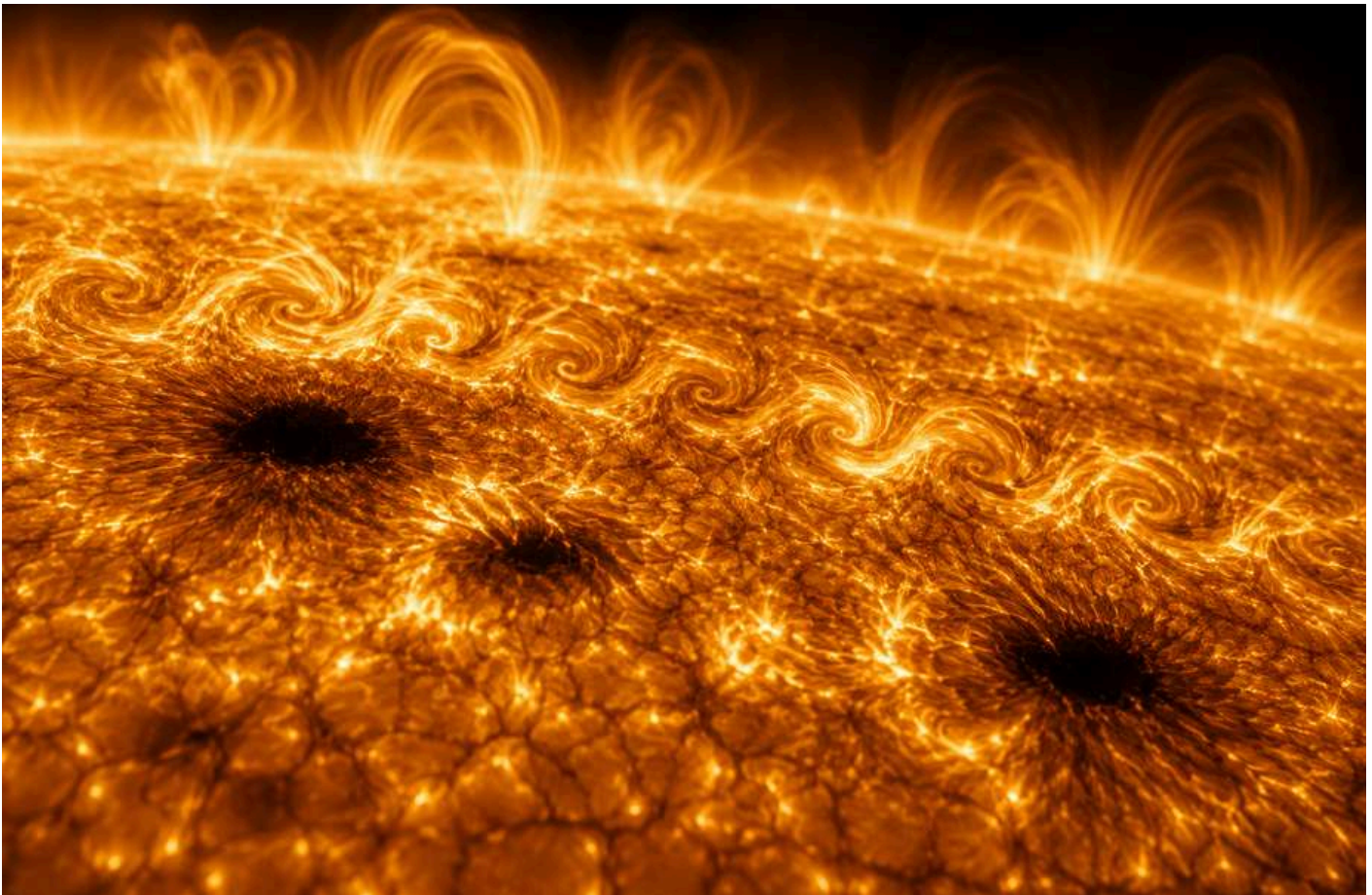
 | By **Dr. Sudha Shankar**

HIDDEN TURBULENCE ON THE SUN: HOW TINY VORTICES SHAPE SOLAR PLASMA

High above the clouds on the Hawaiian island of Maui, a young solar scientist named Maui entered the control room of the Daniel K. Inouye Solar Telescope. Beside her was her colleague Haleakala, named after the volcano where the telescope stands. They were studying the Sun, but not its enormous flares or spectacular eruptions. Instead, they were interested in something much smaller the constantly moving photosphere, the visible surface of the Sun. This region is made of extremely hot plasma threaded by magnetic fields. Scientists had long predicted that tiny whirlpools called Kelvin–Helmholtz instabilities (KHIs) could form where plasma flows at different speeds along magnetic boundaries. Similar rolling waves occur when two layers of air or water move past each other at different speeds. KHIs had been observed elsewhere in the solar atmosphere, but structures this small had remained beyond the reach of previous telescopes. “Maybe they have always been there,”

Maui wondered, “and we simply couldn’t see them.” That changed when Maui and Haleakala examined remarkably detailed observations from DKIST, the world’s first 4-metre-class solar telescope. They studied a magnetically active region near a sunspot at a wavelength of 416 nanometres. DKIST could distinguish structures only about 19 kilometres across on the Sun, revealing details previously blurred together. Instead of smooth magnetic boundaries, Maui saw tiny curls, ripples and narrow streaks. The team examined 47 vortices and found that the typical distance between neighbouring vortices was about 65 kilometres, with measured scales ranging from approximately 25 to 170 kilometres. These structures also travelled rapidly along magnetic boundaries, with apparent speeds of around 0.67 to 3 kilometres per second. The observations revealed that the photosphere was much more finely structured than scientists could previously see. Something important appeared to be happening where moving plasma encountered strong magnetic regions.

However, seeing curling structures was not enough to prove that they were Kelvin–Helmholtz instabilities. Haleakala therefore turned to a sophisticated computer model called MURaM, which simulates plasma and magn-



 | By **Dr. Sudha Shankar**

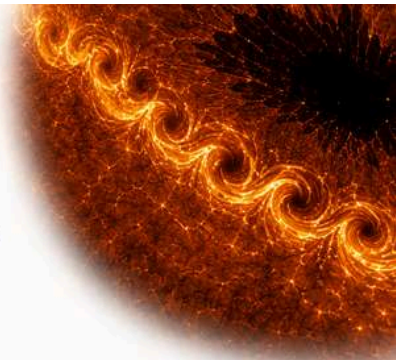
etic fields in the solar atmosphere. The simulations produced curls and striations remarkably similar to those observed by DKIST. More importantly, they revealed what was happening to the plasma. Strong horizontal velocity shear developed along the edges of magnetic regions, meaning that neighbouring plasma was moving at different speeds. Haleakala described it simply: “Imagine two streams flowing beside each other at different speeds. Their boundary begins to ripple, and those ripples eventually roll into vortices.” The magnetic field was mainly vertical while the shear flow was horizontal, meaning the field could not completely suppress the instability. The close agreement between telescope observations, simulations and theoretical predictions provided strong evidence that the tiny structures were indeed Kelvin–Helmholtz instabilities.

The discovery became more interesting when Maui examined what happened after the vortices formed. They quickly became complicated. Some merged, while smaller vortices appeared around larger ones, eventually producing turbulence. This turbulent motion allowed plasma from weakly magnetized regions to mix with strongly magnetized plasma, potentially transporting mass, energy, momentum and magnetic flux across the solar surface. The simulations also showed that these vortices were not limited to the visible photosphere. They extended vertically for hundreds of kilometres and continued beneath the visible surface. In deeper layers, the instability became stronger and could fragment magnetic regions into smaller structures. A magnetic feature that appeared to be one continuous object at the surface could therefore consist of several magnetic strands underneath. The researchers also found that KHIs could explain fine dark striations previously observed around magnetic features. These streaks may therefore be visible signatures of magnetic boundaries continuously being distorted by turbulent plasma motions.

Standing in the observatory, Maui realized that these tiny vortices could have consequences far beyond their small size. Magnetic structures rooted in the photosphere extend upward into the solar atmosphere and contribute to features such as spicules, prominences and coronal loops. If KHIs continually disturb magnetic fields at their roots, their effects could influence higher layers of the Sun. The vortices may also contribute to magnetic flux braiding, where magnetic fieldlines become twisted and interwoven. These tangled fields can store energy that may later be released through magnetic reconnection. Such processes are important for understanding how energy moves through

gh magnetic reconnection. Such processes are important for understanding how energy moves through the solar atmosphere and may contribute to the long-standing mystery of why the Sun’s outer corona is extraordinarily hot. The study does not claim that KHIs alone explain coronal heating, but it reveals a previously unresolved and widespread source of plasma mixing and magnetic disturbance. Looking at the tiny curls captured by DKIST, Maui understood their importance: structures only tens of kilometres across could help shape processes extending thousands of kilometres through the solar atmosphere. These tiny instabilities show that even the smallest motions on the Sun can influence its vast magnetic environment, offering scientists a new window into how solar energy is transported and transformed.

A solar scientist observes the edge of a magnetic feature on the Sun using a very high-resolution telescope. She sees many small, rolling whirlpool-like structures along the boundary.



Computer simulations show that these structures form when fast-moving plasma flows past a magnetic region with slower plasma, creating velocity shear.

Which phenomenon are the scientist most likely observing?

- A** Magnetic reconnection between opposite magnetic fields.
- B** Kelvin–Helmholtz instabilities at the magnetic boundary.
- C** Large-scale solar flares releasing energy into space.
- D** Pressure-driven shock waves from the Sun’s core.



REFERENCE

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 | By Dr. Sourav Kumar

HOW SOCIAL INEQUALITY SHAPES OUR BIOLOGICAL AGE

In Berlin, Germany, a young health researcher named Lina was fascinated by a simple question: why can two people of exactly the same age seem to age so differently? She imagined two 50-year-old neighbours. One had spent much of life with stable housing, good education, financial security and easy access to resources. The other had experienced financial hardship, uncertain employment and stressful living conditions. Both had celebrated the same number of birthdays, but had their bodies aged at the same speed? Scientists have developed tools called epigenetic clocks, which examine patterns of DNA methylation—small chemical marks associated with DNA to provide clues about biological ageing. Working with colleagues connected with Berlin and New York, Lina wondered whether these clocks could reveal something remarkable: could the social conditions in which people live leave measurable marks on biological ageing?

To investigate, Lina and her colleague Brooklyn gathered evidence from research conducted around the world. Instead of relying on one experiment, they brought together 140 studies involving 65,919 people, producing more than a thousand statistical comparisons. Participants came from 79 cohorts across 23 countries and ranged from newborn babies to adults aged 86. Researchers assessed socioeconomic status using measures such as income, wealth, education, occupation and neighbourhood conditions. They then compared these circumstances with three generations of epigenetic clocks. Brooklyn described them as increasingly sophisticated watches. First-generation clocks were mainly designed to estimate chronological age from DNA methylation. Second-generation clocks incorporated biological information related to health and mortality. Newer third-generation clocks were designed to measure something particularly important—the pace at which the body is ageing. Lina wanted to know which clocks could best detect the biological signatures associated with social disadvantage. When the results were combined, a clear pattern emerged. People with lower socioeconomic status tended to show ol-



 | By **Dr. Sourav Kumar**

der biological age or faster biological ageing than those with higher socioeconomic status. However, the strength of the relationship depended on the clock being used. First-generation clocks showed relatively weak associations, second-generation clocks showed stronger relationships, and third-generation clocks showed the strongest overall associations. Measures including GrimAge, DunedinPoAm and DunedinPACE were particularly sensitive to socioeconomic differences. “The newer clocks are detecting something the older clocks were not designed to capture,” Brooklyn explained. Importantly, these patterns could begin early in life. Children growing up in lower socioeconomic conditions tended to show faster biological ageing on newer clocks. Adults who had experienced socioeconomic disadvantage during childhood also showed signs of accelerated biological ageing decades later. This suggested that circumstances experienced early in life may remain connected with biological ageing long into adulthood.

Another researcher in their imagined team, Harlem, examined findings concerning race and ethnicity. Lina knew these results required careful interpretation because all studies included in these comparisons came from the United States. Black participants tended to show faster biological ageing than white participants when newer epigenetic clocks were used, with the largest differences appearing in third-generation measures. First-generation clocks showed little overall difference. Comparisons between Latinx and white participants followed a similar pattern, with DunedinPACE showing particularly clear differences. But Harlem emphasized an essential point: these results did not mean that racial identity itself biologically causes faster ageing. Race and ethnicity exist within social environments shaped by differences in economic opportunities, neighbourhood conditions, environmental exposures, discrimination and access to resources. The researchers therefore viewed these findings through the broader framework of social determinants of health. Epigenetic differences may provide a way to study how unequal social experiences become associated with biological processes rather than representing fixed biological differences between racial groups.

Back in Berlin, Lina realized that the study revealed a much larger story about ageing. Our biological clocks may respond not only to the number of years we live but also to the conditions under which those years are lived. The meta-analysis could not prove that social disadvantage directly causes accelerated epigenetic ageing or identify one pathway responsible for the association. The research-

ers also acknowledged important limitations: many studies came from wealthy countries, particularly the United States, making the global evidence uneven.

Nevertheless, across tens of thousands of participants, a consistent message emerged: social disadvantage was associated with faster biological ageing, and newer epigenetic clocks detected this relationship more clearly than older clocks. Lina imagined these tools eventually helping scientists study whether improving childhood conditions, neighbourhoods or access to resources might also be accompanied by healthier biological ageing.



Researchers are studying how social conditions early in life may influence biological ageing. They measure DNA methylation using different epigenetic clocks in children growing up in families with lower versus higher socioeconomic status (SES).

Which outcome would best support their hypothesis that social disadvantage leads to faster biological ageing?

- A** Children from lower-SES families show higher epigenetic age acceleration than those from higher-SES families, especially on newer clocks.
- B** Children from lower-SES families show no difference in epigenetic age acceleration across all clocks.
- C** Children from higher-SES families show faster epigenetic ageing than those from lower-SES families.
- D** All clocks show the same strong association with chronological age but not with SES.

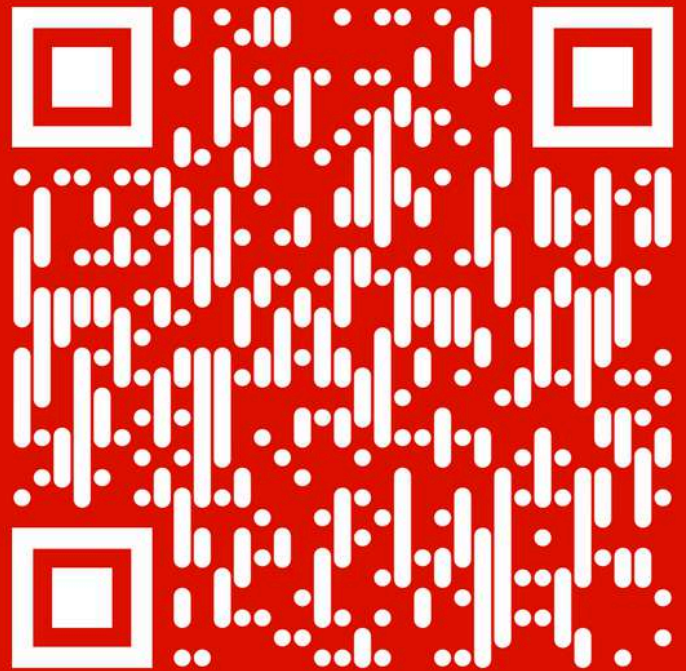
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 Max Planck Research Group Biosocial – Biology, Social Disparities and Development, Max Planck Institute for Human Development, Berlin, Germany.

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Engineering Peptide Nanofibrils to Outsmart Superbugs-Toward Targeted Antibacterial Strategies for Drug-Resistant Infections

OUTLOOK

Antibiotic resistance is making some bacterial infections increasingly difficult to treat. One important example is MRSA, a type of *Staphylococcus aureus* bacterium that is resistant to several commonly used antibiotics. The problem becomes even more difficult when these bacteria form biofilms protective communities that help them survive treatment. Researchers are therefore exploring new ways to target harmful bacteria more precisely. In this Science Desk conversation, Prof. Yu-Chie Chen discusses how self-assembling peptides small protein-like molecules that can organize themselves into tiny structures can recognize and attack specific bacteria, and what this approach could mean for the future of drug-resistant infection management.



Prof. Yu-Chie Chen

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AREAS OF EXPERTISE

Antimicrobial strategies • bacterial detection • mass spectrometry • nanotechnology

and then concentrates its antibacterial activity directly on the bacterial surface? We were particularly interested in *S. aureus* because we had identified a short peptide sequence, DVFLG, with the ability to preferentially recognize this bacterium. We therefore explored whether this targeting motif could be engineered into an antibacterial peptide while retaining its recognition capability. This led us to combine bacterial targeting with another powerful molecular phenomenon, i.e., self-assembly. By carefully modifying the peptide sequence, we developed D4W, a peptide capable of both recognizing *S. aureus* and assembling into fibril-like nanostructures. Our goal was to use molecular recognition to bring the antibacterial peptide to its target and self-assembly to enhance its local antibacterial effect. This combination ultimately provided the foundation for our targeted peptide nanofibril strategy.

Q What inspired your team to explore self-assembling peptide nanofibrils as a new strategy to combat drug-resistant bacteria?

A The rapid spread of antibiotic-resistant bacteria has made many infections increasingly difficult to treat. Methicillin-resistant *Staphylococcus aureus* (MRSA), for example, can cause persistent infections in wounds, implanted medical devices, and hospital settings. These challenges motivated us to explore antibacterial strategies that work differently from conventional antibiotics. Our research began with a simple question: instead of developing another agent that broadly attacks bacteria, could we design a peptide that first recognizes a particular bacterium a-

Q Many readers are familiar with antibiotics, but not with antimicrobial peptides. What are they, and why are they considered promising alternatives to conventional antibiotics?

A Antimicrobial peptides, commonly called AMPs, are short chains of amino acids that can kill or inhibit microorganisms. Many occur naturally as part of the innate immune systems of humans, animals, plants, and other organisms, where they provide a first line of defense against microbial infection. Conventional antibiotics often act by inhibiting a specific bacterial enzyme or biochemical pathway. Bacteria can eventually develop resistance through genetic mutations, modification of drug targets, production

of antibiotic-degrading enzymes, or other mechanisms. Many antimicrobial peptides operate differently. They can interact directly with bacterial surfaces and membranes, causing rapid structural damage that is more difficult for bacteria to overcome through a single genetic change. Peptides also offer an important advantage from an engineering perspective. Because their amino acid sequences can be systematically modified, we can tune properties such as charge, hydrophobicity, bacterial recognition, self-assembly, and biocompatibility. This makes peptides attractive molecular building blocks for developing new antibacterial agents. However, antimicrobial peptides also face challenges, including limited stability, potential toxicity, and manufacturing cost. The objective should therefore not simply be to discover more peptides, but to engineer them rationally so that they become more selective, stable, and effective.

Q *Your study introduces self-assembling peptide nanofibrils rather than free peptides. How does self-assembly improve their antibacterial performance and make them more effective against MRSA?*

A Self-assembly is a fascinating process in which individual molecules spontaneously organize into larger, ordered structures through non-covalent interactions. Nature uses this principle extensively to construct complex biological structures. In our study, we incorporated tryptophan residues into a *Staphylococcus*-targeting peptide to promote both antibacterial activity and self-assembly. The resulting D4W peptide can form fibril-like aggregates under appropriate conditions. The key concept is that self-assembly changes how the peptide interacts with bacteria. Instead of relying only on individual peptide molecules, assembly produces nanoscale structures that can maintain strong and prolonged contact with the bacterial surface. When combined with the targeting ability of the peptide, this creates a high local concentration of antibacterial molecules where they are needed. Our experimental observations indicated that these fibril-like peptide structures preferentially accumulated around *S. aureus* and MRSA cells and produced strong antibacterial activity. This suggests a synergistic mechanism: molecular recognition helps localize the peptide to the bacterial surface, while self-assembly strengthens and extends the interaction. We therefore view self-assem-

bly not simply as a structural feature, but as a functional component of antibacterial peptide design.

Q *One remarkable aspect of your work is its ability to inhibit bacterial biofilms. Why are biofilms such a major obstacle in treating infections, and how do your peptide nanofibrils help overcome this challenge?*

A Biofilms are organized communities of bacteria surrounded by a protective extracellular matrix. They commonly develop on wounds, catheters, artificial joints, and other implanted medical devices. Once established, biofilms can be extremely difficult to eradicate. The biofilm matrix acts as a physical and chemical barrier that can reduce the penetration and effectiveness of antimicrobial agents. Bacteria within biofilms can also enter physiological states in which they grow more slowly and become less susceptible to antibiotics. Consequently, biofilm-associated infections may persist despite conventional treatment and can sometimes require removal of an infected medical device. Our peptide strategy is particularly interesting in this context because D4W combines recognition of *Staphylococcus* with antibacterial activity and supramolecular assembly. By preferentially associating with the bacterial surface and forming peptide aggregates, D4W can interfere with bacterial growth and biofilm development at relatively low concentrations. Preventing biofilm formation is especially important. Once a mature biofilm becomes established, treatment becomes much more difficult. Therefore, targeted peptide nanomaterials may eventually be useful not only for treating infections but also for preventing bacterial colonization of susceptible surfaces.

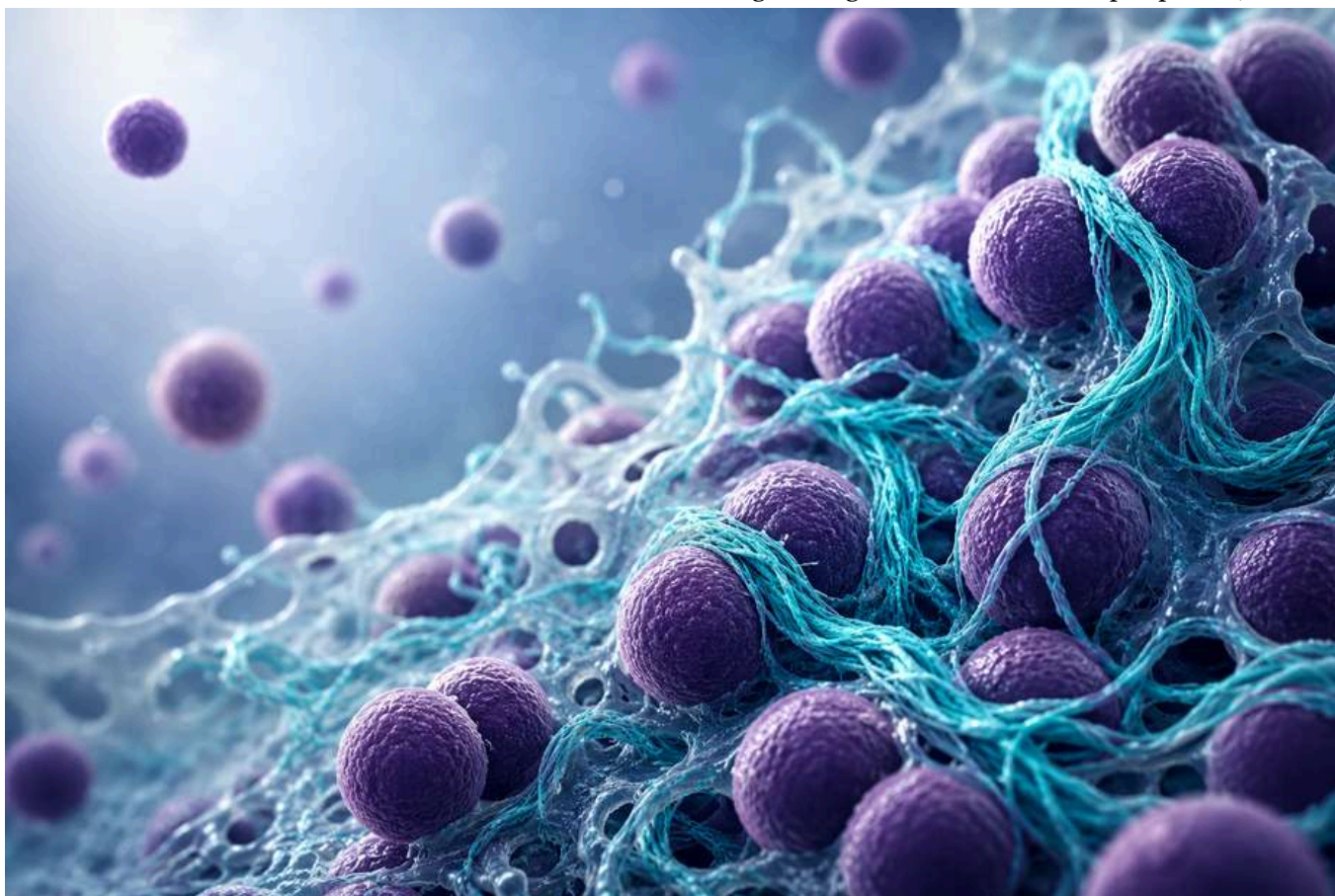
Q *A major concern with new antibacterial agents is their safety. How did your team ensure that these peptide nanofibrils selectively target bacteria while minimizing harm to healthy mammalian cells?*

A Antibacterial potency alone is not sufficient for developing a useful therapeutic agent. Selectivity and biocompatibility are equally important. Our design strategy takes advantage of differences between bacterial and mammalian cell surfaces. The DVFLG sequence provides preferential recognition toward *Staphylococcus*, while careful control of the peptide composition helps balance antibacterial activity with compatibility toward mammalian cells. We evaluated

this experimentally using several complementary approaches. Hemolysis assays were used to determine whether the peptide damaged red blood cells, while mammalian-cell compatibility was assessed to examine potential cytotoxicity. We also extended the evaluation beyond simple cell-based assays by examining antibacterial performance in biologically relevant models. The results showed that the peptide maintained strong antibacterial activity while exhibiting low hemolytic activity and favorable biocompatibility under the tested conditions. These findings are encouraging, although considerably more extensive toxicological and pharmacological evaluation should be required before any clinical application could be considered. For us, this balance between bacterial targeting and host compatibility is one of the most important principles for future antimicrobial peptide engineering.

Q *Your study demonstrates promising results in laboratory, ex vivo, and in vivo models. What are the next scientific and translational steps required before this technology could be considered for clinical applications?*

A There remains a considerable distance between demonstrating an effective antibacterial material in experimental models and developing a clinically approved therapy. One important next step is to understand the molecular mechanism of bacterial recognition more precisely. We know that the targeting sequence preferentially interacts with *Staphylococcus*, but identifying the specific bacterial surface components responsible for this recognition could enable us to design even more selective and effective peptides. In addition, identifying the specific targeting sites of our peptide on *S. aureus* could provide deeper insights into its antibacterial mechanism. This is an area where computational approaches are becoming increasingly valuable. Artificial intelligence (AI)-assisted structural prediction, molecular docking, and molecular dynamics simulations can help us investigate peptide–bacteria interactions at the molecular level. Combined with experimental validation, these approaches may allow researchers to move from empirical peptide screening toward more rational, computationally guided antimicrobial peptide engineering. From a translational perspective, future



studies must also evaluate peptide stability in complex biological environments, pharmacokinetics, long-term toxicity, immune responses, manufacturing scalability, and efficacy in more advanced animal infection models. The optimal mode of delivery will also depend on the intended application. For example, local delivery through wound dressings or antimicrobial coatings may present different opportunities and challenges from systemic administration. We therefore regard the current work as an important proof of concept rather than an endpoint. The ultimate goal is to understand the relationships among molecular recognition, peptide sequence, self-assembly, antibacterial activity, and biological safety well enough to design future antimicrobial materials predictively rather than largely through trial and error.

Q *Looking ahead, how do you envision self-assembling peptide nanomaterials shaping the future of antimicrobial therapies and helping society tackle the growing threat of antibiotic resistance?*

A We believe the future of antimicrobial peptide research will involve a transition from simply searching for molecules with stronger antibacterial activity toward designing multifunctional systems with precisely controlled biological behaviours. Self-assembling peptides are particularly attractive because their amino acid sequences encode both molecular function and material properties. A single peptide can potentially be engineered to recognize a pathogen, assemble into a functional nanostructure, disrupt bacterial viability, inhibit biofilm formation, and minimize interactions with healthy cells. At the same time, advances in AI and computational biology are changing how these molecules can be discovered. In the future, AI may help generate promising peptide sequences, structural prediction can reveal their three-dimensional conformations, molecular docking can identify potential bacterial targets, and molecular dynamics simulations can evaluate the stability of peptide–target and peptide–membrane interactions. Experimental studies can then validate the most promising candidates and provide data for further computational optimization. We envision this integration of molecular recognition, computational modelling, supramolecular self-assembly, and experimental microbiology as an important direction toward precision antibacterial therapy. Such approach-

es are unlikely to replace conventional antibiotics entirely. Instead, they may provide complementary tools for situations in which antibiotic resistance, biofilm formation, or the need for pathogen-selective treatment makes conventional therapy insufficient. Potential applications could include infected wounds, localized treatment of biofilm-associated infections, and combination therapies with existing antibiotics. For decades, antimicrobial peptide research has largely focused on discovering molecules with greater bactericidal activity. The next stage may be defined by something broader: understanding how peptides recognize pathogens, predicting their behaviour computationally, and programming their supramolecular organization to achieve specific biological functions. By bringing these capabilities together, we may eventually transform antimicrobial peptides from naturally inspired molecules into rationally engineered precision therapeutics for combating drug-resistant infections.



ABOUT THE AUTHORS

Prof. Yu-Chie Chen is a Professor in the Department of Applied Chemistry at National Yang Ming Chiao Tung University (NYCU), Taiwan. Her research combines analytical chemistry, mass spectrometry, and nanotechnology to address biological and medical challenges. Her work includes developing new methods for detecting and targeting harmful bacteria, particularly antibiotic-resistant pathogens. Her research also explores how peptides and advanced nanomaterials can be designed for more precise antibacterial applications, contributing to new strategies for fighting difficult-to-treat infections.

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Engineering Gold Nanoparticles for Smarter Blood Typing

OUTLOOK

Blood transfusions save millions of lives, but finding the right blood match involves more than the familiar A, B, AB and O blood groups. RhD is another important blood-group marker, particularly for patients who require repeated transfusions, as mismatches can trigger unwanted immune reactions. Researchers are therefore exploring simpler ways to identify blood-group genes accurately. In this Science Desk conversation, Dr. Parikshit Moitra and his research team discusses how a programmable gold nanoparticle NanoNet can detect the RHD gene without PCR amplification, and what this approach could mean for the future of safer and more accessible blood-group testing.



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AREAS OF EXPERTISE

Chemical Biology • Biomedical Engineering • Biosensors • Nanotherapeutics • Biomedical Imaging



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AREAS OF EXPERTISE

Transfusion Medicine

Q *Blood transfusions save millions of lives every year, yet ensuring the right blood match can still be challenging. What inspired your team to develop a new nanotechnology-based approach for RhD blood typing, and what clinical problem were you hoping to solve?*

A Indeed, blood transfusion saves millions of lives if an accurate group of blood is provided. While most people are familiar with the ABO blood groups, the RhD blood group is equally important. An incorrect RhD match can trigger an immune response in patients, complicating future transfusions. Our motivation was to explore whether we could utilize nanotechnology for a simple and efficient way to detect the RhD gene. The plan was simple: designing a Gold-oligo nanonet assembly to detect the RhD gene directly without fluorescence and PCR amplification. Although this technology is in a proof-of-concept stage, we have tried to build the foundation for a faster and more accurate platform for specific blood typing. We are working in the direction of modifying the design to adapt to more suitable point-of-care diagnostics.

Q *Many readers may not be familiar with RhD blood typing. Could you explain why accurately identifying RhD blood groups is so important, particularly for patients who require repeated blood transfusions?*

A Yes, in terms of blood grouping, ABO is much more common, but RhD is just as important as the other for safe blood transfusion. If a RhD-negative patient receives RhD-positive blood, the recipient will recognize the donor RBCs as a foreign entity and will start producing antibodies against them. This process, known as alloimmunization, will create serious concern for future transfusions and pregnancies. The problem is not restricted to RhD alone but extends to other minor Rh system antigens such as C, c, E, and e. This process is highly important for patients with thalassemia, sickle cell disease, and bone marrow failure syndromes, where blood transfusion is almost a regular necessity throughout life.

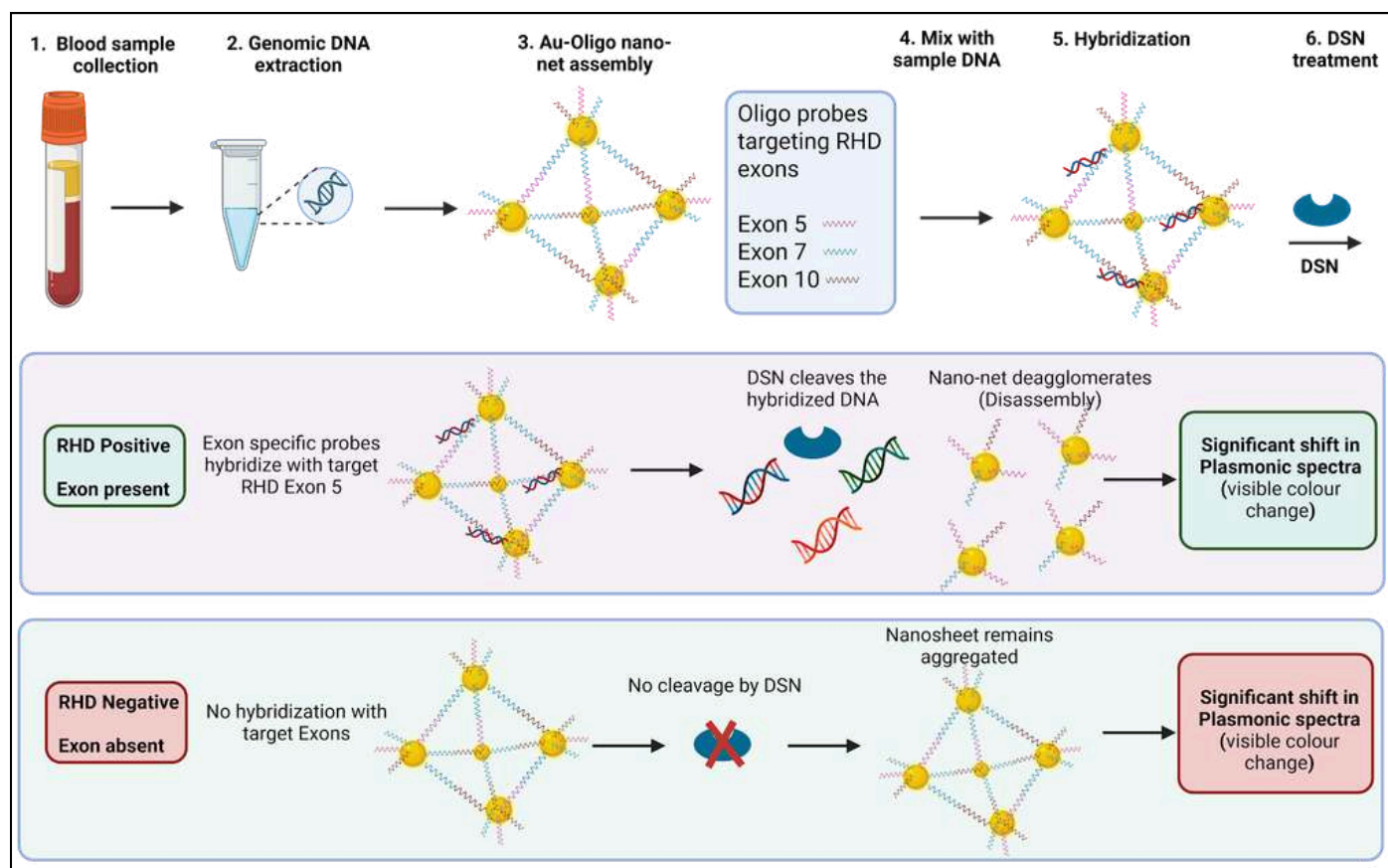


Figure 1. Schematic representation of the gold nanoparticle–oligonucleotide NanoNet platform for differentiating RHD genotypes.

That is why precise RhD typing is very crucial. With the long-term goal of making molecular blood typing more dependable and accessible, our research attempts to help achieve this goal by creating a straightforward nanotechnology-based technique for identifying the entire gamut of Rh genotypes with better specificity.

Q Your study introduces a unique "gold NanoNet" platform. In simple terms, how does this technology work, and what makes it different from conventional blood typing methods?

A Imagine our "Gold NanoNet" as a small fishing net composed of gold nanoparticles (AuNPs) as the beads and complementary oligonucleotides as the thread to connect the beads. We have introduced this supramolecular AuNP-oligonucleotide nanonet as a new plasmonic diagnostic tool for genotyping the RhD blood group. We aimed to detect the RhD gene directly from genomic DNA instead of using conventional serological typing. Our main goal was to create a simple, PCR-free plasmonic biosensor that can differentiate between RhD-positive and RhD-nega-

tive individuals by targeting the RHD gene. This approach reduces reliance on complex molecular labs. The differences in AuNPs assembly in the presence of the target RhD DNA form the basis of the biosensor. In the course of DNA addition, RhD DNA hybridizes with complementary oligonucleotides if the patient is RhD positive. Duplex-specific nuclease (DSN) recognizes and cleaves the DNA, resulting in deaggregation of the nanonet and a significant change in optical properties. Conversely, when DNA from RhD-negative patients is present, there is no complementary hybridization with the "Gold-NanoNet" assembly, and hence no change in aggregation and optical properties. Conventional blood typing involves protein detection on the surface of RBCs, while molecular detection techniques, such as PCR, necessitate complex laboratory equipment, include a large number of steps, prolonged sample-to-result time and skilled personnel, which we mostly tried to minimize in our technology.

Q Gold nanoparticles are at the heart of your sensing platform. What makes these tiny particles particula-

Why suitable for detecting specific genetic markers such as the RHD gene?

A Scientists are fascinated by gold due to its distinct chemical properties. Its remarkable nanoscale behaviour makes it extremely useful in medical diagnostics. The major scientific reason for using gold in our study is its strong localized surface plasmon resonance. Let me explain it in a very general way. Light interacting with tiny gold nanoparticles differs greatly from that of bulk gold. These particles are great signal producers because even slight alterations in their arrangement/ self-organization can result in observable changes in their optical characteristics.

Along with this, the chemical stability, ease to modify with DNA molecules, and high biocompatibility are the reasons that attracted us towards gold and led us to build the sensing platform out of it.

Q *What do you consider the most significant finding of your study, and how could this research contribute to making blood transfusions safer in the future?*

A Our study's most important discovery is that we showed how to use a programmable network of gold nanoparticles to identify the RhD genotype in an entirely new method. We demonstrated that a nanostructured material could identify a specific genetic sequence and translate that chemical event into a straightforward optical signal, rather than relying solely on traditional blood typing techniques. This gives molecular blood group diagnostics a new avenue.

Q *Although the results are promising, your platform is currently a proof-of-concept. What are the major challenges that need to be overcome before this technology can become part of routine clinical practice?*

A Although this paper is currently at the proof-of-concept stage, it is still far from being a clinically deployable molecular diagnostic platform. The limited sample size is a problem in this case. However, we understand the room for improvement in this particular work, and a group of students from our lab is working towards it. Designing a multi-oligonucleotide panel covering common D variants, including the DEL phenotype, will make the platform

globally applicable. The same technology will also be used to target four other Rh antigens: C, c, E, and e. This will facilitate extended blood grouping based on genotype for patients who require transfusions. Furthermore, we are working on a point-of-care electrochemical diagnostic platform to perform a direct whole blood assay, which the current nanonet platform lacks.

Q *Looking ahead, could the same programmable gold nanoparticle strategy be adapted to detect other genetic markers or diseases, and how do you envision this technology shaping the future of molecular diagnostics?*

A Absolutely. The greatest strength of our nanoplatform is that it is programmable. In principle, the same sensing strategy can be adapted to recognize different genetic markers of blood typing, infectious disease, or even cancer-causing genetic biomarkers. In the future, I see this technology developing into portable, point-of-care diagnostic tools that are inexpensive, user-friendly, and able to concurrently identify several genetic markers from a single sample. Such flexibility could allow the platform to evolve beyond a single diagnostic application, supporting rapid screening, earlier disease detection, and more accessible molecular testing in clinics and resource-limited settings.

ABOUT THE AUTHORS

Dr. Parikshit Moitra and his team at IISER Berhampur develop programmable nanomaterials for simple and accessible molecular diagnostics. Their research combines nanotechnology, chemical biology and molecular sensing. Working with Dr. Souryadip Roy, an expert in point-of-care diagnostics and biosensing, and Dr. Suvro Sankha Datta, Head of Transfusion Medicine at Tata Medical Centre, Kolkata, the team combines nanotechnology with clinical expertise to develop new approaches for Rh genotyping and safer blood transfusion.

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Rajeev, R., M, N.K., Mohanty, P. et al. (2026). A molecular diagnostic platform devised from supramolecular gold-oligo NanoNet assembly for differentiating RhD genotypes among transfusion-dependent patients. *ACS Applied Bio Materials*, 9, 5530–5544. [DOI](#)

GABARAPL2 and Alix mediate reciprocal regulation of autophagy and exosome pathways to facilitate cellular homeostasis

OUTLOOK

Cancer cells are remarkably good at surviving difficult conditions and resisting treatment. They use different systems to recycle damaged material, remove waste, and communicate with nearby cells. This research shows that two of these systems autophagy and exosome secretion can work together, helping cancer cells adapt when one system is blocked. In this Science Desk conversation, Dr. Bhawana Bissa explains how this connection works, the role of proteins called GABARAPL2 and Alix, and why targeting both systems together could offer a new direction for future cancer treatments.

Q *Cancer cells often survive treatments that would normally kill healthy cells. What makes cancer cells so resilient, and why is understanding their survival mechanisms so important?*

A In healthy cell physiology, cellular life and death are governed by strict regulatory checkpoints. When a normal cell encounters catastrophic DNA damage, nutrient starvation, or toxic stress, programmed cell death (apoptosis) is activated to protect the organism. Cancer cells, however, dismantle these safeguard checkpoints. They survive harsh hypoxic microenvironments, high metabolic demands, and cytotoxic chemotherapy regimens that would rapidly destroy healthy tissue.

What makes cancer cells so remarkably resilient? The answer lies in their adaptive metabolic plasticity and intracellular homeostatic mechanisms. Rather than relying on a single survival pathway, malignant cells



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AREAS OF EXPERTISE

Autophagy • Exosome • Cancer Biology



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AREAS OF EXPERTISE

Autophagy • Exosomes • Breast Cancer

rewire their internal waste-management, energy-generating, and intercellular signaling networks. When faced with therapeutic stress, they adapt and recycle damaged organelles for immediate fuel, expel toxic drug molecules, and secrete chemical signals to niche tissues for invasion and metastasis.

Understanding these survival mechanisms is one of the most critical frontiers in modern molecular oncology. Conventional monotherapies/single-agent therapy frequently fail because cancer cells exploit compensatory pathways; when one survival route is blocked, the cell reroutes its stress response through another. By mapping the precise molecular machinery that underpins cellular homeostasis, researchers can identify hidden vulnerabilities and design combination therapies that eliminate the cell's backup options, preventing recurrence and chemoresistance.

Q *Your study focuses on two cellular processes—autophagy and exosome secretion. Could you*

explain, in simple terms, what these processes are and how they help cancer cells survive?

A **Autophagy** (literally "self-eating") is the cell's internal recycling system. When a cell experiences nutrient deprivation or oxidative stress, it encapsulates damaged proteins, misfolded aggregates, and worn-out organelles into double-membrane vesicles called autophagosomes. These vesicles fuse with lysosomes, where their contents are broken down into basic amino acids and fatty acids. Cancer cells exploit autophagy as a crucial energy reservoir and quality-control mechanism, allowing them to endure starvation and clean up toxic debris generated by chemotherapy.

Exosome secretion serves as the cell's long-range communication and waste-export network. Exosomes are nano-sized, membrane-bound extracellular vesicles formed inside endosomal compartments known as multivesicular bodies (MVBs). Once MVBs fuse with the cell's outer membrane, exosomes are released into the extracellular space. Packed with signaling proteins, lipids, and nucleic acids (such as non-coding RNAs), exosomes allow cancer cells to communicate with neighboring stromal cells, suppress immune responses, facilitate metastasis, and dump intracellular metabolic waste.

Together, these two pathways function as a dual-action survival network: autophagy maintains internal quality and metabolic balance, while exosome secretion reshapes the external environment and assists in intercellular communications.

Q *One of your key findings is that these two pathways work together. Why was discovering this connection important, and how does it change our understanding of cancer biology?*

A For years, cell biologists largely studied autophagy and exosome secretion as distinct, parallel pathways. However, emerging research—including our recent study published in *Molecular Biology Reports*, reveals that these two systems are deeply interconnected in a dynamic, reciprocal regulatory loop.

When we blocked the exosome biogenesis pathway in aggressive breast cancer cells (MDA-MB-231), the cells did not simply stop communicating; instead, they upregulated core autophagic machinery, specifically elevating key autophagy-related proteins such as ATG5 and ATG16L1. Conversely, when we pharmacologically inhibited autophagy, the cells compensated by significantly increasing the secretion

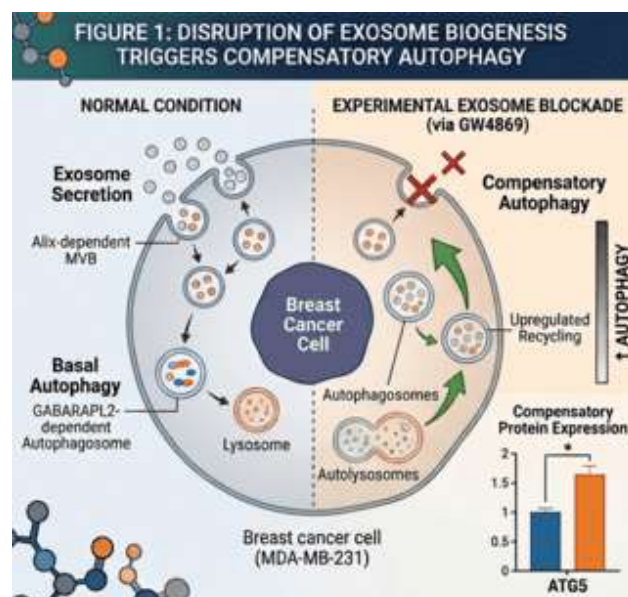


Figure 1. Schematic representation of reciprocal crosstalk. In MDA-MB-231 breast cancer cells, inhibition of exosome secretion via GW4869 blocks the release of "Alix-dependent MVB" (multivesicular body)-derived exosomes, concurrently triggering "Compensatory Autophagy."

of exosomes into their surrounding environment. This discovery fundamentally alters our understanding of cancer biology.

It proves that multivesicular bodies (MVBs) serve as a central molecular traffic junction, routing cellular cargo toward either lysosomal degradation or extracellular release based on real-time stress signals. Because the cell maintains an active "sensing" system between internal recycling and external secretion, targeting only one side of this equilibrium simply pushes the cell to rely more heavily on the other.

Your research identified the proteins GABARAPL2 and Alix as important regulators. What role do these molecules play, and why could they become promising targets for future cancer therapies?

Our study identified a novel mechanism uniting these two factors.

A GABARAPL2 acts as a master regulator modulating the levels and secretion of Alix. When autophagy is inhibited, cellular levels of Alix drop while exosome secretion surges; remarkably, knocking down GABARAPL2 prevents this decrease in Alix, highlighting GABARAPL2's crucial role in governing Alix-dependent exosome packaging and release. Because GABARAPL2 and Alix operate at the interse-

ction of cellular degradation and intercellular signaling, they represent attractive targets for therapeutic intervention. Small molecules or RNA-based therapeutics capable of disrupting the interaction between GABARAPL2 and Alix could shut down the cell's ability to switch between recycling and secretion, dismantling its primary survival safety net.

Q Your team found that blocking both pathways together was much more effective than targeting either one alone. Why is this combination strategy so promising?

A One of the most significant findings of our research is that single-pathway inhibition is largely ineffective at curbing aggressive cancer cell growth. When we blocked exosome biogenesis alone, breast cancer cells actually exhibited an increase in proliferation, driven by compensatory autophagic activity. Similarly, inhibiting autophagy in isolation produced negligible effects on restricting tumor cell growth, as the cells compensated by dumping excess metabolic stress via exosomes.

However, when we implemented a dual-inhibition strategy—simultaneously suppressing both autophagy and exosome biogenesis—the result was a striking reduction in breast cancer cell proliferation.

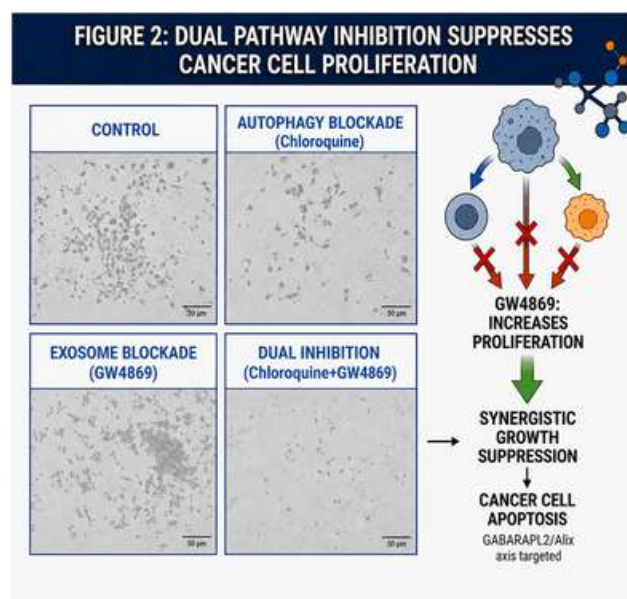


Figure 1. Representative phase-contrast images of MDA-MB-231 cells showing distinct responses to different treatments over time. Simultaneous blockade of both autophagy and exosome secretion caused a dramatic and widespread collapse of the cell population and cell death.

This combination approach works by trapping the cancer cell in a state of unresolvable metabolic stress. Blocking autophagy prevents the cell from clearing damaged mitochondria and protein aggregates internally, while blocking exosome secretion stops it from expelling waste products or signaling for external support. Unable to clean, recycle, or communicate, the cancer cell experiences metabolic collapse.

Q How could discoveries like yours contribute to the development of more effective and personalised treatments for breast cancer in the future?

A Breast cancer is a highly heterogeneous disease, with subtypes like Triple-Negative Breast Cancer (TNBC) presenting significant clinical challenges due to high recurrence rates and limited targetable receptors. TNBC cells rely heavily on robust autophagy and dense exosome secretion to thrive in nutrient-deprived tumor microenvironments.

Discoveries centering on the GABARAPL2-Alix axis provide a blueprint for precision medicine:

- 1. Biomarker Stratification:** Patient tumors can be screened for baseline expression levels of GABARAPL2, Alix, ATG5, and exosomal markers (CD63). High expression profiles could identify patients whose tumors depend heavily on this reciprocal survival loop.
- 2. Combination Drug Cocktails:** Instead of administering single-agent autophagy inhibitors (like chloroquine), oncologists could combine autophagy inhibitors with exosome-blocking agents (such as neutral sphingomyelinase inhibitors or novel Alix inhibitors).
- 3. Overcoming Chemoresistance:** Standard chemotherapy often induces autophagy as an unintended stress response. By pairing conventional chemotherapy with dual autophagy-exosome blockade, clinicians can prevent cells from developing drug resistance and metastasizing.

Q Looking ahead, what are the next steps for this research, and what challenges need to be overcome before these findings can eventually benefit patients?

A While these findings open exciting possibilities for molecular biology of cancer, several translational hurdles remain before dual-inhibition therapies reach

clinical practice.

The next immediate step for our research group is validating these cell-culture observations in pre-clinical animal models (in vivo xenografts).

We must evaluate whether dual inhibition effectively shrinks tumors and suppresses metastasis in complex physiological environments without causing systemic toxicity. Because healthy cells, particularly neurons, hepatocytes, and immune cells, also rely on basal autophagy and exosome release for physiological maintenance, non-selective systemic inhibition could cause adverse off-target effects.

To overcome this challenge, future work will focus on developing targeted drug delivery vehicles, such as antibody-conjugated nanoparticles, designed to deliver dual-pathway inhibitors specifically to tumor tissues.

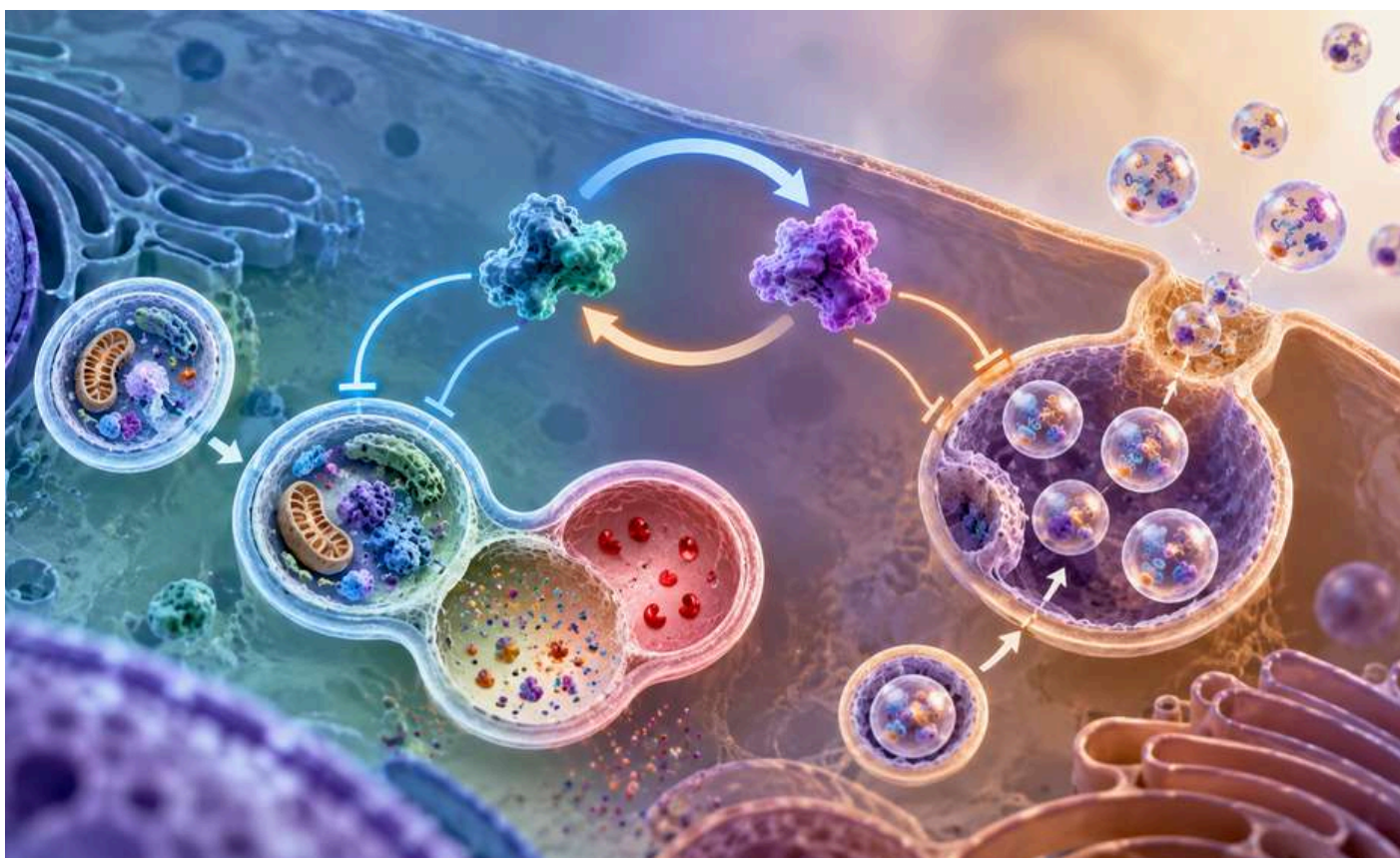
Refining these molecular tools will bring us closer to converting this fundamental biological breakthrough into a viable, life-saving therapeutic reality for cancer patients.

ABOUT THE AUTHORS

Dr. Bhawana Bissa, Naveen Soni, are researchers in Biochemistry at the Central University of Rajasthan, India. Their research focuses on how cancer cells survive, adapt, and resist treatment. They study important cellular processes such as autophagy and exosome communication, which help cells recycle materials and communicate with their surroundings. Their work explores how these systems work together in cancer cells.

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Finding the Genes We Missed: The Next Frontier in Genome Annotation

OUTLOOK

Genome sequencing has transformed biology, but DNA alone cannot always show every gene or which proteins are actually produced. Proteogenomics combines information from DNA and proteins to find missing genes and improve our understanding of how genomes work. In this Science Desk, Dr. Harsh Pawar and Dr. Soumi Chowdhury explain how proteogenomics is helping scientists better understand parasites and other pathogens and could support future advances in disease research and precision medicine.

Q *Most people think that sequencing a genome tells us everything about an organism. What inspired your team to look beyond the genome itself, and why is genome annotation still an important scientific challenge?*

A Our motivation came from years of proteomic and proteogenomic work across parasites including *Leishmania*, *Trypanosoma*, *Entamoeba* and other pathogens at the Institute of Bioinformatics, Bangalore. We kept meeting the same problem: a reference genome never fully captures an organism's true coding potential, however long it has been sequenced. Annotation relies heavily on computational prediction, so genes get missed, boundaries misassigned, and proteins stay "hypothetical" for lack of evidence, especially in parasites, whose genomes are often divergent or species-specific.

Proteomics adds an experimental layer. Identifying peptides by mass spectrometry and mapping them to the genome lets us validate predicted genes and uncover overlooked coding regions. Sequencing gives the scaffold; protein evidence shows how complete our reading of it is. Annotation is evolving, not a one-time exercise; as technologies advance, hidden layers of genome biology become accessible.



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AREAS OF EXPERTISE

Parasitology • Proteogenomic • Proteomics • Vector Biology



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AREAS OF EXPERTISE

Proteogenomics • Metagenomics • Vector Biology • Parasitology

Q *Your study uses a proteogenomic approach to identify previously hidden protein-coding genes. Could you explain what proteogenomics is and how combining proteins with genomic information provides a more complete picture than DNA alone?*

A Proteogenomics integrates genomics and proteomics to characterise a genome's coding potential using computational prediction plus experimental evidence. Sequencing gives the blueprint, but its accuracy depends on whether predicted genes are actually expressed. Across several parasites, well-sequenced genomes still carry incomplete annotations, missed genes, wrong boundaries, and "hypothetical" proteins since prediction struggles with proteins that are short, divergent or absent from reference databases.

Proteomics offers an independent check: mass spectrometry identifies peptides in a sample, and mapping these to the genome reveals coding regions prediction missed or refines known boundaries. This has uncovered unannotated genes and corrected gene

models, giving a stronger basis for studying protein roles in host-parasite interactions.

DNA shows what an organism can potentially encode; proteins show what is actually produced. Proteogenomics moves us from a predicted genome to an experimentally supported one, asking not "what genes are present?" but "what coding potential can we demonstrate at the protein level?"

Q *Your work revealed new genes and corrected existing gene annotations in *Entamoeba histolytica*. Why are these seemingly small improvements so important for understanding the biology and disease-causing mechanisms of this parasite?*

A Annotation underlies nearly every downstream analysis, so small errors distort our understanding of pathways and host-pathogen interactions. We've seen this recur across parasites: initial annotations rarely give a complete picture. A missing gene becomes invisible downstream; an incorrect boundary produces a wrong protein sequence, skewing predicted function and localisation.

In our *E. histolytica* study, combining mass spectrometry with genomic data identified 41 previously unrecognised protein-coding genes and corrected 18 existing gene models, providing evidence that even a well-studied genome holds coding information revealed only by pairing prediction with experiment. Many carried conserved domains hinting at function, some with orthologs in related *Entamoeba* species.

A more accurate coding repertoire lets researchers examine pathways tied to survival and pathogenicity, and revisit datasets for previously missed signals. A new gene adds a missing puzzle piece; a corrected model ensures researchers study the right protein.

Q *Many newly identified proteins were previously labelled as "hypothetical." How can confirming that these proteins actually exist change the way scientists study parasite biology and identify potential therapeutic targets?*

A "Hypothetical protein" reflects a prediction lacking experimental support common across parasite

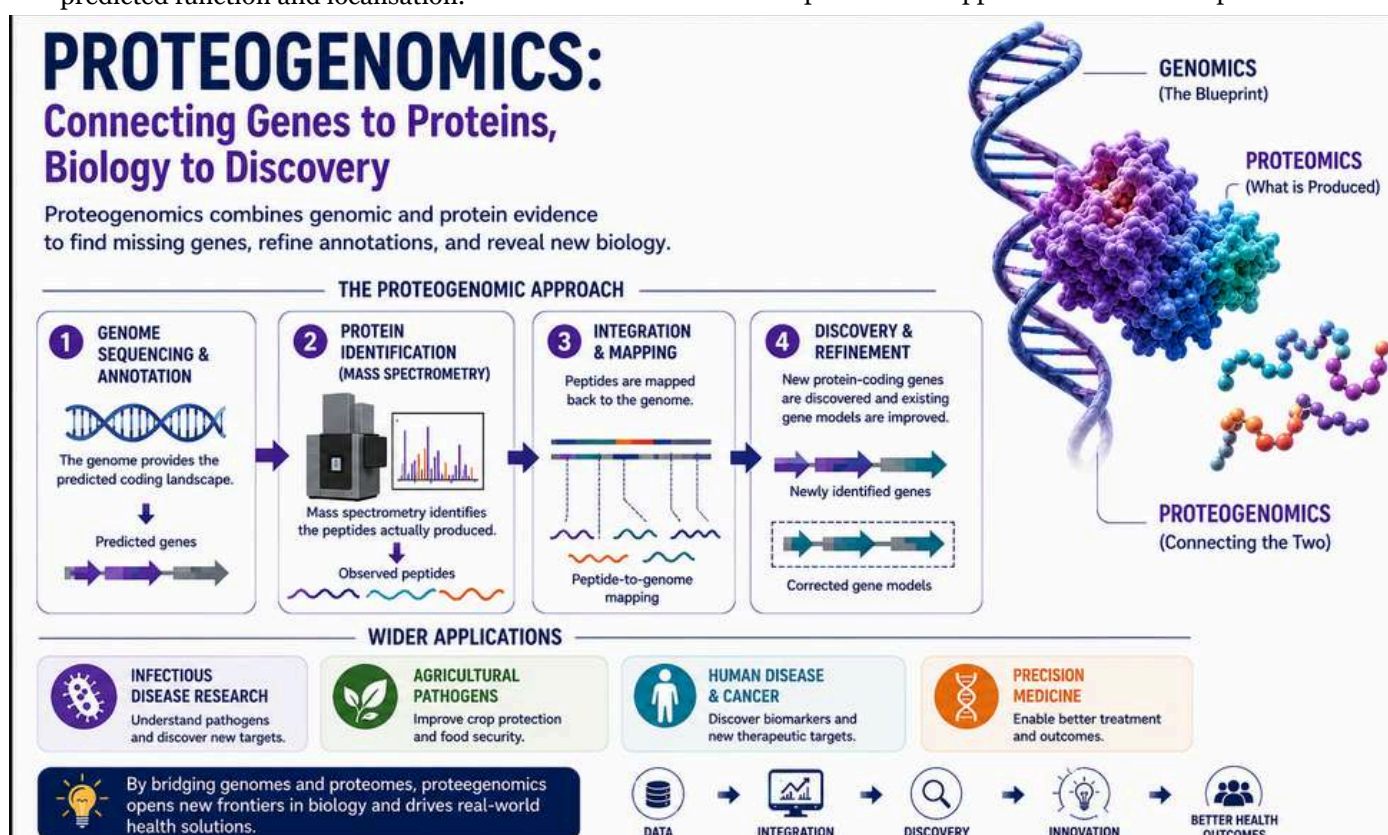


Figure 1. Proteogenomics integrates genome sequencing and annotation with mass-spectrometry-based proteomics to identify previously unrecognised protein-coding regions and refine existing gene models. By mapping experimentally observed peptides back to genomic sequences, the approach can provide evidence for proteins missed or incompletely represented by conventional genome annotation. Proteogenomic approaches have applications across diverse organisms, including parasites such as *Leishmania*, *Trypanosoma* and *Entamoeba*, as well as other infectious organisms, agricultural pathogens and human diseases.

genomes, and heavy in *Trypanosoma* and *Leishmania*.

When mass spectrometry detects a matching peptide, that protein moves from computational guess to confirmed entity. This doesn't reveal function immediately, but opens questions: where and when is it expressed, and what role might it play in metabolism or host interaction?

This matters especially for parasites, whose divergent proteins are easily missed by similarity-based annotation. In our *E. histolytica* study, several new proteins carried conserved domains offering functional clues, moving them toward candidates for functional research.

Confirmation also strengthens target prioritisation: a protein essential for survival or infection becomes a stronger drug-target candidate, though existence alone isn't proof of suitability. Divergence from human counterparts can open opportunities for selective therapies. The greatest value may be expanding the search space: overlooked hypothetical proteins, once confirmed, become starting points for new biology and drug targets.

ometry?

A The core challenge is connecting genomic predictions with mass-spectrometry peptide spectra accurately enough to know which signals genuinely indicate coding regions. Proteogenomics searches beyond annotated databases into regions not flagged as coding, raising discovery potential but also false-positive risk. Confidence requires a match to be statistically robust, biologically sensible and to support a new gene, and whether conserved domains support it.

Genome assembly quality is another constraint, as misassembled repetitive regions make even strong proteomic evidence hard to interpret. No single computational approach works universally, requiring careful integration of genomic, proteomic and comparative evidence.

The field is advancing quickly. Long-read sequencing now produces more complete genome assemblies; mass spectrometry sensitivity keeps improving. Integration with transcriptomics adds independent evidence, and when approaches converge, confidence rises.

Q *Beyond amoebiasis, how could proteogenomic approaches benefit research on other infectious organisms, agricultural pathogens, or even human diseases?*

A Proteogenomics addresses a universal gap between genomic prediction and experimentally observed proteins, making it valuable for any pathogen with divergent or poorly characterised proteins, including bacteria, fungi and viruses with incomplete annotation.

In agriculture, pathogens rely on protein networks for invasion, colonisation and immune evasion; proteogenomic can identify these and inform surveillance, diagnostics and control strategies.

In human disease, though the genome is well annotated, the proteome is still being understood; variants often reveal functional consequences only at the protein level. This matters in cancer, where alterations produce tumour-specific proteins; integrating genomic and proteomic data can identify these as biomarkers or targets for precision medicine.

Q *What were the biggest technical and computational challenges in integrating large-scale proteomic and genomic datasets, and how is this field continuing to evolve with advances in sequencing and mass spectr-*

Q *Looking ahead, how do you envision proteogenomics transforming biological research over the next decade? What exciting discoveries do you think this approach will enable in genome science and precision medicine?*

A We expect proteogenomics to move from a specialised annotation tool to a core part of biological research. Our parasite work shows substantial biology still hidden between genomic prediction and protein-level evidence. As assemblies and mass spectrometry improve, we'll probe previously inaccessible regions, revealing new genes and lineage-specific proteins.

Annotation should shift toward an evolving, evidence-based model that is important for infectious disease, where proteins involved in immune evasion or drug resistance are hard to find through comparison alone. Comparative proteogenomics across strains could reveal which proteins distinguish more pathogenic organisms.

For precision medicine, proteins usually translate genetic change into biological effect. Linking genotype to protein sequence and function could be transformative in cancer, offering new biomarkers and targets. Integration with spatial and single-cell biology will reveal not just which proteins exist, but where and when.

The deeper shift is conceptual: from "what does the genome contain?" to "which regions are expressed and functional?" The most exciting discoveries ahead will likely come from these unexplored connections - moving genome science from reading genomes to understanding what they do.

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Dr. Harsh Pawar is a Faculty Scientist at the Institute of Bioinformatics, Bengaluru, specializing in proteomics, proteogenomics, genomics, and infectious-disease research. His work uses genomic and protein information to better understand parasites and improve genome annotation. Dr. Soumi Chowdhury is a researcher at the Institute of Bioinformatics working on proteogenomics and parasite biology, particularly *Leishmania*. Together, their research helps uncover previously missed genes and proteins and provides a clearer understanding of parasite biology. Their interdisciplinary approach demonstrates how combining genomic and proteomic evidence can reveal hidden biological information, strengthen genome annotations, and support future efforts to understand parasite evolution, infection mechanisms, and potential therapeutic targets.



Shining Light on Artificial Enzymes: How Supramolecular Science Makes Aqueous Organocatalysis Switchable

OUTLOOK

Nature controls chemical reactions with remarkable precision, switching biological processes on and off when needed. Inspired by this principle, scientists are developing artificial enzymes that can be controlled using light. In this Science Desk conversation, Dr. Chandan Maity and Ms. Divya Chauhan explain how simple molecules can organize themselves into catalytic structures in water, how light acts as a molecular switch, and how programmable chemistry could contribute to greener chemical processes, smart materials, and responsive technologies.

Q *What inspired your team to develop a light-switchable artificial enzyme, and what scientific challenge were you aiming to address?*

A Our inspiration came from nature's remarkable ability to regulate chemistry with precision. Nature has been regulating chemistry for billions of years. Photosynthesis is one of its most remarkable examples – plants, algae, and photosynthetic microorganisms capture light energy to drive chemical reactions that transform CO₂ and water into glucose. Yet light does more than power photosynthesis. In living systems, it also helps regulate processes such as plant growth, development, flowering, and responses to environmental conditions. Enzymes are central to this remarkable control. They accelerate chemical reactions with extraordinary speed and selectivity, while their activity can be regulated by environmental signals to ensure that

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(Organic)Materials Science • Supramolecular Chemistry • Aqueous Organocatalysis • Smart Material

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Organic Chemistry • Supramolecular Chemistry • Photoswitchable Materials • Smart catalysis

chemistry occurs at the right time and place. Nature therefore demonstrates a powerful principle: Chemistry becomes more useful when it can be precisely controlled.

Inspired by these strategies, we asked: Can an organocatalytic system operate in water and be reversibly switched ON and OFF using light? Rather than trying to reproduce the enormous complexity of a natural enzyme, we followed a philosophy of “doing more with less.” Could relatively simple molecules organize themselves into a sophisticated functional system?

The answer lies in supramolecular chemistry the science of how molecules recognize one another and assemble through reversible, non-covalent interactions. When simple molecular building blocks work together, they can produce functions far beyond those of the individual molecules.

Q *Your study combines light-responsive molecules, supramolecular assembly, and enzyme-mimetic*

catalysis. Could you explain how these components work together to switch the catalyst between its "ON" and "OFF" states?

A The system works through a coordinated sequence of molecular switching, self-assembly, and molecular recognition. Our design combines an imidazole unit, capable of participating in catalysis, with azobenzene, a well-established molecular photoswitch. The resulting molecule, Azo-Imd, brings catalytic activity and light responsiveness into a single molecular system.

Its most interesting behavior emerged in water. Rather than remaining as individual molecules, Azo-Imd spontaneously organized into vesicular nanostructures. When exposed to light, the azobenzene component underwent reversible trans-to-cis photoisomerization a change in molecular shape that triggered a larger structural transformation from vesicles to micelles. Thus, light did more than change one molecule. A tiny molecular movement was amplified through self-assembly to reorganize the entire catalytic environment.

But structural change alone was not enough. We wanted the catalyst itself to switch between OFF and ON states. The crucial ingredient was β -cyclodextrin (β -CD), a cyclic sugar molecule with a hydrophobic cavity that can selectively host suitable molecules. In the absence of light, β -CD preferentially captures the trans form of Azo-Imd. This effectively hides the catalytic imidazole group from the substrate, placing the catalyst in its OFF state.

Light changes Azo-Imd into its cis form. This shape no longer fits comfortably within the β -CD cavity, so the catalyst is released. It then self-assembles into catalytically active micelles, exposing the imidazole group and switching the system ON. The activated catalyst promotes ester hydrolysis in water. As the photoswitch gradually returns to its original form, the catalyst can again be captured by β -CD, restoring the OFF state.

The entire process can be viewed as a molecular smart home: Light is the remote control, β -CD is the smart lock, and supramolecular assembly creates the catalytic environment. The catalyst is already present—the signal simply controls access to its active site.

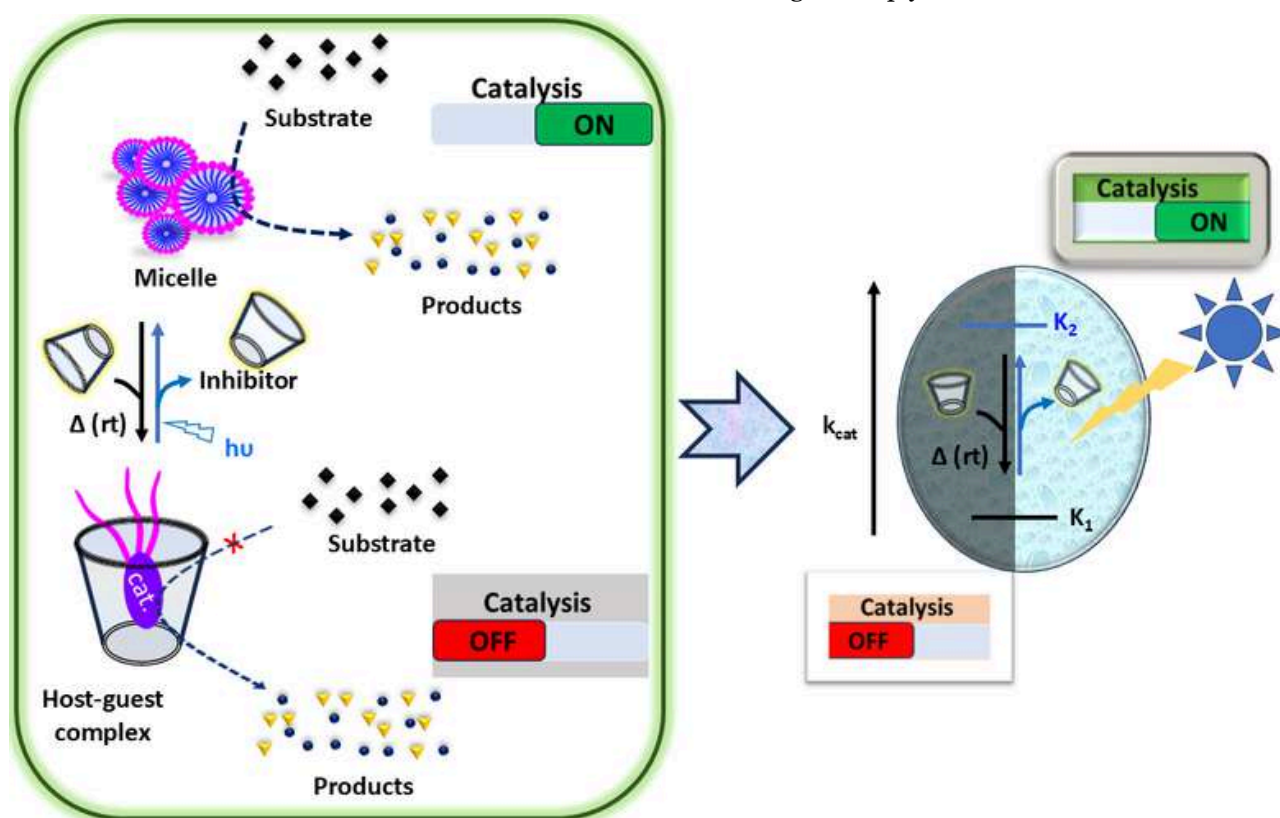


Figure 1. The Azo-Imd organocatalyst undergoes reversible trans–cis photoisomerization upon light irradiation, while β -CD inhibits catalysis by forming a host–guest complex with Azo-Imd, thereby establishing the OFF state (k_1). Upon light irradiation, the weakened host–guest interaction releases cis-Azo-Imd, promotes micelle formation, and restores enhanced catalytic activity in the ON state (k_2).

Q *One of the most intriguing aspects of your work is the ability to control chemical reactions simply by using light. Why is light considered such a powerful tool for regulating catalytic processes compared with conventional chemical triggers?*

A Light is an especially powerful tool for programmable chemistry. Conventional triggers such as acids, bases, or additional chemical reagents can change the reaction environment and may generate unwanted by-products. Light can initiate molecular transformations without adding another chemical reagent.

It can also provide exceptional spatiotemporal control. In principle, a catalyst could be activated precisely when and where it is needed. This makes light-responsive catalysis attractive for developing more adaptive and potentially sustainable chemical processes.

Q *Your artificial catalyst operates in water and mimics certain features of natural enzymes. How closely does this system resemble biological enzymes, and what advantages does it offer over traditional synthetic catalysts?*

A Our system is not intended to replace biological enzymes. Natural enzymes are extraordinarily sophisticated molecular machines refined through billions of years of evolution. Instead, our goal was to capture some of their most useful principles. The artificial catalyst operates in water, creates a localized catalytic environment through supramolecular organization, and displays Michaelis–Menten-type kinetics, a framework commonly used to describe enzyme-catalyzed reactions. Most importantly, its catalytic activity can be reversibly controlled by an external stimulus.

The lesson is that sophisticated function does not necessarily require a sophisticated molecule. Here, molecular recognition, self-assembly, and photoswitching work together to generate enzyme-like behavior.

Q *What are the most promising real-world applications of light-switchable catalytic systems? Could they eventually contribute to greener chemical manufacturing, smart materials, or biomedical technologies?*

A The present work is fundamental research, but the concept points toward exciting possibilities. In green chemistry, catalysts that operate only when required could eventually help reduce unwanted reactions and

chemical waste. In smart materials, similar systems could contribute to responsive coatings, polymers, hydrogels, and other materials whose chemical behavior can be programmed.

There may also be opportunities in biomedical technologies, including responsive therapeutic materials and controlled molecular systems. However, these remain future possibilities rather than demonstrated applications of the present catalyst.

Q *Every breakthrough comes with challenges. What are the current limitations of this technology, and what improvements are needed before similar systems can be applied beyond the laboratory?*

A Important challenges remain. The current system has been demonstrated using a model reaction under controlled laboratory conditions. Future systems will need to work with a broader range of chemical transformations while offering greater efficiency, stability, and robustness. A particularly important goal is developing catalysts that respond effectively to visible light or sunlight, rather than ultraviolet irradiation. Researchers must also understand how these systems behave in complex chemical and biological environments. These challenges are not simply barriers they are opportunities to make programmable catalysis increasingly practical.

Q *Looking ahead, how do you envision the future of programmable catalysis and artificial enzyme systems? What exciting developments should scientists and the public watch for in the coming years.*

A The broader significance of this work lies in its design philosophy. By combining simple molecular building blocks with supramolecular self-assembly, we can create chemical systems capable of responding dynamically to their surroundings. Future artificial enzymes may incorporate multiple molecular switches, respond to several environmental signals, perform more complex catalytic reactions, or become integrated into adaptive materials and reaction networks.

Nature teaches us that extraordinary functions can emerge when relatively simple components work together in precisely organized ways. Our light-switchable artificial enzyme offers a small but compelling demonstration of that principle. Light becomes the remote control. Supramolecular assembly becomes the molecular machinery.

Chemistry becomes programmable capable of turning ON when needed and returning to OFF when the job is done.

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ABOUT THE AUTHORS

Dr. Chandan Maity and Ms. Divya Chauhan are researchers at Vellore Institute of Technology (VIT), India. Dr. Maity leads research on supramolecular chemistry, artificial enzymes, catalysis, and responsive soft materials, exploring how simple molecules can organize themselves to perform useful functions. Ms. Chauhan is a research scholar working with him on light-responsive molecular systems and supramolecular assembly. Together, their research explores how external signals such as light can control chemical reactions, with potential applications in sustainable chemistry, smart materials, and adaptive catalytic systems.



Tiny Plastics, Big Consequences: What Fish Reveal About Freshwater Pollution

OUTLOOK

Microplastics are increasingly finding their way into rivers, lakes, and the organisms that live in them even in remote mountain ecosystems. Their presence in freshwater fish raises important questions about ecosystem health, pollution sources, and possible movement through the food chain. In this Science Desk conversation, Dr. Syed Talia Mushtaq and Mr. Ganesh Chiranji explain what the Golden Mahseer reveals about microplastic contamination in Himalayan waters, how these particles enter and accumulate in fish, and why better monitoring and pollution control are essential for protecting freshwater ecosystems and the communities that depend on them.

Q *Microplastics have become a growing environmental concern worldwide. What inspired your team to investigate their presence in the Golden Mahseer, and why is this species important for monitoring freshwater ecosystem health?*

A Microplastics - plastic particles smaller than 5 mm - have become one of the most pervasive pollutants in aquatic ecosystems, and they persist, travel long distances, and bioaccumulate through food webs. Yet most evidence comes from marine and estuarine fish, while Himalayan freshwater systems remain poorly studied. We were struck by how little was known about these mountain waters, which are vital freshwater resources and home to many endemic and endangered species. The Golden Mahseer (*Tor putitora*) is a culturally and economically important fish of these rivers and lakes, and it is widely regarded as a reliable bioindicator of environmental contamination. By examining where microplastics accumulate inside its body, we could obtain an early, sensitive signal of ecosystem health. Our study is among the first organ-level assessments of microplastic contamination in Himalayan freshwater fish.



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AREAS OF EXPERTISE

Fisheries Resource Management • Fish Biology • Freshwater ecology • Fish migration



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AREAS OF EXPERTISE

Fish Biology • Microplastic pollution

Q *Your study found microplastics in the gills, gut, and even the muscle of the fish. What does this tell us about the extent of plastic pollution in Himalayan freshwater ecosystems?*

A We detected microplastics in every tissue we examined - gills, gastrointestinal tract, and even muscle - in fish from all three sites. This tells us that plastic pollution has already reached deep into Himalayan freshwater ecosystems, which are often assumed to be pristine because of their low industrial activity. The presence of particles in muscle is especially telling, because it shows that microplastics do not simply pass through the gut; some move into body tissues. Compared with other systems, the contamination we found was moderate - other researchers reported 4 to 10 particles per fish on the Tibetan Plateau and up to 12 in the Indus basin - but it is ecologically significant. It confirms that even remote mountain catchments are not insulated from plastic pollution, most likely because particles arrive through atmospheric deposition and are transported

across the wider catchment.

Q One of your key findings is that the gastrointestinal tract contained the highest levels of microplastics. Why do these particles accumulate mainly in the gut, and what does this reveal about how fish are exposed to plastic pollution?

A The gastrointestinal tract clearly carried the heaviest burden - on average 5.53 plus or minus 4.26 microplastics per individual, compared with 3.50 plus or minus 2.58 in the gills and just 0.08 plus or minus 0.02 in muscle - and these organ differences were statistically significant. This pattern points to ingestion as the main route of exposure. Microplastics suspended in the water column are swallowed during feeding or taken in accidentally with food particles. The Golden Mahseer is a benthic feeder that forages close to the sediment, exactly where microplastics tend to settle and accumulate, so it readily consumes particles along with prey and detritus. Similar gut-dominated patterns have been reported in other freshwater fishes such as common carp and snow trout. The higher counts in gills also indicate a respiratory pathway, meaning fish are exposed both through what they breathe and what they eat.

Q Most of the microplastics you identified were small fibers, many of them black or blue in color. Where do

these particles most likely come from, and what human activities are contributing to their presence in rivers and lakes?

A Fibers were by far the most common shape (49.6%), ahead of fragments (27.9%) and pellets (22.5%), and more than 74% of all particles were black or brown and blue or violet. Most were small - about 71% were 500 micrometres or less. This combination is a fingerprint of everyday human activity rather than heavy industry. Dark fibers of this kind typically come from weathered synthetic textiles and laundry wastewater, from domestic sewage, from tire-wear debris carried in road and urban runoff, and from fishing gear such as nets and lines. Comparable fiber-rich, dark-coloured profiles have been reported in the Yangtze and Brahmaputra river systems, where domestic wastewater and urban runoff were identified as major sources. It is important to stress, however, that because we used visual and morphological identification rather than FTIR or Raman spectroscopy, these source links remain informed inferences rather than confirmed polymer identifications.

Q Although only small amounts of microplastics were detected in the edible muscle, should consumers be concerned? What do we currently know, and what remains uncertain about the implications for food safety and human health?

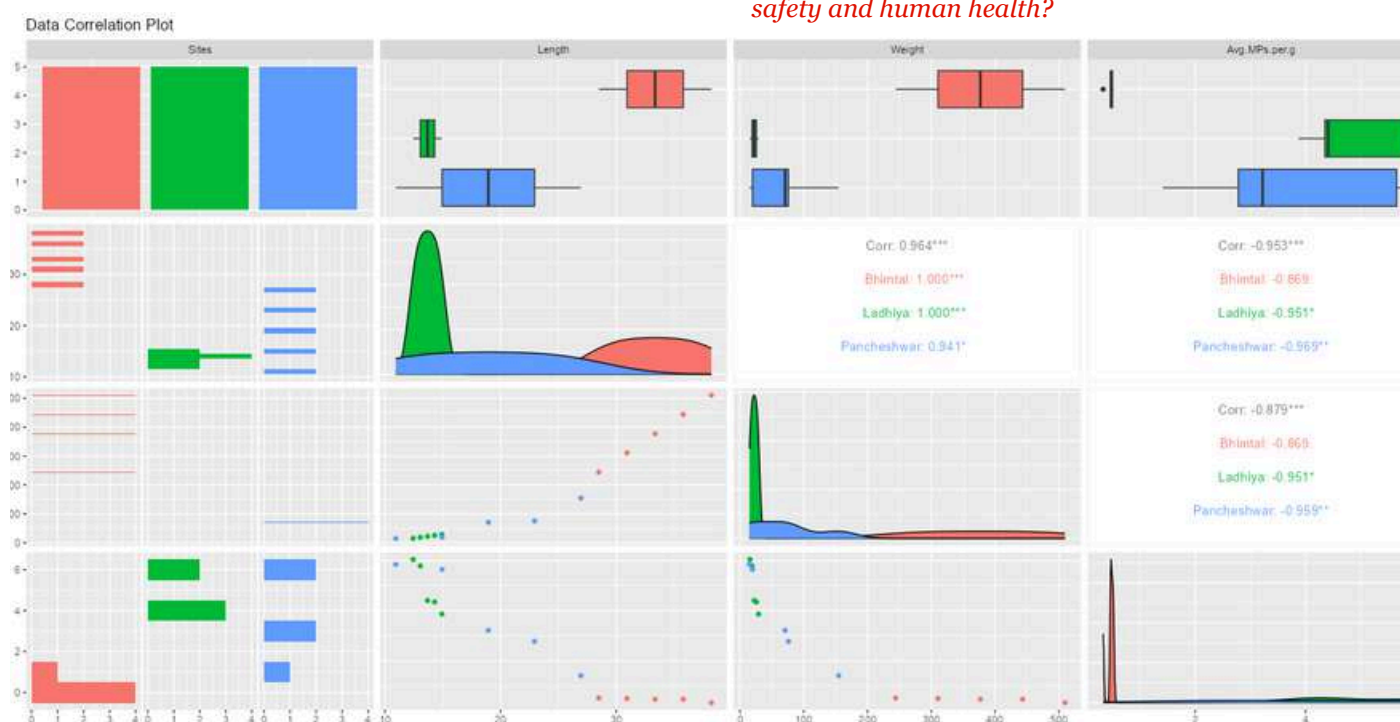


Figure 1. Microplastic abundance in the gastrointestinal tract and muscle tissue of *Tor putitora* across sampling sites

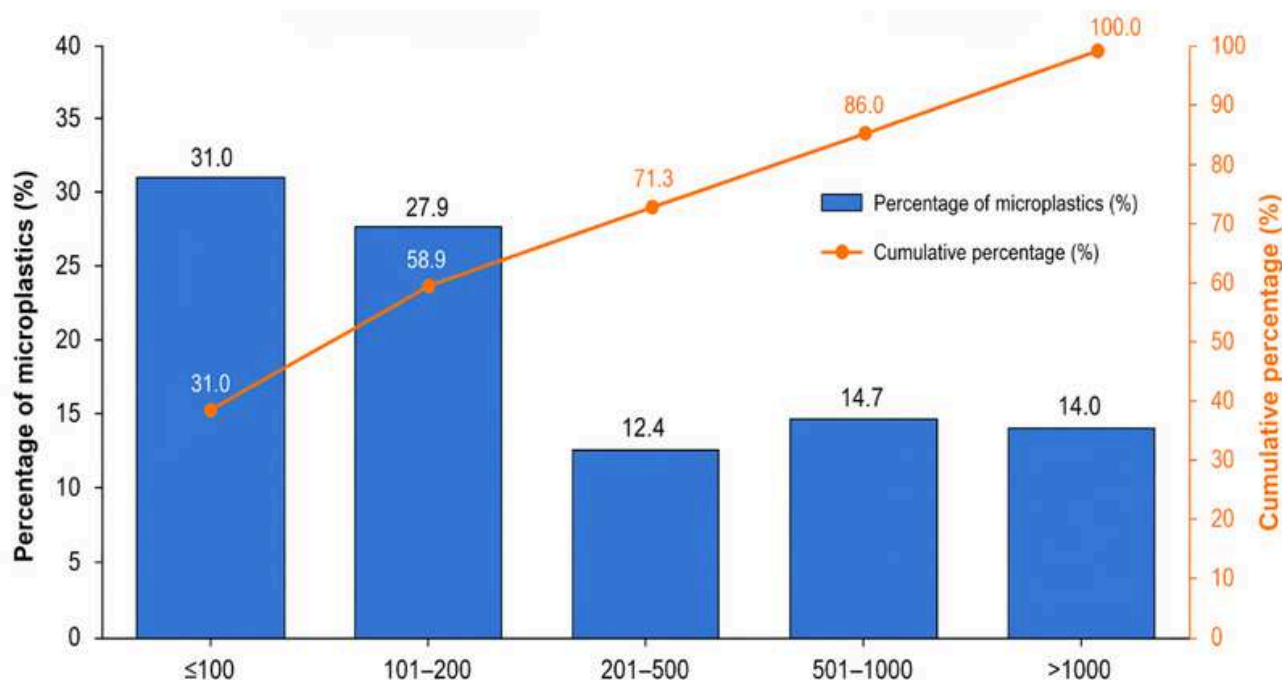


Figure 2. Percentage of microplastics per size class with cumulative percentage. Particles 500 micrometres or smaller accounted for 71.3% of all microplastics, with the smallest size classes most abundant.

A Consumers should be thoughtful rather than alarmed. We found only trace amounts in edible muscle (0.08 plus or minus 0.02 particles per fish), but the fact that any particles reach muscle matters, because the Golden Mahseer is widely eaten by local communities. Laboratory and field studies suggest that very small microplastics - below about 500 micrometres - can cross epithelial barriers, move into tissues, and trigger oxidative stress and inflammation in aquatic organisms, which raises legitimate questions about transfer up the food chain to people. What remains genuinely uncertain is the human health picture: our study did not measure toxicological effects or actual dietary risk, and visual identification can overestimate counts by including natural fibers. So the honest message is that microplastics are present in the food chain and deserve attention, but the real implications for food safety cannot yet be quantified and require dedicated toxicological and exposure research.

Q Your study highlights differences in microplastic contamination among the three sampling sites. What do these variations tell us about the influence of tourism, urbanization, and local human activities on freshwater pollution?

A The three sites told very different stories. The Ladhiya River carried the highest overall load (4.89 plus or

minus 2.26 particles per fish), followed by Pancheshwar (3.77 plus or minus 2.06), while Bhimtal Lake was strikingly lower (0.45 plus or minus 0.16). The elevated contamination at Ladhiya reflects concentrated human pressure - tourism, urban runoff, and effluent discharges - entering a relatively confined river stretch. Pancheshwar, at the confluence of the Kali and Saryu rivers, showed lower counts most likely because higher flow and dilution reduce particle retention, consistent with reports that faster mountain rivers retain fewer microplastics. In other words, contamination tracks local human activity and hydrology rather than being uniform across the landscape. This variation is a useful message for managers: pollution hotspots form where tourism and urbanization concentrate, so targeted, site-specific interventions are likely to be more effective than blanket measures.

Q Looking ahead, what actions should researchers, policymakers, and the public take to reduce microplastic pollution and better protect freshwater ecosystems and the species that depend on them?

A Reducing microplastic pollution will require coordinated action. Researchers should move beyond counting particles to confirming polymer types with FTIR or Raman spectroscopy, analyse water and

sediment alongside fish to trace sources, and study toxicological effects such as oxidative stress, histopathology, and metabolic disruption.

Policymakers should prioritise improved wastewater treatment, better solid-waste and plastic regulation in Himalayan catchments, and effective management of tourism, which our data link to local contamination. Sustained, standardized monitoring is essential so that trends can be tracked over time.

The public also has a direct role - reducing single-use plastics, disposing of waste responsibly, and limiting the shedding of synthetic fibers from clothing. Because vulnerable species like the Golden Mahseer act as sentinels of ecosystem health, protecting them and their habitats ultimately safeguards the freshwater resources and communities that depend on these rivers and lakes.

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ABOUT THE AUTHORS

Dr. Syed Talia Mushtaq works in fisheries, freshwater ecosystems, and environmental pollution. She supervised this study on microplastics in the Golden Mahseer, an important fish of Himalayan rivers. Her research helps us understand how plastic pollution enters fish and affects freshwater environments. Mr. Ganesh Chiranji contributed to the study of microplastic contamination in the Golden Mahseer. Together, their work provides useful information for protecting freshwater fish, reducing pollution, and conserving Himalayan rivers and aquatic ecosystems.



How Do Plants Survive Stress? The Science Behind Stronger Crops

OUTLOOK

Nature controls chemical reactions with remarkable precision, switching biological processes on and off when needed. Inspired by this principle, scientists are developing artificial enzymes that can be controlled using light. In this Science Desk conversation, Dr. Chandan Maity and Ms. Divya Chauhan explain how simple molecules can organize themselves into catalytic structures in water, how light acts as a molecular switch, and how programmable chemistry could contribute to greener chemical processes, smart materials, and responsive technologies.

Q *Plants cannot move away from heat, drought or salty soil. How do they protect themselves when conditions become difficult?*

A Plants are remarkably adaptable organisms. Unlike animals, they cannot move to a more favorable environment when drought, heat, salinity or other stresses occur. Instead, they must sense the changing conditions and rapidly adjust their physiology, metabolism and growth. One of the first responses is to control water balance. During drought, plants reduce water loss by closing microscopic pores on their leaves, called stomata. They can also increase the production of protective molecules such as osmolytes, antioxidants and stress-related proteins. These molecules help maintain cellular water balance and protect proteins, membranes and other cellular components from damage. At the same time, plants modify their root systems to explore available water more efficiently and alter their metabolism to conserve energy. They also activate sophisticated molecular defense systems that regulate gene expression and cellular signaling. So, plant stress tolerance is not regulated by a single gene or protein mechanism. It is a coordinated response involving stress perception, signaling, gene regulation, metabolism, growth adjustment and cellular protection.



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AREAS OF EXPERTISE

Plant Molecular Biology • Plant Abiotic Stress • Plant-Environment Interactions



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AREAS OF EXPERTISE

Plant Biotechnology • Genetic Engineering • Biotic and Abiotic Stress

Q *What happens inside a plant when it first senses environmental stress?*

A The first step is stress perception. A plant cell continuously monitors its surroundings, including water availability, temperature, salt concentration and changes in cellular conditions. When an environmental disturbance occurs, it triggers rapid changes inside the cell. These may include alterations in calcium levels, production of reactive oxygen species (ROS), changes in protein phosphorylation and activation of hormone signaling pathways. Plant hormones such as abscisic acid (ABA), jasmonic acid (JA), salicylic acid (SA) and ethylene can participate in coordinating these responses, depending on the type and severity of stress. These early signals eventually reach the nucleus and influence transcription factors and other regulatory proteins. As a result, specific stress-responsive genes are activated or repressed. What makes this system particularly fascinating is that plants do not simply respond passively. They continuously integrate diffe-

rent signals and adjust their responses according to the intensity and duration of the stress.

Q Why can protecting itself from stress sometimes come at the cost of plant growth and crop yield?

A A plant has limited resources. Energy and carbon that could be used to produce new leaves, roots, flowers and seeds may instead be redirected toward survival. For example, under severe drought, plants may close their stomata to reduce water loss. This protects the plant, but it also restricts carbon dioxide entry into the leaves and can reduce photosynthesis. Similarly, plants may invest energy in producing antioxidants, osmoprotectants, protective proteins and other stress-response molecules rather than biomass. This creates an important biological trade-off: Survival and growth are often competing priorities.

s. A highly stress-responsive plant may survive a difficult environment but produce less biomass or fewer seeds. Conversely, a rapidly growing plant may perform extremely well under favorable conditions but become vulnerable when environmental conditions deteriorate. Therefore, one of the major goals of modern plant science is not simply to make plants "stress resistant." It is to develop plants that can balance stress protection with continued growth and productivity.

Q Your recent work discusses WD40 proteins. In simple terms, what are these proteins, and why are they important for plants?

A WD40 proteins can be thought of as molecular platforms or scaffolds inside cells. The name comes from the presence of characteristic WD repeats, which

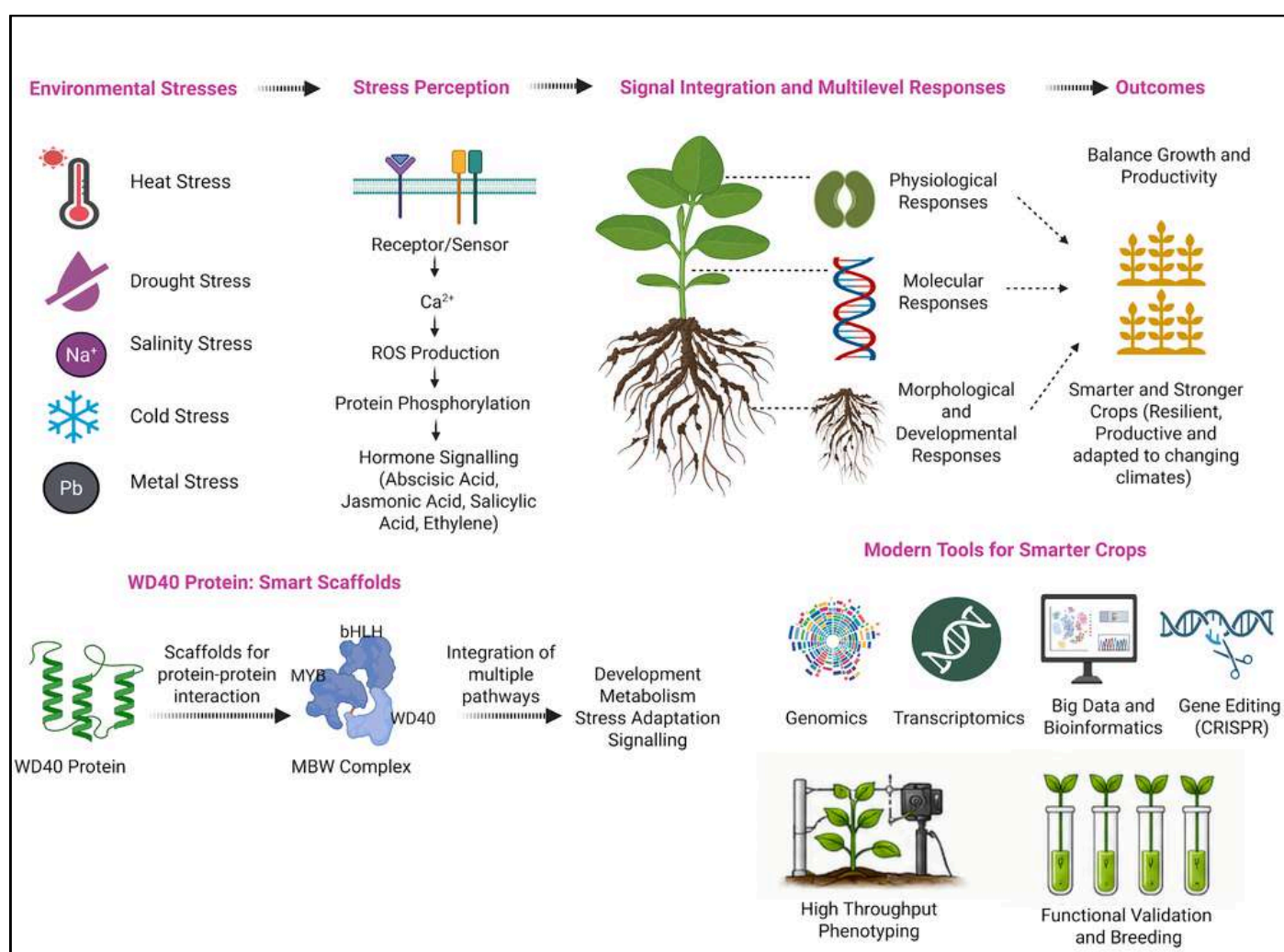


Figure 2. WD40 proteins act as molecular scaffolds that integrate plant development, metabolism and stress signaling, coordinating physiological and molecular responses to environmental stress and supporting growth and productivity.

often contain tryptophan (W) and aspartic acid (D). Rather than acting like a single-purpose enzyme, many WD40 proteins help bring other proteins together. They can therefore participate in protein–protein interactions and help organize molecular complexes involved in diverse cellular processes. In plants, WD40 proteins are associated with processes including development, hormone responses, transcriptional regulation, protein modification, metabolism and responses to environmental stresses. Their importance comes from their ability to act as molecular coordinators. A WD40 protein can help connect different regulatory components, allowing a plant cell to integrate information from several signaling pathways.

This makes WD40 proteins particularly interesting when we think about environmental stress. Plants must coordinate their stress responses with growth and development, and molecular scaffolds such as WD40 proteins can contribute to this complex regulatory network.

Q *Can understanding how plants naturally respond to stress help us develop crops that survive drought, heat and salinity better?*

A Absolutely. Nature has already provided plants with an enormous toolbox for coping with environmental challenges. Different plant species, and even different varieties of the same crop, can possess different levels of stress tolerance. By understanding the molecular mechanisms behind these natural differences, researchers can identify genes, proteins and regulatory pathways associated with improved resilience. For example, we can investigate how tolerant plants regulate water use, root development, antioxidant defense, osmotic adjustment and stress-responsive gene expression. The next step is to determine which mechanisms can be translated into crop improvement without causing undesirable effects on growth or yield. This is especially important because stress tolerance is usually a complex trait controlled by many genes and interacting pathways, rather than by one "stress-resistance gene." The ultimate goal is therefore to understand the regulatory networks that allow plants to remain productive under stress, rather than simply allowing them to survive.

Q *How are modern tools such as gene editing and genomics helping scientists develop stronger and m-*

ore resilient crops?

A Modern genomics has transformed the way we study plant stress responses. Genome sequencing, transcriptomics, proteomics and other "omics" approaches allow scientists to examine thousands of genes and molecular changes simultaneously. These approaches can reveal which genes become activated when plants experience drought, heat or salinity and can help identify naturally occurring genetic variation associated with stress tolerance. Gene-editing technologies, particularly CRISPR-based approaches, provide another powerful opportunity. Once an important regulatory gene or pathway has been identified, researchers can precisely modify it and test whether the change improves plant performance under stress. However, the objective should not simply be to switch stress-response genes permanently on. That could impose a substantial energy cost on the plant. A more promising strategy is to understand when, where and how strongly a stress response should be activated. In this way, future crop improvement could focus on fine-tuning regulatory networks so that plants respond rapidly when stress occurs but maintain normal growth when conditions are favorable.

Q *As climate change creates new challenges for agriculture, what developments in plant science give you the most hope for protecting future food production?*

A What gives me the most hope is the growing ability to connect fundamental plant biology with practical crop improvement. We are moving from simply identifying stress-responsive genes toward understanding complex molecular networks that coordinate growth, development and environmental adaptation. The integration of genomics, gene editing, computational biology, high-throughput phenotyping and advanced molecular biology will allow us to examine plant responses at unprecedented resolution.

I am particularly optimistic about approaches that combine natural genetic diversity with modern molecular technologies. Instead of looking for a single universal solution to drought or heat stress, we can identify mechanisms that are naturally successful in different environments and use that knowledge to develop crops suited to changing climates. The future of crop resilience will likely depend on precision rather than simply stronger stress responses—developing plants that can sense environmental chan-

changes, adjust their physiology efficiently, protect themselves when necessary, and return to normal growth when conditions improve. Climate change presents an enormous challenge, but plants have already evolved sophisticated mechanisms for surviving environmental stress over millions of years. Our task as plant scientists is to understand these mechanisms and translate that knowledge into sustainable agricultural solutions. Ultimately, the science of stronger crops is not only about helping plants survive. It is about helping them remain productive, efficient and resilient in an increasingly unpredictable environment.

Reference

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ABOUT THE AUTHORS

Dr. Salman Sahid, Dr. Shuvobrata Majumder, and Dr. Chandan Roy study how plants survive difficult environmental conditions such as drought, heat, and salty soil. Their research looks at how plants use genes and proteins to protect themselves, adjust their growth, and continue developing when conditions become stressful. By understanding these natural survival mechanisms, their work can help scientists develop stronger crops that can better cope with changing climates and challenging growing conditions.



Beyond Pneumonia: Recognising the Hidden Danger of Leptospirosis

OUTLOOK

Leptospirosis is a bacterial infection that can spread through water or soil contaminated by infected animals. In some people, it can affect the lungs and become life-threatening very quickly, sometimes looking like ordinary pneumonia at first. In this Science Desk conversation, Dr. Praveen Kumar Dubey and Dr. Bhoomika Kaushik explain how exposure to waterlogged areas can increase the risk, what warning signs doctors should recognize, and why early diagnosis, proper treatment, and greater awareness are important for preventing serious complications.

Q *What is leptospirosis, how is it transmitted, and why is it an important public health concern?*

A Leptospirosis is a bacterial infection caused by *Leptospira* species. The bacteria are commonly shed in the urine of infected animals, particularly rodents and livestock, and can contaminate soil and water. People become infected mainly through contact with contaminated water or wet soil, especially when the bacteria enter through cuts or abrasions in the skin or through the eyes, nose, or mouth.

Farmers and agricultural workers are particularly at risk because of frequent contact with soil, standing water, crops, and animals. Heavy rainfall and flooding can increase the risk by spreading contaminated water over a wider area. This makes working in waterlogged fields after heavy rain an important exposure to recognise.

Leptospirosis can range from a mild febrile illness to severe disease involving multiple organs. In some patients, the lungs can be severely affected, leading to pulmonary haemorrhage and life-threatening respiratory failure.

Q *Why can leptospirosis be mistaken for ordinary pneumonia, and what clinical clues should prompt doctors to look beyond the obvious diagnosis?*

A Leptospirosis can initially resemble pneumonia beca-



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AREAS OF EXPERTISE



Pulmonary Medicine • Tuberculosis • Critical Care
Medicine • Interventional Pulmonology • Severe
Respiratory Infections



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AREAS OF EXPERTISE



Histopathology • Cytopathology • Hematopathology
• HPLC

use fever, cough, breathlessness, and lung opacities can occur in both conditions. The warning sign is often how quickly the patient deteriorates.

In our patient, the initial chest X-ray showed left lower-zone consolidation and he was treated for pneumonia. Within 24 hours, he developed severe breathlessness, profound hypoxaemia, hypotension, and bilateral pulmonary opacities. His haemoglobin and platelet counts also fell, with evidence of liver involvement. Such rapid progression should prompt clinicians to reconsider the diagnosis. A history of heavy rainfall, flooding, agricultural work, or exposure to waterlogged fields can provide an important clue. In our case, the history of working in waterlogged wheat fields after heavy rainfall helped point towards leptospirosis.

Q *How does exposure to contaminated water increase the risk of leptospirosis, and which groups are most vulnerable?*

A *Leptospira* can contaminate water and moist soil aft-

er being shed in the urine of infected animals. Heavy rainfall and flooding can spread this contamination through standing water and waterlogged fields.

Farmers and agricultural workers are particularly vulnerable because they may have prolonged contact with wet soil and standing water. People involved in flood-related work, sewage and sanitation, and animal handling may also be at increased risk. The risk is especially relevant during and after the rainy season. In our patient, exposure to waterlogged wheat fields following heavy rainfall was an important epidemiological clue.

Q What happens in the lungs during leptospirosis-associated pulmonary haemorrhage, and why can it become life-threatening so quickly?

A In severe leptospirosis, inflammation can damage the small blood vessels of the lungs and increase the permeability of the alveolar-capillary barrier. Blood then leaks into the air spaces, causing diffuse alveolar haemorrhage. This is thought to result mainly from an immune-mediated process rather than direct destruction of lung tissue by the bacteria. As blood fil-

ls the alveoli, oxygen exchange becomes severely impaired, leading to profound hypoxaemia and respiratory failure. The bleeding can also cause a rapid fall in haemoglobin. In our patient, the initial localized lung opacity progressed to bilateral pulmonary opacities within 24 hours, accompanied by severe hypoxaemia and falling haemoglobin and platelet counts. This rapid progression is what makes pulmonary haemorrhage such a dangerous complication.

Q How did early diagnosis, antibiotics, respiratory support, and corticosteroid therapy contribute to the patient's recovery?

A Early recognition allowed us to address both the infection and the rapidly developing pulmonary complication. *Leptospira* IgM was positive, while investigations for important mimics, including dengue, malaria, tuberculosis, and pulmonary vasculitis, were negative. The patient received antimicrobial therapy, including doxycycline initially and ceftriaxone subsequently. Because of severe hypoxaemia, he required non-invasive ventilation with BiPAP and high inspired oxygen. Once severe pu-

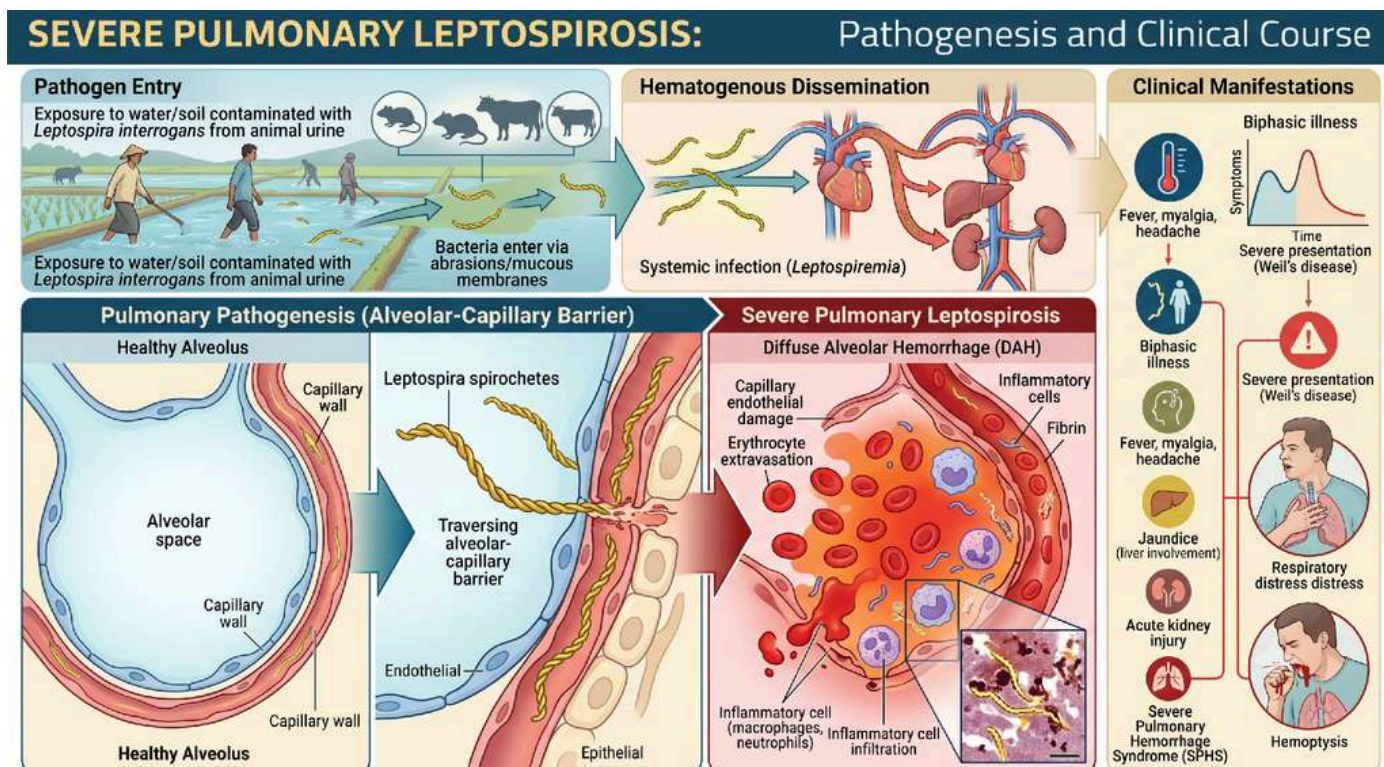


Figure 1. Pathogenesis and clinical course of severe pulmonary leptospirosis. Following environmental exposure and hematogenous spread, *Leptospira* spirochetes disrupt the alveolar-capillary barrier to cause diffuse alveolar haemorrhage (DAH), presenting with rapidly worsening respiratory distress and hemoptysis (SPHS).

monary haemorrhage was established, intravenous methylprednisolone was given, followed by oral prednisolone. He improved substantially within 48 hours, was weaned from ventilatory support by day 5, and showed marked radiological improvement. The steroid response was encouraging, although a single case cannot establish the effectiveness of corticosteroids for all patients.

Q *What practical lessons does this case offer to healthcare professionals when a patient deteriorates rapidly despite treatment for presumed pneumonia?*

A The key lesson is to reassess the diagnosis when a patient deteriorates much faster than expected. Clinicians should review the exposure history and look for falling haemoglobin or platelet counts, worsening oxygenation, rapidly increasing bilateral infiltrates, and evidence of other organ involvement. These findings may indicate pulmonary haemorrhage rather than uncomplicated pneumonia. A few targeted questions about occupation, recent rainfall, flooding, and contact with standing or contaminated water can provide an important diagnostic clue. At the same time, conditions such as dengue, malaria, tuberculosis, and pulmonary vasculitis should be considered when clinically appropriate. The practical message is simple: when presumed pneumonia progresses unusually quickly, stop and reassess the diagnosis.

Q *Looking ahead, what improvements in awareness, diagnosis, or treatment could help reduce illness and deaths from severe leptospirosis?*

A Greater awareness among both healthcare professionals and communities could help identify leptospirosis earlier, particularly during and after periods of heavy rainfall and flooding. Farmers and others who regularly work in wet or waterlogged environments should be made aware of the risk. For clinicians, recognising leptospirosis when a febrile illness develops severe or rapidly progressive respiratory involvement can reduce diagnostic delay. Better access to timely and reliable diagnostic testing, particularly in rural and resource-limited settings, would also be valuable.

In severe pulmonary haemorrhage, early respiratory support and appropriate antimicrobial treatment are important. The potential role of corticosteroids should continue to be studied, as our patient's response was encouraging but cannot establish treatment efficacy.

At the public health level, education before and during the rainy season, together with measures that reduce exposure to contaminated water and soil, may help prevent infection and encourage earlier medical attention.

ABOUT THE AUTHORS

Dr. Praveen Kumar Dubey is a doctor and researcher at AIIMS Raipur, India, who studies lung diseases, respiratory infections, and breathing problems. Dr. Bhoomika Kaushik also works at AIIMS Raipur, in Pathology and Laboratory Medicine, where she studies tissues, cells, and blood to help diagnose diseases. Their work together highlights severe leptospirosis affecting the lungs, particularly dangerous lung bleeding. Through their research, they emphasize the importance of recognizing environmental exposure, identifying rapid worsening of symptoms, and providing early diagnosis, antibiotics, breathing support, and appropriate treatment.

Reference

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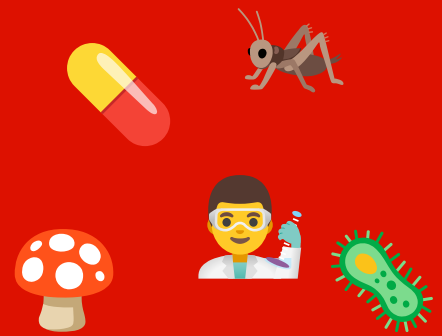
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Answers here – don't peek!

SCRATCH-N-SCIENCE!

QUIZ BUZZERS



Q1

What can DNA help researchers learn about Thar Desert communities?

- A. Their migration history
- B. Tomorrow's weather
- C. The age of desert sand
- D. The amount of rainfall next year

Q2

What do molecular chaperones help protect when plants face extreme heat?

- A. Soil minerals
- B. Proteins
- C. Flower colours
- D. Rainwater

Q3

What useful material can be made from discarded fruit peels?

- A. Glass
- B. Steel
- C. Activated carbon
- D. Plastic bottles

Q4

Do ideas of beauty change across cultures and time?

- A. No, they are always the same
- B. Yes, they can change
- C. Only during childhood
- D. Only in one country

Q5

How can conflict harm children who are not directly injured?

- A. By making the days shorter
- B. By disrupting healthcare, food and clean water
- C. By changing their blood type
- D. By stopping the seasons

Q6

Which part of the brain do the electronic devices in the article aim to imitate?

- A. Synapses
- B. Bones
- C. Muscles
- D. Blood vessels

Q7

What habit does the article encourage for healthy ageing?

- A. Avoiding exercise
- B. Exercising only as a child
- C. Regular physical activity
- D. Sleeping all day

Q8

What does robotic telesurgery allow a surgeon to do?

- A. Operate from a distant location
- B. Perform surgery without a patient
- C. Work without any equipment
- D. Replace every member of the surgical team

DISCOVERY HIGHLIGHTS

CANCER SCIENCE &
PRECISION THERAPEUTICSAI REVEALS HIDDEN STEM-LIKE
CELL STATES LINKED TO CANCER
OUTCOMES

Artificial intelligence has revealed cancer stem-like cell patterns associated with tumor survival and response to immunotherapy. Researchers developed ACSCeND, a deep-learning framework that identifies different stem-like cell states using single-cell and bulk RNA sequencing data. Applying it to more than 25,000 tumor profiles, they found that greater abundance of cancer stem-like cells was associated with poorer disease-free survival and reduced response to immunotherapy. The analysis also uncovered distinct molecular programs linked to different stem-like states, providing clues to how tumors maintain diversity and evolve. By combining individual-cell information with large tumor datasets, the approach offers a view of cancer stemness. The findings suggest that these cellular states could become biomarkers for understanding disease progression and predicting differences

in treatment response.

Chowdhury D. et al., NAR Cancer, 2026.

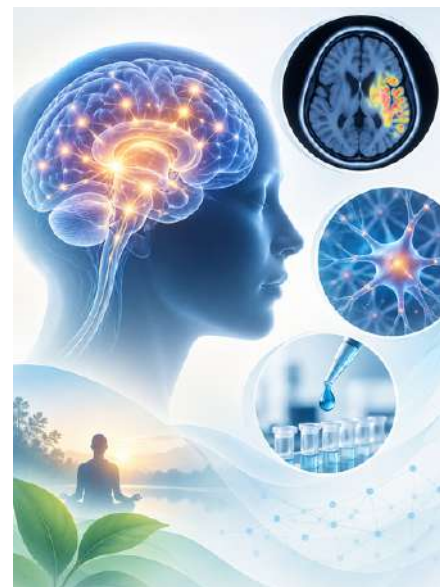
A CANCER DRUG RELEASES ITS
PAYLOAD AND LIGHTS UP AT THE
SAME TIME

Researchers have created an anticancer prodrug that activates under cancer-associated conditions while simultaneously producing a fluorescent signal. Called RK-251, the molecule responds to reactive oxygen species, which are often elevated in cancer cells. Activation releases NBDHEX, an inhibitor of GSTP1, a protein that can contribute to drug resistance. Remarkably, the same reaction switches on near-infrared fluorescence, allowing researchers to track drug release. In laboratory experiments, RK-251 showed potent activity against triple-negative breast cancer cells compared with nonmalignant cells. Fluorescence activation was also demonstrated in developing zebrafish embryos without noticeable acute toxicity. The finding shows that treatment and imaging can be incorporated into one molecule, providing a strategy for anticancer agents whose activation and drug release could be monitored during treatment.

Kesarwani R. et al., Journal of Medicinal Chemistry, 2026.

BRAIN HEALTH &
DIAGNOSTICSA FLUORESCENT PROBE BRINGS
SMARTPHONE-BASED ALZHEIM-
ER'S DETECTION CLOSER

Researchers have developed a fluorescent probe that detects amyloid- β , a marker of Alzheimer's disease, and pairs its signal with



smartphone-based analysis. Called TZ-48, the probe lights up when it binds amyloid- β and can track changes as the protein aggregates. In Alzheimer's-model mice, TZ-48 crossed the blood-brain barrier and enabled researchers to visualize amyloid accumulation in the brain. It also detected amyloid- β in blood serum and distinguished samples from Alzheimer's-model mice from healthy controls. The team then developed ADxFluor, a smartphone-enabled platform that measures the fluorescence signal to assess serum amyloid. The finding demonstrates how molecular sensing and technology could be combined for simpler Alzheimer's assessment. However, the approach remains preclinical and requires validation in humans before becoming a diagnostic test. If successfully translated to human testing, this approach could support more accessible, minimally invasive Alzheimer's screening and potentially help identify disease-related changes at earlier stages.

Bhagavath K. K. et al., ACS Chemical Neuroscience, 2026.

DISCOVERY HIGHLIGHTS

A PORTABLE SENSOR DETECTS MULTIPLE TOXICANTS IN MINUTES

Researchers have developed a compact point-of-care device that can detect iron, chromium, fluoride and lead without relying on large laboratory instruments. The system uses specific colour-producing chemical reactions and measures the resulting optical signals using a light source, photoresistor and microcontroller. Each contaminant reacts with a selected reagent, allowing the device to identify different toxicants with good selectivity. Importantly, its detection limits were below World Health Organization threshold levels. Researchers tested the system using more than 2,000 spiked and field samples and found good agreement with conventional laboratory-based spectroscopic measurements. Its portable design and rapid measurements could make it particularly useful in resource-limited areas, providing a practical approach for environmental and healthcare monitoring closer to where testing is needed.

Kashyap S. et al., *IEEE Sensors Journal*, 2026.

MICROBES, IMMUNITY & DRUG RESISTANCE

CITY LIFE CHANGES GUT MICROBES DIFFERENTLY ACROSS SOUTH ASIA

Urbanization changes the human gut microbiome, but a South Asian study found no single microbial signature of moving from village to city life. Researchers examined gut bacteria from 575 adults across ten diverse communities, comparing pe-



ople in ancestral villages with those in urban centres. Although urbanization was associated with increases in some disease-linked microbes, many changes differed between communities. Surprisingly, geography and community membership shaped microbiome composition more strongly than lifestyle. Researchers also identified microbial functions associated with wheat and dairy consumption in some populations, suggesting gut microbes may contribute to adaptation to local diets. The findings reveal that modernization does not reshape everyone's microbiome equally: culture, geography and food traditions continue leaving distinct biological signatures within the human gut.

Ramachandran S. L. et al., *Gut Microbes*, 2026.

AN ENGINEERED GAUZE BREAKS DOWN BACTERIAL BIOFILMS TO HELP WOUNDS HEAL

Researchers have developed a bioactive wound dressing that attacks the protective biofilm surrounding bacteria rather than directly killing

the microbes. The team identified CRhAB, an enzyme that breaks down the polysaccharide-rich matrix formed by *Acinetobacter baumannii*, a WHO critical-priority pathogen. Removing this protective barrier disrupted mature biofilms and allowed macrophages to infiltrate and clear bacteria more effectively, without directly affecting bacterial viability. Researchers then attached the enzyme to clinical-grade gauze, creating a stable dressing that retained its biofilm-breaking activity. In a mouse infection model, the engineered gauze reduced bacterial colonization and accelerated wound healing. Because the strategy targets biofilm architecture rather than bacterial survival, it could offer a resistance-agnostic approach for developing wound-care materials against difficult biofilm-associated infections.

Ramakrishnan R. et al., *npj Biofilms and Microbiomes*, 2026.

MATERIALS & INNOVATION

A THIN FILM BREAKS EXPECTED LIMITS FOR TURNING HEAT INTO VOLTAGE

A crystalline semiconductor has produced a thermoelectric response far beyond expectations for conventional electronic conductors. Researchers created 200-nanometre-thick scandium nitride films containing high concentrations of charged dopants. Their uneven distribution generated large fluctuations in the material's electronic potential, changing how electrical charges moved through it. Near room temperature, the films produced a Seebeck coefficient exceeding -124 millivolts per kelvin, a scale more commonly associated with ionic systems than crystalline semiconductors. The response became even stronger in ultrathin films, where electrical interactions amplified these fluctuations. Remarkably, the solid material displayed electrolyte-like thermopower while remaining crystal-

DISCOVERY HIGHLIGHTS



line. The discovery challenges expectations for thermoelectric transport and reveals an unusual strategy for designing materials generating exceptionally large electrical responses from relatively small differences in temperature.

Karanje R. et al., *Science*, 2026.

MACHINE LEARNING SPEEDS THE SEARCH FOR MATERIALS THAT CAN RECYCLE CO₂

Researchers have used machine learning and computational modelling to identify promising two-dimensional materials for converting carbon dioxide into useful carbon monoxide. The team screened 56 high-entropy MBenes, materials containing combinations of five metals and boron. By combining quantum-mechanical calculations with a machine-learning model, they narrowed thousands of possible surface environments to 18 viable catalysts. Three compositions emerged as particularly promising, showing favourable CO₂-to-CO conversion without requiring additional applied potential in the co-

mputational analysis. The researchers found that interactions between different metals helped stabilise an important reaction intermediate, overcoming limitations commonly seen in simpler catalyst surfaces. The study demonstrates how machine learning can accelerate the discovery of complex catalysts for CO₂ conversion, although experimental validation will be required to confirm their predicted performance.

Bharadwaj H. S. H. & Ranganathan R., *npj Computational Materials*, 2026.

PLANTS, FOOD & AGRICULTURAL INNOVATION

CHANGING INDIA'S CROP MIX COULD SAVE WATER AND REDUCE FERTILISER POLLUTION

Researchers have found that restructuring India's crop production around nitrogen efficiency could deliver several environmental benefits without reducing calorie production. Using an integrated analysis of nutrients, water, greenhouse-gas emissions, economics and interstate food trade, the study found that nitrogen-focused crop restructuring could reduce excess nitrogen by 13.4% and agricultural water use by 18.6%. It could also lower greenhouse-gas emissions by 8.7% while reducing the economic gap in cereal returns. The researchers estimated that lower nitrogen pollution could reduce associated socio-environmental costs by around US\$1.19 billion. The restructuring would also increase interstate trade



in alternative cereals. The findings show how changing where and which crops are grown could simultaneously improve resource efficiency, reduce pollution and strengthen the sustainability of India's food system.

Goyal S. S. et al., *Nature Communications*, 2026.

A PLANT'S REFUSAL TO SELF-POLLINATE COULD HELP IMPROVE MUSTARD CROPS

Researchers have uncovered key genes controlling self-incompatibility in *Brassica rapa*, a natural mechanism that prevents a flower from fertilising itself. Studying the important Indian oilseed varieties toria and yellow sarson, the team identified SRK, FER and ARC1 as key components regulating self-incompatibility, while SRK, FER and MLPK were linked to reactive oxygen species signalling. By comparing gene sequences, structures and expression patterns, researchers found that these components are conserved with previously known self-incompatibility systems. Preventing self-fertilisation encoura-

DISCOVERY HIGHLIGHTS

ages cross-pollination, helping maintain genetic diversity and enabling breeders to exploit hybrid vigour. Understanding this reproductive system could therefore provide a foundation for developing improved Brassica rapa varieties and combining valuable agricultural traits through hybrid breeding.

Bhalla H. et al., Frontiers in Plant Science, 2026.

ATMOSPHERE, CLIMATE & ENVIRONMENT

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Bhalla H. et al., Frontiers in Plant Science, 2026.



AN UNUSUAL OZONE-RICH LAYER APPEARS OVER THE BAY OF BENGAL

Scientists detected an unusually enhanced ozone layer high above the North Bay of Bengal, showing how atmospheric movement can temporarily reshape stratospheric ozone. Winter measurements identified the ozone-rich region at about 21–23 kilometres altitude, where ozone pressure was approximately 50 nbar higher than the typical profile over eastern Indian subtropics. The layer was around 2.1–2.4 kilometres thick and persisted for more than 24 hours. Weather balloons, ground-based radar, satellites and atmospheric datasets independently supported the observation. Researchers suggest that compression of air masses or movement of ozone-rich air from mid-latitudes may have caused the enhancement. The finding provides new evidence that atmospheric circulation can create substantial, short-lived redistributions of ozone, improving understanding of changes in Earth's protective stratospheric ozone layer.

Das S. S. et al., Earth and Space Science, 2026.

WILDFIRES CAN BRIEFLY BOOST FOREST SOIL FERTILITY BUT THERE IS A COST

Wildfires can temporarily enrich forest soils, but repeated burning may ultimately threaten their health. Researchers studied 12 fire-affected sites in the dry deciduous forests of West Bengal, comparing burned soils with nearby unburned areas. The strongest changes occurred within the upper five centimetres of soil, where fire-derived ash increased available nitrogen by 42%, potassium by 74%, organic carbon by 36% and electrical conductivity by 82%. Soil pH also increased, while bulk density declined slightly. These short-term improvements largely resulted from ash produced by incomplete burning of surface vegetation. However, the researchers caution that recurrent fires can increase surface erosion and subsequent nutrient loss, potentially degrading soils and undermining long-term forest sustainability despite the temporary fertility boost.

Mallick K. et al., Environmental Research Communications, 2026.

HIDDEN LIFE & BIODIVERSITY

A NEW UNDERGROUND FISH EMERGES FROM INDIA'S HIDDEN WATERS

Scientists have discovered a remarkable new fish living entirely underground in the alluvial aquifers of Bihar's Indo-Gangetic Plain. Named *Gangaichthys indonepalicus*, the tiny earthworm eel represents both a new genus and new species and is the first subterranean member known from its fish family. All three specimens were recovered from borewells, revealing an aquatic ecosystem hidden beneath one of India's most densely populated regions. Adapted to permanent darkness, the fish has reduced eyes, la-

DISCOVERY HIGHLIGHTS



cks body pigmentation and shows several unusual skeletal features. Genetic analysis confirmed its placement within the Chaudhuriidae family while revealing substantial divergence from related genera. The discovery highlights how poorly explored groundwater ecosystems can harbour highly distinctive species and underscores the importance of documenting and protecting subterranean biodiversity.

Khandekar A. et al., ZooKeys, 2026.

A NEW PLANT SPECIES EMERGES FROM TAMIL NADU'S SCRUBLANDS

Researchers have described a new plant species from the scrub vegetation of Cuddalore District in Tamil Nadu, adding to India's rich botanical diversity. Named *Schoenoplectiella cuddalorensis*, the species belongs to the sedge family, Cyperaceae. Although it resembles the closely related *Schoenoplectiella erecta*, researchers identified several distinctive features that establish it as a separate species. These include the absence of perianth bristles and a ligule, a well-developed creeping underground stem called a

rhizome, oblong-shaped seeds and a leaf sheath with a characteristically truncated opening. The discovery demonstrates that even relatively familiar scrub habitats can harbour plant species that remain undocumented. Careful botanical surveys and detailed comparisons of plant structures therefore remain important for revealing biodiversity and improving knowledge of India's regional flora.

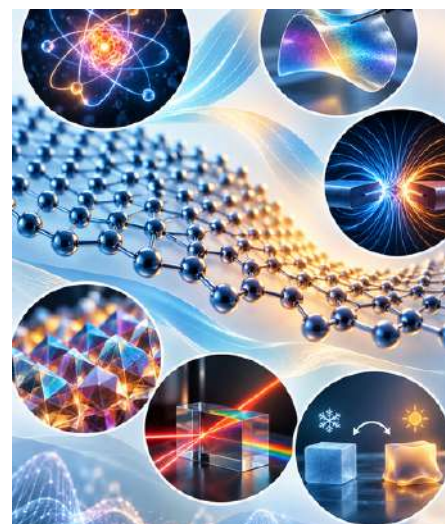
Lincy J. et al., Feddes Repertorium, 2026.

Ancient Earth & Deep Ocean

PHYSICS & RESPONSIVE MATERIALS

SOFT MATERIALS REVEAL A PHYSICAL MEMORY OF THEIR TEMPERATURE HISTORY

Researchers have shown that a soft material can retain a memory of how it was heated and cooled. The team studied packed PNIPAM microgel particles, which change size in response to temperature. When the suspensions were heated and cooled at different rates, their elasticity did not simply follow the same path back. Instead, the material's recovery depended on its thermal journey, revealing a history-dependent memory effect. Measurements showed that microscopic rearrangements of particles dissipated energy and influenced how strongly this memory persisted. Researchers could tune the effect by changing both temperature ramp rate and particle concentration. The findings reveal that soft glass-like materials depend on both present conditions and their past, offering a way to control memory in responsive materials.



Kawale S. V. et al., Journal of Colloid and Interface Science, 2026.

JUST 1% SOLVENT SWITCHES ON ELECTRICITY IN PEPTIDE NANOFIBERS

Adding only 1% of a cosolvent transformed electrically inactive peptide nanofibers into materials with a pronounced piezoelectric response. Researchers found that a peptide formed elongated nanofibers in pure water but showed neither large-scale chirality nor significant piezoelectric activity. Surprisingly, adding just 1% DMSO or DMF reorganized the molecular assembly, producing a chiral, or handed, structure while switching on its ability to generate an electrical response to mechanical stress. Spectroscopy, microscopy and molecular simulations linked this chirality with the emergence of piezoelectric behaviour. The discovery shows that new properties can arise without redesigning the molecule itself; changing its assembly environment can be enough. This offers a new strategy for creating responsive peptide materials for self-powered biosensors, biomedical devices and future bioelectronics.

DISCOVERY HIGHLIGHTS

Ramesh A. et al., *Angewandte Chemie International Edition*, 2026.

SPACE & SOLAR SCIENCE

MAGNETIC RECONNECTION EMERGES AS A DRIVER OF SOLAR ERUPTIONS

Scientists have uncovered a close connection between magnetic reconnection and the acceleration of powerful solar eruptions. Using three-dimensional computer simulations alongside observations of a real solar event, researchers followed twisted magnetic structures called flux ropes as they rose through the Sun's atmosphere. As a flux rope moved upward, surrounding magnetic fields stretched and compressed, eventually triggering magnetic reconnection, where field lines rearrange and release stored energy. The study found that changes in reconnection rate closely followed acceleration of the erupting structure, indicating that reconnection helps determine how rapidly these eruptions develop. Because coronal mass ejections can disrupt satellites, communications and technologies around Earth, the finding provides insight into solar eruptions and could improve better future models of hazardous space-weather events.

Maity S. S. et al., *The Astrophysical Journal*, 2026.

SOLAR WAVES REVEAL HOW ERUPTIONS DRIVE SHOCKS THROUGH THE SUN'S ATMOSPHERE

Researchers have found a strong connection between fast-moving ext-



reme-ultraviolet waves on the Sun and type II radio bursts, which are produced by shock waves travelling through the solar atmosphere. Using high-resolution observations from the Solar Dynamics Observatory together with radio measurements, the team compared the speeds of fast EUV wavefronts with shock speeds inferred from metric type II radio bursts. They found a clear linear relationship, with a correlation coefficient of **0.77**, suggesting that both signals originate from different parts of the same CME-driven shock. The findings also indicate that the slower coronal EIT waves described in earlier studies are unlikely to represent the fast shock component. The work helps clarify how solar eruptions generate large-scale shocks and improves interpretation of space-weather signatures.

Chandra R. et al., *Scientific Reports*, 2026.

QUANTUM SCIENCE

ONE WELL-TIMED ACTION CAN CHANGE HOW LONG QUANTUM ENTANGLEMENT SURVIVES

Researchers have demonstrated that the timing of a quantum operation can determine whether entanglement disappears early, survives longer or avoids sudden collapse altogether. Ent-

anglement is vulnerable to its surroundings and can abruptly vanish through "entanglement sudden death," creating challenges for quantum technologies. Researchers showed theoretically that applying a single local operation at different moments redirects the system along paths of entanglement decay without modifying its environment. They demonstrated the principle experimentally using a photonic interferometer, achieving avoidance, delay and acceleration of entanglement loss in one platform. The study also showed that this single-shot approach is optimal among broad local control strategies. The discovery establishes timing as a quantum-control resource: preserving quantum connections can depend on when scientists choose to act.

Behera S. R. et al., *Physical Review A*, 2026.

QUANTUM LIGHT MAKES FORBIDDEN SIGNALS APPEAR IN GRAPHENE

Researchers have shown theoretically that the quantum nature of light can unlock optical signals in graphene that would normally remain forbidden. The team studied graphene driven by specially structured quantum light containing two counter-rotating frequencies. When one component was placed in a squeezed quantum state, its fluctuations broke the symmetry that normally suppresses certain high-harmonic signals, allowing these "forbidden" harmonics to appear. The researchers also found distinctive polarization patterns and unusually strong photon-number fluctuations, showing that the emitted harmonics retain information about the quantum statistics of the incoming light. The findings suggest that these signals could act as sensitive probes of quantum light.

Prabhu K. & Dixit G., *Physical Review B*, 2026.

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SCIENCE IN FOCUS

**INDIA-AUSTRALIA PARTNERSHIP
INDIA LOOKS TO THE DEEP OCEAN TO
SECURE ITS CRITICAL MINERAL FUTURE**

India is taking steps to develop deep-sea mining as a future source of critical minerals needed for clean energy, electric mobility, advanced manufacturing and high-performance computing. On 8 September 2026, the Ministry of Earth Sciences and the National Institute of Ocean Technology (NIOT), with EY and NITI Aayog, organized an industry workshop to explore the strategic and commercial potential of deep-sea mining. India holds an International Seabed Authority exploration contract covering 75,000 square kilometres of the Central Indian Ocean Basin, estimated to contain around 366–380 million tonnes of polymetallic nodules. These nodules contain strategically important metals including nickel, cobalt, copper and manganese. India also holds exploration contracts for polymetallic sulphides. Technology development is progressing under the ₹4,077 crore Deep Ocean Mission. NIOT has already demonstrated indigenous deep-sea mining crawler systems at depths exceeding 5,000 metres in the Indian Ocean, highlighting India's growing capabilities in subsea engineering. Developing these resources could eventually create a broader "mine-to-metal" ecosystem involving marine robotics, offshore engineering, shipbuilding, metallurgy and battery manufacturing. The initiative also seeks to connect research institutions, technology developers, investors and industry to prepare future commercial projects. However, commercial mining of polymetallic nodules in international waters cannot begin until the International Seabed Authority finalizes its Exploitation Code.

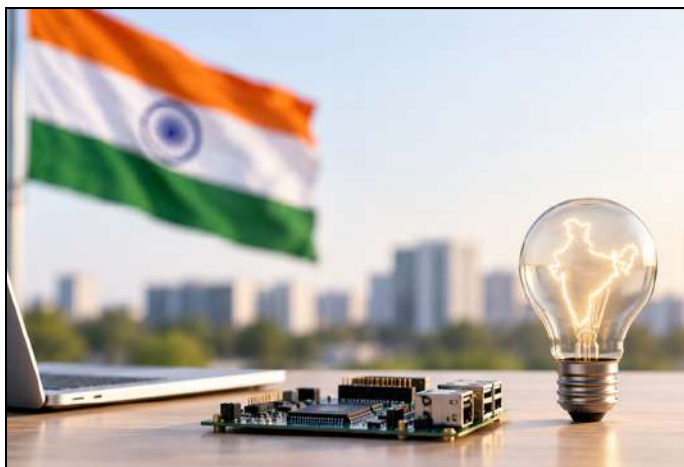
**CYBER FRAUD
TECHNOLOGY STOPS ₹5,000 CRORE IN
CYBER FRAUD BEFORE THE MONEY IS
LOST**

India's Financial Fraud Risk Indicator (FRI) has helped prevent more than ₹5,000 crore in suspected cyber-fraud transactions within just 15 months, demonstrating how technology can stop financial crime before citizens lose their money. Launched by the Department of Telecommunications in May 2025, FRI uses telecom intelligence to assess whether a mobile number is likely to be associated with financial fraud. Numbers are classified as medium, high or very high risk using information from citizen reports, cybercrime databases, telecom operators, banks and other sources.

These risk signals are shared in real time with banks, payment platforms and other financial institutions, allowing suspicious transactions to be flagged or stopped before money leaves an account. By August 2026, prevented losses had reached ₹5,043.73 crore, compared with ₹660 crore during the programme's first six months.

The system demonstrates a shift from investigating cybercrime after losses occur to preventing fraud at the transaction stage, highlighting how shared digital intelligence and institutional cooperation can strengthen protection in India's expanding digital economy. As cybercriminals adopt increasingly sophisticated methods, tools such as FRI could become essential for building public trust in digital payments while creating a faster, coordinated defence against evolving financial threats.

SCIENCE IN FOCUS



SOFTWARE POWERHOUSE FROM SOFTWARE POWERHOUSE TO HARDWARE INNOVATOR: INDIA EXPANDS ITS ELECTRONICS STARTUP AMBITION

India is expanding its ambitions in electronics and hardware innovation, aiming to turn more home-grown ideas into commercially competitive products. At the Electropreneur Summit 2026, Software Technology Parks of India launched an Open Challenge Programme to identify and support promising startups in Electronics System Design and Manufacturing (ESDM). The initiative builds on Electropreneur Park 1.0, which supported 59 startups, generated 129 products and led to 66 patent filings. Its next phase, EP 2.0, has a much larger target: nurturing 500 startups while extending incubation, mentoring and infrastructure support beyond major technology centres into Tier-II and Tier-III cities. Eleven partner institutions across northern India will serve as Spoke Centres, helping innovators gain access to the wider electronics ecosystem. The programme also brings investors, academia, industry and government closer together. The expansion comes as India's electronics production has grown from under ₹2 lakh crore to more than ₹13 lakh crore over the past decade. The larger goal is to convert India's technology talent into intellectual property, hardware products and globally competitive electronics businesses. By strengthening support from early prototyping to commercialisation, the initiative could help more Indian electronics startups scale successfully, create skilled jobs, attract investment and transform innovative ideas into globally competitive technologies and businesses.



NEW PLATFORM INDIA BUILDS A NEW PLATFORM TO PUT MORE ZERO-EMISSION TRUCKS ON THE ROAD

India is taking a major step toward cleaner freight transport with the launch of the Platform for Aggregating Clean Transport (PACT), a NITI Aayog initiative designed to accelerate the deployment of zero-emission trucks across the country. PACT will bring together freight demand from shippers and logistics companies and connect it with vehicle manufacturers, financiers and charging operators. By identifying demand along major freight corridors, the platform aims to make investment in electric trucks and charging infrastructure more commercially attractive and easier to plan. India's electric freight sector is already expanding. Deployments increased more than fourfold, from 201 vehicles in FY25 to 826 in FY26, while more than 3,000 electric medium- and heavy-duty trucks are currently operating nationwide. The initiative also introduced the ZET Marketplace, connecting companies seeking vehicles, financing, charging solutions and technology partnerships. Rather than supporting isolated electric-truck pilots, PACT aims to coordinate demand, infrastructure and investment at scale.

The approach could help reduce freight emissions while strengthening domestic clean-mobility manufacturing, logistics efficiency and India's long-term energy security. By aligning technology, finance and infrastructure, PACT could make zero-emission freight more practical for businesses, helping cleaner trucks move from demonstration projects toward widespread adoption across India's major transport corridors.

SCIENCE IN FOCUS



FISH FARMING LESS FRESH WATER FISH FARMING WITH 95% LESS FRESH WATER: INDIA EXPANDS NEXT- GENERATION AQUACULTURE

India is expanding technology-driven aquaculture using Recirculatory Aquaculture Systems (RAS) and Biofloc technology, opening new possibilities for producing fish with less water and in places where conventional fish farming may be difficult. RAS treats and recirculates water within controlled farming systems, recycling up to 90–95% of it. Biofloc takes a different approach, using beneficial microorganisms to maintain water quality while supporting fish growth. Both technologies can enable intensive, year-round production while improving resource efficiency. Under the Pradhan Mantri Matsya Sampada Yojana, 9,467 RAS and 4,573 Biofloc units have been approved, backed by ₹4,120 crore in investment.

These systems are also supporting high-value species including trout, shrimp and ornamental fish. The shift comes as India's annual fish production has more than doubled, reaching 198 lakh tonnes in 2024–25. Future integration with artificial intelligence, digital monitoring, drones and renewable energy could make these systems even more efficient. Such technology-led aquaculture could strengthen food security, rural livelihoods and seafood exports while reducing pressure on water resources.

By bringing advanced fish farming closer to communities, these systems could also create skilled jobs, encourage entrepreneurship and help farmers produce more reliably despite climate change and increasing water scarcity.



INDIA AND SWEDEN FORCES INDIA AND SWEDEN JOIN FORCES TO TURN AI INTO REAL-WORLD INDUSTRIAL SOLUTIONS

India and Sweden are exploring a deeper technology partnership that could combine India's rapidly expanding artificial-intelligence ecosystem with Sweden's strengths in advanced manufacturing, industrial research and technology. Under the Sweden-India Technology and AI Corridor (SITAC), the IndiaAI Mission and Swedish representatives discussed opportunities for collaboration in industrial AI, trusted data, computing infrastructure, skills and responsible AI. The partnership could lead to joint pilots, testbeds, technology co-development and commercial collaborations between companies from both countries. India brings large-scale digital public infrastructure, a growing AI talent pool and extensive environments for testing and deploying new technologies. Sweden contributes expertise in industrial innovation and advanced manufacturing. The discussions also covered important issues surrounding AI adoption, including data governance, localisation, regulation and market access. IndiaAI's priorities extend beyond developing AI models to building computing capacity, datasets, indigenous AI, startup financing and future skills. By connecting these capabilities with Swedish industry, the initiative aims to move international AI cooperation from dialogue toward practical applications while promoting safe, trusted and responsible technology. Together, these complementary strengths could accelerate real-world AI innovation, strengthen economic ties and create new opportunities for researchers and startups.

SCIENCE IN FOCUS



PARTICULATE POLLUTION

CLEARER SKIES? 108 INDIAN CITIES REPORT A DROP IN PARTICULATE AIR POLLUTION

India's efforts to tackle urban air pollution are showing measurable progress. In 2025–26, 108 cities recorded lower annual PM10 concentrations than in 2017–18. Among them, 72 achieved reductions above 20%, while 26 reported declines exceeding 40%. Fourteen cities met national air-quality standards. Much of this effort is being coordinated through the National Clean Air Programme (NCAP), launched in 2019 and now covering 130 cities. India has also expanded its air-quality monitoring network to 1,646 stations across 603 cities, combining periodic measurements with continuous real-time monitoring.

The strategy goes beyond monitoring. Cities are addressing vehicle and industrial emissions, construction dust, waste burning and crop-residue burning while promoting cleaner transport and green spaces. Digital platforms are also being used to track progress and improve accountability. Challenges remain, particularly because pollution sources differ between cities. The next phase therefore emphasizes source-specific interventions, real-time data, forecasting and scientific modelling moving India's clean-air strategy toward increasingly targeted, evidence-based action.

As monitoring improves and interventions become more locally focused, these efforts could help cities identify pollution hotspots earlier, protect public health and support cleaner, healthier and more sustainable urban environments for millions of people.



BRING VULTURES BACK

INDIA IS WORKING TO BRING ITS VULTURES BACK

India is strengthening efforts to restore vulture populations after their dramatic decline since the 1990s. These scavengers are vital to ecosystems because they rapidly remove animal carcasses, recycle nutrients and reduce the accumulation of potentially disease-carrying remains. A major focus is the Jatayu Conservation Breeding Centre in Pinjore, which breeds three threatened species: White-rumped, Long-billed and Slender-billed vultures. During 2025–26, the centre housed 356 vultures and successfully bred 35 chicks. It also released or contributed 87 vultures for reintroduction and transferred 90 birds to other conservation-breeding facilities. India's strategy is now moving beyond captive breeding toward creating "Vulture Safe Zones" where recovered populations can survive in the wild. This requires safer veterinary practices, reliable uncontaminated food and improved carcass management. The approach reflects an important lesson in conservation: breeding endangered animals is only the beginning. Long-term recovery depends on removing the threats that caused their decline and creating landscapes where reintroduced populations can survive, reproduce and eventually become self-sustaining.

Restoring these remarkable birds could strengthen ecosystem health while reducing risks associated with unmanaged carcasses. Their recovery would also demonstrate how science, conservation breeding and safer landscapes can reverse severe wildlife declines.

SCIENCE IN FOCUS



SPACE HUMAN SPACEFLIGHT

INDIA AND FRANCE EXPAND A SIX-DECADE SPACE PARTNERSHIP TOWARD HUMAN SPACEFLIGHT

India and France are preparing to deepen one of India's longest international space partnerships, with human spaceflight, advanced technologies and greater industry participation emerging as key areas for future cooperation. The two countries have collaborated in space for nearly six decades, including through joint satellite missions such as Megha-Tropiques and SARAL. Their partnership is now looking toward a new generation of activities, including Earth observation, climate applications and India's future human spaceflight programme in Low Earth Orbit. The discussions also highlighted design and manufacturing technologies, space-based connectivity and exploration beyond the International Space Station. Greater interaction between Indian and French space companies is expected to complement cooperation between ISRO and France's CNES. Another important focus is responsible use of space. India and France are discussing sustainable use of outer space, open access to scientific data and international management of communication frequencies. The evolving partnership reflects how space cooperation is changing from primarily joint satellite missions toward human exploration, commercial innovation and technologies that could shape the future space economy. As cooperation expands, the partnership could create new opportunities for scientists, startups and industry while supporting safer space operations and developing technologies needed for future exploration, climate monitoring and a growing global space economy.



BIOTECHNOLOGY INNOVATIONS

FROM LAB TO MARKET: BIO-NIVESH AIMS TO SCALE INDIA'S BIOTECHNOLOGY INNOVATIONS

India has launched BIO-NIVESH, a new platform designed to tackle one of biotechnology's biggest challenges: turning promising laboratory discoveries into products and companies that can reach the market. Biotechnology often requires long development periods, complex regulatory pathways and substantial investment before an innovation becomes commercially viable. BIO-NIVESH aims to bridge this gap by bringing scientists, startups, investors and industry together early in the development process. Its first edition connected 20 biotechnology and deep-tech startups with around 50 investors. Unlike conventional pitching events, the platform is intended to help investors understand the science, intellectual property and regulatory pathways behind emerging technologies, while helping innovators understand investment and market requirements. The initiative is supported by a broader push to attract long-term private capital into research. BIRAC has also been designated a fund manager for biotechnology and allied sectors under India's ₹1-lakh-crore Research, Development and Innovation Fund. BIO-NIVESH is planned as a recurring platform across different cities. Its success will ultimately depend on whether these connections translate into investment, scaled technologies and products reaching real-world markets.

By strengthening connections between science and finance, BIO-NIVESH could help promising Indian biotechnology innovations move faster from laboratories into society.

SCIENCE IN FOCUS



NATIONAL CLOCK

ONE NATION, ONE TIME: INDIA BUILDS A PRECISE NATIONAL CLOCK

India is establishing Indian Standard Time (IST) as the country's common, legally recognised and scientifically traceable time reference under the new Legal Metrology (Indian Standard Time) Rules, 2026. Precise time is far more important than simply keeping clocks accurate. Telecommunications, digital payments, power grids, transportation, data centres and cybersecurity systems depend on synchronised time stamps. Even tiny timing differences can become important when networks must coordinate transactions or reconstruct the sequence of events during a cyberattack. At the heart of the system is CSIR-NPL, which generates IST using an ensemble of atomic clocks. The national time scale is maintained within a few nanoseconds of Coordinated Universal Time, the international reference. India is also creating a distributed timing network, with secondary time scales at five regional laboratories and satellite-based dissemination through ISRO's NavIC. Network technologies and high-precision optical-fibre systems provide additional routes for distributing accurate time. The new framework therefore goes beyond standardising clocks. It treats precise, reliable and resilient time as essential national infrastructure for an increasingly digital economy.

As digital systems become more interconnected, a unified national time standard could improve reliability, strengthen cybersecurity and support emerging technologies that require precise coordination, from financial networks and smart grids to navigation and advanced scientific research.



DRONES AND DEFENCE

INDIA BUILDS INDIGENOUS MICRO GAS TURBINE ENGINES FOR DRONES AND DEFENCE SYSTEMS

India has taken another step towards self-reliance in aerospace propulsion with the unveiling of three indigenous Micro and Small Gas Turbine Engines developed by CSIR-National Aerospace Laboratories. On 25 August 2026, CSIR-NAL introduced the NJ-05, NJ-50 and NJ-100 engines, producing 5 kg, 50 kg and 100 kg of thrust respectively. The compact engines are designed for applications including tactical unmanned aerial vehicles, drone interceptors and small missile systems. Their development required advances in high-speed turbomachinery and high-temperature combustion technologies, areas that are critical for miniaturised propulsion. CSIR-NAL is also positioning itself as a multi-stage integrator for India's expanding drone ecosystem, with domestic aerospace companies and start-ups expected to play an important role in manufacturing these engines at scale. Developing indigenous propulsion systems could reduce dependence on imported critical subsystems while strengthening capabilities in UAVs, defence aerospace and autonomous platforms. The programme also supports a wider domestic ecosystem involving engine design, precision manufacturing, materials engineering, electronics and systems integration. The NJ-05, NJ-50 and NJ-100 therefore represent more than individual engine prototypes; they are part of a broader effort to build national capability in compact gas-turbine technology and strengthen India's technological self-reliance in unmanned defence systems.

INNOVATIONS & PATENTS

Every great invention begins with a bold idea—and a patent to protect it. Innovations drive progress, and patents turn breakthroughs into lasting impact. From lab benches to the marketplace, this is where creativity meets protection.

 By **Dr. Avijit Das**

A SMARTER DRONE THAT CAN SPOT CRACKS WHILE IT FLIES

Inspecting bridges, towers and tall buildings is essential for public safety, but traditional inspections can be costly, time-consuming and dangerous. Drones provide a safer alternative, although onboard computers may struggle to manage flight stability and image analysis simultaneously. A new invention addresses this problem by giving the drone two separate “brains.” One processor controls flight using an inertial measurement unit and continuously adjusts the motors to maintain stability. A second processor independently analyses images captured by the onboard camera. Using a convolutional neural-network-based detection model, it can identify structural defects such as cracks, corrosion and slippage.

Because flying and image analysis occur simultaneously on separate processors, the drone can remain responsive while inspecting structures in real time. An asymmetric fr-

ame also keeps propellers away from the camera’s view. The approach could transform drones from simple flying cameras into safer, faster and more intelligent infrastructure-inspection tools.

This could be particularly valuable for examining difficult-to-reach areas of bridges, communication towers and high-rise buildings without repeatedly exposing workers to hazardous conditions. Faster image processing could also allow potential defects to be identified during the flight rather than after the drone returns. Engineers could then focus detailed inspections on suspicious areas, saving time and resources. By combining stable autonomous flight with dedicated artificial-intelligence-based visual analysis, the system demonstrates how smarter drone design could improve routine infrastructure monitoring and maintenance.

INNOVATION

Chandan S, Choubey V, Upadhyay V. Unmanned Aerial Vehicle with Concurrent Processing for Structural Defect Detection. Indian Patent No. 600715.

 National Institute of Technology Patna, Bihar, India



 | By Dr. Priyanka

A MARINE ROBOT THAT CLEANS WATER AND KEEPS WORKING WHEN IT FLIPS

Plastic bottles, bags, oil and other waste are increasingly accumulating in rivers, lakes, harbours and coastal waters. Removing this pollution is essential for protecting aquatic ecosystems, but conventional approaches often depend on manual collection, nets, skimmers or large cleaning vessels. These methods can be labour-intensive, expensive and difficult to use in smaller or remote water bodies. A new invention proposes a different approach: an autonomous marine robot that can collect floating waste while also monitoring the aquatic environment. What makes the design particularly interesting is its ability to continue functioning even if waves or collisions accidentally turn the robot over. During normal operation, the robot floats across the water using two bi-directional thrusters. Support structures guide floating waste underneath the robot, where a collection net captures it. A

camera helps with navigation, while onboard sensors can measure environmental parameters including water temperature, pH and salinity.

The broader importance of the invention is its dual purpose. It is not simply a floating garbage collector: it combines waste removal, water monitoring, underwater observation and an unusual self-adapting propulsion system in one platform. Ultimately, the technology demonstrates how robotics could make cleaning and monitoring water bodies safer, smarter and less dependent on manual labour, while turning an accidental flip from a potential failure into another useful operating mode.

INNOVATION

Veetil SAP, Sekar K, Areekadan MT, Vasanth BS, Prasannakumar V. An Autonomous Marine Robot with Angular Positioning for Waste Collection and Underwater Surveillance and Method Thereof. Indian Patent Application No. 599420

 National Institute of Technology Calicut, Kerala, India.





System and Method for Portable Capacitive Liquid Level Monitoring with LoRa Transmission



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Areas of Expertise: Green Manufacturing | Sustainable Water Management | Ecofriendly Technologies | Micro-Manufacturing | Systems Engineering | New Product Development



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Areas of Expertise: Rural Technology Development | Engineering Education & Innovation | Technology Design | Prototyping

Managing water levels in storage tanks can be a constant challenge, especially in rural villages, isolated facilities, or large agricultural farms where checking tanks manually is difficult and time-consuming. Traditional monitoring systems often rely on bulky equipment, require continuous electricity, need regular maintenance, or depend entirely on a stable internet connection. To solve these issues, an innovative, portable, and energy-efficient liquid level monitoring system has been developed.

At the heart of this invention is a smart application of physics called capacitive sensing. The system uses lightweight, flexible insulated wires that are dropped directly into a water tank or reservoir. Because water and air alter electrical properties differently, any change in the water level causes a distinct, measurable shift in electrical capacitance. By using a precise charging and discharging measurement technique, the device can accurately calculate the exact height of the liquid in real time while using a minimal amount of battery power.

What truly sets this system apart is how it transmits this data. Instead of relying on Wi-Fi or cellular networks, which are frequently unavailable or highly unreliable in remote regions, the device integrates LoRa (Long Range) wireless technology. LoRa allows the system to send data across distances of several kilometers while consuming very little energy. Because the setup is entirely battery-operated, compact, and standalone, it can function continuously for extended periods without needing a wired infrastructure or connection to an electrical grid.

The applications for this technology are incredibly broad. For municipal corporations and water distribution agencies, it offers an affordable way to track reservoirs spread across vast geographical areas from a single centralized location, helping prevent costly leakages and overflows. In agriculture, it can monitor irrigation tanks and farm reservoirs to promote smarter water utilization. Its portable design even makes it perfect for temporary setups, such as disaster relief camps, construction zones, or emergency operations.

Ultimately, this invention combines flexible sensor technology with long-range wireless communication to deliver a cost-effective, low-maintenance, and highly scalable solution. By removing the barriers of high costs and complex infrastructure, it provides resource-constrained communities and modern industries alike with a practical tool to better conserve, manage, and protect our most vital natural resource.

Patent Reference:

System and Method for Portable Capacitive Liquid Level Monitoring with LoRa Transmission” (Patent No. 586408).



Smart and Sustainable Roads: Zinc-Coordinated Porphyrin-Integrated Geocomposite Systems for Future Pavement Engineering



Dr. Vivek

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Areas of Expertise: Sustainable Pavement Engineering | Geosynthetics | self-healing roads | Carbon-capturing pavements | climate-resilient transportation infrastructure

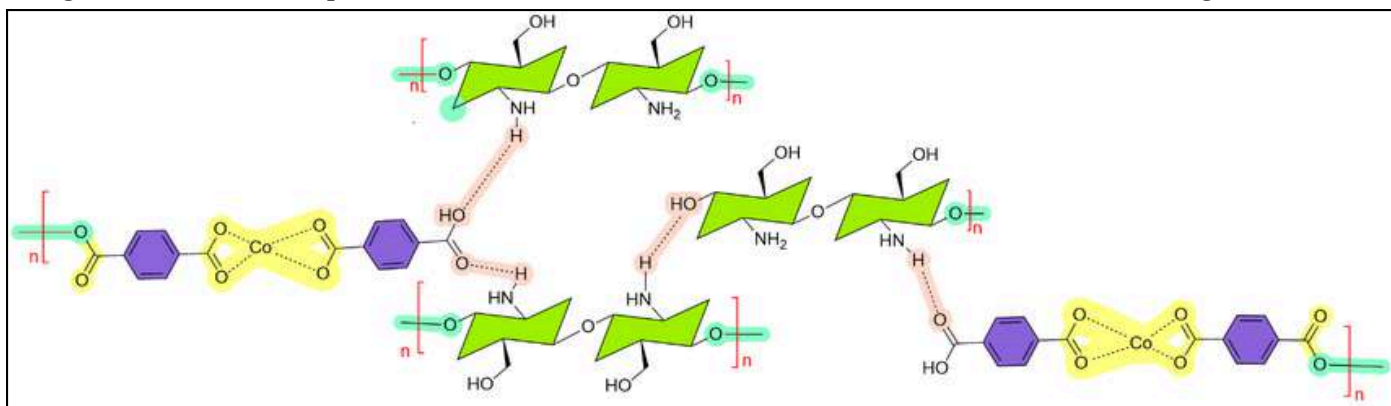
The rapid growth of transportation networks has increased the demand for road infrastructure that is durable, cost-effective, and environmentally sustainable. Conventional pavement systems often experience deterioration due to traffic loading, temperature variations, moisture intrusion, and environmental pollution. These challenges lead to frequent maintenance activities, increased costs, and significant environmental impacts. To overcome these limitations, an innovative technology known as Zinc-Coordinated Porphyrin-Integrated Geocomposite Systems has been developed for sustainable pavement engineering.

This advanced technology combines geosynthetic materials with zinc-coordinated porphyrin structures to create multifunctional pavement systems. Geosynthetics such as geotextiles, geogrids, geomembranes, and geocells are already widely used in road construction to improve soil stability, reinforce weak subgrades, and enhance pavement performance. However, their functionality is primarily structural. The integration of zinc-coordinated porphyrins introduces additional smart features that significantly improve the overall performance and sustainability of road infrastructure.

Porphyrins are naturally occurring organic compounds known for their unique light-absorbing and catalytic properties. When combined with zinc ions, they form stable complexes with enhanced chemical and photophysical characteristics. These zinc-porphyrin structures can be uniformly distributed within geocomposite materials, transforming traditional pavement reinforcement systems into intelligent and environmentally responsive infrastructure components.

One of the most remarkable features of this technology is its self-healing capability. Small cracks and minor damages that develop within pavement layers can be repaired automatically through catalytic reactions triggered by environmental conditions such as sunlight and moisture. This self-healing mechanism reduces the progression of pavement distress, extends service life, and minimizes maintenance requirements.

Another important benefit is pollutant degradation. The zinc-coordinated porphyrin system acts as a catalyst that can break down harmful organic pollutants deposited on road surfaces. Through photocatalytic reactions activated by sunlight, these materials help reduce environmental contamination and contribute to cleaner surroundings.



Patent Reference:

Zinc-Coordinated Porphyrin-Integrated Geocomposite Systems for Sustainable Pavement Engineering” (Patent No. 586895).



The technology also enables solar energy harvesting. Zinc-porphyrins possess excellent light absorption properties, allowing them to capture solar energy and convert it into usable electrical energy. This harvested energy can power embedded sensors, lighting systems, or monitoring devices within the pavement structure, reducing dependence on external power sources and promoting energy-efficient infrastructure.

In addition, the system offers environmental sensing capabilities. The integrated porphyrin structures can detect changes in temperature, moisture, and pollutant concentrations, providing real-time information about pavement conditions and surrounding environmental factors. This capability supports proactive maintenance strategies and facilitates the development of smart transportation networks.

Beyond these advanced functionalities, the geocomposite system continues to provide traditional engineering benefits such as improved load distribution, enhanced soil stabilization, and increased structural durability. By combining mechanical reinforcement with environmental responsiveness, energy generation, and self-healing properties, the technology represents a significant advancement in pavement engineering.

In conclusion, Zinc-Coordinated Porphyrin-Integrated Geocomposite Systems offer a revolutionary approach to sustainable road construction. By creating roads that can sense, heal, clean, and even generate energy, this innovation supports the development of resilient, eco-friendly, and intelligent transportation infrastructure for future generations.



Patent Reference:

Zinc-Coordinated Porphyrin-Integrated Geocomposite Systems for Sustainable Pavement Engineering" (Patent No. 586895).



Beyond the Paper: Communicating the Stories That Shape Plant Science



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Plant Reproductive Biology | Big Data and
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Science Communication

SNAPSHOT

Good research needs clear communication to create a lasting impact. Dr. Neeta Lohani, Assistant Features Editor for Plant Physiology (Oxford University Press), combines scientific expertise with editorial insight. Here, she shares how strong storytelling and clear writing enhance research visibility, engage wider audiences, and amplify the global reach of science.

Q *As an Assistant Features Editor for Plant Physiology, you regularly communicate important discoveries from across the plant sciences. What motivated you to take on this editorial role, and how has it influenced the way you read, interpret, and communicate scientific research?*

A My motivation grew from a realization during my PhD at the University of Melbourne, where I studied how rising temperatures impair sexual reproduction in plants. I saw firsthand how even significant findings can remain invisible if they are not communicated beyond the original publication. Later, as a Research Scientist at the Donald Danforth Plant Science Center, I moved into big data in biology and large-scale omics, leading projects on soybean improvement by analysing thousands of genomes and transcriptomes of wild and cultivated soybean. Participating

in elevator pitch training and competition at Danforth reinforced the importance of distilling complex science into clear, accessible language, and motivated me to invest more deliberately in science communication.

Working across biology and computation strengthened my conviction that impactful science requires the ability to communicate across disciplinary boundaries.

The editorial role has trained me to approach every paper with two questions:

What is the core discovery, and why should someone outside this subfield care?

Q *Your recent editorials span diverse topics, including plant-microbe interactions, climate-driven changes in nitrogen dynamics, genome-wide association studies, seed longevity, epigenetic regulation, and plant development. Despite their diversity, what common scientific themes or emerging trends do you see shaping the future of plant biology?*

A Despite their surface diversity, these topics converge on a deeper intellectual shift in how we understand plants as biological systems. The first theme is interconnectedness: environmental sensing, metabolic reprogramming, epigenetic regulation, and developmental decisions are not discrete pathways but facets of a single integrated network. A plant responding to shortened daylength does not simply reset its clock; it rewires gene expression through plastid-derived signals and deposits heritable epigenetic marks that persist across generations. The second theme is resolution: genomic and multi-omics approaches now let us interrogate this complexity at scales that were unimaginable a decade ago. New reference-quality genomes, for example, are revealing how transposable element dynamics and metabolic pathways have been co-shaped by millions of years of evolutionary pressure, connections that only become visible at chromosome-scale resolution. Third, there is a gro-



wing convergence between fundamental discovery and translational application, whether the system is a model species or a major crop like soybean, rice, or canola.

Q *Every year, thousands of plant science papers are published. From your editorial perspective, what qualities distinguish a study that simply reports new findings from one that has the potential to transform the field?*

A Transformative studies ask questions that bridge scales, linking a molecular mechanism to an organismal phenotype or an agricultural outcome. They employ integrative strategies, combining genetic screens with transcriptomics, imaging, or computational modeling. Rather than reinforcing established frameworks, they challenge prevailing models, for instance by uncovering entirely unexpected layers of regulation within signaling pathways that the community assumed were well understood. Equally important is framing: a study that explains why a gene matters for crop architecture or food security will always resonate more widely than one that simply catalogues a new sequence.

Q *One of the greatest challenges in science communication is making complex discoveries accessible without sacrificing scientific accuracy. What principles guide your writing when translating cutting-edge research for a broad scientific audience?*

A Three principles guide my writing when I translate cutting-edge research for a broader audience. First, lead with the question, not the method; readers engage when they

understand what problem is being solved. Second, use analogies carefully: they can illuminate a concept, but they should never replace the underlying biology. Third, preserve uncertainty honestly. Good science writing acknowledges what remains unknown, because that is often where the most exciting future work lies. Above all, I try to let the data tell a story rather than imposing a narrative onto it.

Q *Many of the studies you have featured illustrate how different biological processes, from environmental sensing and nutrient metabolism to development and epigenetic regulation, are deeply interconnected. How important is it for today's researchers to adopt a more integrative view of plant biology?*

A An integrative view is not just useful, it is essential, and some of the most striking findings I have written about emerged precisely because researchers looked across traditional boundaries. Hormones long associated with a single function are now known to govern entirely unrelated processes when examined in new developmental contexts. Organelle-to-nucleus signaling connects environmental cues to heritable epigenetic change that persists across generations. Genomic approaches, similarly, are revealing how plants coordinate their interactions with beneficial soil microbes through shared regulatory modules rather than independent pathways. None of these connections would have surfaced within a single-pathway framework. As plant biology increasingly relies on multi-omics and systems-level data, the ability to think across subdisciplines is the foundation of

discovery.

Q *Based on the many exciting discoveries you have highlighted, which areas of plant science do you believe are likely to have the greatest impact on sustainable agriculture, food security, and climate resilience over the coming decade?*

A Three areas are poised to reshape the relationship between laboratory science and agricultural practice. First, climate-adaptive crop reproduction: my own work on pollen thermotolerance has revealed how acutely vulnerable crop yields are to even modest temperature increases during flowering, a physiological bottleneck that demands urgent mechanistic understanding. Second, the engineering of plant-microbe symbioses, which offers a path toward reduced dependence on synthetic inputs by leveraging co-evolved biological partnerships for nutrient acquisition. Third, big-data-driven breeding strategies that can mine the deep reservoir of genetic diversity locked in thousands of wild and cultivated accessions to accelerate the development of climate-resilient varieties.

Q *Emerging technologies such as artificial intelligence, multi-omics, genome editing, advanced imaging, and high-throughput phenotyping are rapidly transforming plant research. Which of these advances do you think will have the most profound influence on future discoveries?*

A Among these technologies, artifi-



ificial intelligence and machine learning stand out not merely as faster tools but as fundamentally different ways of interrogating biological complexity.

From my own work on AI-driven dissection of epistasis and causal gene networks in soybean to community-wide efforts in genotype-to-phenotype modeling, AI is enabling us to ask questions about higher-order interactions that were previously intractable. That said, AI derives its power from the quality of the data it learns from, which is why parallel advances in multi-omics, CRISPR-based functional genomics, and bioinformatics platforms like SPDEv3.0 are equally critical. It is the convergence of these technologies, rather than any single advance, that will define the next decade of plant science.

Q *Scientific publishing continues to evolve through open science, preprints, AI-assisted writing, and new publishing models. How do you see the role of scientific editors changing in this evolving landscape, and what responsibilities will remain most important?*

A The role is shifting from gatekeeping toward curation, contextualization, and quality assurance. In a world where anyone can post a preprint and AI tools can generate fluent prose, the responsibilities that remain most important are precisely the ones that require human judgment: evaluating the significance of a finding within its broader scientific context, identifying emerging narratives that connect disparate fields, and ensuring that the communication of science is accurate, fair, and accessible.

Q *Many early-career researchers aspire to publish impactful work but often struggle to communicate its broader significance. Based on your editorial experience, what advice would you offer young scientists to improve their scientific writing, storytelling, and the visibility of their research?*

A I would offer three pieces of advice drawn from my own experience. Read beyond your immediate subfield; breadth of knowledge is what distinguishes a scientist who generates connections from one who generates data. Invest in your writing as deliberately as you invest in your bench or computational skills; clear prose is not a luxury but a tool for impact. And seek out editorial and communication opportunities early. Reviewing manuscripts, writing scientific commentaries, and engaging with public audiences will sharpen your thinking and expand your professional network in ways that purely research-focused training cannot.

Q *Finally, looking ahead, what excites you most about the future of plant science, and what message would you like to share with the next generation of researchers who will shape the future of this discipline?*

A What excites me most is the dissolution of traditional disciplinary boundaries. Computational biologists are working alongside breeders; epigeneticists are in dialogue with ecologists; data scientists are partnering with field researchers to test hypotheses across thousands of genomes. This convergence, coupled with a growing societal urgency around food security and climate resilience, means that discoveries made in plant laboratories today can

travel from bench to field faster than at any point in history. To the next generation, I would say: pursue problems that connect molecular mechanisms to real-world outcomes, maintain scientific rigor, and invest in communicating your findings beyond your immediate subfield. Effective science communication is not peripheral to research; it is what enables a discovery to have real impact.

ABOUT THE AUTHORS

Dr. Neeta Lohani is an Assistant Professor at Thapar Institute of Engineering and Technology. A plant biologist specializing in biotechnology, genomics, and bioinformatics, her research focuses on heat tolerance and climate-resilient crops. She previously conducted big-data soybean research at the Danforth Center and serves as an Assistant Features Editor for *Plant Physiology*.

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Krishna AchutaRao

India has lost one of its most respected voices in climate science. Prof. Krishna Mirle AchutaRao, climate scientist and professor at the Centre for Atmospheric Sciences at IIT Delhi, passed away on 4 September 2026 at the age of 62. Over a career spanning climate modelling, extreme-weather attribution, climate-risk assessment and adaptation, he helped scientists and society better understand one of the defining questions of our time: how is human-caused climate change altering the world around us?

Prof. AchutaRao's path to climate science was remarkably interdisciplinary. He completed a bachelor's degree in Mechanical Engineering and a master's degree in Mathematics from BITS Pilani in 1986, before moving to the United States for further study. He earned a master's degree in engineering and a PhD from Tulane University in New Orleans. He subsequently worked at the Lawrence Livermore National Laboratory in California, including with the Program for Climate Model Diagnosis and Intercomparison, before returning to India in 2007 to join IIT Delhi.

At IIT Delhi, Prof. AchutaRao built a career around understanding how Earth's climate responds to both natural influences and human activities. His research covered regional climate change, climate variability, extreme weather, climate-model evaluation, long-term climate change, risk assessment and adaptation. He also served the institution in leadership positions, including as Head of the Centre for Atmospheric Sciences and Dean (Faculty).

Among his most important scientific contributions was his work in climate attribution. When a devastating heatwave, unusually intense rainfall or another extreme event occurs, an increasingly important question follows: *what role did climate change play?* Attribution science uses observations, climate models and statistical methods to examine whether human-induced warming has altered the probability or intensity of such events. Prof. AchutaRao helped advance this field in India and brought greater attention to the regional consequences of global climate change.

This work has profound practical importance for a country such as India. Climate change is not experienced only as a

**REMEMBERING
KRISHNA
ACHUTARAO: THE
SCIENTIST WHO
HELPED INDIA
UNDERSTAND A
CHANGING CLIMATE
(1964 – 4 September 2026)**



gradual increase in average temperature. It can influence the frequency and intensity of heat extremes, rainfall patterns and other hazards that affect agriculture, cities, infrastructure, health and livelihoods.

Understanding how those risks are changing can help governments and communities prepare for a future in which historical climate patterns may no longer provide a sufficient guide.

Prof. AchutaRao's scientific influence extended well beyond India. He had been associated with the Intergovernmental Panel on Climate Change (IPCC) Working Group I since 2001 and served as a Lead Author for both the Fifth and Sixth Assessment Reports. These assessments represent one of the world's largest scientific efforts to evaluate what is known about climate change and provide the scientific foundation for international climate discussions and policy.

His contribution to international climate science continued through the World Climate Research Programme (WCRP). He served on scientific groups associated with WCRP and, beginning in January 2025, became a member of its Joint Scientific Committee. He also contributed to India's Monsoon Mission through its Scientific Review and Monitoring Committee. These roles reflected the breadth of his expertise and the respect he commanded within both Indian and international climate-science communities.

Yet Prof. AchutaRao was concerned not only with identifying climate change, but also with what societies could do about it. He was instrumental in establishing IIT Delhi's Centre of Excellence for Climate Change Adaptation, an initiative concerned with translating climate knowledge into risk assessment and adaptation planning. Its work addresses challenges including heat extremes, monsoon variability and climate risks faced by vulnerable communities.



This emphasis on adaptation reflected an important dimension of his scientific outlook. Climate science becomes particularly valuable when it can help society make better decisions. Knowing that temperatures are rising is important; understanding who will be exposed, which systems are vulnerable and what actions can reduce the resulting risks is equally important. Prof. AchutaRao worked across these boundaries between climate modelling, risk, adaptation and policy.

He was also an effective communicator of climate science. Complex climate models and probabilistic attribution can be difficult subjects to explain outside specialist circles, yet he regularly engaged with journalists and the public. He emphasised that India's development offered both a challenge and an opportunity: the country needed to continue improving living standards while avoiding the high-emission development pathways followed historically by many industrialised nations.

His colleagues remembered another quality that is less visible in lists of publications and professional appointments: his insistence on scientific rigour. Fellow climate scientist Roxy Mathew Koll recalled his scientific temper, extraordinary attention to detail and sense of humour, noting that Prof. AchutaRao would keep questioning an argument until he was convinced that it could withstand scientific scrutiny. The World Climate Research Programme similarly remembered him as both an excellent scientist and a valued colleague.

His influence also lived through teaching and mentorship. At IIT Delhi he helped train researchers entering a field that has become increasingly important for India. His academic contributions were recognised with IIT Delhi's Teaching Excellence Award in 2019. His students worked on subjects including climate-change detection and attribution over India and uncertainties in future climate projections—areas closely connected with the questions that shaped his own scientific career.

The significance of Prof. AchutaRao's work becomes clearer with every extreme weather event. When temperatures break records, monsoon behaviour changes or communities confront unfamiliar climate risks, society needs more than forecasts. It needs scientists who can carefully distinguish natural variability from long-term change, quantify uncertainty and explain what the evidence actually allows us to conclude.

Prof. AchutaRao devoted his career to precisely those questions. His work helped strengthen the scientific foundations for understanding how the climate is changing, why it is changing and what those changes mean for people.

For young researchers, his career also offers a broader lesson about the role of a scientist. Scientific contribution is not measured solely by publications. It can also be found in building institutions, improving international assessments, mentoring students, questioning weak evidence, communicating complicated ideas clearly and ensuring that scientific knowledge reaches decisions that affect society.

Climate change will remain one of India's greatest scientific and developmental challenges for decades to come. Meeting that challenge will require better observations, stronger models, careful attribution of extreme events, effective adaptation and scientists willing to communicate uncertainty without diminishing urgency. Prof. Krishna AchutaRao helped build that capacity.

His passing is a significant loss to Indian and international climate science. But his legacy remains in the climate research he advanced, the global assessments he helped shape, the institutions he strengthened and the scientists he trained. Most importantly, it remains in a principle that ran through his work: understanding a changing climate is not merely an academic exercise—it is essential for helping society prepare for the world ahead.



By
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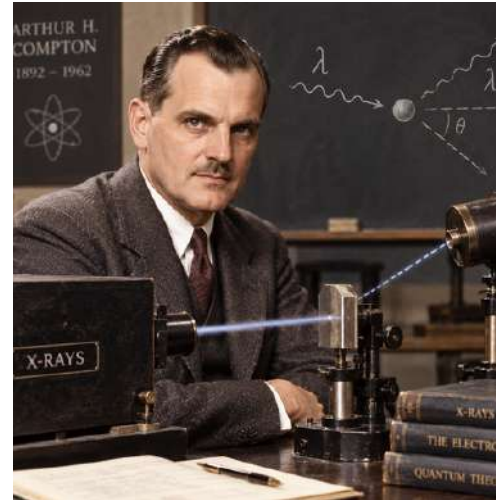
SCIENCE NEWS & OPPORTUNITIES

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10 September 1892 — Arthur Compton

01 Arthur Compton was an American physicist famous for discovering the Compton effect. He showed that when X-rays collide with electrons, they lose some energy and change wavelength. This could be explained if light behaved as tiny packets of energy called photons. His experiment therefore provided strong evidence that light can behave like particles as well as waves. The discovery became an important foundation of quantum physics and changed our understanding of light and matter. Compton received the 1927 Nobel Prize in Physics.



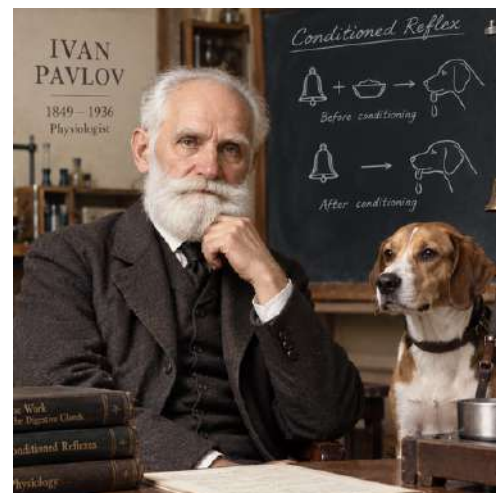
12 September 1897— Irène Joliot-Curie

02 Irène Joliot-Curie was a French scientist who, with Frédéric Joliot-Curie, discovered artificial radioactivity. They showed that stable elements could be changed into radioactive forms by bombarding them with particles. The newly created atoms continued releasing radiation even after the original radiation source was removed. This discovery made it possible to produce radioactive isotopes in laboratories. Such isotopes later became important in medicine, biology and scientific research. The couple received the 1935 Nobel Prize in Chemistry for this groundbreaking discovery.



14 September 1849 — Ivan Pavlov

03 Ivan Pavlov was a Russian physiologist famous for discovering classical conditioning. While studying dogs, he noticed that they could learn to associate a signal, such as a sound, with food. After repeated training, the sound alone could make the dogs salivate. This demonstrated how the brain learns by connecting one stimulus with another. Pavlov's work became fundamental to understanding learning, behaviour and reflexes. He received the 1904 Nobel Prize in Physiology or Medicine for his important research on digestion.



15 September 1861 — M. Visvesvaraya

04 Sir M. Visvesvaraya was one of India's most celebrated engineers. He developed innovative automatic water-control gates that helped regulate reservoir water levels and improve irrigation and flood management. The gates could respond to changing water levels, allowing better storage and control of water. His engineering ideas contributed greatly to India's infrastructure, agriculture and industrial development. He received the Bharat Ratna in 1955. His birthday, 15 September, is celebrated as Engineers' Day in India in recognition of his remarkable contribution to engineering.



16 September— World Ozone Day

05 The International Day for the Preservation of the Ozone Layer, or World Ozone Day, is observed on 16 September. It commemorates the Montreal Protocol, adopted in 1987 to control chemicals that damage the ozone layer. The ozone layer protects life from harmful ultraviolet radiation. Global action has successfully reduced many ozone-depleting substances, making this an important example of science guiding international environmental action.



20 September 2004 — EDUSAT Launch

06 On 20 September 2004, India launched EDUSAT (GSAT-3), the country's first satellite built specifically for education. Developed by ISRO, it used satellite communication to connect classrooms and educational institutions, including those in remote areas. EDUSAT supported distance education, teacher training and interactive learning. The mission demonstrated how space technology could be used not only for scientific exploration but also to improve access to education.



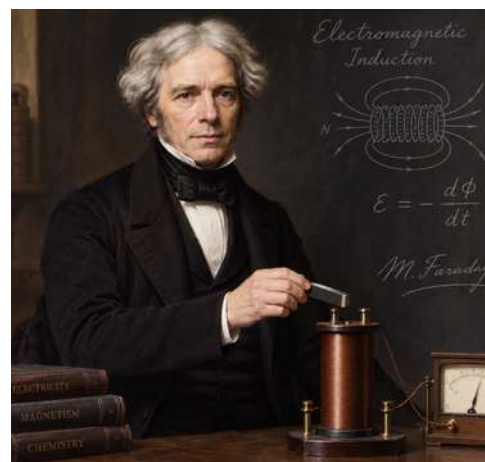
21 September — World Alzheimer's Day

07 World Alzheimer's Day is observed on 21 September to increase awareness of Alzheimer's disease and other forms of dementia. Alzheimer's gradually damages brain cells, affecting memory, thinking and everyday activities. Scientists are studying how abnormal proteins, including amyloid and tau, contribute to brain-cell damage. The day emphasizes early recognition, better care and continued research toward improved diagnosis, prevention and treatment of dementia.



22 September 1791 — Michael Faraday

08 Michael Faraday was a British scientist whose work helped make modern electricity possible. He discovered electromagnetic induction, showing that moving a magnet near a coil of wire can produce electric current. In simple terms, a changing magnetic field can generate electricity. This principle is the basis of electric generators and transformers. Faraday also made major contributions to electrochemistry and our understanding of electric and magnetic fields. His discoveries continue to power much of the technology we use today.



28 September — World Rabies Day

09 World Rabies Day is observed on 28 September, the anniversary of the death of Louis Pasteur, who helped develop the first successful rabies vaccine. Rabies is a deadly viral disease that spreads mainly through bites from infected animals. Once symptoms appear, it is almost always fatal, but it is preventable through animal vaccination and rapid treatment after exposure. The day promotes the global goal of eliminating human rabies deaths.



Guide SCIENCE TOMORROW

From the dark depths of our oceans to the farthest reaches of the cosmos, countless mysteries remain unsolved. Science continues to push the boundaries of the known, revealing just how much is still left to uncover. What lies beyond our current understanding may reshape the future of humanity.



EMERGING INSIGHT

Spatiotemporal Precision in Targeted Therapeutics: Supramolecular and Peptide-based Innovations Against Neurodegenerative Pathology



Prof. Prof. Amitava Das

Indian Institute of Science
Education and Research Kolkata

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AREAS OF EXPERTISE

Supramolecular Chemistry and Molecular Recognition • Nanostructured Functional Molecules and Materials for Therapeutic Applications • Functional Materials for Sustainable Chemistry and Environmental Applications

WHY IT MATTERS

Diseases such as Alzheimer's, cancer, and drug-resistant infections can be difficult to treat because medicines do not always reach or act exactly where they are needed. Scientists are therefore developing smart materials that can find and act on specific disease-causing molecules. In this Science Tomorrow article, Prof. Das explains how specially designed peptide materials could stop harmful proteins from coming together, break down existing protein deposits, and deliver treatments more precisely, offering new possibilities for safer and more effective therapies in the future.

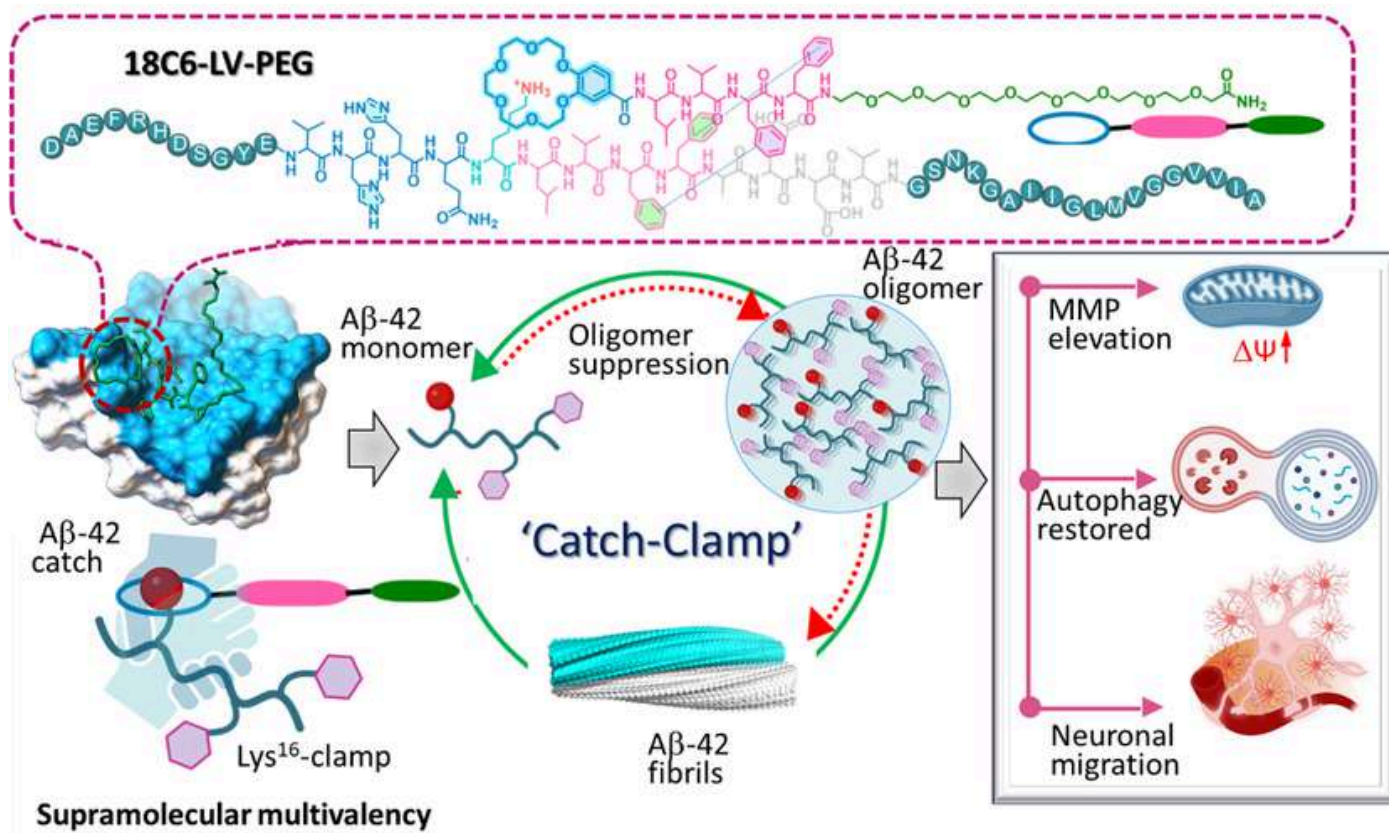
A central, unresolved paradigm in modern pharmacology is achieving the localization of therapeutic agents with high spatial and temporal precision at targeted disease sites. Conventional small-molecule drugs and biologics often suffer from rapid systemic clearance, off-target toxicity, and an inability to maintain therapeutic concentrations within localized, pathological microenvironments. To address these limitations, researchers have increasingly turned to synthetic chemistry, nanoscience, and non-covalent supramolecular design to construct systems capable of recognizing, responding to, and modulating specific biochemical niches.

Among these strategies, peptide-based supramolecular materials have

emerged as exceptionally versatile candidates. By leveraging multivalent, dynamic, and reversible non-covalent interactions, chemically programmable peptide assemblies offer elegant solutions to structural and functional challenges in complex disease pathways spanning neurodegenerative disorders, oncology, and multidrug-resistant infectious diseases.

Globally, over 55 million people live with dementia, alongside a massive burden from cancer and antimicrobial-resistant ESKAPE pathogens. In neurodegeneration, particularly Alzheimer's disease (AD), conventional drug development has faced notorious attrition rates due to the biological complexity of central nervous system (CNS) disease pathways. Historically,

the amyloid cascade hypothesis positioned the deposition of mature, β -sheet-rich fibrillar species of amyloid- β (Ab) as the primary therapeutic checkpoint. However, contemporary clinical and mechanistic insights strongly indicate that transient, soluble prefibrillar/oligomeric species of (Ab-42) generated via enzymatic cleavage of amyloid precursor proteins (APPs) by β - and γ -secretases under physiological conditions are the true primary drivers of synaptic disruption and neurotoxicity. Despite the shift toward targeting transient Ab-42 oligomers, major challenges remain in designing therapies that can navigate their dynamic structural heterogeneity without static binding pockets while achieving precise spatiotemporal delivery. A truly



Jana, A., Jash, M., Sen, S. et al. *Angew. Chem. Int. Ed.* 65, e5919230 (2026).

transformative strategy must move beyond simple aggregation inhibition to provide dual action simultaneously halting toxic oligomerization and actively destabilizing existing mature fibrils through smart, non-covalent sequestration.

To tackle the structural and mechanical complexity of toxic protein species, recent years have witnessed a renaissance in molecular and supramolecular strategies. Prof. Stupp and coworkers (*J. Am. Chem. Soc.* 2025, 147, 17710-17724) demonstrated the copolymerization of a trehalose-conjugated amphiphilic glycopeptide (TPA) with Ab-42 monomers/oligomers, arresting aggregation by altering the self-assembly landscape. Prof. Raskatov and colleagues (*J. Am. Chem. Soc.* 2024, 146, 2634-2645) introduced an Aa isoform chaperone

system that co-assembles with Ab-42 to selectively interrupt toxic oligomer formation. Prof. Knowles, Prof. Kassiou, and coworkers designed Perphenazine-Macrocycle conjugates (*ACS Chem. Neurosci* 2023, 14, 87-98) that modulate the pathological aggregation pathway by sequestering Ab-42 monomers and converting them into non-toxic amorphous aggregates. Prof. D.S. Eisenberg and coworkers (*Nature* 2025, 644, 1020-1027) pioneered the concept of stereochemically mismatched peptide sequences that exert severe mechanical torque on the protein fibril lattice, successfully dismantling mature Tau fibrils. Prof. Takuzo Aida and colleagues (*Nat. Commun.* 2022, 13, 5424) introduced a multivalent salt-bridging molecular glue, demonstrating how non-covalent logic can reconstitute dynamic proteins like microtubules into high-

er-order capsule structures. While contemporary literature offers pioneering tactics for either oligomerization inhibition or structural reconstitution, a chemically programmable supramolecular strategy backed by comprehensive mechanistic validation for simultaneous oligomerization inhibition and mature fibril destabilization has remained elusive. Recognizing that the central core domain (17-21LVFFA) and C-terminal residues (33-42Ab-42) govern hydrophobic self-assembly, while the adjacent Lys16 residue plays a pivotal role in proteotoxicity during oligomerization, our group engineered a targeted supramolecular conjugate (18C6-LV-PEG) comprised of 18-Crown-6, a short peptide LVFF and PEG chain (*J. Am. Chem. Soc.* 2026, 148, 27260-27281).

This conjugate, 18C6-LV-PEG catches Ab-42 via specific hydrophobic interactions of LVFF, clamps Lys16, and halting Ab-42 oligomerization. PEG chain imparts biocompatibility, extends circulation half-life in vivo, and aids translational feasibility of this construct. By pairing sequence-specific hydrophobic recognition (LVFF) with site-directed macrocyclic clamping of Lys16, the system not only prevents the formation of toxic oligomeric species, modulates ROS, restores impaired autophagy and ameliorates cognitive deficits but also actively destabilizes established mature Ab-42 aggregates.

Beyond Alzheimer's therapeutics, our research group leverages localized, spatiotemporally controlled peptide self-assembly pathways to tackle other urgent healthcare challenges. Utilizing the diphenylalanine (Phe-Phe) motif, we designed host-guest supramolecular adducts, and coacervates vesicles responsive to ALP and ALP mediated host-guest disassembly/rupture of coacervates vesicles lead apoptosis through 'Phe-Phe' fibrillization and therapeutic release respectively (Sarkar et al., Adv. Healthcare Mater. 2024, 14, 2403243 and Sarkar et al., Adv. Mater. 2026, 38, e73804). Our group also deployed gelatinase-responsive peptide self-sorting pathways followed by localized self-assembly to selectively combat resistant ESKAPE pathogens (Bose et al., J. Am. Chem. Soc. 2025, 147, 37398–37413).

Looking forward, the treatment of complex pathologies like Alzheimer's disease will increasingly rely on smart, bio-orthogonal supramolecul-

ar materials rather than traditional single-target pharmacology.

We anticipate the key avenues that will shape the next generation of advanced therapeutics include supramolecular traps, molecular glues and stimuli-responsive dissipative peptide self-assembly.

By bridging synthetic chemistry with biological architecture, the continued exploration of chemically programmable supramolecular platforms holds immense promise for developing non-invasive nanomedicines, tissue regeneration frameworks, and localized therapies capable of reversing disease progression at its fundamental molecular root.

ABOUT THE AUTHORS

Prof. Amitava Das is a researcher at the Indian Institute of Science Education and Research (IISER) Kolkata, working in supramolecular chemistry, molecular recognition, nanocarriers, and smart drug-delivery systems. His research develops molecules and materials that can recognize specific biological targets and deliver treatments more precisely. His recent work explores new approaches for Alzheimer's disease, cancer, and drug-resistant bacterial infections, including peptide-based materials that respond to biological signals. His research aims to translate innovative chemistry into safer and more targeted therapeutic strategies.

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EMERGING INSIGHT

Rethinking H3K4me3: A Consequence, Not a Cause, of Active Transcription



WHY IT MATTERS

Our genes need to be turned on and off at the right time for our cells to work properly. Scientists have long believed that a chemical mark called H3K4me3 helps switch genes on. But new research suggests that this mark may actually appear after a gene becomes active. In this Science Tomorrow article, Dr. Sabarinadh Chilaka explains why this discovery could change our understanding of how genes work and, in the future, help scientists develop more precise treatments for cancer and other diseases.

Inside eukaryotic cells, the genome is hierarchically organized into a higher-order chromatin structure rather than existing as unconstrained DNA. DNA wraps around an octameric complex of core histones (H2A, H2B, H3, H4) to form nucleosomes—the fundamental subunits of chromatin. While the hydrophobic octamer core stabilizes the particle, N-terminal histone tails protrude outward into the nuclear environment, exposing them to enzymatic machinery (Figure 1). This exposure allows site-specific post-translational modifications (PTMs)—including acetylation, methylation, phosphorylation, and ubiquitination—to be dynamically deposited by "writers," removed by "erasers," and interpreted by "readers." Within the 'histone code' framework, these modifications regulate local chromatin accessibility through distinct modes: lysine acetylation neutralizes positive charges to promote chromatin opening, whereas histone methylation acts in a context-dependent manner to foster either open or condensed chromatin states. Together, these modifications

regulate local chromatin spatial accessibility: highly condensed heterochromatin sterically occludes cis-regulatory elements (such as promoters and enhancers), preventing transcription factor binding to enforce gene silencing, whereas localized chromatin remodeling opens euchromatin to permit transcriptional engagement (Figure 1).

Extensive research has identified hundreds of distinct histone PTMs on canonical and variant histones, forming a coordinated network that fine-tunes cell-type-specific gene expression. Crucially, dysregulation of these epigenetic mechanisms drives diverse human pathologies, including cancer, autoimmune conditions, and chronic inflammatory disorders. Because histone PTMs are dynamic and reversible, targeting their regulatory pathways offers a powerful strategy for epigenetic therapy and drug discovery. Global initiatives—such as the ENCODE project and the Roadmap Epigenomics Consortium—have systematically mapped these



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Epigenetics • Chromatin Biology • Gene Regulation • Inflammation

functional landscapes across diverse cell types and disease states. Building on these foundational maps, elucidating the precise mechanisms governing histone PTM deposition remains essential for decoding gene regulation and identifying novel therapeutic targets.

Out of the vast repertoire of histone PTMs, trimethylation of histone H3 at lysine 4 (H3K4me3) has emerged as one of the most extensively studied marks, featured in over 4,000 PubMed publications to date and widely considered a hallmark of active promoters. Mapping precisely to transcription start sites (TSSs) across eukaryotic evolution, early foundational studies framed H3K4me3 as an instructive driver of gene expression. In this model, H3K4me3 was thought to actively

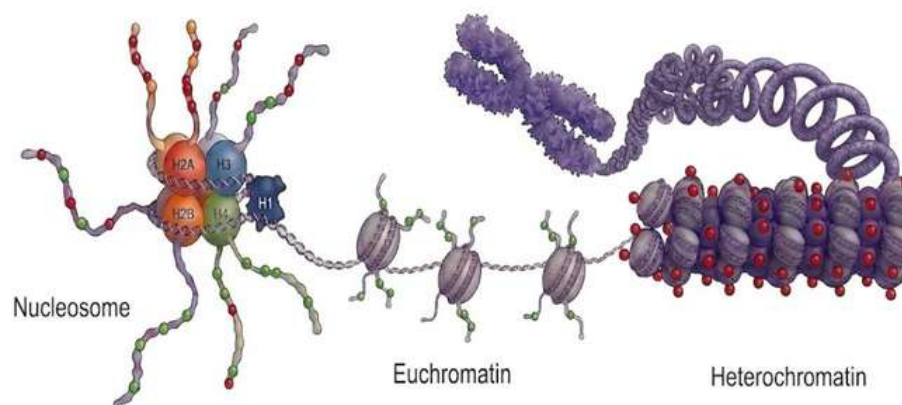


Figure 1: The nucleosome core consists of an octamer of histone proteins wrapped by DNA, with protruding N-terminal histone tails bearing various post-translational modifications (PTMs, indicated by colored dots). Active PTMs (green dots) promote an open, relaxed nucleosome arrangement characteristic of transcriptionally accessible euchromatin. Conversely, repressive or silent PTMs (red dots) mediate nucleosome compaction into dense, transcriptionally inactive heterochromatin. Created with Google Gemini [Generative AI visual tool], August 12, 2026, Google.

trigger transcription initiation by maintaining open promoter architecture and recruiting chromatin remodelers and basal machinery to assemble RNA Polymerase II (Pol II). However, accumulating evidence challenges this instructive paradigm. Genetic knockout or catalytic inhibition of major MLL/COMPASS family methyltransferases depletes global H3K4me3 without causing a corresponding collapse in steady-state transcription. Likewise, targeted promoter demethylation frequently leaves ongoing transcript synthesis intact. These paradoxical observations create a classic "chicken-and-egg" paradigm: Is H3K4me3 an instructive cause that drives transcription initiation, or a reactive consequence deposited by transcriptional activity?

Resolving this paradox required a model system to overcome a long-standing experimental deadlock. Most chromatin studies rely on con-

stitutively active genes or slow induction paradigms, where transcription and histone modifications change synchronously over extended timeframes, obscuring cause and consequence. Determining whether H3K4me3 deposition precedes, accompanies, or follows transcription demanded high temporal resolution with rapid activation and shutdown. We strategically targeted the inducible human tumor necrosis factor alpha (TNF- α) and interleukin 1 beta (IL-1 β) genes, two key inflammatory cytokine genes that exhibit a well-characterized, highly dynamic 'off-on-off' expression profile upon lipopolysaccharide (LPS) stimulation, in THP-1 human monocytic cells. Their rapid induction, short mRNA half-lives, and swift resolution provided an ideal experimental window to delineate the precise sequence of molecular events. Evaluating this strategy across two independent genes at their native genomic locati-

ons on distinct chromosomes ensured that the observed kinetic trends reflected generalizable biological principles rather than locus-specific artifacts.

Leveraging this temporal framework, our work published in Life Science Alliance (DOI: 10.26508/lsa.202503511) revealed that H3K4me3 accumulates hours after peak transcription rather than coinciding with it, directly challenging models that position this mark as an early requirement for Pol II assembly. Our study provided three distinct lines of evidence supporting this model: First, kinetic analysis revealed clear temporal separation between activation machinery and mark deposition: while NF- κ B occupancy, p300 recruitment, histone acetylation (H3K27ac/H4K8ac), and Ser5/Ser2-phosphorylated Pol II correlate peak transcription, MLL1-the methyltransferase responsible for H3K4me3 in these cells-recruitment and H3K4me2/3 accumulation lag significantly behind. Second, we showed that this delayed deposition is strictly transcription-dependent, as pharmacological inhibition of NF- κ B (via TPCA-1) or global transcription (via actinomycin D) blunted H3K4me3 accumulation-confirming that active elongation, not static activator binding, triggers its writing. Third, MLL1 knockdown depleted H3K4me3 without compromising TNF- α or IL-1 β induced transcription, showing that loss of H3K4me3 does not limit or impair transcriptional output. Together, these findings demonstrate that H3K4me3 operates as a post-transcriptional record of past synthesis rather than an instructive driver.

Using an inducible gene system, this study provides the first report in human gene models that H3K4me3 accumulation requires and strictly follows active transcription. While similar temporal lag between transcription and H3K4me3 deposition have been noted in non-human systems—such as yeast metabolic cycling and mouse liver circadian rhythms—our transcriptional perturbations and MLL1 knockdown experiments establish the precise functional sequence during acute human gene induction. By demonstrating that H3K4me3 accumulation occurs downstream of transcription, these findings reaffirm H3K4me3 as a post-transcriptional event rather than an instructive trigger. This framework offers a cohesive mechanism to address a long-standing paradox in chromatin biology: why acute depletion or catalytic knockout of H3K4me3 methyltransferases consistently fails to block initial gene activation or primary Pol II recruitment. Viewing H3K4me3 as a post-transcriptional consequence rather than a prerequisite trigger offers a plausible framework to help reconcile prior conflicting observations across eukaryotic systems.

A fundamental question arising from our study is whether delayed H3K4me3 loading is restricted to acute, inducible genes or operates similarly at constitutively active loci. Our kinetic dissection relied on the sharp "off-on-off" transcriptional burst of inflammatory loci, providing a clear window to uncouple transcription from histone modification. In contrast, assessing these kinetics at constitutively expressed genes presents a methodological challenge, as contin-

uous transcription and delayed H3K4me3 exist in steady state rather than a resolvable pulse. While our transcriptional shutdown experiment at the constitutively active MYC locus sought to test whether delayed H3K4me3 deposition persists post-inhibition, the sustained mark presence observed after arrest could suggest this phenomenon. However, this persistence could reflect either continued active deposition or merely slow mark turnover and delayed clearance. Ultimately, determining whether post-transcriptional H3K4me3 accumulation is a universal principle across steady-state genomic regions will require future approaches combining metabolic pulse-chase histone labeling with rapid catalytic inhibition of methyltransferases or transcription.

If H3K4me3 does not drive primary initiation, what is its real post-transcriptional role? While our observation of delayed H3K4me3 loading does not definitively prove a singular downstream function, it raises compelling hypotheses regarding how this mark operates after transcription has commenced. Based on existing literature and our kinetic observations, we speculate that post-transcriptional H3K4me3 may contribute to several non-mutually exclusive processes: (i) preserving an open promoter architecture around the TSS to prevent the encroachment of repressive marks for chromatin barrier maintenance; (ii) genome integrity protection, by safeguarding exposed, open DNA at highly active promoters against transcription-induced damage; (iii) transcriptional memory, by serving as a molecular record of recent synthesis to "prime" the locus for more efficient reactivati-

on during subsequent stimulation; and (iv) temporal reader recruitment, by acting as a late beacon to recruit nuclear reader proteins that coordinate splicing, elongation efficiency, or chromatin resetting upon termination.

Overall, our findings in human inducible gene models indicate that H3K4me3 deposition is temporally uncoupled from initial transcription at TNF- α and IL-1 β , pointing toward a post-activation role rather than an instructive driver of initiation. These results provide a strong rationale for future studies to systematically evaluate whether similar kinetic uncoupling operates across broader genomic contexts and to define its precise post-transcriptional functions. Countless disease-profiling studies—spanning cancer, autoimmune conditions, and neurodegenerative disorders—have documented extensive H3K4me3 dysregulation. While our findings stem from acute response loci, this delayed-loading perspective offers a nuanced lens through which existing disease datasets can be re-interpreted. Applying this kinetic framework to disease-associated H3K4me3 patterns may offer valuable insights into disease mechanisms, gene aberrations, and chromatin locus resetting.

Ultimately, H3K4me3 represents just one mark within a vast landscape of PTMs, whose functional roles in diverse nuclear mechanisms remain incompletely understood. While comprehensive mapping initiatives have catalogued these marks across the genome, systematically decoding how PTMs dynamically coordinate these multi-step nuclear processes represents a critical frontier for epigenetic research and translational

applications.

However, translating these fundamental insights into targeted epigenetic therapies is currently hindered by the limited genome-wide specificity of conventional inhibitors, which can cause off-target toxicity and drug resistance.

Overcoming these clinical barriers will require developing highly selective small-molecule chemical inhibitors targeting specific classes or domains of epigenetic modulators, as well as deploying locus-specific precision tools and cell-targeted formulations to restrict chromatin engineering strictly to disease-driving loci.



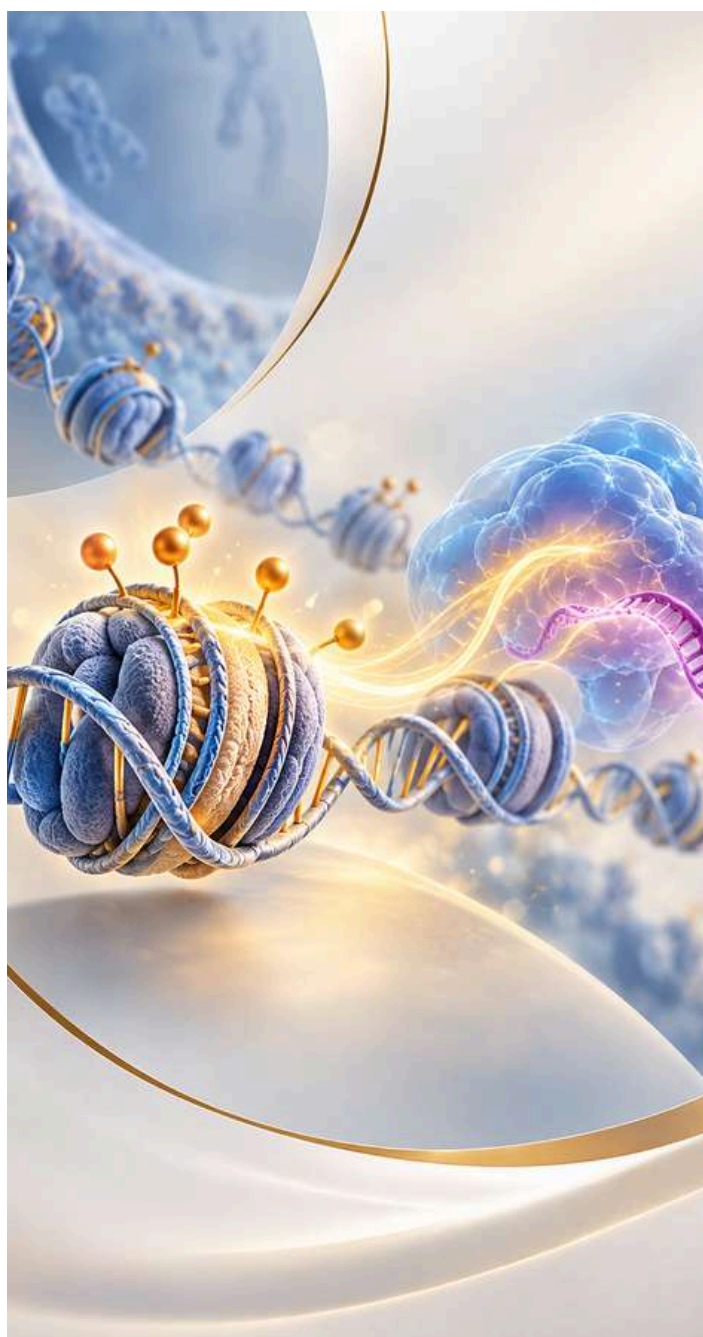
Dr. Sabarinadh Chilaka and his PhD student, Ms. Komal Paresh Walvekar, authors of the H3K4me3 study discussed.

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Dr. Sabarinadh Chilaka and Ms. Komal Paresh Walvekar are researchers at the CSIR–Indian Institute of Chemical Technology (CSIR-IICT), Hyderabad, India. Their research focuses on understanding how genes are turned on and off inside our cells and how these changes can affect health and disease. Their recent work studies a chemical mark called H3K4me3 and shows that it may appear after a gene becomes active rather than switching the gene on. Their research helps us better understand how our cells control gene activity.





EMERGING INSIGHT

When Deep Wounds Refuse to Heal



WHY IT MATTERS

Some wounds, especially diabetic and other chronic wounds, can remain unhealed for weeks or even months because inflammation does not switch off at the right time. Future treatments may work differently not simply by blocking inflammation, but by guiding immune cells from inflammation toward healing. In this Science Tomorrow article, Prof. Mirza S. Baig and Sk Rameej Raja explain how targeting signals inside immune cells, together with smart local drug-delivery systems, could lead to faster and more precise treatments for difficult-to-heal wounds.

Wound healing is a carefully coordinated process. In the early stage, inflammation is necessary. It helps the body clear damaged tissue, dead cells, and invading microorganisms from the wound. After this initial response, inflammation should gradually subside, and the wound should progress toward repair and tissue remodeling. Complications arise when this transition fails to occur. If inflammation persists too long, immune cells remain active and can cause further tissue damage. As a result, the wound's transition to the repair stage may be delayed. This prolonged inflammatory state is characteristic of many chronic wounds, including diabetic wounds, where persistent macrophage activation can interfere with the transition from inflammation to tissue repair.

Are We Dealing with Wounds the Right Way?

For many years, researchers have tried to control chronic inflammation by targeting inflammatory molecules such as TNF- α , IL-1 β , and IL-6. These molecules are important in ch-

ronic wound inflammation, but targeting them individually has not been enough to restore normal healing. The reason is that chronic wounds are complex. More than one process is usually affected at the same time. Inflammation, immune responses, and tissue repair can all become disturbed. Macrophages are an important part of this process. They respond to signals from damaged tissue, microbes, oxidative stress, and other factors in the wound environment. These signals can activate pathways such as Toll-like receptors, NF- κ B, and MAPKs. When these pathways remain active for too long, macrophages may continue to produce inflammatory responses rather than shift toward functions that support tissue repair. This raises an important question: instead of blocking inflammatory molecules after they are produced; can we control the signaling pathways that drive macrophages to produce them in the first place?

A New Way to Think About Wound Healing

The aim is not to stop inflammation altogether. Some inflammation is ne-



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Macrophage Signaling • Chronic Inflammation • Cancer Biology & Therapeutics



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AREAS OF EXPERTISE

Host-pathogen interaction • *Leishmania donovani* • Macrophage signalling pathways

eded at the beginning of wound healing to clear damaged tissue and harmful microorganisms and to prepare the wound for repair. The problem arises when this response continues for too long. Macrophages are important in this process because the signals they receive can determine whether they continue to promote inflammation or begin supporting tissue repair. Treatment could also be delivered directly to the affected area. Hydrogels, nanoparticles, biomaterials, and controlled-release systems could be used to deliver compounds that modulate macrophage signaling at the wound site while reducing their effects elsewhere in the body.

Adaptor Proteins: The Signals Behind Inflammation

Adaptor proteins are key components of cell signaling. They link activated receptors to other proteins inside the cell and help relay signals from one part of the cell to another. One example is Toll/interleukin-1 receptor domain-containing adaptor protein, or TIRAP. TIRAP helps transmit signals from Toll-like receptors and can influence pathways including NF- κ B, AP-1, STAT1, and IRF3. TIRAP has been studied extensively in immune responses, but we still know relatively little about its role in macrophages during wound healing. This potential role of TIRAP-mediated signaling in macrophage responses provides a rationale for exploring whether modulation of this pathway could influence wound repair. Our recent work with the novel sulfonamide-based compound DRZ-V provides one example of this approach. In our study, DRZ-V was associated with modulation of inflammatory responses in macrophages and enhanced wound

repair, with the findings implicating TIRAP-mediated signaling in this response.

This work suggests that altering macrophage signaling may help reduce prolonged inflammation and allow the wound to progress toward repair.

Moving from Inflammation to Healing

The therapeutic challenge is not to eliminate inflammation, but to restore its appropriate timing and resolution. Macrophages are central to this transition, and understanding the signaling mechanisms that regulate their inflammatory and reparative functions may provide new opportunities to influence chronic wound healing.

Our findings with DRZ-V provide an example of this approach, with modulation of TIRAP-mediated signaling associated with changes in macrophage inflammatory responses and wound repair.

ABOUT THE AUTHORS

Prof. Mirza S. Baig and Sk Rameej Raja are researchers at the Indian Institute of Technology Indore (IIT Indore). Prof. Baig studies inflammation, immune cells, and the development of new treatments for disease, while Sk Rameej Raja, his research scholar, works with him on understanding how inflammation affects wound healing. Their research explores how immune cells called macrophages can be guided from causing prolonged inflammation toward helping the body repair damaged tissue, with the goal of developing better treatments for chronic and difficult-to-heal wounds.

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EMERGING INSIGHT

How Plants Talk Under Attack: The Future of Natural Crop Protection



WHY IT MATTERS

Plants cannot run away when insects attack, but they can send warning signals from one part of the plant to another and prepare for further damage. In this Science Tomorrow article, Dr. Archana Kumari and Shivani Pawar explain how scientists are beginning to understand this hidden communication system. In the future, technologies such as precision gene editing and real-time plant monitoring could help strengthen these natural defenses, leading to crops that better resist pests while reducing the need for chemical pesticides.

When an insect damages one leaf, information about the attack must rapidly reach undamaged tissues, allowing distant parts of the plant to defend against further attack. Plants achieve this through an interconnected communication network involving calcium, reactive oxygen species, changes in electrical activity, and defense hormones such as jasmonate. However, important question remains about how these signals are coordinated in space and time. Our work on the plasma membrane H^+ -ATPase 1(AHA1) highlights the importance of this coordination: the autoinhibitory C-terminal tail of AHA1 regulates proton-pump activity, the duration of wound-induced slow wave potentials, and downstream jasmonate responses in both local-wounded and distally connected tissue. However, we still lack a complete understanding of how changes in proton transport and membrane potential are translated into hormonal and metabolic defense outputs. The next major advances will likely come from technologies

that allow us to monitor and manipulate these processes with greater spatial and temporal precision. Real-time electrophysiological recording (probably using voltage sensors), tissue-specific genetic manipulation, live reporters for jasmonate and other signaling molecules, and spatially resolved metabolomics could help connect electrical signals with hormonal activation and metabolic reprogramming. The demonstrated importance of phloem-specific AHA1 activity suggests that understanding where a signaling component acts may be as important as understanding how much it is activated. Together, these approaches could reveal the molecular “language” through which plants communicate damage and coordinate systemic defense. Such knowledge may ultimately allow us to manipulate plant signaling pathways in a tissue-specific and inducible manner, strengthening natural defense responses while minimizing growth penalties. The broader goal is to move from simply understanding

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Plant Stress Biology • Plant Signaling
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plant defense to harnessing the plant's own communication network for sustainable crop protection.

The Missing Pieces in Plant Defense

Despite growing evidence that plants use electrical, hormonal, and metabolic signals to coordinate defense, it remains unclear how these signals interact together to create a rapid and effective whole-plant response.

How strength, duration, and spatial distribution of signals determine specific responses. It is also crucial to understand how plants distinguish between different types of stresses and adapt their responses accordingly, and balance rapid defense with continued growth. Ultimately, the field needs to move beyond identifying individual signals toward understanding the integrated language of plant communication—how information is encoded, transmitted, and decoded into responses.

Further, several gaps stand out in th-

is work. First, the precise molecular link between membrane electrical signaling (the slow wave potential) and downstream metabolic reprogramming is still unclear. The study shows a strong correlation among SWP duration, JAZ10 expression, and glucosinolate accumulation, but the direct mechanistic link between proton pump regulation and systemic hormone and metabolite induction remains unresolved. Another important question is why the precise level and location of AHA1 activity are so critical for defense. Increased AHA1 activity through C-tail truncation compromises systemic defense, whereas tissue-specific expression in phloem cells can restore electrical signaling and largely alleviate growth defects. This raises the possibility that plants require tightly controlled, cell-specific modulation of proton-pump activity rather than simply increasing or decreasing its activity. Ultimately, we need to determine whether this AHA1-electrical signal-

ing-jasmonate-metabolic network operates similarly across different plant species and agriculturally important crops.

New Tools to Unlock Plant Defense

Recent cross-linking mass spectrometry and covalent-labelling studies on AHA2 (Blackburn et al. 2025) have provided insight into how the C-terminal regulatory domain physically contacts the pump's catalytic domains in three dimensions and how those contacts shift during activation. Extending this kind of structural resolution to AHA1 and capturing it in real time during wounding would allow researchers to observe the release and re-imposition of autoinhibition. Comparable gene-editing precision applied to AHA1's C-tail phosphosites could dissect exactly which phosphorylation events matter for defense versus growth, instead of removing the whole regulatory module. Better tools for cell-type-resolved electrophysiology are also needed. Current surface

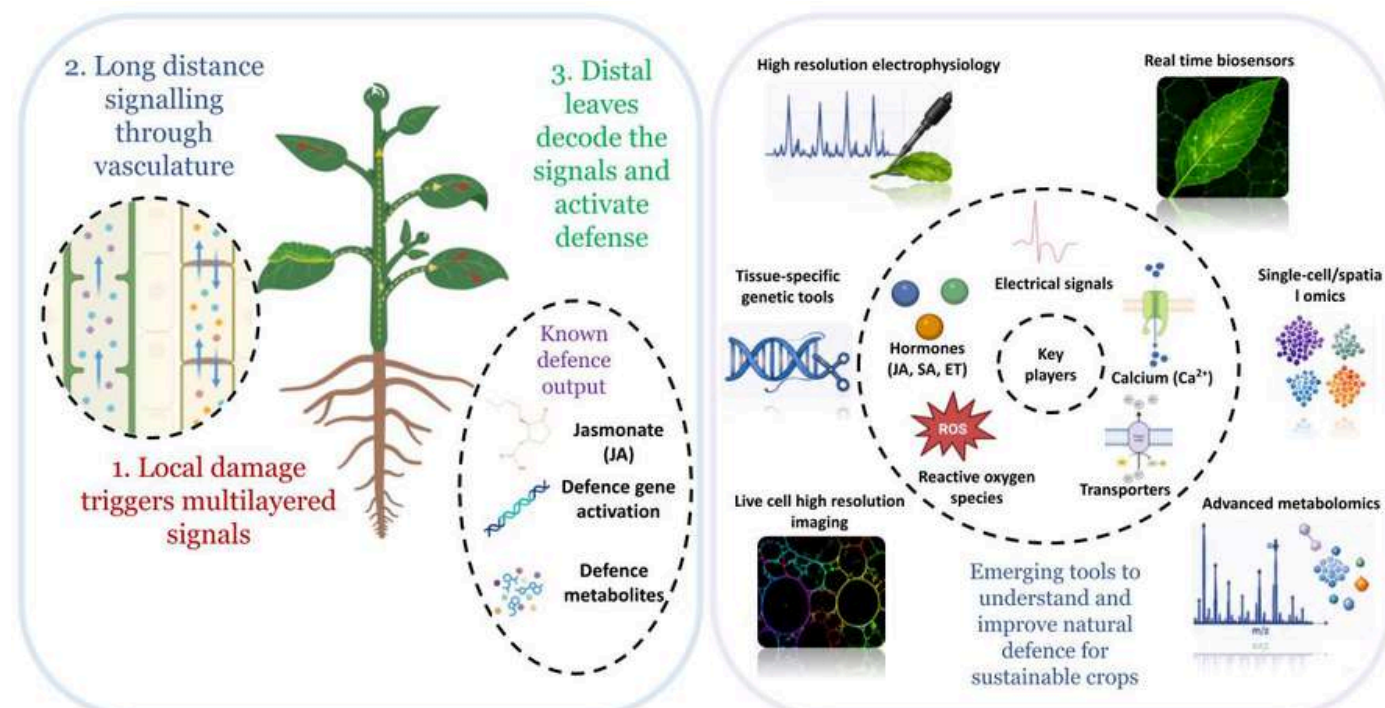


Figure 1: Long-distance signaling with emerging technologies to better understand natural plant defense.



potential measurements capture aggregate signals across whole petioles; more precise, non-invasive methods to record membrane potential changes specifically in sieve elements during herbivory would give more details, like the aphid-electrode intracellular recordings used in earlier phloem signaling work (Salvador-Recatalà et al. 2014).

Finally, genome editing pipelines for introducing precise, tissue-restricted regulatory changes (not just knockouts) in crop species would be needed to translate the promoter-restricted expression strategy used here in *Arabidopsis* into applied breeding programs. Further, small-molecule modulation of proton pumps could provide a promising strategy for enhancing plant resilience and engineering crops with tailored stress responses while minimizing growth penalties.

The Rise of Precision Crop Protection

The most promising trend illustrated by this paper, is precise, targeted genetic engineering rather than whole-plant or whole-gene modification. Using cell-type-restricted promoters (like GLR3.3 for phloem) to fine-tune AHA1 activity in one tissue avoided the growth penalties seen with constitutive C-tail truncation-mirroring the broader shift seen elsewhere in the field, such as the CRISPR-edited GLR3.3 desensitization allele that boosted herbivore defense by altering a single feedback mechanism rather than removing the whole channel (Shao et al. 2024).

Multi-omics integration is another

clear trend: combining electrophysiology, transcriptional reporters, and untargeted metabolomics in a single study, as done here, gives a far more complete systems-level view than any single technique could- and recent reviews (Li et al. 2025) increasingly frame plant systemic defense as a coordinated multi-signal network (electrical, calcium, glutathione, ROS) rather than a single linear pathway, which pushes the field toward integrated experimental designs.

There is also growing interest in identifying conserved "master regulators" that act across species and even across land-plant evolution. Work showing that the AHA R-domain itself is an evolutionary innovation tied to plant terrestrialization (Stéger et al. 2022) and that GLR-based long-range signaling is broadly conserved from mosses to flowering plants (Watanabe et al. 2024) suggests these regulatory modules are promising, evolutionarily robust targets for crop engineering. There's also growing interest in exploiting proton pump regulators as targets, taking inspiration from how animal biology already targets ATPases pharmacologically- a translational bridge between basic membrane biophysics and applied crop protection.

The Next Decade of Plant Defense Research

We expect the field to move from establishing that individual components- AHA1, GLR3.3, calcium channels- matter for defense (much of the last decade's work, including this study), toward a quantitative model of how these co-

ponents interact as an integrated network. Recent reviews already frame wound signaling as running through parallel, interacting channels of electrical, calcium, ROS, and glutathione signals (Li et al. 2025). and we expect the field to increasingly build predictive, system-level models rather than studying each signal in isolation.

We also expect stronger convergence between structural biology and physiology. As cryo-EM and cross-linking methods resolve exactly how regulatory domains like AHA's C-tail or GLR's desensitization loop physically regulate activity (Blackburn et al. 2025), researchers will be able to design far more targeted point mutations or small molecules instead of blunt truncations or knockouts- reducing the growth trade-offs that studies like this one still report. Translational work will likely accelerate too: the demonstrated success of precision editing in boosting defense without major fitness costs (as with the GLR3.3 desensitization allele) provides a template that crop scientists are likely to test in tomato, rice, Brassica, and other economically important species over this timeframe, moving the field from *Arabidopsis* proof-of-concept toward field-deployable traits.

Finally, given increasing climate pressure on crops, we think proton pump and electrical signaling research will be studied less as a "herbivory-specific" topic and more as a general stress-integration node, since AHAs and GLR channels are already implicated in drought, salinity, and pathogen responses alongside insect defense.



Researchers will likely build detailed regulatory maps that show exactly which kinases and 14-3-3 interactions govern AHA activity for each specific stimulus. We also expect a stronger push toward translational work- testing whether the same C-tail regulatory logic holds in crop plants like tomato, rice, or Brassica species, and whether tissue-restricted engineering strategies can be deployed without unacceptable trade-offs in the field.

Toward Smarter, More Resilient Crops

The major developments expected in this rapidly advancing field will likely focus on precision engineering of AHA1 rather than complete removal of its regulatory C-tail. Specific phosphosites within the C-tail could be modified to determine whether defense responses can be enhanced while avoiding growth penalties.

It will also be important to test whether AHA1's phloem-specific regulatory mechanism and the broader glutamate-calcium-electrical signaling network operate similarly in crop species under field conditions, moving beyond Arabidopsis and controlled laboratory environments. Structural studies examining the dynamic conformation of the AHA1 C-tail could further clarify how pump activation is linked to downstream signaling.

Finally, small molecules that target proton pumps or their regulatory domains could provide an inducible, non-genetic approach for enhancing plant defense.

ABOUT THE AUTHORS

Dr. Archana Kumari, Assistant Professor at Gujarat Biotechnology University, Gandhinagar, and Shivani Pawar, Ph.D. Scholar at CSIR–National Chemical Laboratory, Pune, study how plants protect themselves when attacked by insects. Their research explores how a damaged leaf sends warning signals to other parts of the plant, helping activate natural defenses. Their work could contribute to developing stronger, pest-resistant crops and more sustainable approaches to crop protection.

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EMERGING INSIGHT

Can Nature Help Defeat Oral Cancer?

The Future of Plant-Based Cancer Therapies



WHY IT MATTERS

What if some of the starting points for future cancer treatments are hidden in plants around us? Plant compounds can influence how cancer cells grow, survive, and interact with the immune system. In this Science Tomorrow article, Dr. Subhayan Sur explores how compounds found in tea, bitter melon, and other plants are being studied against oral cancer. With advances in molecular research, computer-based screening, and targeted drug delivery, these natural molecules could someday contribute to safer, more precise ways to prevent or complement the treatment of oral cancer.

Imagine that some molecules capable of influencing cancer biology are already growing around us, in tea leaves, bitter melon, grapes, broccoli and many other plants. This does not mean that drinking tea or eating vegetables can cure cancer. Rather, it raises an intriguing question: Could nature provide valuable starting points for safer and more effective approaches to prevent and treat oral cancer?

Plants produce thousands of biologically active compounds that can influence inflammation, cell growth, metabolism, immune responses and programmed cell death. Nature has already contributed several important anticancer medicines. The challenge now is to identify promising plant-derived molecules, understand their mechanisms and determine whether they can be developed into reliable preventive or therapeutic strategies.

Oral cancer: a persistent challenge

Oral squamous cell carcinoma (OSCC), which develops from the epithelial lining of the oral cavity, accounts for more than 90% of oral cancers. Despite advances in surgery, radiotherapy, chemotherapy, targeted therapy and immunotherapy, it remains a major clinical challenge.

Globally, cancers of the lip and oral cavity accounted for approximately 452,205 new cases and 194,108 deaths in 2022, with Asia carrying the greatest burden (GLOBOCAN 2022). In the United States, cancers of the oral cavity and pharynx are estimated to cause about 60,480 new cases and 13,150 deaths in 2026.

The burden is particularly concerning in countries such as India, where tobacco and alcohol use, together with other environmental and lifestyle factors, contributes substantially to disease development. Many patients are diagnosed after in-

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AREAS OF EXPERTISE

Cancer Biology

vasion of surrounding tissues or lymph-node involvement, while recurrence and second primary tumors remain important concerns.

Modern treatments have made significant progress. Surgery remains central, while radiotherapy and chemotherapy are commonly used for advanced disease. Targeted therapies against molecules such as epidermal growth factor receptor (EGFR) and immune checkpoint inhibitors targeting PD-1/PD-L1 have expanded treatment options. However, tumor heterogeneity, treatment resistance and the complex tumor microenvironment continue to limit therapeutic success.

This complexity has encouraged interest in natural products and phytochemicals as potential complementary approaches.

Nature's chemical library

Plants have been used in traditional medicine for thousands of years. Modern research has revealed their remarkable chemical diversity, including polyphenols, flavonoids, alkaloids, terpenoids and other bioactive molecules. Nature has already contributed directly to oncology. Vinca alkaloids such as vincristine and vinblastine, the taxane paclitaxel and compounds related to podophyllotoxin originated from natural sources and became important anticancer drugs. Common foods such as cruciferous vegetables, garlic, onion, green tea, citrus fruits, soybeans, tomatoes, berries, turmeric and ginger also contain phytochemicals that have attracted attention for their potential role in cancer prevention. The scientific interest lies in understanding how these molecules influence cancer-associated pathways.

Tea: more than a comforting beverage?

Tea contains numerous biologically active compounds, including the green-tea polyphenol epigallocatechin gallate (EGCG) and theaflavins found in black tea. Our research first investigated whether black tea could influence biological damage associated with tobacco exposure, a major risk factor for oral cancer.

In a population-based study involving 308 individuals, regular black-tea consumption was associated with lower tobacco-induced reactive oxygen species (ROS) generation and DNA damage in buccal mucosa compared with individuals without a tea-drinking habit. In addition, both EGCG and theaflavin reduced tobacco-associated multi-organ carcinogenesis in tongue and liver of mice simultaneously, with EGCG showing a stronger preventive effect.

The compounds also reduced cancer-cell proliferation, promoted apoptosis and decreased CD44-posi-

tive cancer stem cells. EGCG and theaflavin further influenced self-renewal pathways such as Wnt/ β -catenin and Hedgehog/Gli1. Other studies have similarly reported that EGCG can influence oral cancer proliferation, migration, apoptosis and tumor growth through pathways including PI3K/AKT, MAPK and NF- κ B.

Tea therefore provides an example of how dietary phytochemicals may influence multiple processes associated with cancer development and progression.

Bitter melon: a potential cancer-preventive plant

Another interesting example is bitter melon (*Momordica charantia*), widely cultivated in tropical and subtropical regions, including India. Traditionally consumed as food, bitter melon contains several biologically active compounds.

Our studies investigated whether bi-

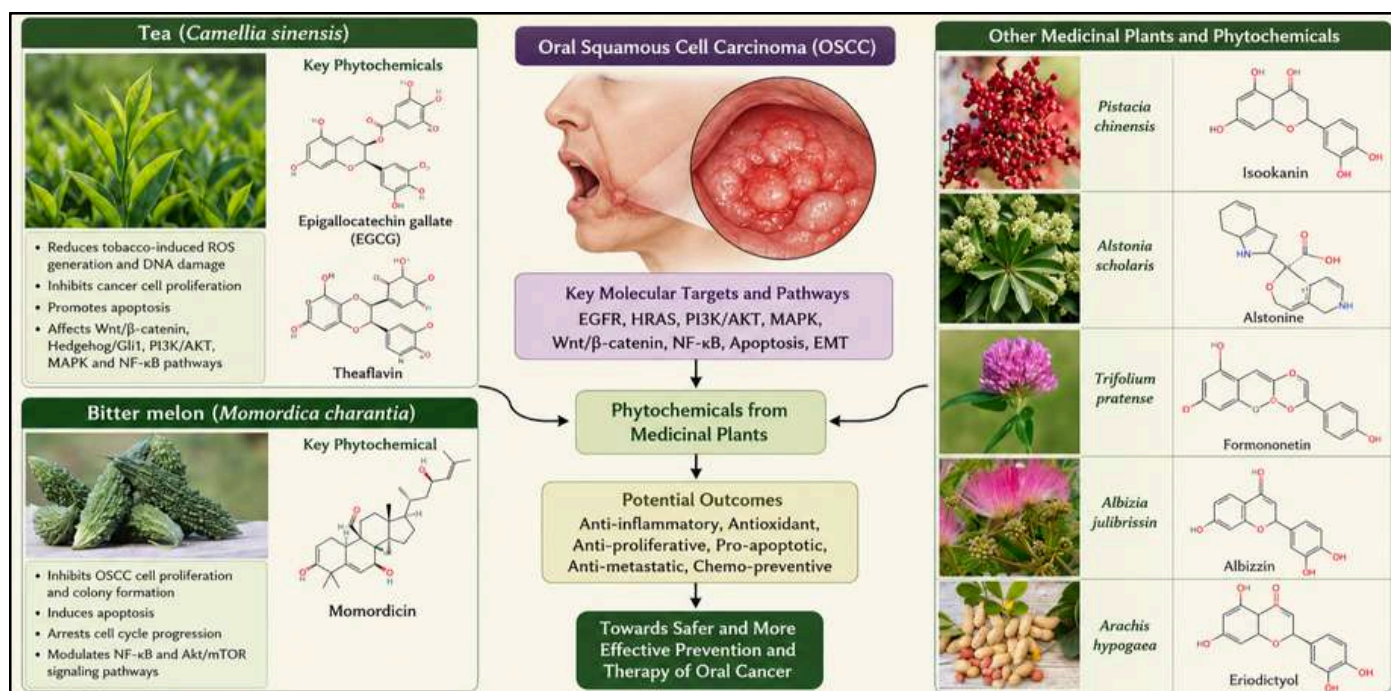


Figure 1. Representative plants and their bioactive phytochemicals with potential anti-oral-cancer activity, highlighting their effects on key molecular pathways and therapeutic processes in oral squamous cell carcinoma (OSCC)



tter melon extract could influence oral carcinogenesis in animal model. Regular administration significantly reduced the incidence of tongue squamous cell carcinoma induced by 4-nitroquinoline 1-oxide (4NQO) in mice, without significant pathological changes in otherwise normal tongue tissue. Next-generation RNA sequencing showed that bitter melon treatment altered 4,482 genes compared with the cancer group. Pathway analysis highlighted immune-related changes, including reductions in pro-inflammatory genes such as S100A9, IL23A and IL1 β . The treatment also influenced PD-1 and MMP9, which are involved in immune regulation and tumor progression.

Bitter melon also affected cancer metabolism, altering genes involved in glycolysis and lipid metabolism and changing pyruvate, lactate and membrane phospholipid production. These findings suggest that plant extracts may influence cancer through interconnected mechanisms involving inflammation, metabolism and immune regulation.

Finding the molecule behind the effect

Plant extracts contain numerous compounds, making it important to identify those responsible for biological activity. Using liquid chromatography coupled with high-resolution mass spectrometry, we identified momordicine-I, a cucurbitane-type triterpene, as an important bioactive component of bitter melon. Momordicine-I reduced human oral cancer cell viability in a dose-dependent manner while showing relatively limited toxicity toward normal cells in experimental studies. Mechanistic

investigations identified c-Met signaling as an important target. In mouse xenograft models, momordicine-I inhibited tumor growth and demonstrated a favorable experimental pharmacokinetic profile.

Cancer is more than a collection of abnormal cells; it is an ecosystem involving tumor, immune and stromal cells. We therefore examined whether momordicine-I could influence the immune environment surrounding oral tumors. Using immunocompetent mouse models and single-cell RNA sequencing, we observed changes in tumor-associated macrophages (TAMs), which can sometimes adopt an immunosuppressive, tumor-supporting phenotype. Momordicine-I altered macrophage-associated molecular programs, including reduced expression of Sfln4 and Cxcl3. Further experiments suggested changes consistent with shifting macrophages away from an M2-like, tumor-supportive state toward a more antitumor M1-like phenotype. Treatment also reduced immune-regulatory molecules including PD-1, PD-L1 and FoxP3 in tumors.

These findings highlight a broader concept: future cancer strategies may need to target not only tumor cells but also tumor metabolism and the surrounding immune microenvironment.

Mining Nature's Chemical Library Through Computational Screening

Nature contains an enormous chemical library, and computational biology can help narrow the search. In our recent OSCC research, RNA sequencing of patient tumors identified the MAPK signaling path-

way as significantly altered. EGFR and HRAS emerged as potential therapeutic targets. We then used molecular docking to screen approximately 17,000 phytochemicals against these targets.

Four molecules: Pratenol B, Eriodictyol, Losbanine and Isookanin, emerged as promising candidates. Pratenol B was particularly interesting because of its potential interactions with both EGFR and HRAS. Additional computational analyses suggested favorable binding, stability, pharmacokinetic characteristics and toxicity.

However, these findings represent an early discovery stage, not proof of clinical efficacy. Computational predictions require validation through laboratory experiments, animal studies and ultimately well-designed clinical trials.

From promising molecules to real medicines

The journey from phytochemical to medicine is complex. Many phytochemicals have limited solubility, poor absorption, rapid metabolism or low bioavailability. Researchers are therefore exploring nanoparticles, targeted delivery systems and other technologies to improve their stability and delivery. Standardization is equally important because plant extracts can vary with species, cultivation, geography, harvesting and extraction methods. Most importantly, natural does not automatically mean safe. Rigorous toxicological, pharmacological and clinical evaluation remains essential.

What might the future look like?

The most exciting possibility may

not be replacing conventional cancer treatment with plant compounds. Instead, the future could involve combination strategies.

A phytochemical might prevent early events in carcinogenesis, another could affect tumor metabolism, while a targeted natural molecule might influence EGFR or HRAS signaling. An immune-modulating compound could potentially reshape the tumor microenvironment. Such approaches may eventually complement conventional therapies or immunotherapy.

This is particularly relevant to oral cancer, where prevention and early intervention could have enormous impact. Identifying high-risk individuals, detecting potentially malignant lesions early and developing scientifically validated chemopreventive strategies could potentially reduce progression to advanced disease.

Nature may therefore not provide a single “magic bullet.” Instead, it may offer a vast library of molecular tools from which future cancer-prevention and treatment strategies can be developed.

The road ahead

Tea polyphenols, bitter melon compounds, momordicine-I and newly identified phytochemicals such as Pratenol B illustrate how plant-derived molecules can influence apoptosis, cancer stem cells, metabolism, inflammatory signaling and the immune microenvironment. The next challenge is translation: Can these molecules be optimized and delivered efficiently? Can their safety be established? Can they complement existing treatments? Most importantly, can their benefits be demonstrated in well-designed

clinical trials?

So, can nature help us fight oral cancer?

The scientifically responsible answer is that nature may contain important pieces of the puzzle, but we are still learning how to put them together. The future of plant-based cancer research will not depend on replacing modern medicine with nature. Rather, it may depend on using modern science to understand nature more deeply. And among the thousands of molecules produced by plants, there may still be important anticancer discoveries waiting to be uncovered.

ABOUT THE AUTHORS

Dr. Subhayan Sur is an Associate Professor at the Dr. D. Y. Patil Biotechnology and Bioinformatics Institute. His research focuses mainly on oral cancer and cancer biology. He studies how oral cancer develops, searches for new biomarkers that could help detect the disease, and investigates natural plant compounds that may help prevent or control cancer. His work also explores non-coding RNAs and molecular pathways involved in cancer, with the broader goal of finding better approaches for cancer diagnosis, prevention, and treatment

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EMERGING INSIGHT

Decoding a bacterial weapon: A new structural blueprint for future antimicrobial strategies



WHY IT MATTERS

As more bacteria become resistant to antibiotics, infections that were once easy to treat could become much harder to control. Scientists are therefore looking for completely new ways to fight harmful bacteria. In this Science Tomorrow article, Bidisha Chakraborty and Dr. Saumen Datta explore a tiny natural weapon used by bacteria, called the Type VI Secretion System (T6SS). They explain how understanding and redesigning this system could someday help disarm dangerous bacteria or deliver targeted treatments directly to harmful microbes.

Microbes have been competing with each other for billions of years over nutrients, space, and survival. This relentless inter-microbial competition has been a powerful force in shaping bacterial evolution, driving bacteria to develop new strategies and increasingly sophisticated weapons to outcompete their rivals. The type VI secretion system (T6SS) is one such weapon found in many Gram-negative bacteria, and provides immense advantage in the microbial warfare. It is a nanoscale protein delivery system embedded in the bacterial cell envelope, made up of multiple conserved structural components. The T6SS remarkably resembles the tail of a bacteriophage in both its architecture and mechanism of action.

The primary function of the T6SS is to deliver toxic effector proteins directly to a neighbouring microbe or to a eukaryotic host cell. These effect-

or toxins attach to some of the core components of the T6SS secretion machinery either by non-covalent bonds, or are translated as a fused part of the secretion system component. When the T6SS fires, the inner tube and the associated effector payload is delivered to the target simply by brute force. Once delivered, the effectors unleash their toxic activities, including disruption of cell walls and membranes, degradation of proteins and nucleic acids, and ultimately damaging or modulating the target.

Over the past two decades, since the discovery of the T6SS in 2006, structural biology techniques—particularly X-ray crystallography, high-resolution cryo-EM, and in situ cryo-electron tomography (cryo-ET) – have been employed extensively to understand the atomic details of individual T6SS component proteins across different bacterial species, as well as to reveal the overall architect-

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Structural biology • Secretion
systems • Bacterial pathogens

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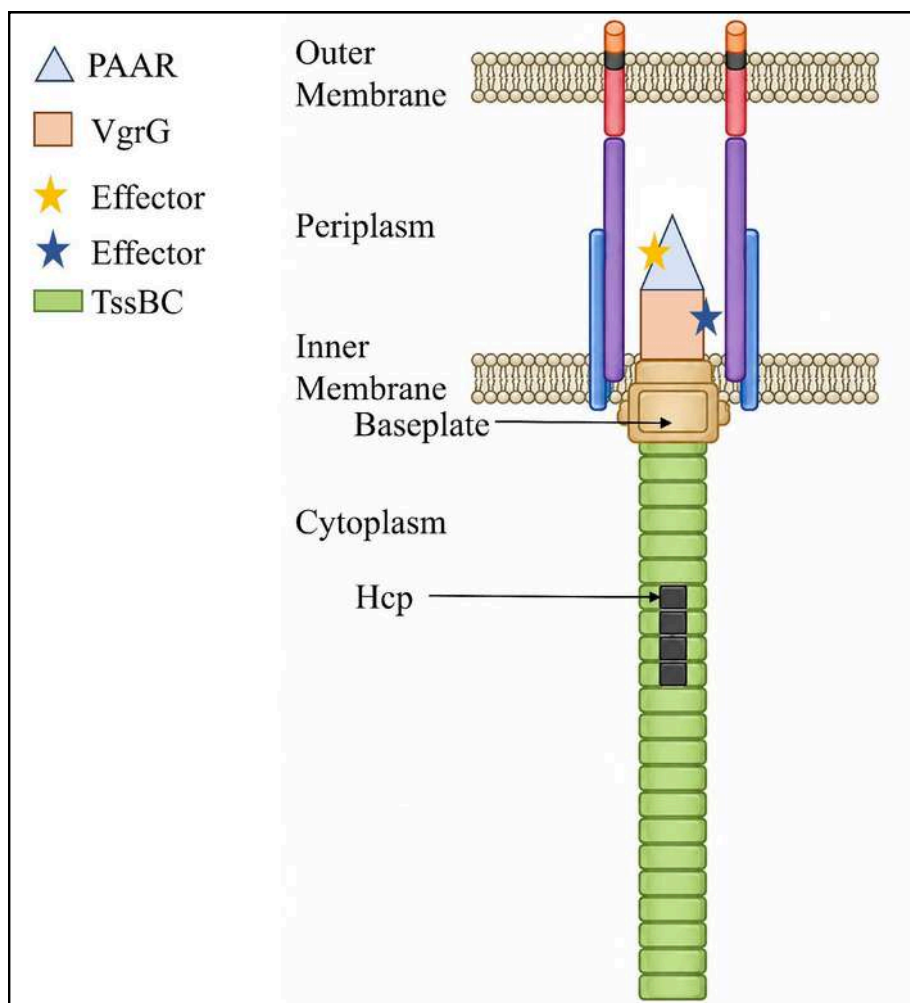


Figure 1. Schematic representation of the T6SS secretion apparatus with different components highlighted.

ure of the secretion apparatus.

Years of rigorous research have also generated extensive biochemical and bioinformatic knowledge about the diverse types of T6SS effectors found across pathogenic and commensal bacterial species, including *Vibrio cholerae*, *Salmonella* spp., and the infamous drug-resistant ESKAPE pathogens.

The basic architecture of the T6SS can be divided into three major structural sub-complexes: a cytoplasmic baseplate complex which serves as a nucleation point for other components to assemble, a membrane complex which spans the

bacterial inner and outer membranes and anchors the secretion machinery to the cell envelope; and a bacteriophage tail-like tail complex which has two concentric tubes capped by a cone-shaped spike that functions as a puncturing device. The inner tube, composed of hexameric rings of Hcp proteins, encloses smaller effector proteins while the spike components VgrG and PAAR repeat containing proteins can carry relatively larger effectors. When the T6SS is fully assembled and ready to fire, the outer tail-tube undergoes rapid contraction. This propels the inner Hcp tube, along with the VgrG-PAAR spike and their associated eff-

ector payload, towards the target.

This extensive structural and biochemical understanding of the T6SS could prove invaluable in the 'post-antibiotic' era that we are rapidly approaching. Since the discovery of penicillin, the overuse and misuse of antibiotics have driven the rapid spread of antimicrobial resistance, giving rise to drug-resistant pathogens that can render conventional treatment options useless. This growing threat highlights the urgent need for alternatives to conventional antibiotics. In this context, the T6SS offers two promising avenues for developing new antimicrobial strategies.

Firstly, the idea of antivirulence, targeting or blocking the virulence factors of pathogens, thereby disarming them without essentially threatening their survival, thus minimizing the selection pressure that leads to development of resistance.

T6SS, with its high structural conservation across species, widespread presence in pathogenic bacteria, and crucial role in infection establishment, is a prime target for antivirulence strategies. Developing a broad-spectrum T6SS inhibitor could become an attractive antivirulence strategy in future.

The second option is perhaps even more intriguing: repurposing the T6SS as an antimicrobial delivery platform to transport selected toxins directly into target pathogens in a controlled manner. Through bioengineering, the T6SS of a non-pathogenic bacterium could potentially be transformed into an efficient delivery vehicle capable of



transporting a cocktail of antimicrobial proteins. These could include canonical T6SS effectors from different bacterial species, as well as non-T6SS toxic proteins with diverse antibacterial and antifungal activities. When coupled with advances in omics and synthetic biology, this approach could provide a highly customizable platform for delivering tailored combinations of toxins against specific microbial targets. Such a strategy offers several potential advantages. It could be used to selectively eliminate harmful pathogens in clinical settings or reshape polymicrobial communities by suppressing undesirable species while promoting the growth of beneficial microbes. The potential applications extend beyond medicine to areas like agriculture and environmental management.

However, though several proof-of-concept studies have shown highly promising results in this context, there are limitations regarding the size of the toxic protein, their stability in the required settings, and their toxic effects in the delivery bacterium.

To sum up, recent advances in our understanding of T6SS structure, coupled with the use of this knowledge to develop alternative antimicrobial strategies, hold significant promise in an era of rising drug resistance and emerging superbugs. T6SS-based antimicrobial applications are still in their infancy, and several major challenges remain to be addressed. However, with continued advances in structural biology, bioengineering, and omics, the T6SS could evolve into a powerful and highly customizable tool in the fight against antimicrobial resistance.

ABOUT THE AUTHORS

Ms. Bidisha Chakraborty and Dr. Saumen Datta are researchers in structural biology at CSIR–Indian Institute of Chemical Biology, Kolkata. Their research explores how disease-causing bacteria use tiny molecular systems to interact with and attack other cells. Their recent work revealed the structure of Tla3, a protein involved in the Type VI Secretion System (T6SS) of *Pseudomonas aeruginosa*. By understanding these bacterial systems at the molecular level, their research could help guide the future development of new strategies to fight drug-resistant bacterial infections.

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EMERGING INSIGHT

The Human Side of Healing: Spirituality, Hope, and Modern Healthcare



WHY IT MATTERS

Modern medicine has become increasingly powerful, but healing is about more than treating the disease. Serious illness can also affect a person's emotions, relationships, hope, and sense of meaning. In this article, Dr. Kamala K. Chandak explores how spirituality, compassion, psychology, and emotional support can complement evidence-based medical care. She explains why listening to patients' values and beliefs can help healthcare become more compassionate and patient-centered, while ensuring that spiritual support never replaces proven medical treatment.

Modern medicine has radically transformed our understanding and treatment of serious illness, offering unprecedented interventions and diagnostic capabilities. Yet, illness is never purely biological. A severe diagnosis echoes far beyond physical symptoms, profoundly impacting a person's emotional state, family dynamics, sense of identity, core values, beliefs, and expectations for the future.

Increasingly, clinical practice recognizes that caring for the whole person requires addressing these human dimensions alongside evidence-based medical treatment. Spirituality, psychology, compassion, and the medical humanities offer essential layers of support provided they are integrated responsibly, ethically, and with deep respect for individual patient belief systems.

Role of Spirituality in Coping with Illness

Personal beliefs and spirituality frequently serve as vital emotional and psychological anchors when

individuals face serious illness. They provide structure and comfort, helping patients and their families navigate overwhelming uncertainty, process grief, and deliberate over complex medical decisions.

Serious illness invariably prompts existential questions that clinical medicine alone cannot answer: Why is this happening to me? How can my family and I cope with this uncertainty? Where do I find internal strength? What gives my life meaning now? Facing this level of personal vulnerability tests every emotional and spiritual reserve. Under such conditions, abstract spiritual concepts and personal beliefs convert into concrete, daily coping strategies.

Practices such as prayer, meditation, mindfulness, or religious rituals offer tangible benefits by helping to reduce anxiety, depression, and feelings of isolation. They lower physiological stress levels, promote comfort, and foster a sustained sense of hope, whether that hope is directed toward

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physical recovery, inner peace, or a meaningful life transition. Furthermore, the experience of illness often impels individuals to resolve lingering past conflicts, extend forgiveness, and deepen personal relationships, bringing a profound sense of emotional completion.

Ultimately, the primary contribution of spirituality is not that it provides a guaranteed explanation or cure for illness, but that it helps individuals discover meaning, connection, comfort, and hope within circumstances they cannot control. Spirituality may not alter the medical diagnosis itself, but it fundamentally transforms how a person experiences, frames, and responds to that diagnosis. Family members similarly draw strength from shared

beliefs, collective prayer, quiet presence, and the supportive network of a faith community.

“Spirituality may not change the medical diagnosis, but it can change how a person experiences and responds to that diagnosis.”

Integrating Spirituality, Psychology, and Conventional Medicine

Whole-person healthcare relies on understanding the distinct yet complementary roles played by different disciplines: **Conventional Medicine:** Focuses primarily on the physical body, providing the scientific foundation for diagnosis, medical treatment, disease prevention, and physical symptom management. **Psychology:** Focuses on the mind and behavior, assisting patients in processing complex emotions, building healthy coping mechanisms, reworking negative thought patterns, and working through psychological trauma. **Spirituality:** Focuses on meaning, purpose, and values, restoring hope, resolving existential distress, and

strengthening a sense of broader connection. Rather than competing, these approaches form what modern healthcare identifies as the Biopsychosocial-Spiritual Model. Instead of treating illness in isolation, this comprehensive framework treats the individual as an integrated whole body, mind, and spirit. In specialized clinical settings such as oncology, palliative care, and chronic disease management, multidisciplinary teams comprising physicians, nurses, therapists, social workers, and chaplains collaborate to support the patient at every stage of disease progression. This integrated care ensures that while medicine stabilizes the physical body, psychology and spiritual care safeguard emotional well-being and personal purpose.

Maintaining Hope Without Unrealistic Expectations

Hope is essential to human resilience, but clinical practice must distinguish realistic hope from false reassurance. Healthcare professionals bear a professional and moral obligation to communicate

honestly about diagnosis, prognosis, treatment risks, and uncertainties. Patients and their families deserve clear, truthful information, even when the truth is difficult to convey.

Simultaneously, maintaining hope does not require promising a medical cure. While a patient may initially hope for successful treatment or remission, hope is dynamic and evolves throughout the illness journey. Hope can refocus toward achievable, deeply meaningful outcomes: relief from physical pain, spending quality time with loved ones, preserving personal autonomy, reconciling family relationships, or achieving a peaceful end-of-life experience. Hope does not depend on clinical certainty; it empowers people to find possibility, dignity, and meaning even in the presence of uncertainty.

“Hope does not require certainty. It allows people to find meaning and possibility even in the presence of uncertainty.”

Lessons from Contemplative and Compassionate Traditions

Long before the advent of modern healthcare systems, diverse cultural and spiritual traditions developed practices to help individuals face suffering, illness, and mortality. These historical traditions offer contemporary medicine valuable insights regarding presence, community support, compassion, and self-reflection.

While modern medicine excels at technical interventions and biological diagnostics, it can struggle with the relational and existential dimensions of patient care. Contemplative practices offer centuries of practical wisdom that

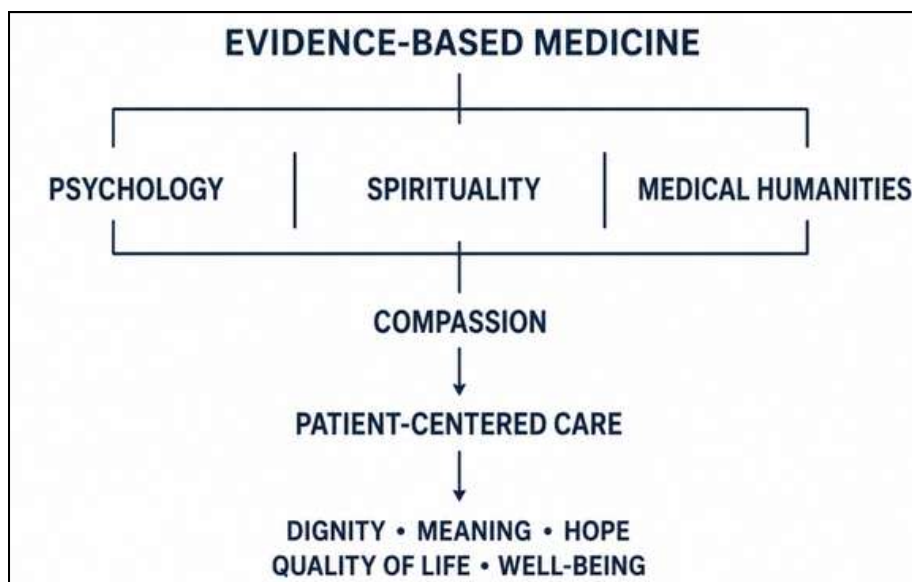


Figure 1: Integrative healthcare model combining scientific medicine with psychological, spiritual, and humanistic support.



can convert transactional medical interactions into holistic healing environments. Emerging research in psychoneuroimmunology highlights that practices like meditation, prayer, and mindfulness help down-regulate the sympathetic nervous system, reducing stress responses and acting as a resilience engine during medical crises.

However, incorporating these concepts into clinical settings requires strict professional boundaries. Spiritual care must always remain voluntary, non-coercive, and centered entirely on the patient's values. Healthcare providers must never impose their personal beliefs. Instead, clinicians should evaluate practices by asking: What does this practice mean to the patient? Does it provide comfort? Is it safe? Can it be safely integrated alongside evidence-based medical treatments?

Current Scientific Research on Spiritual Well-Being

A growing body of scientific literature explores the relationship between spiritual well-being, resilience, and clinical outcomes. A major systematic review published in JAMA demonstrated substantial evidence that spirituality is positively associated with better quality-of-life outcomes in serious illness, recommending its consideration within person-centered care models. Research in palliative and end-of-life care indicates that structured spiritual-care interventions measurably improve spiritual well-being, alleviate psychological distress, and enhance overall quality of life. Studies demonstrate that spiritual practices help facilitate psychological recovery and coping

following severe stress or major medical diagnoses. Despite these positive associations, researchers emphasize that results must be interpreted carefully. Methodologies vary, and association must not be confused with causation. Current research supports spirituality as an effective resource for coping, emotional resilience, and quality of life, but it does not support claims that spiritual practices cure physical diseases like cancer or serve as a substitute for standard medical care.

Addressing Spiritual Needs in Evidence-Based Practice

Healthcare professionals can address spiritual needs while upholding rigorous evidence-based practice through respectful curiosity and active listening. Clinicians can open communication by asking simple, non-judgmental questions about whether personal beliefs, culture, or spirituality play a role in how patients handle their health and well-being.

Medical providers do not need to act as religious experts. When specialized support is required, clinicians should collaborate with trained chaplains, social workers, psychologists, and recognized community faith leaders. This collaborative approach is critical during advanced illness or end-of-life planning, where spiritual beliefs heavily influence views on suffering, medical decisions, and personal dignity.

Core Principle: Evidence guides medical treatment; patient values guide individualized care.

Spiritual practices should always complement scientific medicine rather than replace it. Clinicians

must maintain transparency regarding medical possibilities while offering genuine empathy, recognizing that true compassion does not require making promises that medicine cannot fulfill.

The Future of Integrative Healthcare

The future of medicine relies on establishing an equilibrium where scientific excellence and humanistic care are valued as equally essential components of health services.

As medical technology continues to advance through artificial intelligence, precision medicine, complex diagnostics, and specialized therapies, preserving authentic human connection becomes increasingly vital. The future healthcare delivery model will rely on interdisciplinary teams physicians, nurses, psychologists, social workers, palliative specialists, and spiritual care providers working collaboratively to address individual patient needs.

In this framework, the medical humanities (literature, philosophy, ethics, narrative medicine, and the arts) play a vital role. They train healthcare providers to look beyond medical charts to understand the human story behind the illness. Ultimately, integrative healthcare does not mean endorsing unproven therapies; it means combining scientific rigor, clinical expertise, patient values, and compassionate support. The overarching goal is not merely to become more efficient at treating diseases, but to become far more effective at caring for human beings.

Conclusion

The human side of healing serves as



a constant reminder that illness is simultaneously a biological, emotional, social, and existential experience. Modern medicine provides indispensable tools for diagnosing and curing disease, while spirituality, psychology, compassion, and the humanities protect meaning, emotional resilience, dignity, and personal voice.

The challenge facing modern healthcare is not choosing between scientific rigor and human spirituality. The true challenge is ensuring that continuous scientific and technological progress remains dedicated to the fundamental purpose of medicine: helping human beings live, cope, heal, and, when physical cure is no longer attainable, experience care with unyielding dignity and compassion.

ABOUT THE AUTHORS

Dr. Kamala K. Chandak is an Associate Professor in the Department of Pharmacognosy and Phytochemistry at Smt. Kishoritai Bhojar College of Pharmacy, Kamptee, Nagpur, Maharashtra. She has extensive academic and research experience in pharmacy, with her work focusing particularly on pharmacognosy, phytochemistry, medicinal plants, and natural product. She also writes about the human dimensions of healthcare, including spirituality, hope, compassion, and emotional well-being during serious illness, emphasizing their complementary role alongside evidence-based medical care.

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EMERGING INSIGHT

The Future of Anti-Cancer Drug Discovery: From Molecular Innovation to Precision Medicine



WHY IT MATTERS

Cancer treatment is moving toward a future where medicines could be designed for the specific molecular features of each patient's tumour. In this Science Tomorrow article, Prof. M. Vijjulatha and Dr. P. Saikiran Reddy explain how artificial intelligence, molecular modelling, medicinal chemistry, and precision medicine are transforming anticancer drug discovery. By combining these technologies, researchers could identify promising drugs faster, overcome drug resistance, reduce unwanted side effects, and ultimately develop more precise and personalized cancer treatments.

Cancer therapeutics at present is undergoing a transition from traditional chemotherapy to more advanced mechanism based molecularly driven and patient specific treatment. The scope of anti cancer drug discovery in future is largely depended on the integration of molecular modeling, medicinal chemistry, structural biology, artificial intelligence, genomics, chemical biology and precision medicine. The primary objective is to design specific therapeutic drug candidates which recognize diseases related molecular vulnerabilities while minimizing toxicity effects rather than simply identifying molecules that can kill the cancer cells. Our research demonstrates this transformation through design and synthesis of anticancer scaffolds through molecular docking, 3D QSAR, molecular dynamics simulations and biological evaluation.

Molecular innovation as the basis for next generation cancer therapeutics

The discovery of new potent anticancer agents starts with molecular innovation. The privileged heterocyclic scaffolds, molecular hybrids and structurally modified analogues continue to provide crucial chemical foundation for discovery of new potent molecules. Triazole, thiadiazole, thiazolidinedione, Indole, Azaindole, pyrazole and related heterocyclic entities are highly valuable because of their physicochemical and electronic properties which can be modified systematically to achieve improved selectivity, target recognition and biological activity.

Our recent research particularly demonstrated this strategy well. We reported Meldrum's acid based 7-azaindole based 1,2,3- triazole hybrids and evaluated their anticanc-



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er properties against various cell lines, combining chemical synthesis and biological activity. In another study we reported indole 1,3,4, thiadiazole schiff based hybrids as anticancer agents which showed potent and selective cytotoxicity against cancer cell lines while showing lower toxicity towards normal cells, demonstrating the significance of chemical optimization for achieving a therapeutic window. The same is evident in another study involving 1,2,3-triazole based thiazolidine-2,4-dione derivatives, where synthesis, molecular docking and anticancer/antimicrobial evaluation were combined into a single discovery. These investigations illustrate that molecular innovation is most powerful when synthesis, computational prediction and experimental validations are done recursively rather than isolated stages.

From one drug one target to interconnected network pharmacology

The scope of cancer drug discovery in future will require a paradigm shift from single target to understanding the interconnected signalling networks. Cancer cells generally develop resistance by mutating active site where the drug binds, modifies apoptosis signalling, alters microenvironment or activating alternative pathways. Therefore, inhibition of one protein produces only limited or temporary therapeutic benefit.

Molecular modeling approaches can help in identifying the crucial nodes within cancer associated signalling networks. Our research included molecular modeling studies on various kinase targets relevant to ca-

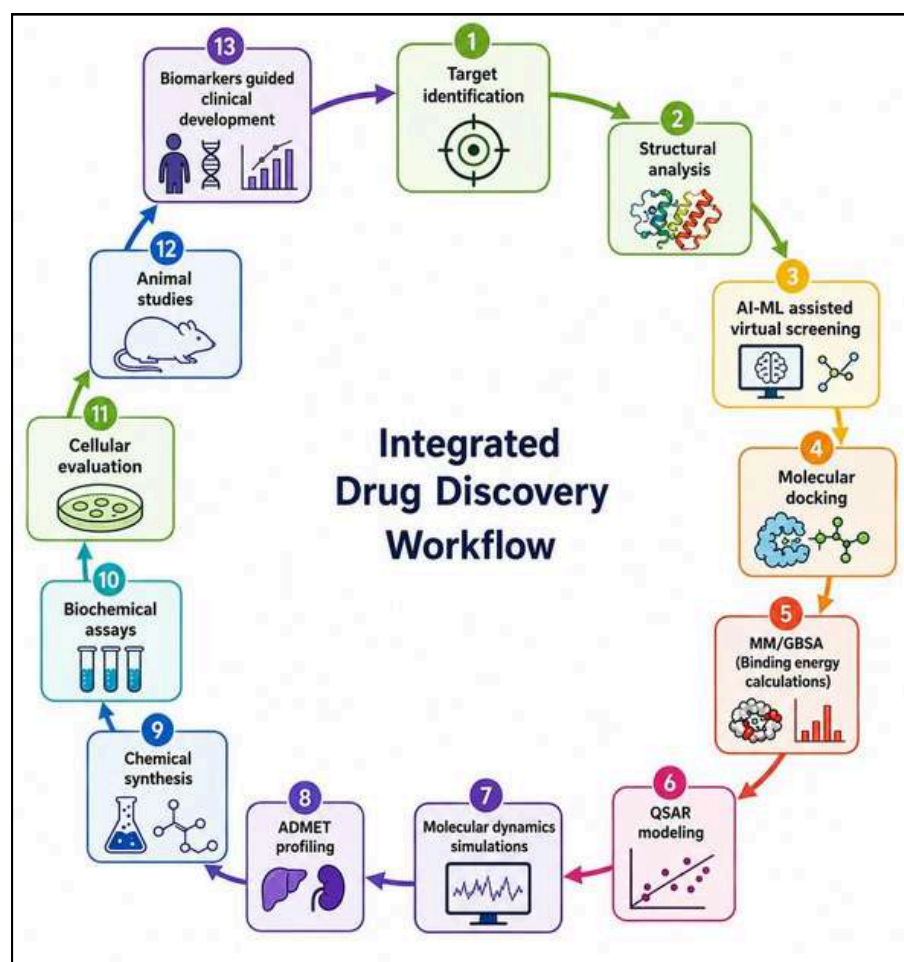
ncer. For example, an insilico study was carried out on Akt inhibitors using computational approaches. Akt is an important component of PI3K/Akt/mTOR signalling pathway which is known to regulate survival, proliferation metabolism and is often dysregulated in cancer.

Earlier we also investigated B-Raf kinase inhibitors through integrated molecular design and computational approaches. All these studies show that computational chemistry is not merely used to rank the compounds but understand how modifications at molecular level influence the target engagement, pathway modulation and even resistance mechanisms.

Artificial Intelligence-Machine learning (AI/ML) and computational drug discovery

Artificial Intelligence and Machine learning are sophisticated tools that are expected to drive next generation anticancer drug discovery. Current medicinal chemistry approaches require synthesis and biological evaluation of millions of compounds where as advanced AI-assisted protocols can prioritize promising leads even before synthesis by predicting biological activities, ADMET profiles, protein-ligand interactions, physicochemical and electronic properties.

The integrated molecular modeling approaches along with machine learning techniques provides a powerful structural framework that can narrow down the chemical space. This computational evolution is reflected in one of our publications involving Molecular docking, MM/





GBSA, 3DQSAR, Pharmacophore modeling and Molecular dynamics simulations. Our work on pim-3 inhibitors involving pragmatic pharmaco-informatics strategy is one of the classic examples of using computational techniques for indentifying new potent anticancer agents.

An important future development in this area is integration of generative AI with structure-based drug design. Generative models rather than searching only existing molecular libraries can propose novel molecular entities or chemical probes optimized simultaneously for selectivity, solubility, potency, synthetic accessibility and metabolic stability.

Medicinal chemists will continue to play essential role because AI-generated molecules must still meet synthetic feasibility, safety, biological relevance and require expert prioritization, retro synthetic planning, experimental validation to be satisfied as a useful drug candidate.

Precision Medicine: Administering the right drug to the right patient at the right time

The paramount goal of molecular innovations is precision medicine. Cancer is not a single disease but rather a collection of molecularly different diseases. Two patients with same anatomical cancer diagnosis may harbour entirely different genetic alterations, drug sensitivities and signalling dependencies. As a result, future anticancer therapy will eventually depend on the molecular characterization of individual tumours.

Proteomics, metabolomics, transcri-

ptomics, genomic sequencing can identify actionable alterations and therapeutic vulnerabilities. Computational approaches can then link molecular signatures with suitable targets and drug candidates. In our previous study we explored the relationship between cancer mutations and drug sensitivity/resistivity. In particular, we investigated how mutations in Epidermal Growth Factor Receptor (EGFR) can influence differential sensitivity towards kinase inhibitors, substantiating the relevance of molecular variation to therapeutic response.

This approach will become gradually important for the causes that are driven by heterogeneous mutations. Instead of specifying treatment solely on the basis of tumour location, future clinical decision making will slowly consider the molecular topology of the tumour. Companion diagnostics, liquid biopsy, circulating tumour DNA and real time molecular monitoring may authorize clinicians to identify emerging resistance before it becomes clinically apparent.

Overcoming Drug resistance

One of the greatest challenges in oncology even today is drug resistance. Cancer cells continue to evolve under therapeutic pressure, causing highly effective targeted therapies fail. Therefore, it is essential for future anticancer discovery to envision resistance at the early stages of molecular design.

One of the promising strategies is development of molecular entities that are capable of identifying mutant forms of therapeutic targets. Other strategies include developme-

nt of covalent inhibitors, allosteric inhibitors, multi target directed ligands and molecular degraders. Combination therapy can simultaneously suppress shared survival pathways and decrease the probability of resistant clones arising thereof.

In this context design of molecular hybrids is an attractive strategy. Medicinal chemists and researchers can generate potential compounds capable of interacting with more than one disease relevant mechanism by integrating pharmacologically relevant structural motifs into a single molecular framework. Our work on azaindole-triazole and thiadiazole containing compounds and relevant heterocyclic hybrids is perfect example of this molecular hybridization approach.

This concept may be further extended in future by proteolysis targeting chimeras, (PROTACS) molecular genes and other targeted protein degradation strategies. These technologies remove or destabilize the pathogen protein itself rather than inhibiting a cancer associated protein.

From insilico predictions to invivo validated medicines

One of the major challenges in the process of computational drug discovery is translation of predicated activity into reproducible experimental and clinical outcomes. Docking score or binding energy values alone cannot establish whether a compound can become a successful drug (or) hit molecule. Various parameters such as solvent effects, protein flexibility, cellular permeability, ADMET profiling and

tumour heterogeneity must all be considered. Therefore, a closed loop discovery model would be ideal for future workflow.

The strength of our research lies in the interconnection mechanism where interdisciplinary areas of molecular modeling and medicinal chemistry are connected. Our recent studies combine computational studies, synthetic chemistry and biological testing, providing a combined route from the molecular hypothesis to the experimentally endorsed lead compounds.

The next decade: Towards insightful and patient –specific oncology

The next decade of anticancer drug discovery will be increasingly defined by convergence. Molecular modeling will converge with high through-put experimentation, medicinal chemistry with synthetic biology, drug discovery with genomic medicine and artificial intelligence-machine learning with structural biology. The convergence will enable researchers worldwide to design molecules precisely for defined molecular vulnerabilities rather than identifying broadly cytotoxic compounds. The next generation may involve single cell sequencing, patient derived tumour organoids, computationally generated disease models and spatial transcriptomics. These sophisticated techniques not only help in identifying which mutation is present but also determine which tumour cell population depends upon a particular pathway. Drug like candidates can be thereafter evaluated in biologically relevant patient derived models before entering into clinical trials. Our recent work demonstrates this conti-

nuing evolution of the above research. Our publication on 7-azaindole linked imidazole-1,2,3-triazole hybrids in 2026 combines computational screening, synthesis and antiproliferative evaluation depicting the continuing integration of molecular design and computation in anticancer drug discovery.

Conclusion

The future course of anticancer drug discovery will be determined by the capacity to translate molecular understanding into adaptive, selective and patient specific therapies. The impact of molecular innovation will be amplified through artificial intelligence, computational chemistry, precision medicine, systems pharmacology and structured biology.

Our research contributions substantiate how heterocyclic molecular design, hybridization, computational modeling, QSAR studies, molecular docking, binding free energies, molecular dynamics simulations and biological evaluation can be altogether integrated to address the contemporary and future challenges in drug discovery. The fundamental idea is not to discover a greater number of anticancer molecules, but to develop therapeutics which can exclusively exploit the molecular weakness of individual tumours, overcome resistance, minimize toxicity and improve quality of life.

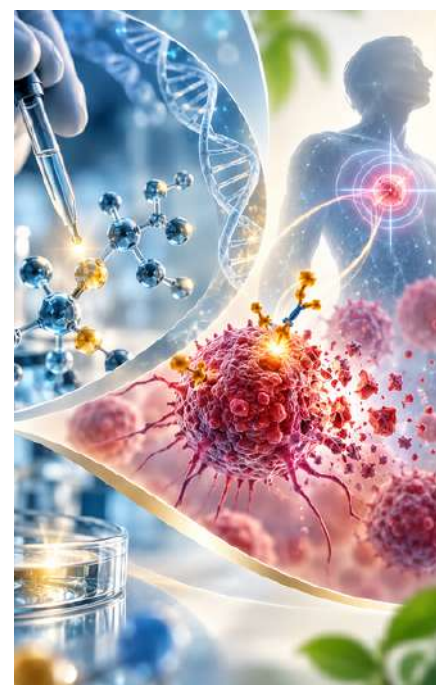
Therefore, it is obvious that future oncology paradigm will increasingly depend on the continuous integration of molecular innovation with precision medicine.

ABOUT THE AUTHORS

Prof. M. Vijjulatha and Dr. P. Saikiran Reddy are researchers at Osmania University, Hyderabad, working on the discovery of new medicines. Their research combines chemistry and computer-based technologies to design and study potential drug molecules before they are tested in the laboratory. They use tools such as molecular modelling, artificial intelligence, and computer simulations to understand how medicines may interact with disease-related targets. Their work has a particular focus on developing new and more precise approaches to cancer drug discovery.

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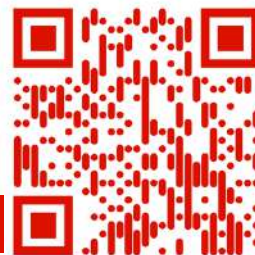
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A Researcher Showcase is a platform designed to highlight the innovative work and contributions of researchers across various fields. It provides an opportunity for scholars to present their findings, exchange ideas, and foster collaborations. RFCSR's showcases helps researchers with networking opportunities to celebrate and support academic and scientific progress.



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RFCSR considers science experts' advice & directions as the foremost priority to impact the science research community. The organization maintains strong connections with over twenty thousand PhD and post-PhD experienced scientific researchers, including scientists, advanced researchers, and both national and predominantly international experts across diverse fields of expertise. Nominate the experts to advise RFCSR. Scientific advisors are specifically focused to advise RFCSR to build and initiate innovative activities.



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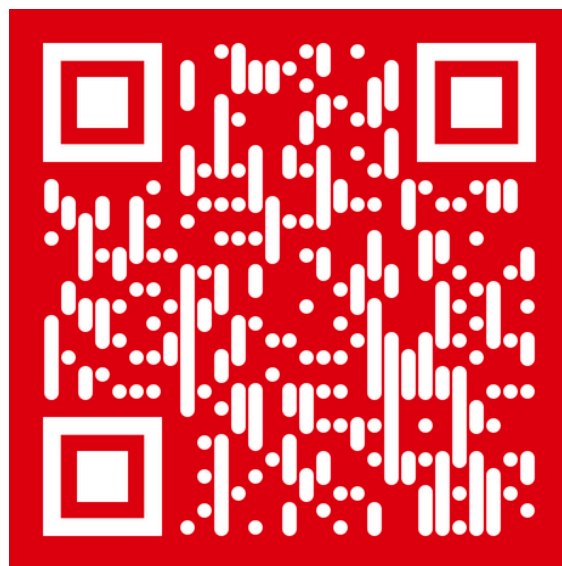
Education and research are the foundation of social progress.

A community grows stronger when everyone has equal access to knowledge, quality education, and the benefits of research. At our organization, we believe in creating opportunities where learning and innovation are accessible to all. By associating with us, you'll help bridge the gap—empowering individuals, supporting education, and contributing to a more inclusive and developed society.

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Global Outreach members are individuals currently residing full time in a resource-constrained country studying or working in sciences and research.

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At Rosalind Franklin Council of Scientific Research (RFCSR), we recognize that the pursuit of science is both inspiring and demanding. Alongside the excitement of discovery, researchers often face unique challenges—intense workloads, high expectations, uncertainty about the future, and at times the discouraging experience of non-cooperation within their professional field or the feeling of being stuck in their career path. Such moments can leave even the most dedicated scientists questioning their way forward.



RESEARCHERS LIFELINE RESEARCH HEALTH



back to school



CURIOUS KID'S

NAME: Chitrakshi Hota

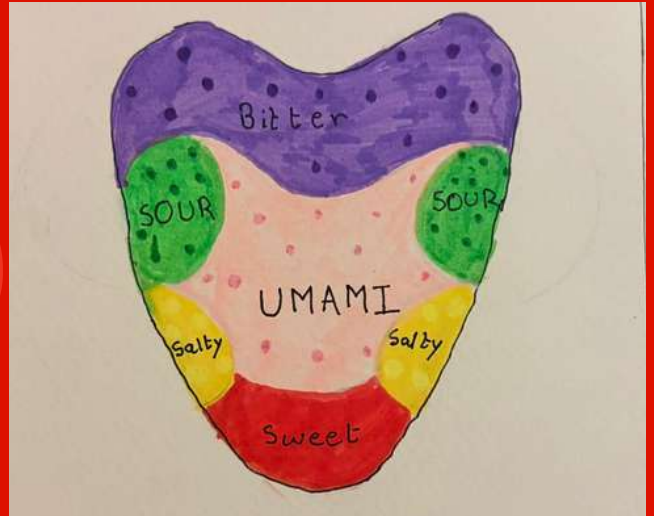
Grade: 4

SCHOOL: VIBGYOR High International School

FOCUS:

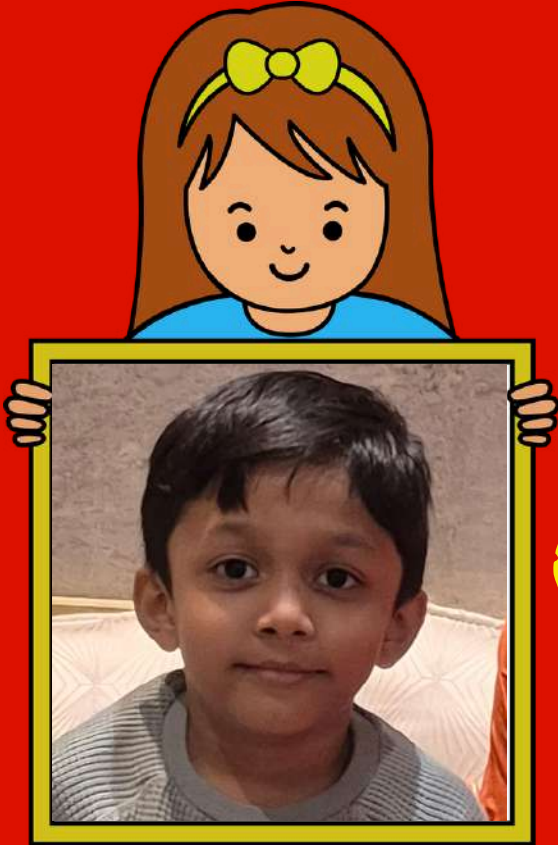
How Does My Tongue Know What I'm Eating?

Have you ever wondered how your tongue can tell the difference between ice cream, lemon, chips, and vegetables? My painting explores the five basic tastes sweet, salty, sour, bitter, and umami. Tiny taste buds on our tongue act like little scientists, detecting these flavors and sending messages to the brain. Together, they help us enjoy food, stay safe from harmful substances, and discover the amazing science hidden in every bite!

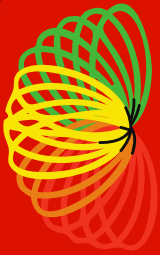


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back to school



CURIOUS KID'S



NAME: Parth Shreyas

Grade: Class 1

SCHOOL: DAV UNIT VII

FOCUS:

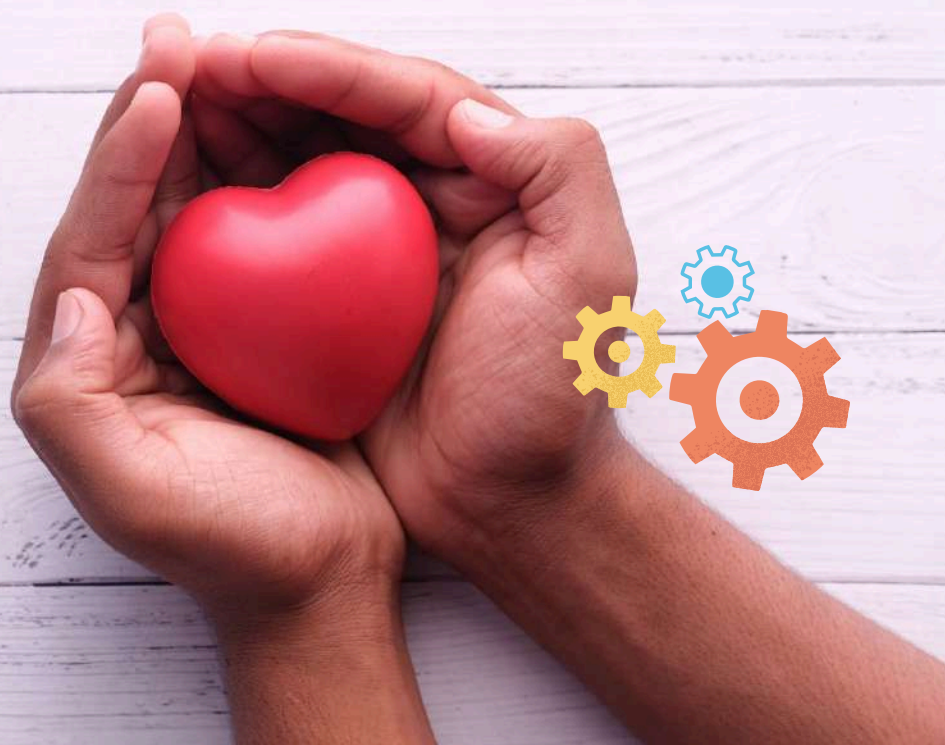
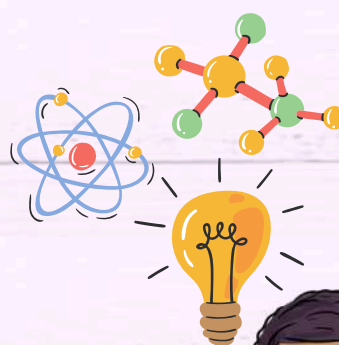
How Fast Does Sunlight Travel?

Have you ever wondered how sunlight reaches us from so far away? My drawing shows the Sun shining light toward Earth. Light travels incredibly fast about 300,000 kilometers every second! Even at this amazing speed, sunlight takes about 8 minutes and 20 seconds to travel the 150 million kilometers between the Sun and Earth. This means when we look at the Sun, we are actually seeing it as it was more than 8 minutes ago. My painting reminds us that light connects distance, time, and life on Earth in a fascinating way.



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