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Healthy corals helping bleached neighbours



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Healthy corals helping bleached neighbours recover | p13

Butterfly wing patterns creating misleading motion cues | p15

A full marathon on a single battery charge | p17



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"In a world flooded with information, *Science Factors* stands out for its clarity, creativity, and commitment to truth. It brings the latest discoveries from top global journals into classrooms, cafés, and conversations—without losing the wonder that makes science so human. I believe this magazine will inspire not just students, but scientists too, to see their work through fresh, curious eyes."



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LETTER *from the* EDITOR

Dr. Animesha Rath
The Editor-in-Chief

Dear Readers,

Every scientific discovery begins with a question. Sometimes it comes from observing something unusual in nature. Sometimes it begins with a problem that needs a solution. What makes science remarkable is our ability to turn these questions into knowledge that can change how we understand the world.

In this November issue of Science Factors, we celebrate that spirit of curiosity and discovery. Our cover story explores how healthy corals can help their bleached neighbours recover, reminding us that nature still has many surprising lessons to teach. We also discover how butterfly wings can confuse predators and how a four-legged robot completed a marathon on a single battery charge. These stories show that inspiration can come from anywhere.

This issue also brings together important perspectives on human health, agriculture, biotechnology and emerging technologies. From understanding the tiny microorganisms that support plant growth to exploring new approaches to gene editing, medicine and sustainable materials, each article offers a different way of looking at the challenges around us.

But science is not only about remarkable discoveries. It is also about the people behind them: researchers who spend years asking questions, students who are just beginning their journeys, and innovators who work to turn ideas into practical solutions. Their experiences remind us that progress requires patience, collaboration and the courage to explore the unknown.

At *Science Factors*, we believe scientific knowledge should reach beyond laboratories and academic journals. Our goal is to make science understandable, interesting and inspiring for everyone, especially young minds who may one day become the scientists and innovators of tomorrow.

I sincerely thank our authors, contributors, reviewers and editorial team for their dedication. To our readers, thank you for being part of this journey and for keeping your curiosity alive.

As you turn these pages, I hope you find something that makes you curious, encourages you to ask a new question, or inspires you to explore an idea of your own. After all, every great discovery begins with someone who dares to wonder.

Happy reading!



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Fuel discovery, inspire the future.

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. Preeti Sharma

HEALTHY CORALS HELPING BLEACHED NEIGHBOURS RECOVER

FEATURED

One quiet morning at Hopkins Marine Station in Pacific Grove, California, Tessa Morgan noticed something troubling in a tank of seawater. A small coral branch that had once glowed with rich brown and golden colors now looked pale and almost lifeless. “It looks as if someone has drained the color right out of it,” she told her colleague, Luis Ortega. The coral was experiencing bleaching, a condition that can happen when unusually warm water stresses a coral and causes it to lose tiny living partners called symbionts. These microscopic organisms live inside coral tissue and use sunlight to make food, sharing much of that energy with their host. Without enough of them, a coral can struggle to survive. Tessa knew that some bleached corals recover when their remaining symbionts multiply or when new ones arrive from the surrounding water. But this process can take months, and some corals die before it happens. As she watched the pale branch, a question began to form in her mind: what if a healthy coral could help a bleached neighbor recover much faster simply by touching it?

Luis was curious, too, but he wanted evidence rather than hope. The researchers prepared small fragments of Pocillopora damicornis, a coral species found on Indo-Pacific reefs, and placed bleached fragments beside healthy ones. Some pairs were allowed to touch directly, while other bleached fragments were kept just a few millimeters away. The team carefully watched both groups over the following weeks. At first, the differences were subtle. Then the pale corals that touched healthy partners began showing signs of change. Their color slowly returned, and the living polyps the tiny individual animals that make up a coral colony started recovering. Under the microscope, Tessa saw something even more exciting: symbionts were appearing in the bleached coral, beginning near the point where the two fragments met. The fragments that remained apart told a very different story. Algae spread over their weakened surfaces, and some eventually died. “They are almost next to each other,” Luis said, looking at the separated fragments, “but that isn’t enough.” The experiment suggested that closeness alone could not explain the recovery. Something important was happening through direct contact.

The team next asked how long that contact needed to last. Did the healthy coral have to stay beside its struggling partner for weeks, or could a brief meeting be enough? They connected coral fragments for different periods, then carefully separated them and continued observing the ble-



| By Dr. Preeti Sharma

ached ones. The results surprised them. A week of contact could provide enough symbionts for a bleached fragment to continue recovering on its own. Some fragments showed signs of recovery after only three days of contact, although that shorter period did not reliably lead to lasting, complete recovery. In the successful cases, the transferred symbionts multiplied and spread through the recipient coral, and full recovery followed over the weeks that came after separation. Tessa watched the microscope images as the tiny organisms appeared first in one small area and then spread farther through the coral tissue. But how were they crossing from one coral to the other? When the researchers separated certain pairs after longer contact, they found matching tears in the tissue of both fragments. The marks suggested that their tissues had joined, forming tiny living bridges. Through these connections, symbionts could pass directly from the healthy coral into the bleached one. It was not simply a matter of borrowing microscopic partners from the water. The corals themselves had created a pathway.

Then came a discovery that made the researchers more cautious. If contact could help one bleached coral recover, could any healthy coral serve as a donor? The team tested pairs that came from different genetic types, known as genets. These corals might look similar, but their tissues could recognize one another as different. Instead of forming helpful connections, the mismatched pairs often reacted aggressively. Thin structures called mesenterial filaments appeared at their meeting points, and the healthy coral could overgrow the weakened fragment. The bleached corals in these mixed pairings did not achieve the same recovery. Tessa realized that the method had an important limit: successful, large-scale transfer depended on compatible corals of the same genet. The experiments also showed that a few symbionts could move between mismatched partners, probably through a slower process involving uptake by coral polyps, but this was not enough to restore the whole fragment. The team had uncovered a natural recovery process, not a universal cure. Their work, published in *Science Advances* in 2026, demonstrated that direct contact with a healthy, genetically matching coral could rapidly restore bleached coral fragments under controlled laboratory conditions. Whether the approach could work reliably across different coral species and in the changing conditions of natural reefs still needed to be tested.

As Tessa recorded the final observations, the once-pale fragments had become living branches again, their color returning as their symbionts multiplied. The finding offered a new way to think about coral restoration: perhaps healthy corals could act as living sources of microscopic partners for nearby bleached relatives. One day, researchers might investigate whether carefully chosen donor corals could help damaged reefs recover after severe bleaching. They might also explore whether this process could work with more coral types or across larger areas. But Tessa understood that the ocean was far more complicated than a laboratory tank. Rising seawater temperatures would continue to threaten reefs, and brief contact between compatible coral fragments could not solve the wider causes of bleaching by itself. Still, the experiment had revealed a possibility that had been easy to overlook: recovery might begin not in the distant water, but at the tiny place where two living branches touch. As she switched off the microscope, Tessa wondered what other hidden acts of cooperation might be taking place beneath the waves and what else a struggling reef might teach scientists about finding its way back to life.



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| By Dr. Priyanka

BUTTERFLY WING PATTERNS CREATING MISLEADING MOTION CUES

FEATURED

One quiet morning in a garden in France, a young butterfly researcher named Élodie noticed something strange. A butterfly with bright, contrasting patterns on its wings suddenly took off, fluttering into the air. Its wings suddenly took off, fluttering into the air. Its wings flashed with every movement, making it easy to see against the green background. “If a bird can spot it so easily, why hasn’t nature made its wings less noticeable?” she wondered. For years, scientists had tried to understand why many butterflies carried such bold patterns. Some patterns warned predators that an animal might be dangerous to eat, while others helped it blend into its surroundings. But these explanations did not seem to answer every question. Élodie began to wonder whether the butterflies’ colourful wings were hiding a different kind of defence not by hiding their bodies, but by confusing the eyes of their hunters.

At the University of Exeter in the United Kingdom, fictional researcher Élodie and her colleague Romain decided to investigate this mystery. They knew that a moving animal could be much harder to catch than a still one, especially if its movements confused the predator’s vision. They wanted to discover whether butterfly wing patterns could make a hunter misjudge the direction or speed of a flying butterfly. To find out, the researchers needed to study the wings in motion, not simply look at pictures of them. They filmed butterfly take-offs using a high-speed camera that recorded about 1,000 frames every second. Then they compared the butterflies’ natural patterns with versions in which the wings appeared plain. The team used a computer model inspired by how animals detect movement. It measured motion signals in different directions, including forwards, backwards and sideways. “Perhaps the wings are not just colourful decorations,” Romain suggested. “Perhaps their patterns make the butterfly’s movement harder to read.” The first results supported their suspicion: butterflies with their natural wing patterns produced greater motion confusion than the



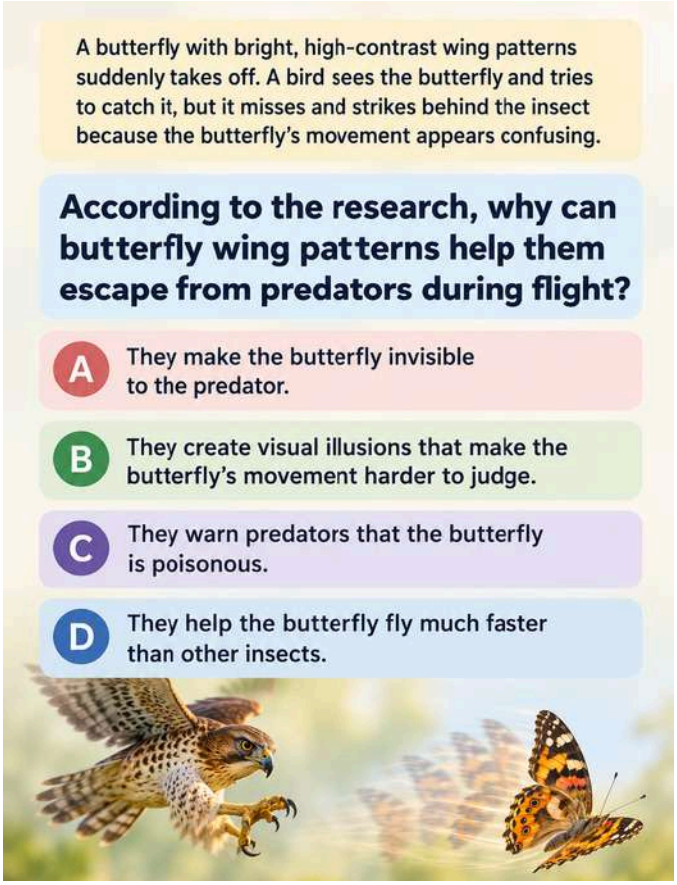
| By Dr. Priyanka

unpatterned versions.

But one butterfly could not solve the whole mystery. Were these effects unusual, or had they developed across many kinds of butterflies? The researchers turned to a much larger investigation, using computer simulations of 757 different wing forms from 397 European butterfly species. They recreated flapping and gliding flight, examining how wing patterns, contrast, shape and other features affected the motion signals. A surprising clue emerged. Strong contrasts, vertical stripes and uneven patterns could increase motion confusion. Some butterflies also had unusual hindwings, including small tails or rough edges, that could contribute to the effect. The way a butterfly moved mattered, too. Flapping wings could create confusing signals about forward movement, while gliding could still produce strong confusion about sideways movement. Romain stared at the colourful images on the screen. “So the secret is not only in the pattern,” he said. “It is in the pattern working together with the wings as they move.” The researchers had found evidence that these effects appeared across many European butterfly species, although their strength varied between species.

There was still an important question: could these confusing patterns actually affect where a hunter aimed? To investigate, the team invited 100 human participants to act as virtual predators, completing thousands of attempts to catch butterflies shown on a high-speed touchscreen. The butterflies moved along realistic flight paths, and their wing movements and patterns were carefully reproduced. The results supported the computer models: butterflies with stronger forward-motion confusion caused attacks to be directed farther behind them, as if the participants had misjudged how quickly the butterflies were moving. Next, the researchers explored whether similar patterns could emerge through digital evolution. They created 57,600 artificial butterfly patterns using computer algorithms that mimicked natural selection. In these experiments, patterns that produced greater motion confusion were selected over generations. Remarkably, some evolved patterns became similar to those found on real European butterflies. This did not prove that every butterfly pattern evolved for this reason, but it provided another line of evidence that motion confusion could help explain the diversity of butterfly wings. The researchers now had several pieces of evidence pointing towards the same possibility: a butterfly’s bright markings could make it harder for a predator to aim accurately.

As the investigation drew to a close, Élodie imagined a bird diving towards a butterfly, only to strike the empty air behind it. The butterfly’s wings had not made it invisible; instead, their patterns and movements may have made its flight harder to judge. The study suggested that this visual defence could be widespread among butterflies, working alongside other possible functions of their wing patterns, such as signalling and temperature control. Yet the mystery was far from solved. The researchers still needed to examine more flight conditions, viewing angles, backgrounds and patterns on the undersides of wings. They also suggested that similar effects might occur in other moving animals, including birds, lizards and fish. In the future, understanding these natural tricks might even help scientists design better motion-detection systems for robots. Élodie looked once more at the butterfly resting in the garden, its wings folded quietly together. What other secrets might nature be hiding in plain sight, waiting for someone to watch a familiar creature move in an entirely new way?



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| By Dr. Ipsita Mohanty

A FULL MARATHON ON A SINGLE BATTERY CHARGE

FEATURED

One chilly morning in Daejeon, South Korea, Minjun Park stood inside a robotics laboratory, staring at a small machine with four mechanical legs. Outside, rain tapped against the windows, and the laboratory smelled faintly of warm electronics. The robot looked almost like a metal dog, but Minjun had a question that made it very different from an ordinary machine. “How far could you walk,” he whispered, “if you had only one battery and nowhere to recharge?” His colleague, Seo-yeon Kim, looked up from her computer. Robots could already climb over difficult ground, run at impressive speeds, and help people explore dangerous places. Yet there was a problem: their batteries often ran out long before their journeys were complete. Imagine a robot sent into a disaster zone to search for survivors. What would happen if it stopped moving halfway through its mission? Minjun and Seo-yeon knew that making a robot faster would not solve everything. They needed to make every step count. At the Korea Advanced Institute of Science and Technology, known as KAIST, researchers were working on a four-legged robot called RAIBO2. Their challenge was not simply to build stronger legs or install a bigger battery. It was to discover how the entire machine could waste less energy, from the electrical circuits inside its body to the moment its feet touched the ground.

At first, the problem seemed straightforward to Minjun: perhaps the robot needed a more powerful motor. But Seo-yeon pointed out that a powerful motor could still waste energy. “Think about running in heavy boots,” she said. “Your legs must work harder every time you lift your feet.” A robot faced a similar challenge. Its joints used electricity to support its body, its gears created friction, and its feet lost energy when they struck the ground. Even the electronics controlling its movements consumed power. Worse, fixing one problem could make another worse. Changing the gears might reduce the electricity needed by a motor but make the robot’s legs heavier and harder to swing. Raising its body could reduce some electrical losses while increasing the energy lost when its feet collided with



| By Dr. Ipsita Mohanty

the ground. The team needed to understand how all these effects worked together. They studied the machine's energy losses and examined how its mechanical parts, electrical circuits and walking behaviour influenced one another. They designed lighter legs, improved the motors and reduced resistance in the motor-driving circuits. They also trained a computer-based control system using reinforcement learning, a method in which a system improves its behaviour through practice and feedback.Instead of simply rewarding the robot for moving forward, the researchers taught it to consider slipping, foot impacts and electricity consumption. Each step became a problem to solve: how could the robot move confidently without wasting the energy stored in its battery?

After weeks of calculations and testing, RAIBO2 began behaving differently. Before each foot touched the ground, its controller reduced the approaching foot's speed, limiting energy lost during impact. The robot could also manage energy across different phases of movement. When travelling downhill, it could recover some mechanical energy instead of wasting it.

But would these improvements work outside the laboratory?

A robot might perform beautifully on a smooth floor yet struggle on roads covered with leaves, slopes and uneven surfaces. The researchers needed a demanding real-world test. Their answer was a marathon.

They entered RAIBO2 in the 22nd Sangju Gotgam Marathon in South Korea. The course covered 42.195 kilometres, including uphill and downhill sections, slippery patches of fallen leaves and a total elevation gain of 286 metres. As the event approached, Minjun imagined the battery indicator falling towards empty, leaving the robot stranded before the finish line. The team had improved the machine in the laboratory, but the road would deliver the final verdict. When the marathon began, RAIBO2 set off alongside human runners. Its four mechanical legs carried it forward while its control system continuously managed movement and energy consumption. Some slopes reached 18.4 degrees, demanding careful coordination of its legs.

Minjun watched anxiously as the distance increased and the battery's stored energy decreased. Yet the robot continued moving. Finally, the result arrived. RAIBO2 had completed the entire 42.195-kilometre marathon in 4 hours, 19 minutes and 52 seconds, consuming only 1,280 watt-hours from a battery capable of storing 1,930 watt-hours.

"We thought the challenge was making a robot walk farther," she said. "Perhaps the real challenge was learning where all its energy was going."

Minjun smiled. Every footstep had once seemed like a simple movement. Now he understood how much science could hide inside it: forces, friction, electricity, timing and decisions made in fractions of a second.

The marathon had demonstrated that a four-legged robot could travel farther by wasting less energy. But it also raised a bigger question: if understanding a single step could carry a robot through a marathon, what might scientists achieve by making every movement of a machine count?



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Beneath the Surface: Understanding Rhizosphere Interactions and Plant Development for Sustainable Agriculture



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Areas of Expertise: Plant Genomics and Computational Biology | Multi-omics | Regulatory Biology | Development and Stress Biology



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Areas of Expertise: Bioinformatics | Host-Microbiome interactions

Beneath every plant lies the rhizosphere, the narrow zone of soil surrounding the roots where plants and microbes constantly exchange chemical signals. Plants release a significant proportion of the sugars they fix through photosynthesis into this zone as root exudates, thereby supporting a dense community of bacteria and fungi. In return, many of these microbes help plants acquire nutrients, defend against pathogens, and tolerate abiotic stresses such as drought and salinity.

High-throughput sequencing enables us to explore these communities directly, without growing each microbe in a lab, which matters because most soil microbes cannot be cultured. Recent findings show that the rhizosphere microbiome is dynamic. Its composition shifts as a plant grows from seedling to flowering to maturity, and it is shaped by soil type, climate and geography as well as by the host itself.

Roots, microbes and the future of food: why the hidden half matters

Plant microbiome research explores the vast communities of bacteria, fungi and other microbes that live in and around plants, especially in the rhizosphere. It sits at the meeting point of microbiology, genomics, ecology and agriculture, and its importance has grown sharply in recent years.

The world must feed a growing population while climate change brings heat, drought and salinity to farmland. For decades, higher yields have relied on synthetic fertilizers and pesticides, but their excessive use degrades soil, pollutes water and harms biodiversity. Microbes offer a gentler alternative. Some fix atmospheric nitrogen, others release locked-up phosphorus, produce growth hormones or shield roots from pathogens.

Harnessing these helpers requires understanding them first: who they are, what they do, and how they respond to the plant, the soil and each other. By decoding these hidden partnerships, researchers aim to design microbial inoculants and farming practices that raise yields while restoring, rather than depleting the soil.

From culturing to metagenomics: milestones in understanding the rhizosphere

| EXPERT OPINION |

The biggest leap came from genome sequencing, which lets us survey entire soil communities without culturing the microbes. Studies across several plants have since shown that the rhizosphere is far from random. Plants shape it through root secretions, and its composition shifts with the plant's growth, species, soil and geography. Comparisons of wild and domesticated crops suggest that breeding may even have changed which microbes plants recruit.

Researchers have also moved from asking "who is there" to asking "what they are doing". Combining gene and gene-activity data reveals microbial functions that are switched on in roots, from nutrient cycling to stress protection. Newer tools can also distinguish individual strains within a species, which matters as closely related species can differ in functions whether they aid in plant development or acts as a pathogen. Finally, scientists have begun to decode the chemical conversations between plants and microbes, including signals that recruit symbiotic partners. Synthetic communities built from selected microbes now allow these interactions to be tested directly.

Mapping the partnership

The rhizosphere is complex and varies enormously between locations, plants and growth stages. Our work has tried to explore and understand this complexity . First, we asked whether plant development influences microbial diversity. By combining sequencing data from a larger number of samples across the globe comprising of eight legume species, we showed that rhizosphere communities shift between the vegetative, reproductive and maturation stages. We identified ten marker bacteria tied to particular stages, several linked to better nodulation, longer roots or earlier flowering. We also found that geography shaped these communities even more strongly than growth stage. By tracking which bacterial genes were active, we moved from a simple census toward understanding function.

Second, we tackled the strain problem. Knowing that a bacterial species, such as Ensifer medicae or Pseudomonas fluorescens is present, tells us little, because one strain may fix nitrogen or protect the plant while its close relative may cause a disease. Yet nearly all strain-tracking tools built were tested on the human metagenomes only, which is far simpler than the plant environment, where diversity is higher, host DNA contaminates samples and many microbes are poorly characterized. So, we benchmarked seven of them on simulated and real plant datasets. Two tools, StrainScan and StrainGE, performed best, yet none excelled everywhere. This gives researchers practical guidance and a clear call for better methods.

Beyond the census: gaps between the lab and the field

Despite rapid progress, the rhizosphere microbiome remains a challenge. A root zone can hold thousands of microbial species, many still unnamed, and its composition

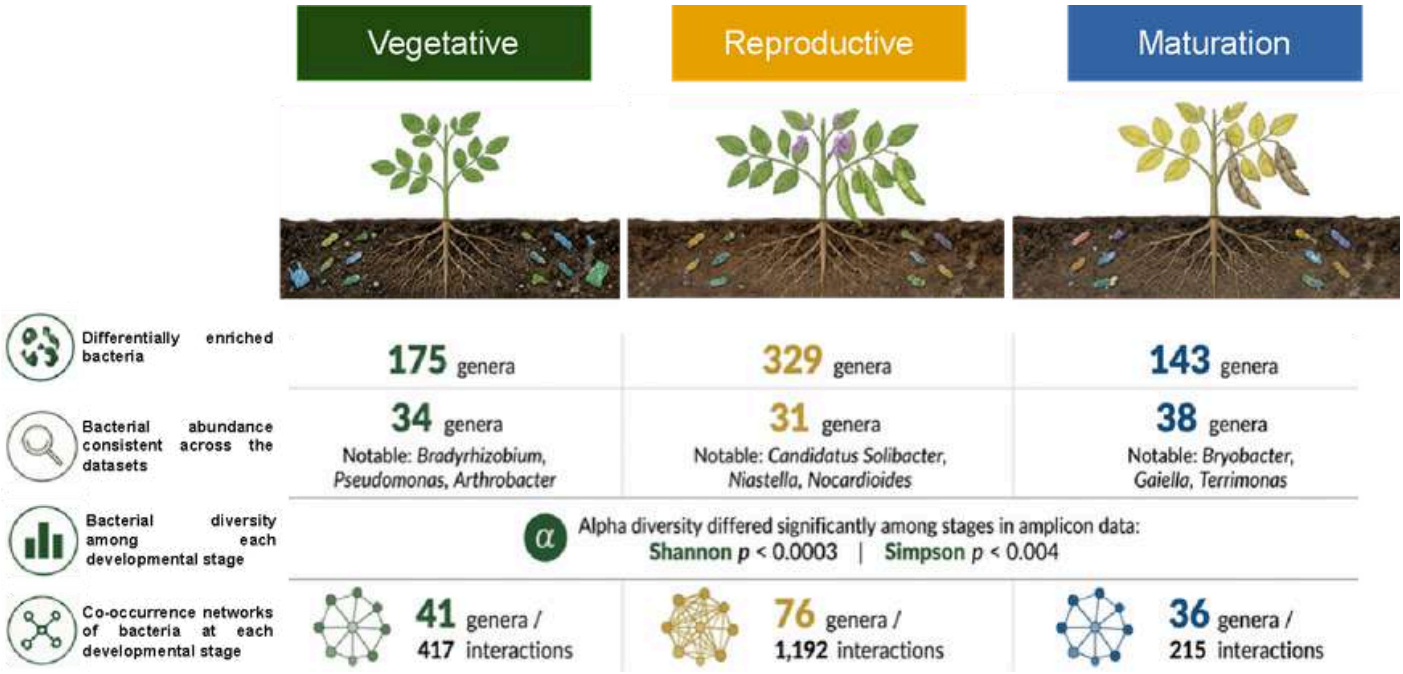


Figure 1: Different plant developmental stages are associated with distinct rhizosphere bacterial communities and interactions among them.

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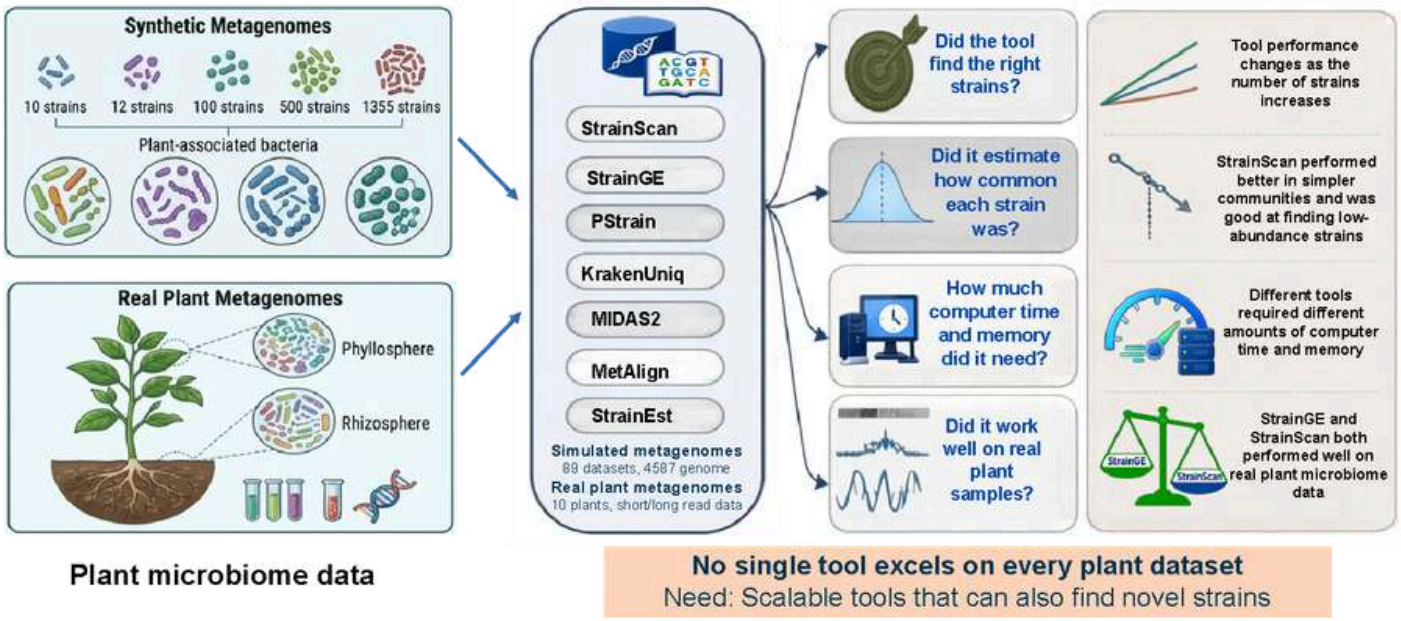


Figure 2: Performance of reference-based tools for strain-level identification of bacteria from complex using simulated and real plant metagenome datasets.

varies with soil, climate, geography and the plant development. Disentangling these overlapping influences requires large, standardized datasets, yet most studies still focus on a single crop at a single site.

A second gap is resolution. Telling strains apart is essential, but available tools were largely designed for the human gut. They rely on reference genomes, so they cannot recognize strains that have never been sequenced, a serious limitation in soils full of unknown organisms. Their accuracy also falls as communities grow more diverse, and some demand days of computing time or very large memory.

Third, association is not causation. Many microbes correlate with better growth, but proving what they cause, requires controlled experiments. Moreover, sequencing shows presence, while measuring activity in the field remains harder. Finally, moving from discovery to application is slow. Microbial inoculants often perform inconsistently outside the lab, and newer ideas, such as using nanoparticles to attract helpful microbes, raise unanswered questions about how they work, whether they accumulate in soil, and how they affect it over many years.

Promise with patience: reading the field honestly

Plant microbiome research is a young field with real promise, but we should treat it as a work in progress rather than a ready-made solution. A plant is no longer seen as a lone organism growing in lifeless dirt, but as one half of a partnership with the life around its roots. This idea is now well supported, and it is changing how we think about plant health, nutrition and resilience.

It helps to separate what is settled from what is still emerging. Settled: microbes influence how plants absorb nutrients and resist disease, and plants in turn actively shape their microbial neighbors. Emerging: which partners matter at which moments of a plant's life, and how the chemical signals between them work. Still speculative: deliberately engineering these relationships at scale.

We should also know that progress is collective. It draws on biologists, chemists, soil scientists, computer scientists and farmers, and depends on researchers openly sharing data so that findings can be compared across crops and geographical locations. The field's greatest gift so far is a new way of seeing agriculture, one that treats soil as living infrastructure worth protecting.

> *"Rhizosphere microbiome is not fixed. Its composition shifts as a plant develops from seedling to maturity."*

| EXPERT OPINION |

ABOUT THE AUTHORS

Prof. Mukesh Jain, a faculty member at Jawaharlal Nehru University, New Delhi, uses genetic and computational tools to study how genes regulate plant growth, development, and environmental stress responses. Dr. Rishav Sahil, an ANRF National Post-Doctoral Fellow at Banaras Hindu University, Varanasi, investigates how beneficial root-associated microorganisms enhance plant health. Together, their research explores plant-microbe interactions to improve crop growth and support sustainable agriculture.

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Inside a Legume Root Nodule: Building the Network for Nitrogen Fixation and Sustainable Agriculture



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Areas of Expertise: Biological Nitrogen Fixation | Root Nodule Symbiosis | beneficial plant microbe interaction | Symbiosis



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Areas of Expertise: Root nodule symbiosis | Plant developmental biology | Molecular biology

Nitrogen is one of the essential nutrients required for plant growth. Although nearly 78% of the Earth's atmosphere is composed of nitrogen gas (N_2), it is not present in a from that plants can directly utilize. As a result, agriculture relies heavily on synthetic nitrogen fertilizers to improve crop productivity. However, excessive use of these fertilizers has serious environmental consequences, including water pollution, greenhouse gas emissions, and degradation of natural ecosystems. These anthropogenic activities have significantly disrupted the global nitrogen cycle by adding more than double the amount of reactive nitrogen into the Earth's ecosystems.

Biological nitrogen fixation provides a natural alternative, and one of its most productive forms is root nodule symbiosis (RNS). BNF is the only sustainable player in the global nitrogen cycle. To establish RNS, plants communicate with compatible soil bacteria. Cognate bacterial recognition by the plant ultimately leads to the formation of a new root organ called a 'nodule'. Inside these nodules, rhizobia convert atmospheric nitrogen into forms that can be used by the plant. In return, the plant provides the bacteria with carbon compounds.

Approximately 110 million years ago (MYA), RNS evolved into two main functional forms.

Based on Phylogenomic studies, RNS evolved ~110 MYA and is restricted to a monophyletic nitrogen-fixing clade (NFC). This clade contained four major orders: Fabales (Fa), Fagales (Fa), Cucurbitales (Cu), and Rosales (Ro), as frequently abbreviated using the acronym FaFaCuRo. In the NFC, two types of nodular architecture are mainly observed. Where Fagales, Cucurbitales, and Rosales form root nodules, the organ is structurally and developmentally similar to lateral roots. While the Fabales (Legumes) form an organ 'sui generis', a unique structure that does not have a perfect resemblance to a lateral root, stem, or leaf (Fig. 1).

Reusing existing genes to build a new symbiosis

Recent comparative genomic studies have provided a clearer picture of how this complex trait may have evolved in the NFC clade. For this process, rather than acquiring an entirely new set of genes, nodulation appears to have

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evolved largely through gene duplication, recruitment, and rewiring of genes that already performed other functions in plants. A recent report divided plant gene duplications into four major periods during plant evolution. The first duplication occurred early in the evolution of flowering plants and coincided with an ancient whole-genome duplication event. The second occurred in the common ancestor of core eudicots and was associated with the γ-whole-genome duplication. A substantial number of gene families that later became involved in RNS can be traced back to this evolutionary period. A third major peak of gene duplication occurred in the ancestor of the Papilionoideae legumes and was also associated with a whole-genome duplication event. This later period of duplication may have contributed to further refinement of the legume symbiotic program. Thus, evolutionary innova-

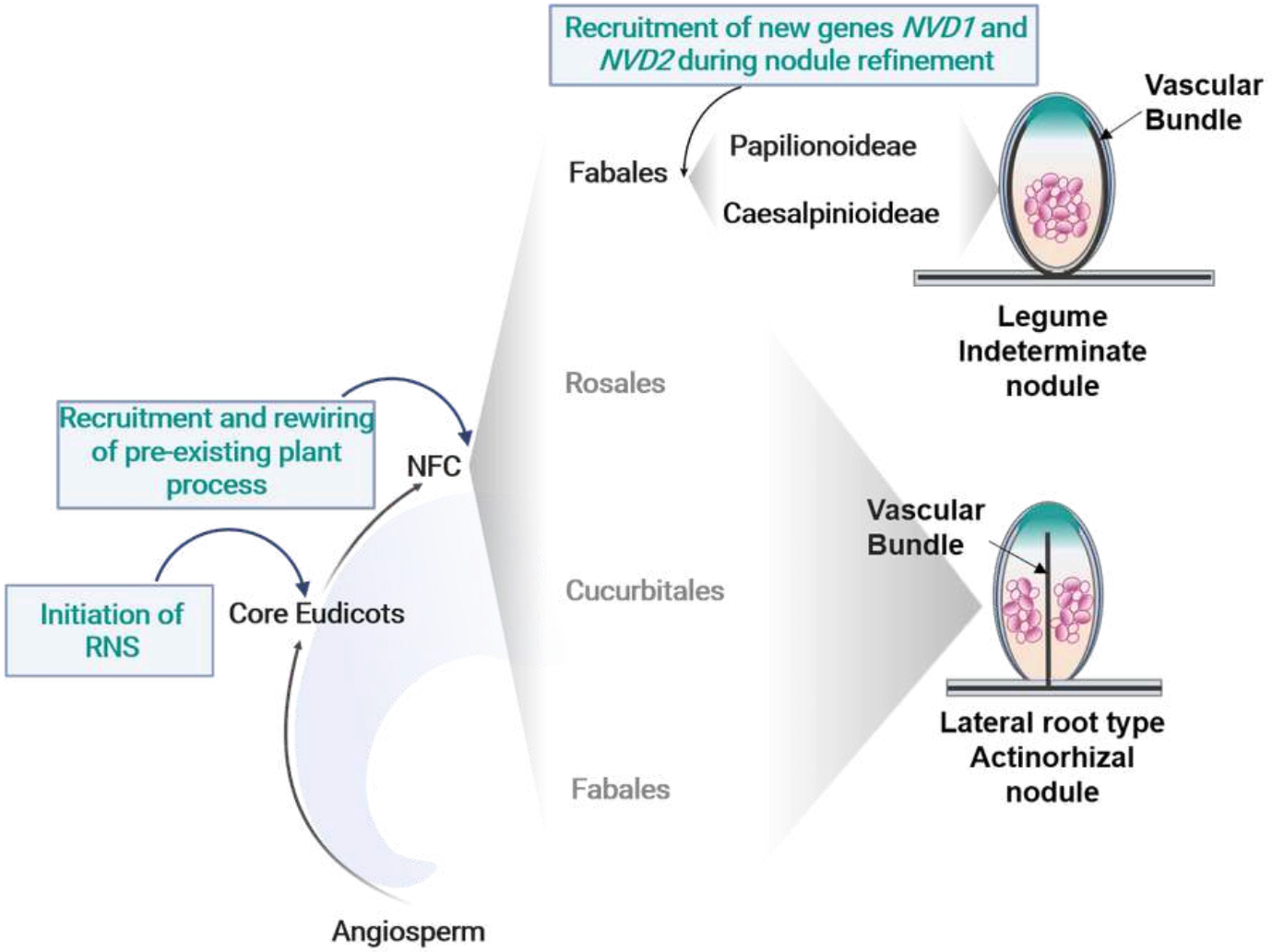


Figure 1: The diagram illustrates the evolution of root nodule symbiosis (RNS), beginning with the emergence of specific nodulation-associated genes in the ancestors of core eudicots, although nodulation itself was not yet established at this stage. The subsequent recruitment and modification of pre-existing plant processes contributed to the evolution of RNS within the nitrogen-fixing clade (NFC), comprising four orders: Fabales, Rosales, Cucurbitales, and Fagales. Among these orders, legumes (Fabales) developed nodules with peripheral vascular bundles, whereas nodules in the other orders exhibit a lateral root-like structure (shown by grey letter), with centrally located vascular tissues. Further recruitment and specialization of genes during legume evolution contributed to the refinement of nodule structure and function. The genes NVD1 and NVD2 are proposed to have been recruited during the diversification of legume lineages, including Papilionoideae and Caesalpinioideae. Their functional roles in regulating peripheral vascular bundle development have been experimentally demonstrated in Medicago truncatula, highlighting their contribution to the structural specialization of legume nodules. The pink oval structure represented the bacteria-filled cells. The root and nodule vasculature is depicted by thick grey lines.

tion continued after the basic RNS program had emerged. Additional genes were recruited during the evolution of legumes, helping to establish features characteristic of legume nodules.

Further refinement of nodulation in legumes

The vascular bundles of legume nodules are arranged in the peripheral region (Fig. 1). These vascular strands connect the nodule to the root and enable the transport of water, nutrients, and fixed nitrogen between the nodule and the rest of the plant efficiently, and also safeguard the enzyme nitrogenase from environmental oxygen, which is localized in the central region of the nodule.

Phylogenomic reconstruction suggests legumes recruited new genes that helped refine nodule development and internal organization, thereby making them a better home for bacteria, and improved plant benefits from symbiosis. Among these are regulators associated with nodule development and tissue organization. Importantly, Nodule Vascular bundle Development (NVD) 1 and NVD2 have been identified as genes recruited at the origin of the legume subfamily, suggesting that they may represent part of the later evolutionary refinement of the nodulation program.

NVD1 and NVD2: Fine-tuning the architecture of the legume nodule

In our recently published work in New Phytologist, we identified two genes, NVD1 and NVD2, and elucidated their molecular mechanisms and functional roles in the Medicago nodule. We identified NVD1, a basic helix–loop–helix (bHLH) transcription factor, as an important regulator of this organization. Disruption of NVD1 caused the vascular strands to shift away from the periphery of the nodule, akin to an intermediate between a 'lateral root-type nodule' and a 'legume-type nodule'. These architectural defects were accompanied by reduced nitrogen-fixation capacity and decreased plant biomass. We further identified NVD2, an HLH transcriptional regulator, as a downstream target of NVD1. Notably, NVD2 lacks the basic region of the DNA-binding domain and thus functions only via protein-protein interaction. NVD1 directly activates NVD2 expression, while NVD2 interacts with NVD1 to regulate its transcriptional activity via a negative feedback loop (or negative feedback autoregulation). Mutations in NVD2 also resulted in abnormal vascular organization. Our work further linked this regulatory module to the plant hormones auxin and cytokinin, thereby demonstrating how transcriptional regulation and hormonal signaling are integrated to establish the internal architecture of the nodule. The complete disruption of this circuit results in a significant reduction in biological nitrogen fixation (BNF), and these nodules are barely capable of BNF. Full disruption of this circuit renders the Medicago root vasculature simple and Arabidopsis-like. Thus, NVD1 and NVD2 are two key evolutionary innovations that refine legume nodules. This refinement created a supportive and comfortable home for the incoming bacterial partner, which is essential to a thriving, mutually rewarding relationship.

From evolutionary history to future crop improvement

The NVD1-NVD2 regulatory module, therefore, adds another layer to our understanding of RNS evolution. The earliest stages in the evolution of nodulation appear to have involved ancient gene duplication and the recruitment of pre-existing signaling pathways. Later evolutionary innovations further refined the development, organization, and function of the legume nodule. Understanding these genetic innovations is important for future efforts to improve sustainable agriculture. In the short term, this newly learned information can be used in the legume breeding program, where these genes and their expression levels can be monitored to identify improved nitrogen-fixing legume nodules.

Further, the long-standing goal in RNS is to reduce cereal crops' dependence on synthetic nitrogen fertilizers by enabling them to obtain a greater proportion of their nitrogen through biological processes. Identifying genes such as NVD1 and NVD2 helps us understand the individual genetic components required to construct and organize this specialized organ. Each newly identified regulator adds a piece to the evolutionary puzzle of how legumes build a sophisticated functional 'home' for nitrogen-fixing bacteria.

> *"Biological nitrogen fixation provides a natural alternative, and one of its most productive forms is root nodule symbiosis (RNS)."*

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ABOUT THE AUTHORS

Dr. Senjuti Sinharoy, a Scientist at BRIC–National Institute of Plant Genome Research, New Delhi, studies how plants partner with soil bacteria to obtain nitrogen. Her team identifies genes guiding bacterial recognition and root nodule formation, helping improve crop nutrition and reduce chemical fertiliser dependence. Dr. Deevita Srivastava, a Postdoctoral Research Fellow at North Dakota State University, USA, studies beneficial plant-microbe interactions. Her doctoral experiments demonstrated how two genes organise the root nodule transport network to facilitate nutrient exchange.

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Beyond Potency: What Defines the Next Generation Selective HDAC8 Inhibitor?



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Areas of Expertise: Medicinal Chemistry | Organic Synthesis | Drug Discovery | Structure-Based Drug Design | Synthesis of Novel Anti-Infective agents/ Bio-active Small Molecules



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Areas of Expertise: Medicinal Chemistry | Organic Synthesis | Drug Discovery | Structure-Based Drug Design | Synthesis of Novel Anti-Infective agents/ Bio-active Small Molecules | Biological Evaluation

Histone deacetylases (HDACs) regulate the acetylation state of histone and non-histone proteins and therefore affect transcription, chromatin organization, cell cycle control and various signalling processes. The human HDAC family is composed of zinc-dependent enzymes of classes I, IIa, IIb and IV and the class III enzymes, sirtuins, which use NAD+ instead of zinc to catalyze the reaction. HDAC8 is a class I enzyme but, with distinct active-site properties and conformational flexibility, is amenable to selective ligand recognition. This makes HDAC8 attractive not only because it can be inhibited, but because selective inhibition provides a route to chemically precise target modulation. Importantly, intracellular substrates, e.g., SMC3, provide a practical means of linking enzyme inhibition to cellular target engagement.

The challenge, however, is not whether HDAC8 can be inhibited. There are already potent inhibitors. The more pertinent question is what should constitute a convincing selective HDAC8 inhibitor. We believe the field should now move beyond a potency-centred strategy to one that integrates zinc recognition, isoform selectivity, intracellular target engagement and pharmacological behaviour.

Why bother with selective HDAC8 inhibition when broad HDAC inhibition is already clinically validated?

The therapeutic tractability of the HDAC family has been demonstrated by broad-spectrum HDAC inhibition. Simultaneous inhibition of multiple HDAC isoforms may also prevent separating a desirable pharmacological effect from the effects of global protein hyperacetylation. This is not to say that pan-HDAC inhibition is inherently undesirable; in some disease settings, concurrent modulation of multiple HDACs may enhance efficacy. But when the biological question concerns a single isoform, selectivity provides a cleaner way to link target inhibition to downstream biology.

Why It's Important?

The HDAC8 catalytic site contains a narrow hydrophobic channel that leads to the catalytic

Zn 2+ center. Flexible surface loops around the entrance to the channel contribute to substrate and inhibitor recognition. These structural features provide opportunities for selectivity, with the cap group interacting with loop- and surface-associated regions, the linker occupying the catalytic channel, and the zinc-binding group oriented toward the metal center.

Aberrant HDAC8 activity is linked to various diseases, especially cancer, including neuroblastoma and acute myel-

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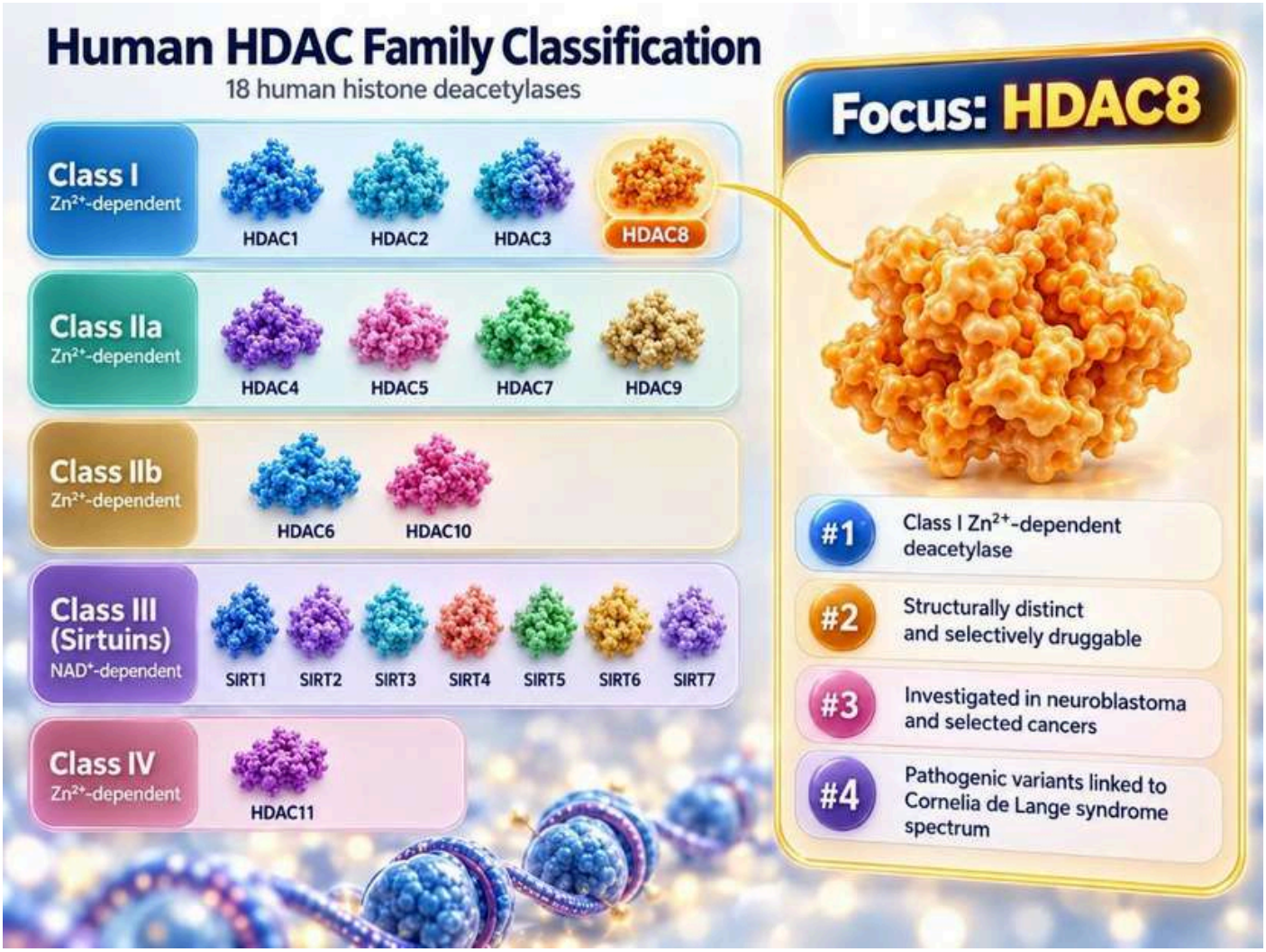


Figure 1: Classification of the human HDAC family and focused representation of HDAC8

oid leukemia. Elevated HDAC8 levels correlate with tumor growth in neuroblastoma, where selective inhibition can curb proliferation and promote differentiation. The challenge lies in identifying selective and pharmacologically credible inhibitors through a comprehensive assessment that includes enzyme activity and intracellular target engagement. HDAC8 can be effectively studied using specific biomarkers like SMC3, which shows increased acetylation after treatment. However, this increase does not imply that all cellular changes are solely due to HDAC8 inhibition.

Have we become too dependent on hydroxamates for zinc recognition?

Most HDAC inhibitors consist of three main regions: a cap group for surface recognition, a linker, and a zinc-binding group (ZBG) near the catalytic Zn2+ ion. Hydroxamic acid, commonly used for its effective zinc coordination and potent inhibitors, raises the question of whether medicinal chemists are over-relying on the ZBG while seeking selectivity through modifications of the cap and linker. Changes to the ZBG can significantly influence binding-site coordination, ligand orientation, and other physicochemical properties. Therefore, exploring alternative ZBGs is not just about replicating the potency of hydroxamates but also about potentially altering the pharmacological behavior of inhibitors through different interactions with catalytic zinc.

Non-hydroxamate approaches such as benzamides, thiols, mercaptoamides, hydrazides and other sulfur containing groups suggest that the answer may be yes. The scientific contribution of these chemotypes is to expand the interaction space available to HDAC medicinal chemistry, rather than to assume that any alternative ZBG will be safer or more selective.

Where does cyanocarbonimidodithioate fit in?

Among these alternatives, cyanocarbonimidodithioate is a

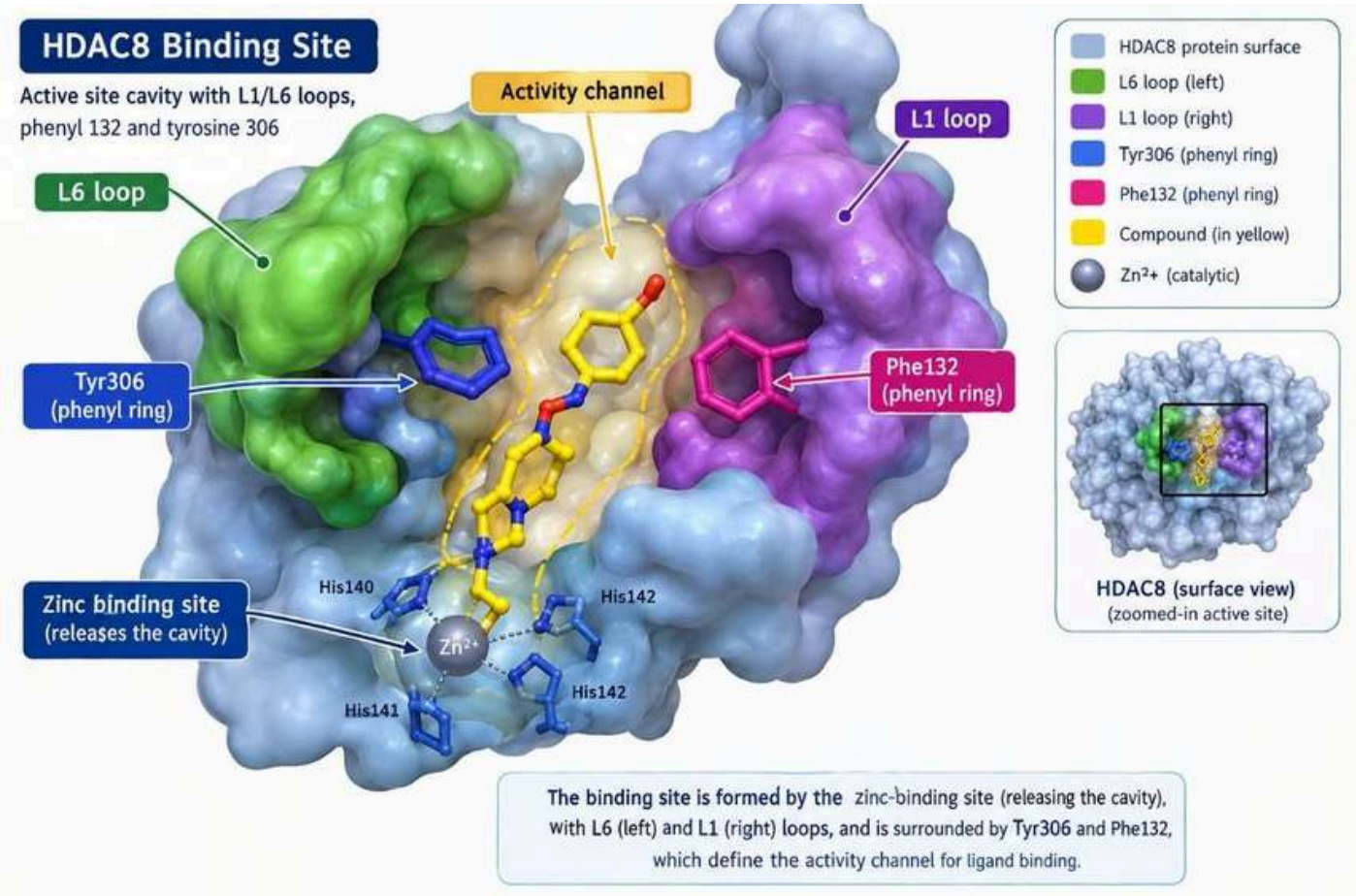


Figure 2: Schematic 3D representation of the HDAC8 active-site architecture.

particularly interesting sulfur-rich metal-binding chemotype. Our recent work provides a clear demonstration of this integrated approach in the design of selective HDAC8 inhibitors. We have reported non-hydroxamate HDAC8 inhibitors as neuroblastoma anticancer agents, not as treatments for all HDAC8-related diseases. In the benzothiazole derivatives containing cyanocarbonimidodithioates, we combined potent biochemical activity with isoform profiling, cellular evaluation and computational studies to understand how to modulate activity with zinc recognition and molecular geometry. The same sulfur-rich zinc binding concept has later been applied to quinoxaline and thieno[3,2-d]pyrimidine scaffolds, which enabled a systematic study of the effects of cap-group and linker on HDAC8 potency, selectivity and cellular behavior. Selected compounds were further evaluated by colony-formation assays, apoptosis and caspase-3/7 studies, cell-cycle analysis, and acetylated SMC3 measurements, which linked enzyme inhibition to intracellular HDAC8-related target engagement. The experiments were also complemented by molecular docking and molecular dynamics simulations, which provided structural hypotheses for ligand recognition within the HDAC8 catalytic pocket. In our studies, selected quinoxaline and thieno[3,2-d]pyrimidine derivatives showed inhibition of proliferation in IMR-32 neuroblastoma cells with supporting mechanistic evidence. Together, these studies demonstrate that the discovery of selective HDAC8 inhibitors is best served by integrating synthetic chemistry, enzymology, cellular pharmacology, and computational modelling rather than executing them as separate stages. Our studies show that molecules with this motif can provide potent HDAC8 inhibition and that its activity is highly dependent on the surrounding cap and linker architecture. Rather than a hydroxamate replacement, cyanocarbonimidodithioate is more useful as a tunable zinc-recognition element that expands the coordination and interaction space in HDAC medicinal chemistry.

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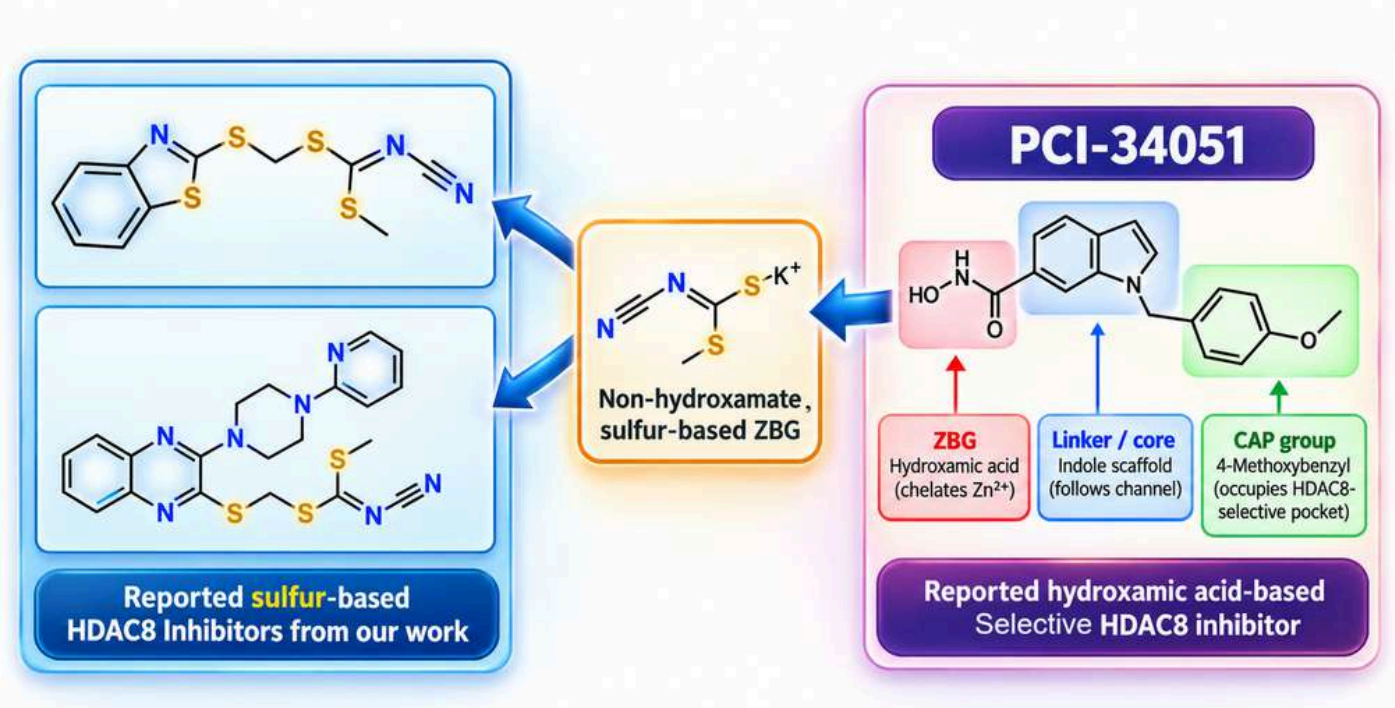


Figure 3: Design rationale for non-hydroxamate sulfur-based zinc-binding groups as alternative HDAC8 inhibitor scaffolds, compared with the reported hydroxamic acid-based inhibitor PCI-34051.

(ZBG) near the catalytic Zn2+ ion. Hydroxamic acid, commonly used for its effective zinc coordination and potent inhibitors, raises the question of whether medicinal chemists are over-relying on the ZBG while seeking selectivity through modifications of the cap and linker. Changes to the ZBG can significantly influence binding-site coordination, ligand orientation, and other physicochemical properties. Therefore, exploring alternative ZBGs is not just about replicating the potency of hydroxamates but also about potentially altering the pharmacological behavior of inhibitors through different interactions with catalytic zinc.

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Computational studies suggest a Zn-associated binding orientation for certain molecules, while biochemical studies indicate preferential HDAC8 activity in specific structures. However, the precise geometry of metal coordination remains experimentally undetermined. This is further complicated by the chemotype's variable isoform behaviour based on the molecular environment. PCI-34051, a selective HDAC8 inhibitor, serves as a benchmark distinguishing HDAC8 from other isoforms. Additionally, our cyanocarbonimidodithioate-based compounds propose an alternative non-hydroxamate zinc-binding strategy, demonstrating selective HDAC8 inhibition, intracellular Ac-SMC3 modulation, and anticancer effects.

If potency is driven by zinc binding, why is the most potent enzyme inhibitor not always the best lead?

This is one of the most useful questions in the field of selective HDAC medicinal chemistry. Biochemical assays offer the inhibitor direct access to purified enzyme under controlled conditions. Cells form additional barriers. The molecule must enter the cell, not be effluxed or metabolized too much, reach sufficient intracellular free concentration and interact with HDAC8 in its physiological environment.

Therefore, enzyme potency and cellular potency do not need to be measured in parallel. In our HDAC8 studies, the compounds that showed excellent biochemical inhibition were not necessarily those that displayed the most balanced cellular behaviour. Potency ranking alone provided less insight for lead prioritization than compounds that combined enzyme inhibition with intracellular readouts such as enhanced Ac-SMC3.

Don't dismiss this kind of discrepancy as bad cellular activity. It is to be taken as diagnostic information. The right question is: where is the biochemical potency being lost? Possibilities include limited permeability, active efflux, metabolism, nonspecific binding or insufficient intracellular accumulation. The explanations should be tested, not assumed.

This change how medicinal chemists ought to assign priority to compounds. A ten-fold improvement in purified-enzyme IC50 may be less valuable than a small improvement in permeability, intracellular exposure or target engagement.

Does molecular docking prove that a novel zinc-binding group binds Zn2+?

Docking and molecular dynamics simulations are valuable for validating inhibitor orientations and stability in the catalytic pocket of HDAC8. These methods assist in hypothesis generation, especially with new zinc-binding groups (ZBGs). However, calculated interactions differ from experimental coordination, particularly for cyanocarbonimidodithioates, necessitating direct structural evidence for accuracy. A co-crystal structure of the protein and ligand would provide the clearest evidence, supported by spectroscopic methods. Claims of improved selectivity must be rigorously validated against both HDAC isoforms and relevant non-HDAC metalloenzymes to confirm the effectiveness of new ZBGs in avoiding nonspecific metal chelation.

> *"soform selectivity should be considered first a mechanistic advantage, and its therapeutic advantage must be demonstrated experimentally."*

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What makes a good HDAC8 inhibitor?

The discovery of HDAC8 should be viewed as a chain of evidence rather than simply a race for potency. An effective development pathway should connect biochemical inhibition, isoform selectivity, physicochemical properties, intracellular exposure, HDAC8 target engagement, relevant phenotype, and experimental ADME/PK. Although not all early studies will conform to this sequence, it provides a more meaningful foundation for determining which molecules to optimize. This perspective also challenges the traditional view of the CAP-linker-ZBG pharmacophore as independent components. Instead, data suggest that the cap's recognition affects surface orientation, the linker's length and flexibility influences passage through the catalytic channel, and the ZBG must achieve proper geometry to engage with the catalytic metal. Therefore, the design focus shifts from identifying the strongest ZBG to combining CAP, linker, and zinc-recognition chemistry for optimal molecular behavior.

Where does the discovery of selective HDAC8 go from here?

The next step forward is unlikely to be based on biochemical potency alone. Other zinc-binding groups are worthy of further investigation but should be optimized when considering complete molecular architectures. Lead optimization requires earlier measurements of cellular target engagement. Design should be guided by structural models, but experiments are needed to validate key binding hypotheses. Claims of selectivity should be backed by broader isoform and metalloenzyme profiling. Increasingly, permeability, stability and pharmacokinetics should influence compound ranking before extensive biological resources are committed.

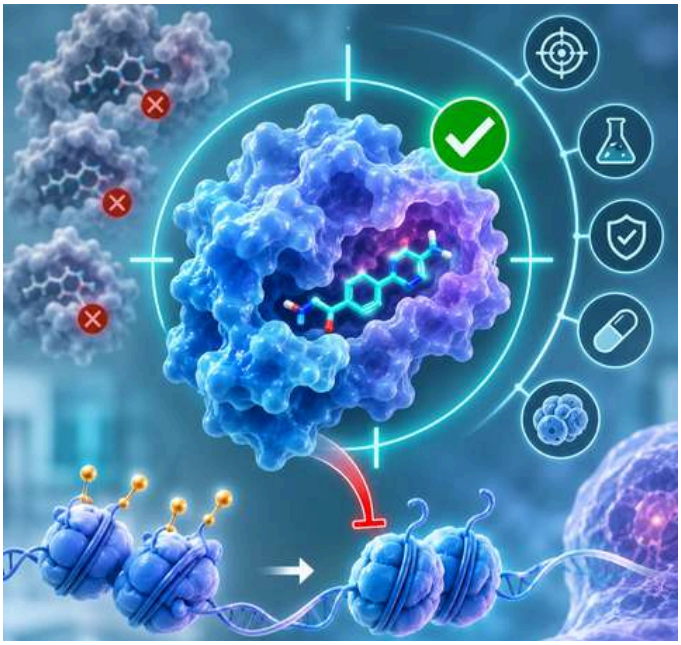
Finally, the disease context matters. The therapeutic utility of a highly selective inhibitor will only be realized if the disease of interest is sufficiently dependent on HDAC8 biology.

The central question of the field has thus changed. We already know that HDAC8 can be inhibited. But the more important questions are: can we control the interaction between the inhibitor and the catalytic zinc? Can we achieve true intracellular isoform selectivity? Is it possible to convert biochemical inhibition into measurable target engagement? And is there a disease context in which that interaction is important for HDAC8 inhibition?

Whether selective HDAC8 inhibition will make the leap from promising medicinal chemistry to meaningful pharmacology will depend on answering those questions, not generating yet another lower IC50.

ABOUT THE AUTHORS

Prof. K. V. G. Chandra Sekhar, Professor in the Department of Chemistry at BITS Pilani, Hyderabad Campus. His contribution to this field lies in advancing medicinal-chemistry strategies for selective HDAC inhibition through the development of new heterocyclic chemotypes and non-hydroxamate zinc-binding approaches. This work helped expand the chemical space available for HDAC8 inhibitor design and generated structure–activity and biological insights that support a more integrated view of zinc recognition, isoform selectivity, and anticancer lead development. Co-author Kosana Sai Chaitanya is a PhD scholar in the same department, working in medicinal chemistry, organic synthesis and drug discovery.



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The Cell's Nuclear RNA Quality Control: Finding Faulty Messages and Fine-Tuning Gene Activity



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Areas of Expertise: RNA Biology | Gene Expression | Yeast Genetics



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Areas of Expertise: RNA Degradation | Gene Expression

In all eukaryotes, mRNA biogenesis consists of the transcription of the protein-coding genes by RNA polymerase II, capping of the primary transcript at the 5′-end, splicing, and an end-maturation event at the 3′-termius of the message. During these events, each transcript interacts and associates with a vast repertoire of mRNA-binding factors and heterogeneous nuclear ribonucleoproteins. Association of the mRNA with these factors dictates the subsequent fates of mRNAs later in their life. Concerted execution of these nuclear events ultimately leads to the formation of an export-competent mRNP (messenger ribonucleoprotein) followed by its nuclear export and subsequent translation in the cytoplasm (Fig. 1). Notably, each of these nuclear events is tightly coupled and linked to ensure formation of productive mRNPs and lowers the risk of formation of erroneous messages. Despite this functional coupling, a substantial amount of non-productive, aberrant mRNPs are continuously produced, raising the possibility of translating these faulty messages, which in turn can produce even a higher amount of aggregation-prone, abnormal or otherwise non-functional polypeptide chains. Accumulation of such aggregation-prone polypeptides eventually increases the probability of having several kinds of disease states such as autoimmune and neurodegenerative diseases. Although this may seem alarming, every eukaryote has evolved highly organized quality-control mechanisms that thoroughly scrutinize the entire biogenesis process, from transcription to export. These mechanisms, collectively called mRNA surveillance mechanisms, rapidly monitor every nuclear event, promptly detect faulty messages, and degrade them selectively. Messenger RNA surveillance is paramount, as it limits the accumulation of aberrant messages, safeguards cells from their detrimental effects, and contributes to the fidelity of the gene-expression pipeline.

mRNA Quality Control System scrutinizes the errors executed in mRNA biogenesis events

Despite the substantial number of faulty messages formed in a healthy cell at any given time, non-functional, aggregation-prone, defective polypeptides are seldom generated from such faulty messages because eukaryotes have a vigilant mRNA quality control system. This system

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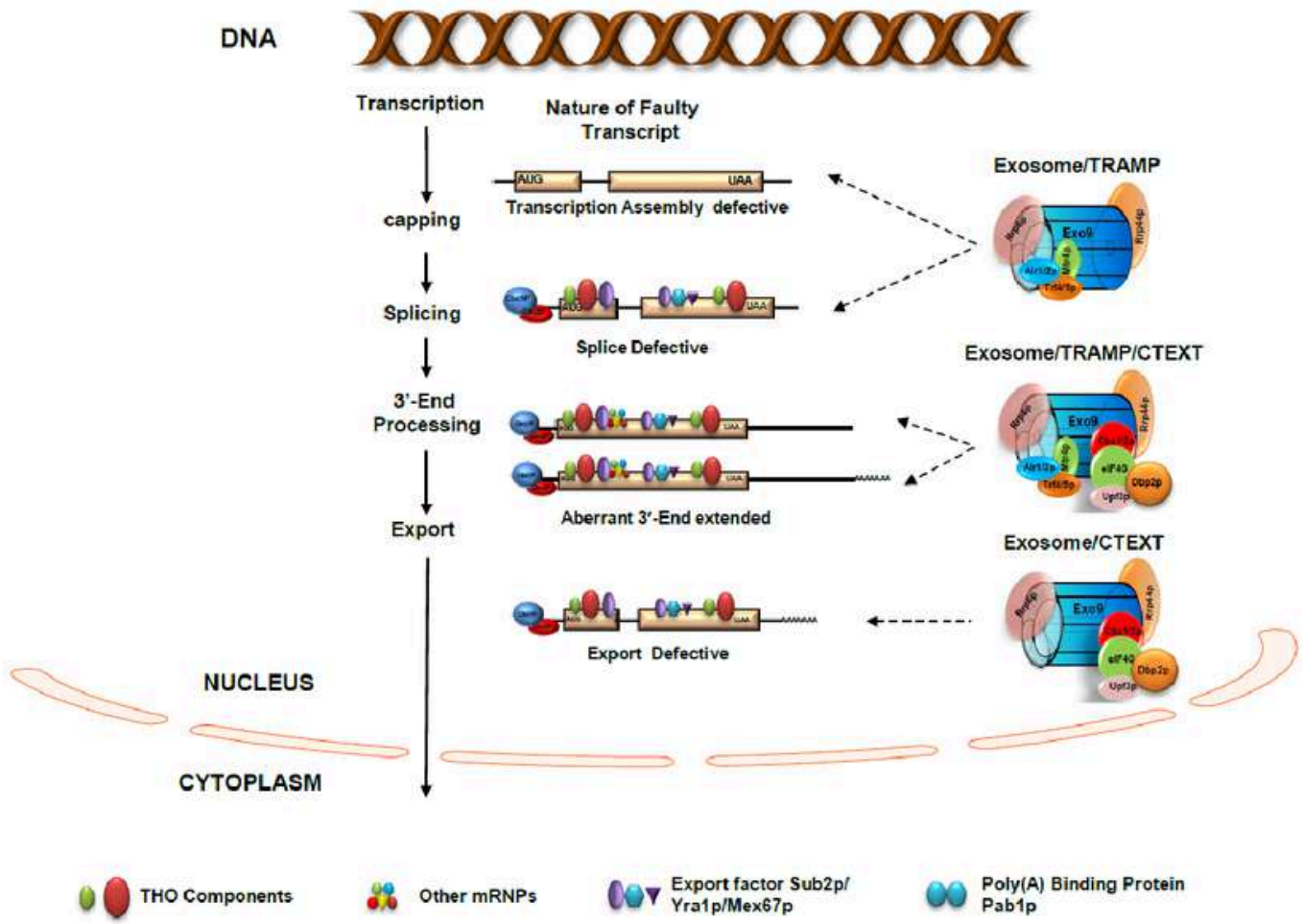


Figure 1:Schematic representation depicting the stages of mRNA biogenesis in the nucleus, each of which is subject to quality control by the nuclear surveillance systems (nuclear exosome/TRAMP/ CTEXT). Normal and functional mRNAs are exported quickly out of the nucleus (indicated in the left half of the figure). Aberrant messages, by contrast, are degraded by the exosome/TRAMP, the exosome/TRAMP/CTEXT, or the exosome/CTEXT. Faulty messages generated in the early, middle and later phases of biogenesis are targeted by the exosome/TRAMP, the exosome/TRAMP/CTEXT and the exosome/CTEXT complex, respectively (see text for details). Proteins binding to maturing transcripts during different stages are schematically indicated by different solid coloured symbols.

critically monitors the entire biogenesis event, detects diverse classes of faulty messages, and promptly targets and degrades them in the nucleus, thereby preventing their export and unwanted translation and precluding the formation of abnormal proteins. Research from various laboratories, including our own, has shown that a highly conserved multi-protein complex called the nuclear RNA exosome is the major machinery in the nucleus involved in targeting and degrading faulty messages. RNA exosome displays extreme conservation in its structure from the simplest eukaryote, baker's yeast, to humans and shows a high degree of similarity in its mode of action. This complex consists of eleven different subunits, of which only two play a vital role in degrading substrate RNAs. These subunits are called Rrp44 (Dis3) and Rrp6, both of which degrade the RNAs from their 3'-terminus in a processive manner.

Remarkably, the nuclear exosome can target and degrade all kinds of RNAs in the cell without assistance and can, in principle, degrade the entire cellular RNA pool. To adapt this molecular machine to target specific mRNAs (such as faulty mRNAs) selectively, the RNA exosome is assisted by a group of protein cofactors called exosomal cofactors. To date, three different exosomal cofactors are reported in the literature: the TRAMP (TRf4/5-Air1/2-Mtr4-Polyadenylation) complex, CTEXT (Cbc1-Tif4631-EXosomal-Targeting) complex, and NNS (Nrd1-Nab3-Sen1) complex (Figure 1). These cofactors help the nuclear exosome scrutinize the entire nuclear RNA pool, preferent-

ially pick up aberrant/faulty mRNAs, and degrade these defective, unwanted messages in the nucleus in a selective fashion. Thus, these cofactors have the important responsibility of distinguishing aberrant/defective messages from normal functional messages.

Recent findings from many laboratories, including our own, indicate that principally four kinds of faulty messenger RNAs are generated in the nucleus of baker's yeast, Saccharomyces cerevisiae, progressively through transcription and various mRNA biogenesis/maturation events. These faulty messages include transcription-assembly-defective, splice-defective, 3'-end maturation-event-defective, and export-defective transcripts. Our laboratory demonstrated that while TRAMP plays a vital role in recognizing and targeting transcription-assembly- and splice-defective messages, CTEXT principally targets and degrades 3'-end maturation-event-defective and export-defective transcripts (Figure 1). Importantly, all aberrant messages display export incompetence and thus cannot be exported efficiently from the nucleus to the cytoplasm, and are largely arrested in the nucleus. This selective nuclear retention helps distinguish them from normal functional messages that are exported readily. Importantly, proper distinction between aberrant and normal functional messages is critical because accidental targeting of the normal messages instead of aberrant ones may lead to cellular catastrophe, which remained an enigma until recently. A recent finding from our laboratory revealed that the third exosomal cofactor, the NNS complex, plays a fundamental role in distinguishing aberrant messages from normal messages. RNA polymerase II preferentially loads the NNS complex onto aberrant transcripts (but not on normal functional messages) in a transcription-dependent manner, thereby marking them as faulty messages.

NNS complex, thus, acts as a "molecular mark" in making the distinction between aberrant and normal messages. The current model thus suggests that aberrant mRNAs are recognized very early during their transcription and biogenesis when the NNS complex is loaded and recruited onto them. Recruitment of the NNS complex leads to the further loading of either the TRAMP or CTEXT complex depending on the phosphorylation status of the long c-terminal domain (CTD) of the largest subunit of RNA polymerase II. During the early phase of mRNP biogenesis, NNS recruits TRAMP onto transcription-elongation-defective and splice-defective messages.

In contrast, NNS recruits CTEXT onto the 3'-end maturation-event-defective and export-defective transcripts specifically during the late phase of mRNP biogenesis.

The mRNA Quality Control System also preferentially degrades a small subset of functional mRNAs, thereby regulating several vital cellular processes.

Interestingly, a recent finding from our lab indicated that the mRNA surveillance machinery, the nuclear RNA exosome/CTEXT, also participates in the selective nuclear degradation of nearly 250 normal functional mRNAs in Saccharomyces cerevisiae, which we termed "special" mRNAs. A global transcriptomic study uncovered these susceptible "special" messages and aimed to determine whether nuclear mRNA surveillance targets and degrades functional messages alongside their aberrant counterparts. Although, the discovery of the finding that mRNA surveillance degrades these small group of functional mRNAs is quite surprising, soon it was realized that the preferential decay of these functional messages reflects a novel mode of regulation of the corresponding genes at the post-transcriptional level that is aimed to regulate the cellular repertoire of these messages under specific environmental signal(s). Experiments designed to understand the reason for the susceptibility of these "special" messages indicated that they were export-inefficient and resemble "aberrant" messages in this context. Understanding the mechanism of their selective nuclear retention is therefore crucial to gaining insight into the regulation of their cellular abundance. Findings from our laboratory revealed that one of the model mRNAs, SKS1 harbours a "nuclear zip code" element in its transcript body that binds, Dbp2, a double stranded RNA helicase that specifically binds to SKS1 (specifically in its nuclear zip code element) and prevent the interaction of SKS1 with export factors Mex67/Yra1, and prevent its nuclear export and promotes its nuclear degradation. Analyses with eight other special mRNAs reveal that all bind Dbp2 and thereby promote their nuclear retention and degradation by the nuclear surveillance machine, exosome/CTEXT. However, the existence of the specific "nuclear zip code" in their transcript body remains to be delineated.

An in-depth, systematic study of the model special mRNA SKS1 revealed that it encodes a signaling kinase whose function is crucial for cellular survival under nutrient-limit-

ing conditions. Consequently, expression of SKS1 is very low under high nutrient levels because the SKS1 mRNA is retained within the nucleus by Dbp2 and undergoes rapid degradation in the nucleus by the exosome/CTEXT. However, under nutrient limiting condition, Dbp2 itself translocates to the cytoplasm thereby permitting the export factors to interact efficiently with the SKS1 mRNA leading to its nuclear export and cytoplasmic translation to produce copious amount of Sks1 protein which is crucial for the uptake/internalization of scarce amounts of glucose/nitrogen from the surrounding medium and cell survival. The nuclear mRNA surveillance system thus plays a vital role in regulating cell survival under nutrient stress.

A parallel study also uncovered that the nuclear surveillance mechanism also regulates the "Unfolded Protein Response" (UPR) pathway – an intracellular signaling pathway activated in response to massive accumulation of unfolded proteins in the endoplasmic reticulum (ER) in response to specific stressors called "ER stress". The transcription factor Hac1 is rapidly activated in the presence of ER stress, which is crucial for rapid activation of downstream genes encoding ER chaperones and heat-shock genes that refold denatured ER proteins and restore cellular homeostasis. Interestingly, the *HAC1* mRNA was found to undergo rapid degradation by the exosome/CTEXT under normal (unstressed) condition.

Our analyses showed that under unstressed conditions, the Rab GTPase Ypt1p is selectively recruited to HAC1 mRNA during transcription and further recruits the NNS complex, CTEXT, and the nuclear exosome sequentially to promote its nuclear decay. However, when ER stress is imposed, the nuclear decay of HAC1 mRNA is diminished because the Ypt1 promptly translocated from nucleus to cytoplasm and in the absence of nuclear Ypt1, the surveillance system fails to recognize HAC1 mRNA thereby leading to its active translation to produce a massive amount of Hac1, which is critical to facilitate expression of downstream ER chaperone genes to restore the cellular homeostasis.

Beyond the roles of the nuclear mRNA surveillance system in yeast survival under nutrient and ER stress, preliminary studies also indicate that the nuclear mRNA quality control system plays a vital role in fine-tuning telomere length regulation under ethanol stress and controlling ribosome biogenesis under nutrient stress. However, further studies are essential to uncover the exact mechanism underlying the regulation of these crucial cellular processes.

Concluding Remarks

All eukaryotes, from yeast to humans, have evolved a nuclear mRNA quality control, or surveillance, system vital for safeguarding cells from the injurious impacts of faulty messages arising spontaneously in healthy cells. The mRNA quality control system is crucial for minimizing the accumulation of aberrant messages in cells, which in turn limits the production of aggregation-prone and otherwise abnormal polypeptide chains. Despite significant advances in our understanding of nuclear mRNA surveillance in simpler model organisms such as baker's yeast, the knowledge base on nuclear mRNA surveillance systems in higher organisms, including metazoans and humans, remains far from complete. For example, an accurate description of the different cofactors of the human nuclear exosome and their respective roles is still needed. Furthermore, a complete picture describing the modes of action of the major exosomal cofactors, hTRAMP, NEXT, and PAXT, concerning their roles and their relative contributions in the nuclear degradation of different kinds of faulty transcripts is currently lacking. Finally, solid evidence that the nuclear exosome and its nuclear cofactors are involved in the regulated nuclear turnover of normal functional transcripts (except for the cytoplasmic decay of AU-rich messages by the human exosome) to control their cellular repertoire in mammals/humans is currently lacking. Further research is necessary to address these unexplored aspects to gain insight into the mechanistic aspects of nuclear mRNA surveillance in humans.

Interestingly, research from various laboratories has presented a large body of evidence linking defects and/or abnormal functions of the surveillance with various disease states, such as neurological disorders, autoimmune diseases, and several kinds of cancers. These mutations map onto various components of the core nuclear exosome, hTRAMP, and NEXT human components. However, our understanding of which specific defects in the surveillance mechanism, owing to each of these mutations, lead to the onset and progression of these diseases remains limited. Further systematic research with a holistic approach is a prerequisite to unraveling mechanistic insights into the nuclear mRNA surveillance system in humans and understanding the biology of these diseases.

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ABOUT THE AUTHORS

Prof. Biswadip Das, Department of Life Science and Biotechnology, Jadavpur University, studies how cells identify and remove faulty messenger RNA using baker's yeast. His laboratory discovered an RNA breakdown pathway and identified CTEXT, a complex that helps remove unwanted RNA. Their research also explained how cells recognise faulty messages and how this quality-control system regulates some normal messenger RNAs. Dr. Satarupa Das is a Research Scientist in the same department at Jadavpur University. Her expertise includes RNA degradation and gene expression.

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> *"The mRNA biogenesis is imprecise leading to the generation of diverse aberrant mRNAs in all eukaryotes."*



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Overcoming Chemotherapy Resistance by Targeting Cancer's Cellular Defences



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| Scientific Profile | Organization Link | Research Lab Page | Factors Press |

Areas of Expertise: Cancer Biology | Multidrug Resistance | Radiation Biology



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Areas of Expertise: Cancer Biology | Redox Biology | Multidrug Resistance Drug | Repurposing

One of the greatest challenges in cancer treatment is not simply finding drugs that kill cancer cells, but understanding why some cells survive treatment. Chemotherapy may initially shrink a tumor, yet resistant cancer cells can persist, multiply and contribute to relapse. Cancer cells exhibit resistance to structurally and functionally different anticancer drug, this phenomenon, known as multidrug resistance (MDR), and it remains a major obstacle to effective cancer treatment. Cancer cells can develop several defense mechanisms. Some use drug transporters to pump chemotherapy agents out of the cell, while others strengthen antioxidant systems, repair DNA damage or alter their metabolism. Together, these adaptations create a complex survival network that allows cancer cells to withstand treatment. Our laboratory has investigated how these defences might be weakened to restore chemotherapy sensitivity. Rather than focusing exclusively on discovering new anticancer drugs, we ask a complementary question: can existing medicines disrupt the mechanisms that protect resistant cancer cells? This approach has guided our research into drug repurposing, thioredoxin reductase (TrxR), NRF2–Keap1 signaling, FOXO3 and P- glycoprotein (P-gp), a transporter associated with drug efflux.

Turning Existing Medicines into New Cancer Tools

Developing a new cancer drug is expensive, time-consuming and uncertain. Drug repurposing offers an alternative by investigating whether medicines developed for one condition could benefit patients with another. Existing pharmacological and safety information may help guide this process, although new indications still require rigorous testing. Our work on drug repurposing in oncology has explored how molecular docking, artificial intelligence (AI), machine learning, transcriptomic analysis and network biology can help identify promising drug–target relationships and potential combinations. Computational predictions, however, are starting points rather than proof of therapeutic effectiveness.

Biochemical experiments, cell based studies and appropriate animal models are needed to establish whether predicted effects occur in biological systems. We are employing multidrug resistant cancer cells and drug-resistant tumor xenograft models for making cancer cells s-

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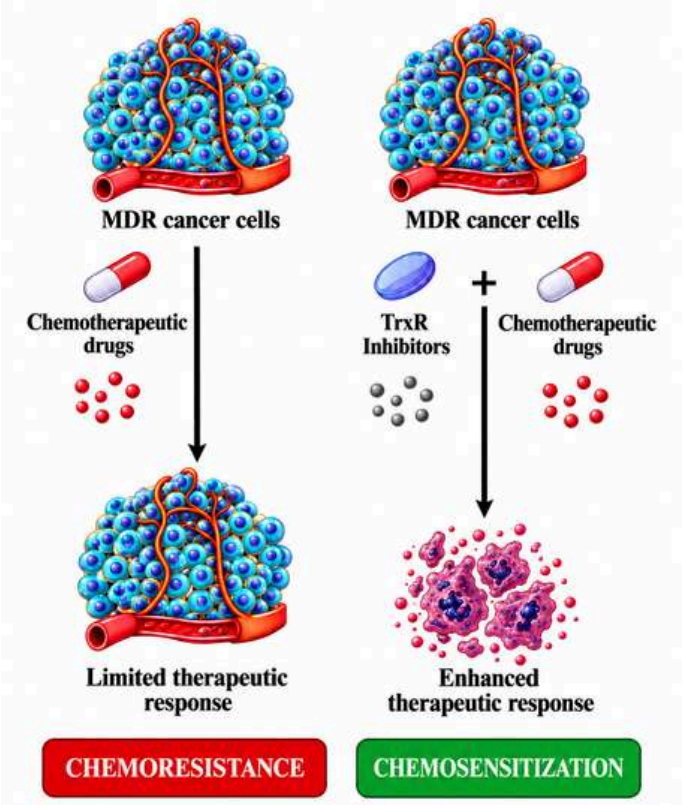


Figure 1: TrxR inhibitors reverse chemoresistance in MDR cancer cells. Chemotherapy alone yields a limited response, whereas co-treatment with TrxR inhibitors enhances therapeutic response through chemosensitization.

ensitive to chemotherapy.

The Redox System: Cancer's Internal Fire-Fighting Network

Reactive oxygen species (ROS) can be compared to cellular sparks. At controlled levels, they participate in normal signaling; when they accumulate excessively, they can damage DNA, proteins, membranes and mitochondria. Chemotherapy can increase oxidative stress, making the capacity to control ROS an important determinant of cancer-cell survival. Two components of this defense network are NRF2 and TrxR. NRF2 regulates genes involved in antioxidant protection and cellular detoxification. Keap1 normally helps control NRF2 activity, but oxidative stress can alter this regulation, allowing NRF2 to activate protective genes. TrxR maintains cellular redox balance and supports antioxidant systems. FOXO3 is another stress-responsive regulator whose effects depend on the cellular context. When these pathways become dysregulated, cancer cells may gain an advantage in surviving treatment. Our research has therefore examined redox regulation as a connected system rather than treating individual antioxidant proteins as isolated targets. The central question is whether disrupting these defences can expose vulnerabilities that chemotherapy alone fails to exploit.

From Auranofin to Ebselen: Exploring Redox Vulnerability

Our more recent experimental work investigated ebselen, a repurposed compound with TrxR-inhibitory activity, in combination with doxorubicin in MDR cells. The combination enhanced doxorubicin activity and increased oxidative DNA damage. It also increased markers of lipid peroxidation and altered iron-related responses while reducing important antioxidant defences, including glutathione peroxidase 4 (GPX4). Experiments using deferoxamine, an iron chelator, and ferrostatin-1, a lipid radical-trapping agent, provided additional evidence supporting the involvement of ferroptosis. Ferroptosis is a form of regulated cell death driven by iron-dependent lipid damage. Unlike apoptosis, it is particularly associated with the failure of systems that protect cellular membranes against lipid oxidation. Our findings suggest that weakening redox defences may make resistant cancer cells more susceptible to this process, alongside other forms of cell death. These results are promising, but they do not establish that ebselen is an effective treatment for patients with resistant cancers. Further research is needed to clarify the mechanisms involved, establish therapeutic selectivity and assess safety and efficacy in clinical settings.

The Other Side of Resistance: Cancer Cells Throw the Drug Away

Another major resistance mechanism involves P-gp, encoded by the ABCB1 gene. This transporter uses cellular energy to remove certain drugs from cells, reducing their intracellular accumulation and potentially limiting their effectiveness. Our ebselen–doxorubicin combination treatment study found reduced ABCB1/P-gp expression alongside increased intracellular doxorubicin accumulation. At the same time, the combination altered TrxR-associated redox defences and increased markers consistent with ferroptotic damage. These observations connect two important aspects of resistance: reduced intracellular drug exposure and enhanced protection against drug-induced damage. Targeting both mechanisms may offer a more comprehensive approach than addressing either one alone. However, changes in transporter expression and drug accumulation do not, by themselves, establish the precise contribution of P-gp inhibition to the overall response.

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A New Way of Thinking About Chemotherapy Resistance

Together, our studies support a broader view of MDR as a network of interconnected defences. Drug efflux can limit chemotherapy exposure; antioxidant pathways can reduce oxidative damage; GPX4 can protect membranes from lipid peroxidation; and iron regulation can influence susceptibility to ferroptosis. Our work with auranofin helped establish the rationale for investigating TrxR as a potential vulnerability. Our research on redox signaling broadened this perspective to pathways involving NRF2, Keap1 and FOXO3. More recently, our ebselen–doxorubicin study linked redox disruption with iron dysregulation, ferroptosis-associated changes and altered P-gp expression. The common principle is that overcoming resistance may require targeting several cooperating survival mechanisms rather than relying on a single molecular target.

From Laboratory Findings to Patient-Relevant Research

Cancer-cell cultures provide valuable mechanistic insights, but they cannot reproduce the complexity of human tumors. Tumor blood vessels, immune cells, connective tissue, oxygen availability and differences between cancer-cell populations can all influence treatment response. Our ebselen–doxorubicin research extended beyond cell culture to a multidrug-resistant xenograft model, where the combination produced substantial tumor-growth suppression under the experimental conditions tested. No significant changes in body weight or evident histopathological abnormalities were observed in the examined organs. These findings provide preliminary in vivo support, but they do not establish long-term safety or clinical effectiveness. Future studies should incorporate more representative models, including three-dimensional tumor cultures, patient-derived organoids and suitable animal systems, to determine whether the observed effects persist in more complex biological environments.

The Future: Treating the Defence System, Not Just the Tumor

The next challenge is to identify which tumors depend most strongly on particular resistance mechanisms. Some may rely heavily on TrxR-associated redox protection, while others may be dominated by P-gp-mediated drug efflux or GPX4-dependent protection against lipid oxidation. Biomarker-guided chemosensitisation could he-

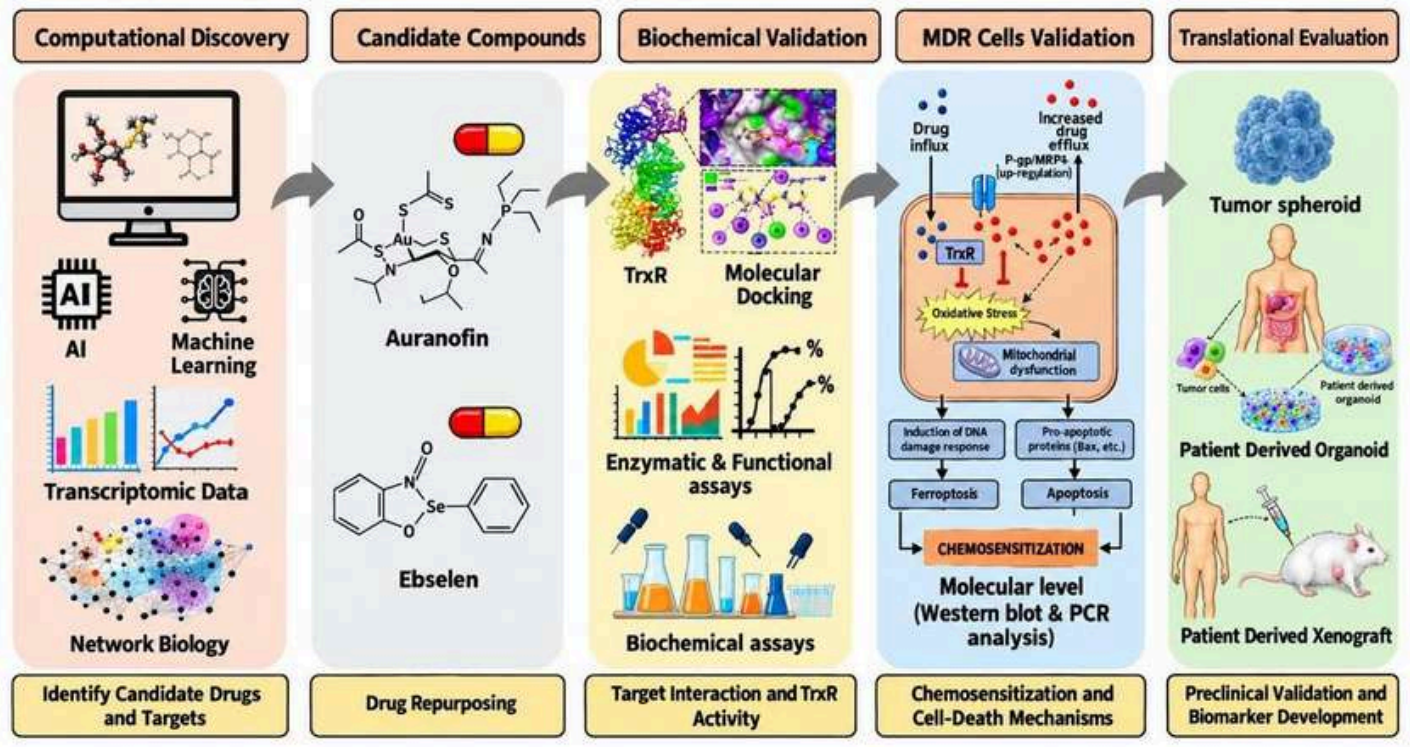


Figure 2: The workflow begins with computational discovery using AI, machine learning, transcriptomics and network biology, followed by drug repurposing to identify auranofin and ebselen as TrxR inhibitors. Biochemical assays validate TrxR inhibition, followed by MDR cell studies examining redox imbalance, NRF2–KEAP1–FOXO3 signaling, P-gp/ABCB1-mediated drug efflux, ferroptosis-associated responses and apoptosis. Finally, tumor spheroids, patient-derived organoids and PDX models evaluate therapeutic efficacy and support biomarker development.

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lp identify tumors most likely to respond to specific combinations. Candidate markers include TrxR activity, NRF2–Keap1 pathway alterations, glutathione status, ABCB1/P-gp expression and ferroptosis-related indicators. Their predictive value must be established through further validation. Across our research, the focus has progressed from investigating repurposed compounds such as auranofin to examining redox signaling and the effects of ebselen combined with doxorubicin. Computational drug discovery provides a framework for extending this work to additional compounds and combinations. Ultimately, the goal is not simply to find another drug that kills cancer cells. It is to understand how resistant cancer cells survive and identify ways to weaken those defences. By combining drug repurposing, redox biology and experimentally validated computational approaches, we hope to contribute to more targeted strategies for overcoming chemotherapy resistance.

ABOUT THE AUTHORS

Dr. N. Rajendra Prasad is a Professor in the Department of Biochemistry and Biotechnology at Annamalai University, with research expertise in radiation biology, cancer biology, and multidrug resistance. His research investigates cellular responses to radiation and the molecular mechanisms underlying cancer progression and therapeutic resistance.

Mr. Sugumar Baskar is a Ph.D. scholar in Biochemistry whose research focuses on overcoming multidrug resistance in cancer cells by targeting cellular redox homeostasis. Their work explores how repurposed drugs, particularly ebselen, may weaken antioxidant defences and enhance chemotherapy sensitivity, highlighting potential strategies for addressing treatment-resistant cancer.

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> *"Chemotherapy resistance is not one lock with one key; it is a network of interconnected cellular defense mechanisms."*

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Beyond Memory Loss: A Metabolic View of Cognitive Decline and Dementia



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| Scientific Profile | | Organization Link | | Research Lab Page | | Factors Press |

Areas of Expertise: Clinical neurology | dementia | cognitive decline | clinical biomarkers



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Areas of Expertise: NMR spectroscopy | clinical metabolomics | biomarker discovery | systems biology

Memory loss is one of the best-known signs of dementia, but it is only the visible part of a much more complex process. Cognitive decline can involve changes in attention, language, planning and everyday function, and different people may reach similar symptoms through different biological pathways. Alzheimer's disease and vascular dementia are not identical conditions, yet both can be accompanied by disturbances in energy use, amino-acid balance, inflammation and lipid metabolism. Understanding these changes may help researchers develop accessible measures that complement neurological examination, cognitive testing and brain imaging.

Why metabolism matters to the brain

The brain has a high and continuous demand for energy. Neurons depend on carefully regulated supplies of mainly glucose and other fuels, functioning mitochondria, and a balanced environment of amino acids and lipids. Inflammation and vascular or metabolic comorbidities can influence these systems. Metabolomics—the systematic study of small molecules in biological samples—offers a way to examine the combined biochemical consequences of genes, lifestyle, ageing and disease. Blood is particularly attractive because collection is relatively straightforward and can be repeated over time. However, a blood profile reflects the whole body; it should not be treated as a direct readout of brain chemistry.

From mild cognitive impairment to dementia: evidence from NMR

Our work using proton nuclear magnetic resonance (^{1}H NMR) spectroscopy has examined circulating metabolic features across different stages of cognitive impairment. In a 2021 study of a North Indian population, plasma from a subset of participants with mild cognitive impairment and healthy controls was profiled using high-field ^{1}H NMR. Lysine, glycine and glutamine emerged as a candidate three-metabolite panel. The study also considered diffusion tensor imaging and cognitive assessment, placing metabolic findings alongside clinical and brain-imaging information. These results supported further investigation of blood-based metabolic markers, but the sample analyzed by NMR was modest and the findings require validation in independent populations.

A broader metabolic signature in cognitive decline

In our more recent study published in Biophysical Chemistry, serum samples from 40 participants with cognitive decline and 54 cognitively normal controls were

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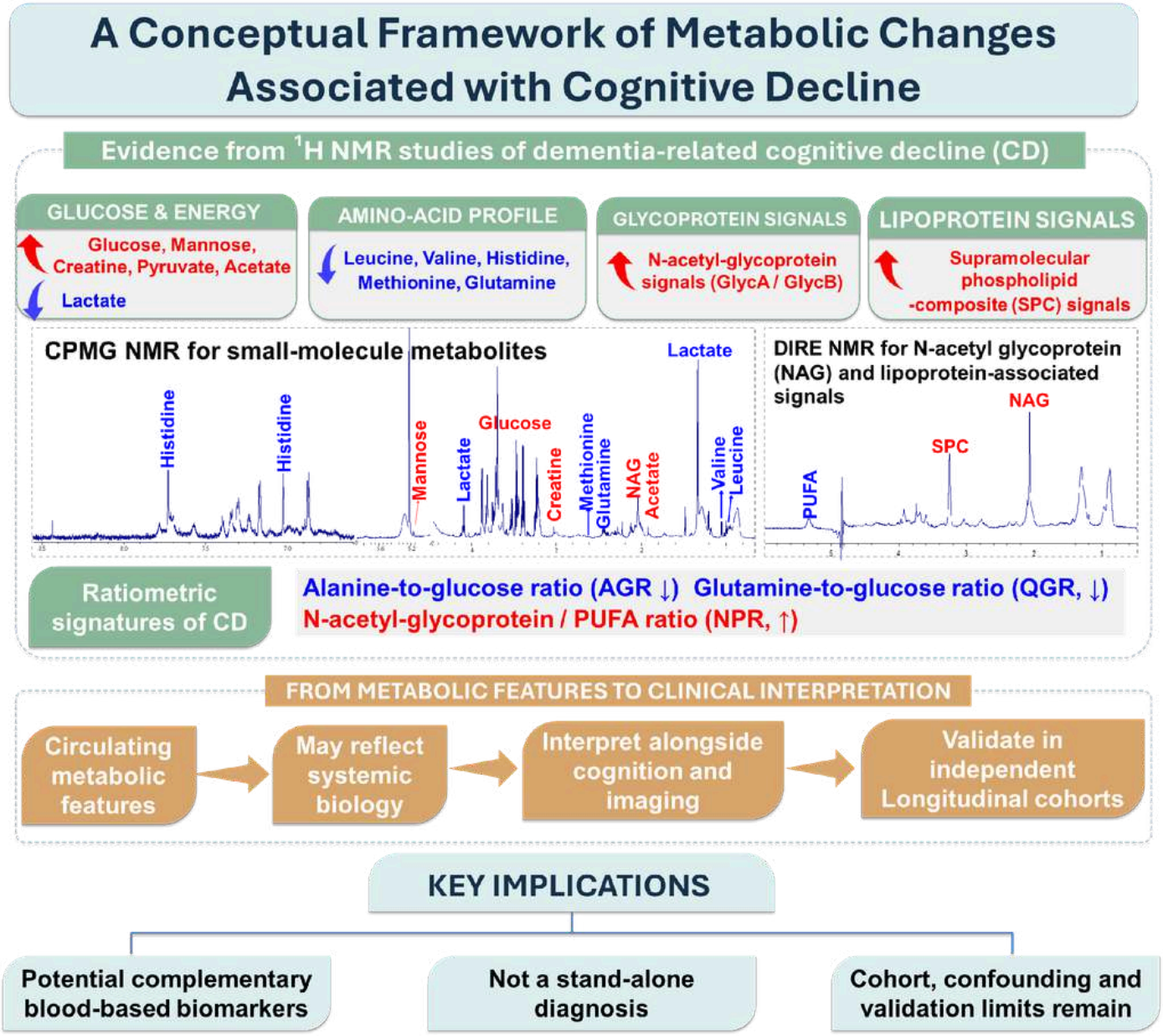


Figure 1: A conceptual framework of metabolic changes associated with cognitive decline illustrating the proposed links among glucose and amino-acid metabolism, glycoprotein-associated inflammatory signals, lipoprotein-related features, and cognitive assessment.

analysed using 800 MHz ¹H NMR spectroscopy. Thirty-three metabolites and selected metabolic ratios were quantified. The cognitive-decline group showed higher glucose, pyruvate, acetate, creatine and mannose, alongside lower levels of several features including lactate, leucine, valine and histidine. The glutamine-to-glucose ratio (QGR) and alanine-to-glucose ratio (AGR) were also lower. AGR was positively associated with Mini-Mental State Examination scores, while AGR and QGR declined with increasing severity in the study cohort. QGR, AGR and the histidine-to-tyrosine ratio showed promising discrimination within that cohort.

Why look at glycoproteins and lipoproteins as well?

Small metabolites are only one part of the circulating biochemical picture. In a separate study currently under review at Clinica Chimica Acta, our team has explored complementary NMR experiments designed to capture both low-molecular-weight metabolites and broader glycoprotein- and lipoprotein-associated signals. The submitted analysis reports higher N-acetyl-glycoprotein signals and supramolecular phospholipid-composite signa-

ls in the cognitive-decline group, together with changes in glucose, mannose, amino acids and metabolic ratios. These findings are preliminary until peer review and independent validation are complete. Nonetheless, they illustrate the value of asking whether several biochemical layers—rather than a single metabolite—can provide a more informative picture of systemic changes accompanying cognitive decline.

What these findings mean—and do not mean

Taken together, the studies support a view of cognitive decline as a condition that may be accompanied by interconnected metabolic changes, rather than a process understood only through memory symptoms. Ratios such as QGR and AGR may be useful because they express relationships between metabolites, not simply the level of one molecule. Glycoprotein-associated signals may add information about systemic inflammatory activity, while lipoprotein-related signals may reflect changes in lipid transport and composition. These are biological interpretations, not proof that a specific pathway caused cognitive impairment. Cross-sectional associations cannot establish whether metabolic changes precede cognitive decline, result from it, or arise partly from other conditions.

The challenges before clinical use

Several hurdles must be cleared before these observations can become clinical tests. First, findings need replication in larger, independent and diverse cohorts, including participants with different educational backgrounds, diets, vascular risks and comorbidities. Second, longitudinal studies should determine whether metabolic profiles change as cognition changes and whether they can predict conversion from mild cognitive impairment to dementia. Third, studies need careful control of factors such as age, sex, fasting status, medication, diabetes, kidney and liver function, sample handling and storage. Dementia is heterogeneous, and a marker that performs well in one group may not generalize to another.

Analytical and statistical standards matter equally. NMR offers reproducible profiling and can measure multiple metabolites in one experiment, but some spectral signals overlap and assignments may remain putative unless confirmed with additional methods. Multivariate models can appear more accurate than they truly are if data are over-fitted or validation is incomplete. Candidate markers should therefore be evaluated with transparent preprocessing, correction for multiple testing, suitable internal validation and external testing. Ultimately, their value must be compared with established clinical assessments and available blood, cerebrospinal-fluid or imaging biomarkers—not merely with healthy controls.

A practical path forward

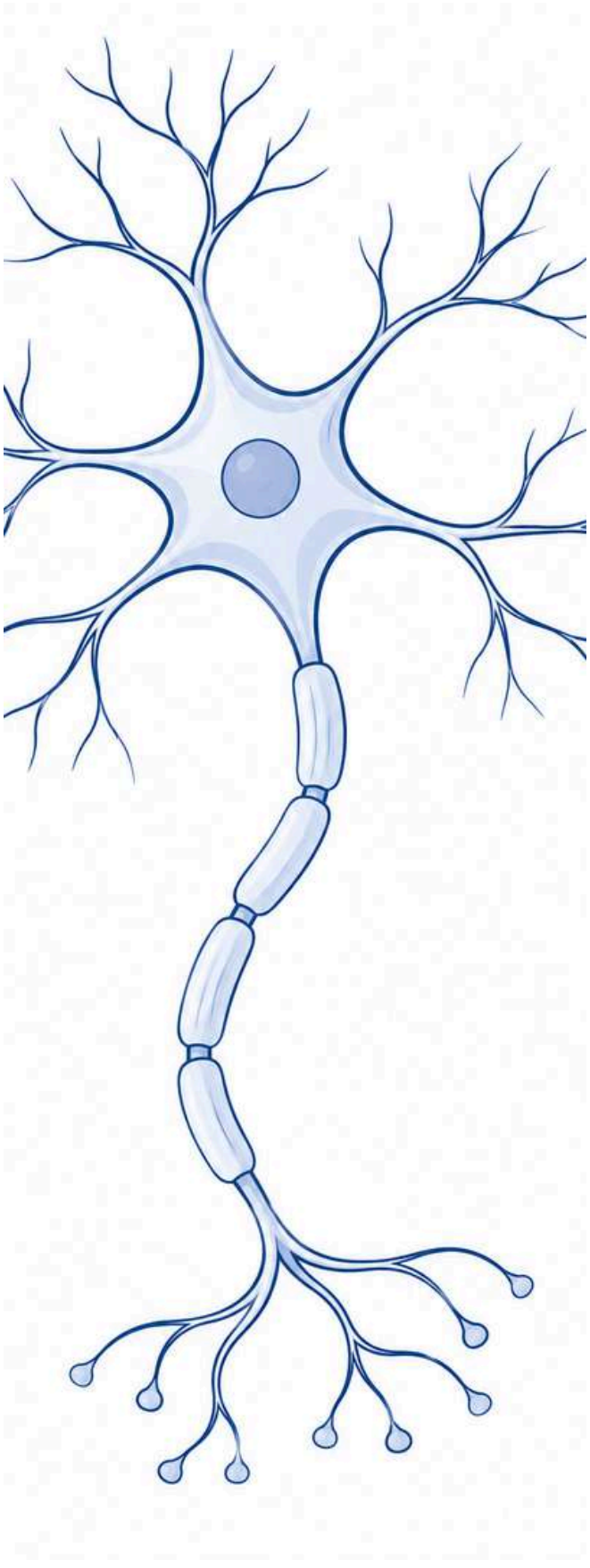
The next step is not to promote a metabolic panel as a stand-alone diagnostic test, but to test whether it adds useful information to existing care. Prospective multicenter studies could combine standardized clinical phenotyping, cognitive scores, brain imaging and established biomarkers with serum or plasma NMR profiles. Where feasible, metabolomics could be integrated with lipidomics, proteomics and other data layers, using machine-learning models that are independently validated and interpretable. Researchers should also examine whether metabolic patterns differ by dementia subtype and whether they reflect modifiable contributors such as vascular risk or nutritional status. The conceptual framework is presented in Figure1.

> *“Cognitive decline may be accompanied by interconnected changes in energy metabolism, amino-acid balance, inflammation and lipid-associated signals.”*

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Key Takeaways

A diagnosis of dementia must remain grounded in a careful clinical evaluation. A blood test based on metabolomics is not currently a substitute for that process. Yet the ability to measure many metabolic features from a small sample offers a promising research route to understanding the biology that accompanies cognitive decline. Our studies—from mild cognitive impairment to broader serum metabolite profiles and exploratory glycoprotein/lipoprotein signals—add to this developing evidence base. The most important task now is rigorous validation and collaboration between neurologists, analytical scientists, statisticians and clinical researchers. Looking beyond memory loss does not mean looking away from patients; it means seeking a fuller biological understanding that may, in time, support more precise assessment and monitoring.



ABOUT THE AUTHORS

Prof. Rameshwar Nath Chaurasia is a faculty member in the Department of Neurology, Institute of Medical Sciences, Banaras Hindu University, Varanasi, India. His clinical and research interests include stroke, dementia, Alzheimer's disease, and tuberculous meningitis. He has contributed to numerous scientific publications on neurological disorders, cognitive impairment, disease-related biomarkers, and treatment outcomes. His research also explores the relationship between diabetes, ageing, and neurodegenerative diseases, aiming to improve diagnosis and patient care. Ms. Rimjhim Trivedi is a UGC Senior Research Fellow at the Centre of Biomedical Research (CBMR), Lucknow, India. Her research focuses on NMR spectroscopy, clinical metabolomics, and biomarker discovery.Dr. Dinesh Kumar is an Additional Professor at CBMR, Lucknow, India. His research focuses on NMR spectroscopy, clinical metabolomics, and systems biology.

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Strengthening Infection Prevention and Responsible Antibiotic Use through Communication and Teamwork



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| Scientific Profile | | Organization Link | | Research Lab Page | | Factors Press |

Areas of Expertise: Infectious diseases | infection prevention and control | antimicrobial stewardship | clinical governance

Consider a patient recovering after abdominal surgery. On the second postoperative day, a nurse notes that the urinary catheter no longer has a clear indication. A pharmacist asks why empirical intravenous antibiotics are continuing without a documented review. The laboratory reports a culture result that would allow a narrower-spectrum drug. Each observation is clinically actionable, but its value depends on whether it reaches someone with the authority to act, and whether that person acts. Each additional catheter-day adds to the risk of catheter-associated urinary tract infection; each unnecessary antibiotic-day adds to the risk of adverse drug effects, Clostridioides difficile infection and selection for resistant bacteria.

Infection prevention and control (IPC) and antimicrobial stewardship (AMS) are delivered through thousands of such exchanges every day. They depend not only on what individual clinicians know, but on how reliably a team moves information to the point of decision. My view is that health systems should treat these exchanges as a component of clinical care that can be designed, resourced and measured: protected time, defined responders and verification that decisions are carried out. A guideline describes what should happen; team processes determine whether it does.

Connect prevention with treatment

The two disciplines act on the same causal chain. Every infection prevented removes a reason to prescribe antibiotics. Every unnecessary antibiotic exposure avoided reduces adverse drug effects and the selection pressure under which resistant bacteria outcompete susceptible ones. Resistance is a property of microorganisms, not of patients: it arises through genetic mutation and the acquisition of resistance genes, and it spreads in hospitals both through antibiotic selection and through transmission between patients via hands, equipment and the environment. Stewardship addresses the first route and infection prevention the second, which is why the two work best as partners rather than as separate programmes.

The strongest quantitative support comes from a meta-analysis of 32 hospital studies covering more than 9 million patient-days. Stewardship programmes were associated with a 51% reduction in the incidence of infection or colonisation (carriage without disease) with multidrug-resistant Gram-negative bacteria, a 37% reduction for meticillin-resistant Staphylococcus aureus (MRSA) and a 32% reduction for C. difficile infection. Effects were larger when stewardship was combined with infection-control measures (pooled incidence ratio 0.69) and largest when those measures included hand hygiene (0.34, roughly a two-thirds reduction). No effect was detected for vancomycin-resistant enterococci. These findings support coordinating the two programmes while preserving the distinct expertise each requires.

These estimates need careful interpretation. The included studies were largely observational, comparing incidence before and after implementation, and so cannot fully separate a programme's effect from background trends or concurrent changes; heterogeneity between studies was also substantial. The programmes were multicomponent,

combining education, prescription audit with feedback, restriction and changes in working practice, so their results cannot isolate the contribution of communication itself. A scoping review of 53 studies of hospital team communication found that structuring the content or process of team discussion was the most common intervention, yet only four studies linked better communication with IPC or AMS outcomes, and the evidence did not allow effectiveness to be estimated. All 53 studies came from high-income countries. Communication is therefore a plausible and important mechanism whose effect size, and transferability to resource-limited settings, remain to be established. We should invest in it while studying it.

Make conversations lead to decisions

A brief, structured daily review can link the two disciplines at the bedside. Four questions cover most of the ground. Does each invasive device, such as a urinary catheter or central venous line, still have a valid indication? What working diagnosis justifies the antibiotic? Have microbiology or other results changed the picture? What must happen today, and who will do it? Assigning each decision to a named person turns discussion into accountable action, and the same structure makes the process auditable.

A formal antibiotic review 48–72 hours after treatment begins, sometimes called an antibiotic time-out, is a sensible default because culture results and the clinical trajectory are usually available by then. Review should happen earlier if new information arrives or the patient deteriorates. The team decides whether to continue, narrow (de-escalate), broaden or stop treatment; whether intravenous therapy can be switched to oral, which also shortens exposure to vascular lines; and what total duration the evidence supports for that infection. Prescribing authority remains with the treating clinician, while nurses, pharmacists and laboratory staff contribute observations that improve the decision.

Stewardship is not the same as restriction. In sepsis and other serious bacterial infections, delay in effective treatment is associated with worse outcomes, so review processes must never obstruct urgent therapy. The counterpart is that empirical treatment, started before the cause is known, should carry a documented plan to reassess both the diagnosis and the prescription.

Laboratory communication needs the same closed-loop discipline used in medication safety. A critical result, such as a positive blood culture, becomes useful only when someone receives it, interprets it in the patient's clinical context and confirms the action taken. If that person is unavailable, a predefined escalation route is needed. Uploading a report to the electronic record is one step in this loop, not its completion.

Diagnostic technology should therefore be judged against the whole pathway, not laboratory speed alone. The FAST randomised trial included 850 patients with Gram-negative bloodstream infection at seven centres in Greece, India, Israel and Spain, all settings with high antimicrobial resistance. Rapid susceptibility testing performed directly from positive blood cultures delivered results in about 7.5 hours, compared with about 44 hours for standard methods, and led to earlier escalation or de-escalation of antibiotics. It was not, however, superior on the primary endpoint, a desirability-of-outcome ranking at 30 days that combined survival, clinical response, discharge status and harms such as kidney injury or acquisition of resistant organisms. Both groups received stewardship review. Faster information is necessary but not sufficient: patient benefit depends on what the clinical system does with it, and has to be measured rather than assumed.

Give every team member a voice

Professional hierarchy is a well-described barrier to safety communication. A junior doctor may hesitate to question a senior colleague's prescription. A nurse may recognise a concern but regard prescribing as outside the nursing role. A pharmacist's recommendation may arrive after the ward round, once decisions have been made. Teams whose members can raise concerns without fear of embarrassment, a condition organisational researchers call psychological safety, are more likely to surface this kind of information. Leaders build it by inviting questions, clarifying roles and responding constructively when concerns are raised.

Shared responsibility needs defined authority. Nurses can prompt review and report changes in the patient's condition; pharmacists can assess dose, drug interactions, adjustment for kidney function and treatment duration; laboratory professionals can explain what a result does and does not establish, for example whether an organism is more likely a contaminant or colonising organism than a cause of infection. The treating clinician integrates these inputs and documents the plan. An unresolved disagreem-

ent should have an agreed route to a senior decision-maker, so that concerns are resolved rather than dropped.

Teamwork must also include staff whose work interrupts transmission directly. Environmental cleaning staff need clear protocols for shared equipment and isolation rooms, and a way to report missing supplies, because contaminated surfaces and equipment are recognised reservoirs for C. difficile spores and multidrug-resistant Gram-negative bacteria. Laboratory staff need relevant clinical information to process and interpret specimens appropriately. At transfer and discharge, receiving teams need the indication for treatment, pending results and the next review or planned stop date; these transitions are points at which information is commonly lost.

Patients and families also need explanations they can use. When antibiotics are not indicated, clinicians should explain the likely cause of the illness (often a viral infection, against which antibiotics have no effect), what will help and which warning signs should prompt a return. When antibiotics are prescribed, the plan and its review point should be explained. Questions should be welcomed without shifting to patients the responsibility for policing their own safety.

Students should practise these conversations across professional boundaries. Interprofessional case discussions can teach future doctors, nurses and pharmacists to disagree constructively, acknowledge diagnostic uncertainty and escalate appropriately. These competencies deserve formal assessment alongside scientific knowledge.

Build support and measure what changes

Communication operates within structural constraints. Overcrowding, inadequate nurse staffing, unreliable water supply, shortages of alcohol-based hand rub and poor access to diagnostics cannot be corrected by training alone; they are upstream drivers of both transmission and empirical prescribing.

Hospital leaders and policymakers should fund these essentials alongside protected time for joint review. In smaller facilities, trained local teams supported remotely by regional specialists may be a workable model, but its effectiveness and cost-effectiveness need formal evaluation.

I would begin with a small, balanced set of indicators. Process measures could include the proportion of device-days with a documented indication, the proportion of antibiotic courses reviewed within 72 hours and the time from a critical result to a documented clinical decision. Outcome measures could include healthcare-associated infection rates per 1,000 device-days or patient-days, C. difficile incidence and, where feasible, resistance trends. Balancing measures guard against unintended harm: time to effective treatment in sepsis, mortality, readmission and staff workload. Comparing units or hospitals requires standardised surveillance definitions and adjustment for case mix, because sicker patient populations have higher infection rates irrespective of care quality.

Teams should review these data regularly, using methods such as statistical process control charts that help distinguish genuine change from random variation. A rise in reported infections may reflect better case detection rather than poorer care, and should be investigated before conclusions are drawn. Reviews should focus on system failures rather than individual blame, and staff should hear what changed as a result of their reports.

For regulators and funders, the relevant question is whether a programme changes care, not merely whether it exists. A committee roster or annual training attendance cannot answer that question. Assessment standards should instead sample individual cases, examine whether recommendations were acted on and test whether staff can raise concerns. Funding should support these functions in community care as well as in hospitals.

Digital systems and artificial intelligence may help flag overdue reviews, identify devices without a documented indication or route urgent results to the right clinician. Their value will depend on data quality, alert burden (too many alerts lead to alert fatigue, and alerts are then ignored) and a clearly accountable clinical response to each alert. Evaluations should use robust designs, such as cluster-randomised or stepped-wedge trials or well-controlled interrupted time-series analyses, and should report patient outcomes, costs and sustainability, particularly in resource-limited settings. The immediate priority is to make structured, closed-loop communication a routine and measurable part of infection prevention and antibiotic care. That means organising daily work so that relevant information is heard, decisions are explained and someone is accountable for follow-through.

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Key messages

Infection prevention and antimicrobial stewardship act on the same chain linking infection, antibiotic exposure and resistance; they should share daily workflows, with clear accountability for acting on concerns and test results. Nurses, pharmacists, laboratory staff and cleaning teams need the training, resources and organisational authority to contribute fully; hierarchy that silences them is a modifiable safety risk. Evaluate team interventions with balanced process, outcome and safety measures, including time to effective treatment, avoidable infections, antibiotic use and staff workload, using study designs that can show whether better communication itself improves patient outcomes.

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Dr. Anup R. Warrier is working as a Group Chief of Medical Services at Baby Memorial Hospitals (BMH) Care Hospital Limited, Ernakulam, Kerala, India. His work focuses on preventing and treating infectious diseases, particularly infections caused by bacteria that are resistant to antibiotics. He has contributed to several scientific publications on antibiotic use, infection prevention, and the treatment of serious infections. He is actively involved in promoting the responsible use of antibiotics and improving infection control in hospitals. His clinical and research experience highlights the importance of teamwork, clear communication, and informed decisions in preventing and treating infections. Through his work, he aims to improve patient care, support healthcare professionals, and raise awareness about the growing challenge of antibiotic resistance.

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> *"Better communication and teamwork help prevent infections and keep antibiotics working longer."*

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Understanding Antibiotic Resistance Through the Structure and Function of Bacterial Enzymes



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Areas of expertise: X-ray crystallography | Protein structural biology | Antimicrobial Resistance | Computational biology Drug discovery



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Imagine having an infection that was once easily treated with antibiotics, but the same medicines no longer work. This is one of the growing challenges facing modern medicine. Antibiotic resistance occurs when bacteria develop the ability to survive medicines designed to kill them or stop their growth.Antibiotics have transformed healthcare, making previously dangerous infections treatable and enabling safer surgeries, cancer treatments and organ transplantation. However, their effectiveness is increasingly threatened by antimicrobial resistance (AMR), which makes infections harder to treat and increases the risk of serious illness. But how can a microscopic bacterium survive a medicine designed to destroy it? The answer lies partly in the remarkable adaptability of bacteria. Some prevent antibiotics from entering their cells, others pump medicines out, while some produce specialised proteins called enzymes that destroy or inactivate antibiotics. Understanding these enzymes is an important step towards understanding antibiotic resistance. Sometimes, the key lies in something invisible to the naked eye: the three-dimensional structure of a protein.

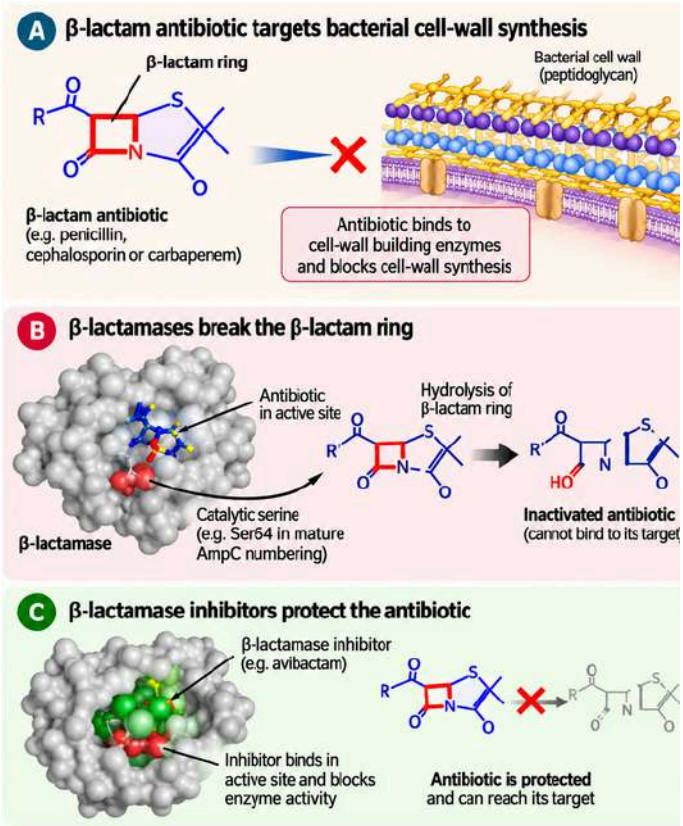
Bacterial enzymes: Tiny machines with a powerful role

Enzymes are proteins that accelerate chemical reactions in living organisms. They perform essential tasks, from helping us digest food to enabling bacteria to grow and survive. However, some bacterial enzymes work against antibiotics. A particularly important group is called beta-lactamases. Penicillins, cephalosporins and carbapenems belong to a major family of antibiotics known as beta-lactams. These medicines work by interfering with the construction of the bacterial cell wall, an essential protective structure. Beta-lactamases defeat this strategy by breaking open a critical chemical ring in these antibiotics, rendering them inactive (Figure 1A). Think of an antibiotic as a key designed to interrupt an essential process in a bacterium. A beta-lactamase acts like a tool that damages that key before it can do its job. Beta-lactamases are diverse and are commonly grouped into four classes (A, B, C and D) based on their molecular characteristics. Most use an amin-

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o acid called Serine64 to break down antibiotics, whereas class B enzymes use zinc ions to facilitate the reaction. Understanding these different mechanisms has been central to developing strategies to counter antibiotic resistance (Figure 1B). The development of beta-lactamase inhibitors represents an important advance in this field. Earlier inhibitors, such as clavulanic acid, sulbactam and tazobactam, helped restore the activity of certain beta-lactam antibiotics against bacteria producing susceptible enzymes. Newer inhibitors, including avibactam, relebactam and vaborbactam, have expanded the range of beta-lactamases that can be targeted (Figure 1C). However, no single inhibitor is effective against every enzyme, and the continuing emergence of new variants presents an ongoing challenge. One important example is Pseudomonas aeruginosa, a bacterium that can cause serious infections, particularly in vulnerable patients. It produces enzymes called Pseudomonas-derived cephalosporinases (PDCs), which belong to the AmpC family of beta-lactamases. As these enzymes evolve, their interactions with different antibiotics may also change. Understanding these changes requires more than knowing which genes a bacterium carries; we need to understand the proteins those genes produce.

Figure 1. How β-lactamases inactivate antibiotics and how inhibitors can block them



Why does the shape of a protein matter?

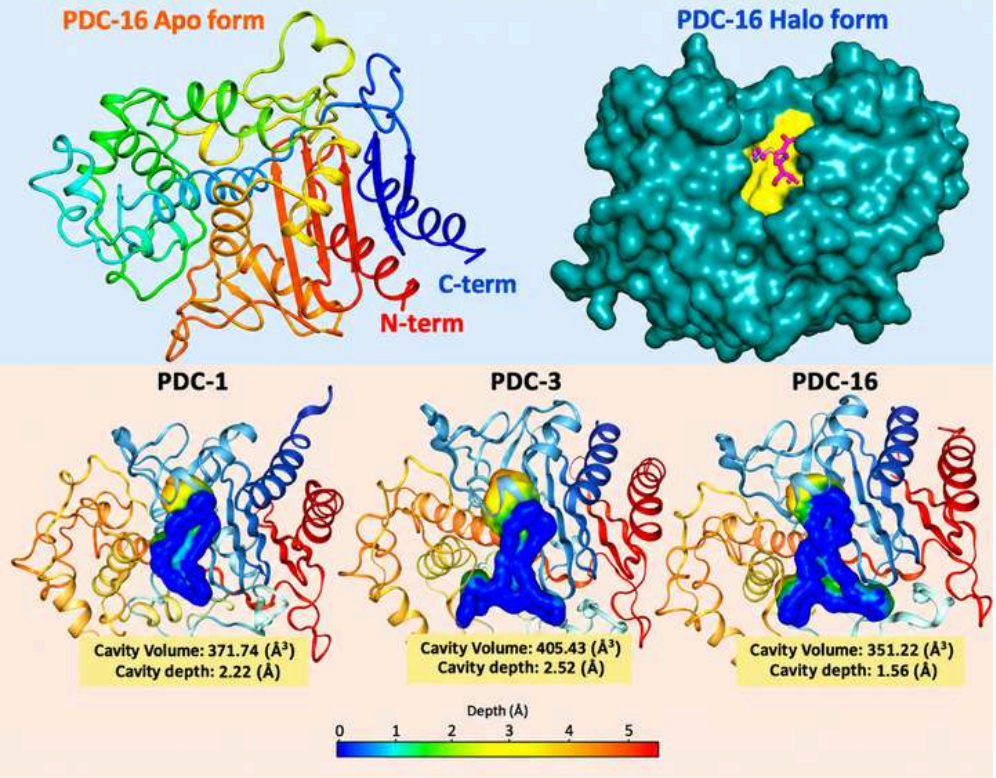
Proteins are not rigid objects. They fold into intricate three-dimensional structures, and their shapes help determine what they can do. Many enzymes contain an active site, a specialized region where a chemical reaction takes place. In beta-lactamases, this region helps recognize and process susceptible antibiotics. Imagine a workspace designed for a particular task. Its size, shape, chemical properties and flexibility all influence how efficiently the task can be completed. An enzyme's active site works in a similar way. Changes in the amino acids that make up a protein can alter the shape or chemical environment of its active site. These changes may influence how an antibiotic enters, how it is positioned and how efficiently the enzyme breaks it down. Importantly, a larger active site does not automatically mean a more effective enzyme, just as a smaller workspace does not necessarily make every task impossible. The outcome depends on the particular antibiotic and the precise arrangement of the enzyme's components. This is where structural biology becomes valuable. Techniques such as X-ray crystallography allow researchers to determine the three-dimensional structures of proteins and investigate how molecular changes may influence their function. When combined with biochemical experiments and computational approaches, structural information provides a more complete picture of how enzymes interact with antibiotics.

A closer look at PDC-16: What our research revealed

Our recent research focused on PDC-16, a variant of the AmpC beta-lactamase associated with carbapenem-resistant P. aeruginosa. Published in the International Journal of Biological Macromolecules (2026Sep 30;383), our study examined the enzyme's structure and function to understand how its molecular architecture relates to its activity against different antibiotics. Using X-ray crystallography, we determined two structures: PDC-16 without an antibiotic bound and PDC-16 with imipenem, a carbapenem antibiotic, bound within its active site (Figure 2). X-ray crystallography uses the diffraction of X-rays by protein crystals to reveal the arrangement of atoms in a protein. In simple terms, it allows scientists to build a detailed three-dimensional picture of a molecular machine that is far too small to see directly. The findings revealed an interesting feature of PDC-16. Its active-site cavity was more constrained than those of the related enzymes used for comparison. Our structural analysis estimated its cavity volume at approximately 351 Å3, compared with 372 Å3 for wild-type PDC-1 and 405 Å3 for cavity expanded PDC-3

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Figure 2: PDC-16 in its apo and halo form and its cavity comparison.



These measurements describe the space available within the enzyme's active site (Figure 2). This observation is interesting because structural adaptation in beta-lactamases does not always involve an expansion of the active site. Changes in the positions of amino acids and the flexibility of nearby protein regions may also influence how an enzyme interacts with different antibiotics. The relationship between active-site architecture and enzyme function is therefore more complex than simply having a larger or smaller cavity. We also observed structural rearrangements in PDC-16 when imipenem was bound. The structure captured a snapshot of the enzyme–antibiotic interaction, including a covalent acyl-enzyme intermediate. Although this provides valuable information about the interaction, further studies are needed to understand the precise molecular movements that occur during the catalytic process. Our biochemical experiments added another important dimension. PDC-16 displayed substrate-dependent kinetic behaviour, with differences in its apparent affinity and catalytic activity across the beta-lactam antibiotics examined. Its behaviour towards one antibiotic could not simply be used to predict its behaviour towards another. This is an important lesson: antibiotic resistance cannot always be explained by labelling an enzyme as simply powerful or weak. Its effects depend on the antibiotic, the molecular features of the enzyme and the broader biology of the bacterium. These findings do not mean that PDC-16 alone explains carbapenem resistance. Other mechanisms, including reduced antibiotic entry and the activity of drug-efflux pumps, can also contribute.

From understanding enzymes to finding better treatments

If enzymes can help bacteria defeat antibiotics, could we develop medicines that stop these enzymes from working? One strategy is to identify beta-lactamase inhibitors. These compounds interfere with the enzyme, allowing a partner antibiotic to retain its

> *"A larger active site does not necessarily make an enzyme more effective; subtle molecular changes can reshape how it interacts with antibiotics."*

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activity against bacteria that would otherwise be able to inactivate it. However, different beta-lactamases respond differently to inhibitors, making it important to understand the molecular features that determine inhibitor recognition.

Our study explored this challenge using computational approaches to identify compounds that might interact with the PDC-16 active site. Although some candidates showed promising predicted interactions, subsequent biochemical experiments demonstrated that favourable computational binding predictions did not necessarily translate into effective enzyme inhibition.

This distinction is crucial. A molecule may appear to fit into an enzyme's active site on a computer but still fail to block its activity in the laboratory. Computational screening is therefore a useful starting point, not proof of inhibitor activity. Candidate molecules must undergo experimental testing to establish whether they inhibit the enzyme, can reach their target inside bacterial cells, are safe and offer meaningful benefits in infection models and, ultimately, clinical studies.

Future perspectives: Where can structural biology take us?

The future of antibiotic resistance research depends on connecting molecular discoveries with practical medical needs.

First, studying more beta-lactamase variants will help researchers understand how bacterial enzymes adapt to different antibiotics. Comparing their structures, activities and evolutionary changes may reveal patterns that are difficult to identify from genetic information alone.

Second, advances in structural biology, computational modelling and artificial intelligence could help scientists identify promising inhibitor candidates more efficiently. These approaches may guide the design of molecules that interact with important regions of an enzyme, including regions that differ between variants.

Third, researchers must investigate how these enzymes function inside living bacteria. A purified protein studied in the laboratory provides valuable information, but bacterial cells are complex systems. Membrane permeability, efflux pumps, gene regulation and other resistance mechanisms can influence whether a treatment succeeds.

Finally, collaboration among structural biologists, microbiologists, medicinal chemists, clinicians and public-health researchers will be essential to translate molecular discoveries into useful treatments.

Conclusion: Small molecular changes, big consequences

Antibiotic resistance is a global challenge, but understanding it begins with fundamental scientific questions:

How does a bacterial enzyme recognise an antibiotic?
How do small changes in its structure influence its activity?
And can these insights help us find better ways to block it?

Our research on PDC-16 illustrates why these questions matter. Its constrained active-site architecture and substrate-dependent kinetic behaviour highlight the complexity of the relationship between protein structure and antibiotic resistance.

Structural biology does not immediately produce new medicines, but it provides essential molecular knowledge that can guide future research and the search for better therapeutic strategies.

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Dr. Immanuel Dhanasingh is an Associate Professor at the Centre for Bioseparation Technology, Vellore Institute of Technology (VIT), Vellore, Tamil Nadu, India. His research focuses on how proteins work and how bacteria develop resistance to antibiotics. He leads a research group studying the three-dimensional structures of bacterial proteins and exploring molecules that could block their activity. His work aims to support the development of better treatments against antibiotic-resistant infections. Ms. Liji Selvanose Susy is a Research Scholar at the same institute. Her research focuses on protein production, purification, and molecular cloning. Together, they study how bacterial enzymes reduce the effectiveness of antibiotics and explore new ways to overcome antibiotic resistance.

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From engineered tissues to organ-on-a-chip: How bioengineering is transforming biomedical research and regenerative medicine



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Biomedical engineering is increasingly at the interface of living and engineered systems. Many biological questions are still difficult to answer using standard two-dimensional (2D) cell culture. Cells in 2D cultures lack the three-dimensional (3D) architecture, cell-cell interactions, extracellular matrix cues, and dynamic physical environment that would be present in a tissue in the body. Animal models are useful, but there are inevitably differences between species that can limit the translation of findings from the animal to the human. This has led to the development of experimental systems that can mimic some of the features of human tissues, while being measurable, controllable, and amenable to engineering design. Tissue engineering and organ-on-a-chip technologies are two approaches to this, which take a very different perspective. Tissue engineering involves the combination of cells, biomaterials, and biochemical or physical cues to generate a tissue-like environment. Organ-on-a-chip systems use micro-fabricated devices and precisely controlled micro-environments to recreate aspects of organ physiology such as fluid flow, mechanical stimulation, and cell-cell interactions. The two approaches together provide a much wider range of opportunities to study disease, assess potential therapies, and explore regenerative strategies.

Engineering the cellular microenvironment

A tissue is more than just a aggregation of cells. Its behavior is determined by the ECM (extracellular matrix), cellular architecture, biochemical signals, and mechanical properties of the tissue. Biomaterials and scaffolds provide a framework for cells to attach to, communicate with each other, and perform their tissue-specific functions. The materials used must therefore be selected with regard to the specific biological application in mind. The research from my lab is a good example of this. We examined soy protein isolate silk-fibroin nanofibrous scaffolds and evaluated their potential for skin tissue regeneration. This

involved the characterization of the scaffolds and assessment of their wound healing potential in an animal model (Varshney et al., 2020). We have also examined psyllium husk-gelatin blends as potential bioinks and used rheological and mechanical characterization to assess those (Biofabrication and 3D bioprinting take this design process further by enabling the precise spatial positioning of cells and biomaterials. However, printability is not the same as biological suitability. A formulation must be printable but also must maintain cell viability, allow for the transport of oxygen and nutrients, and allow for tissue maturation. Rheological and mechanical characterization in conjunction with biological testing is therefore a necessary step. Our FRESH (Freeform Reversible Embedding of Suspended Hydrogels) work demonstrated the use of a chitosan bio-ink to produce complex geometries, including a human tri-leaflet heart valve and a section of a coronary arterial tree. The use of a temporary embedding medium to support the printed structure allows for the maintenance of complex geometries during the fabrication process. This work illustrates how engineering approaches can be used to expand the range of geometries possible with hydrogel-based materials.

Organ-on-a-Chip technologies

Organ-on-a-chip systems combine micro-engineering with cell culture via the use of micro-channels and chambers to control fluid flow, create interfaces between different cell populations, and deliver precisely defined chemical and mechanical stimuli. The degree to which a given system can mimic the relevant features of a particular organ (e.g., liver, lung, intestine, and nervous tissue) will vary according to the design of the system. The importance of being able to control the physical conditions is nicely illustrated by our earlier work using a microfluidic system to study surfactant secretion in alveolar type II epithelial

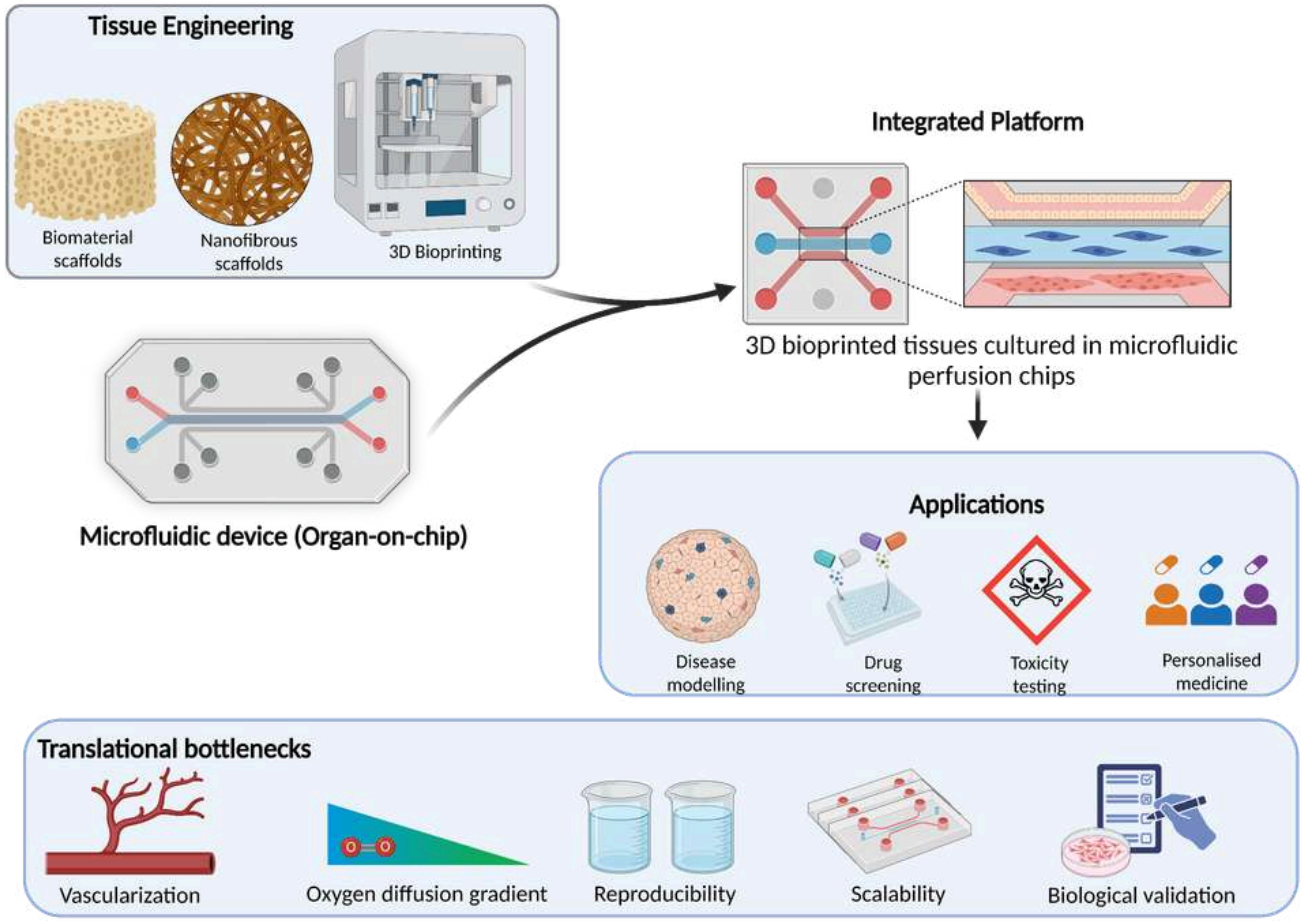


Figure 1: Tissue engineering approaches, including biomaterial scaffolds, nanofibrous scaffolds, and 3D bioprinting, are integrated with microfluidic platforms to develop physiologically relevant tissue models. These platforms support disease modelling, drug screening, toxicity testing, and personalized medicine, while addressing major translational bottlenecks such as vascularization, oxygen diffusion, reproducibility, scalability, and biological validation.

cells. In the study, we revealed that the level of flow-induced wall shear stress could be used to modulate aspects of the surfactant secretory process in these cells, with the effect being different in different cell models. That study is a good example of one of the key benefits of the microfluidic approach, which is, the ability to systematically vary a physical stimulus and observe the resulting cellular response in a controlled manner. Organ-on-a-chip systems are increasingly used for drug screening, toxicity testing, and disease modelling. The effectiveness of the cells depends on their quality, the physiological functions they can reproduce and the validation of these functions against relevant biological references. In this context, studies of brain-on-a-chip demonstrate how microfluidic engineering can advance neuronal modelling, in collaboration with my group, developed a microfluidic platform enables the incorporation of 3D neuronal networks for site-specific neuro-pharmacological treatment and optical monitoring of neuronal activity. Another study by our Poddar et al. (2019) and my group reported on compartmentalized microfluidic devices for low-density primary neuronal culture. This study provided the possibility to study neuronal growth, axonal development and cellular interactions. Together, these studies highlight the potential of microfluidic technologies for creating more functionally relevant and tightly controlled neuronal models for biomedical research and drug discovery.

Organ-on-a-chip systems are being used for a range of applications, including drug screening, toxicity testing, and disease modelling. Their usefulness in any of these areas will depend on the quality of the cells used, the physiological functions that are being represented, and the extent to which they have been validated against appropriate biological references. It is important to note that a chip is not a miniaturized version of a whole human organ. Most systems can only replicate a subset of the features of the organ in question, and other functions may be greatly simplified or entirely absent. The application of the technology and the degree to which it is reproducible will be paramount.

Where the technologies meet

The combination of tissue engineering and organ-on-a-chip design is a promising avenue. Engineered scaffolds and bioprinted tissues can provide the spatial organization and matrix cues that are important, and microfluidic platforms can provide the controlled flow, dynamic stimulation, and defined interfaces between cell populations. The potential is that you can then go on to study how the engineered tissue responds to a more physiologically relevant environment. Our own work in the area of liver tissue engineering is a case in point. We recently looked at the performance of lyophilized, electrospun, and 3D-printed psyllium husk polysaccharide-based scaffolds in the culture of primary rat hepatocytes. All the scaffolds supported cell viability, aggregate formation, and the secretion of liver-specific functional markers (albumin and urea). The level of functional performance was dependent on the scaffold fabrication method. This highlights the need to go beyond simply looking at the look and feel of the tissue and the physical structure to also assess relevant biological function. When combined with microfluidic control, such scaffolds could form the basis for studying the impact of matrix architecture, fluid flow, and cell organization on tissue function. More generally, engineered liver and neural tissues could eventually be used to study selected organ-organ interactions in both health and disease. The added value of such integrated platforms will of course have to be demonstrated through direct experimentation and comparison to appropriate reference models rather than simply being assumed from their complexity.

For biomedical engineering, this convergence means that we need to bring together materials science, cell biology, microfabrication, fluid mechanics, imaging, and quantitative analysis around a common biological question. You have to define what function the model is going to be trying to reproduce, you have to define how you're going to measure that function, and you have to have the evidence that it's actually doing it.

Translational bottlenecks

There are still a whole host of issues in this area. With thick tissues, you can easily get gradients of oxygen and nutrients unless you have appropriate transport mechanisms in place In thick engineered tissues, oxygen and nutrient gradients can readily develop unless adequate transport mechanisms are incorporated to ensure sufficient distribution throughout the tissue. . Vascularization, long-term maturation, and maintenance of tissue-specific function are all still issues. There is a lot of variability in the cell sources, biomaterial batches, fabrication conditions, and device geometries, which will all have an impact on reproducibility. For comparison of results between labs to be meaningful, it is absolutely essential that there are standard protocols and shared be-

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> *"Tissue engineering and organ-on-a-chip technologies are complementary: one organizes cells and materials, while the other provides controlled environments to investigate tissue function."*

nchmarks. There is a need to strike a balance between model complexity and cost, throughput, ease of use, and scalability. You cannot simply assume that more complex models are necessarily more biologically relevant. You need to validate the model for the application of interest. Progress in this area will require working closely with clinicians, regulatory scientists, and end users to ensure that the platforms we develop are actually going to address some real biomedical problems.

Future prospects for more predictive bioengineering

Tissue engineering and organ-on-a-chip technologies are revolutionizing biomedical research by allowing the creation and study of human-relevant biological systems in a more accurate and precise manner. The aim is not simply to build tissue-like structures or miniaturized organs, but to develop tools that can answer biological questions and, when properly validated, inform decisions about therapy and regenerative medicine. In the field of biomedical engineering, the opportunity is to combine engineering control with biological insight and to judge the success of an innovation on the basis of the quality, reproducibility, and relevance of the knowledge that it generates.

A call to action: From engineering innovation to biomedical impact

To truly unlock the potential of tissue engineering and organ-on-a-chip, we need to go beyond individual technologies and work towards integrated, reproducible, and biologically validated systems. The next step involves strengthening collaboration among bioengineers, cell biologists, clinicians, and regulatory scientists to establish shared standards for model validation and ensure that emerging platforms are scalable, reliable and suitable for biomedical applications.

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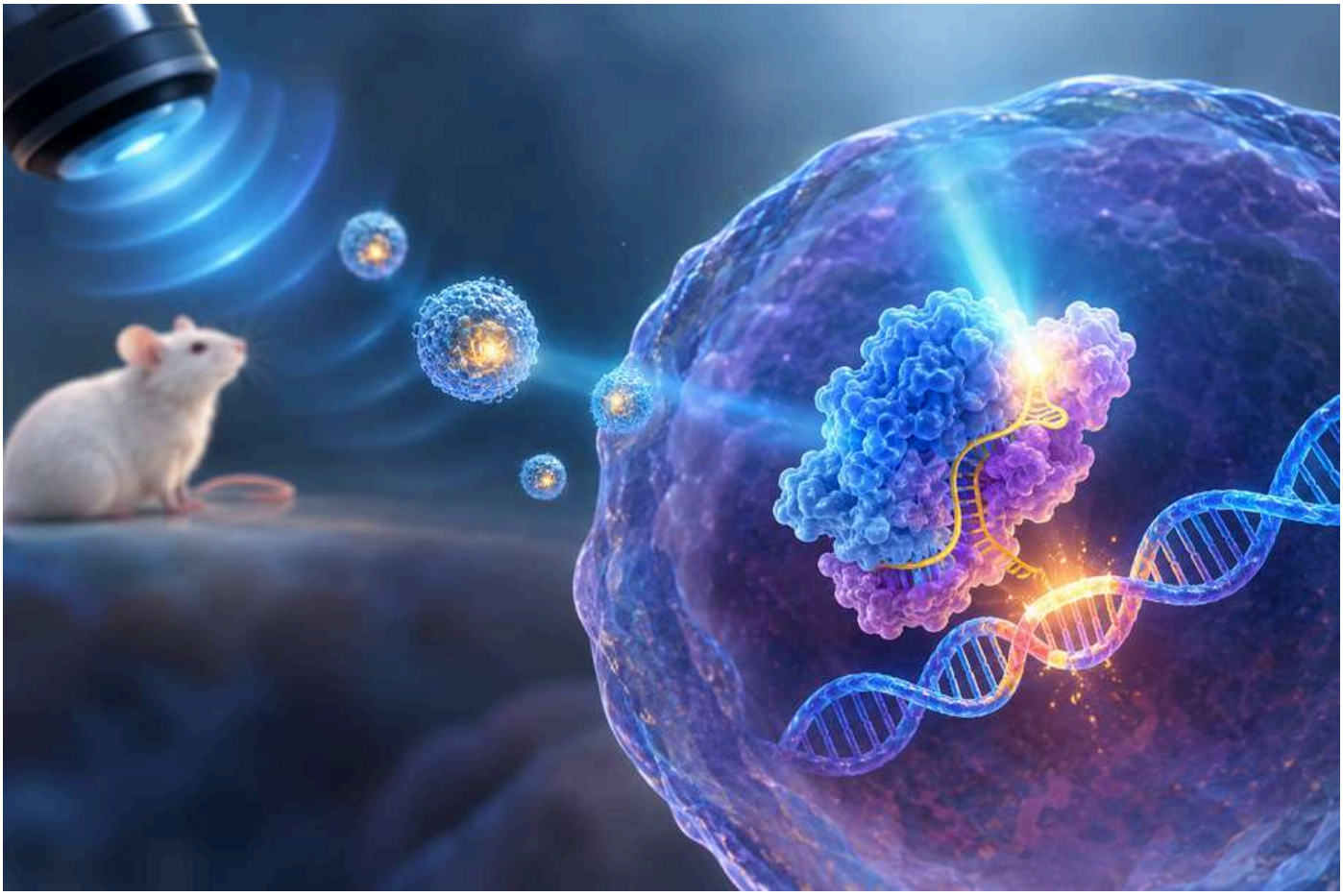
Behind every discovery lies a story of curiosity, perseverance, and wonder. Science unfolds through relentless research and bold explorations into the unknown. These are the journeys that shape our understanding of the world—and beyond.

| By Dr. Manas Prusty

CRISPR ON COMMAND: SWITCHING GENE EDITING ON WITH LIGHT AND SOUND

One quiet morning at Stanford University in California, Emily Reyes noticed something strange on the computer screen in her laboratory. Two groups of mice had received instructions for the same tiny gene -editing tool, but the results were very different. In one group, the tool was already changing DNA. In the other, it seemed to be waiting. “What if we could decide exactly when it starts working?” Emily asked her colleague, Marcus Bennett. They were studying CRISPR, a technology that allows scientists to make changes to DNA, the instruction book inside living cells. It could one day help researchers treat certain diseases, but there was a difficult problem: once a gene editor enters the body, how can scientists control where and when it works? If it edits DNA in the wrong place, unwanted changes may occur. And if researchers want to reach a deep part of the brain, shining light through the skin may not be enough. Emily wrote a question in her notebook: could they build a gene editor that stayed quiet until it received a signal from outside the body?

The team began with a compact gene-editing tool called Cas12f. Like a pair of molecular scissors guided by a set of directions, it can find a chosen DNA sequence and cut it. But the researchers wanted more than scissors; they wanted scissors with an on-and-off switch. They attached Cas12f to a light-sensitive protein called pdDronpa. In darkness, two pdDronpa parts joined together and blocked the gene editor from reaching its target. When cyan light reached the system, the parts separated, opening the way for Cas12f to work. “It’s like putting a cover over the blades,” Marcus explained. “The light lifts the cover.” The team also faced another challenge: fitting the gene editor and its guiding instructions into a tiny delivery vehicle called an AAV, a virus-based carrier used to bring genetic material into cells. Larger gene-editing systems can be difficult to fit into one such vehicle. Because Cas12f was small, the team developed a design that could carry the gene editor and its guide RNA together in a single AAV particle. That meant the pieces could arrive as one package instead of depending on separate deliveries.

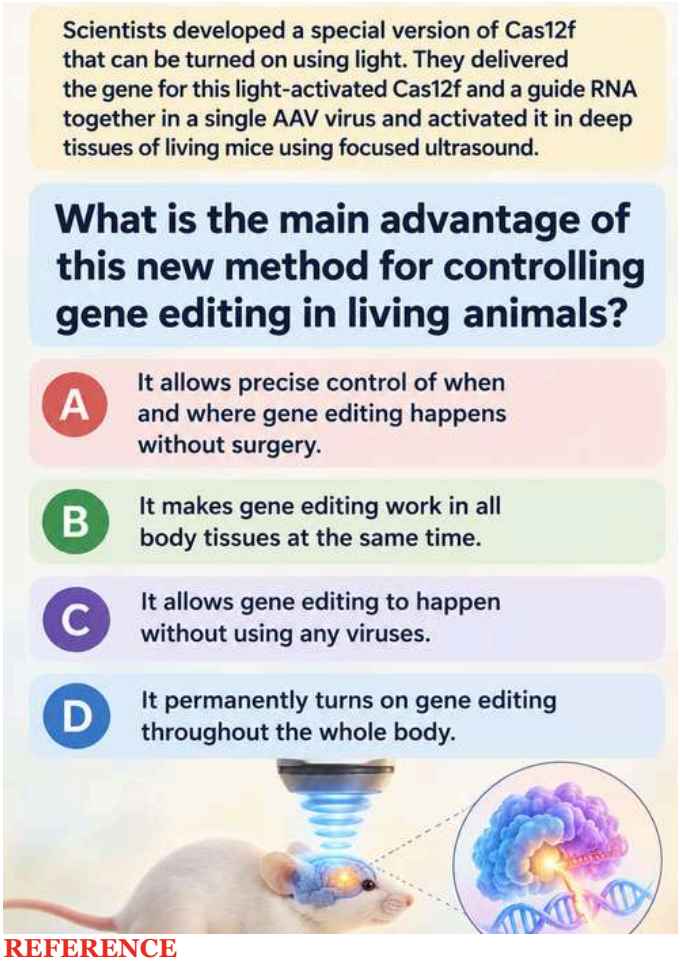


| By Dr. Manas Prusty

At first, the plan worked when the researchers shone cyan light on cells in the laboratory. But Emily kept thinking about the brain, hidden behind skin, bone and layers of tissue. How could light reach a target deep inside a living animal without surgery or an implanted lamp? Then the team explored a surprising partner: focused ultrasound. They used tiny mechanoluminescent particles, which can produce light when stimulated by mechanical force. After these particles were introduced into mice, the researchers directed focused ultrasound at a chosen area. The ultrasound stimulated the particles, creating light where it was needed. That light could switch on the photosensitive gene editor nearby. The team tested the approach in mouse skeletal muscle and found that gene-editing activity rose in the stimulated area. When they directed the ultrasound at one leg, the signal increased there while the other leg remained largely quiet. Later, they targeted specific regions of the brain. The results suggested that a signal sent from outside the body could activate gene editing in selected deep tissues, without needing to implant a light source.

The next challenge was to make the system respond more strongly to light. The first version did not edit DNA as efficiently as the researchers wanted under every condition. So they improved the light-sensitive protein and tested other versions of Cas12f. One improved combination, called ps2-eCas12f1, showed much stronger activity after illumination than the original design. In a muscle experiment, DNA sequencing found changes at the target site in 47.2% of the tested DNA copies after light stimulation, compared with 1.5% without illumination. The researchers also tested a gene called TTR in the liver. It carries instructions for making a protein in the blood, and the team found that stimulating the improved system could reduce that protein. Focused ultrasound and light both activated gene editing, although ultrasound-triggered editing in the liver was generally less efficient than direct cyan-light stimulation. The results were exciting, but Emily knew that a successful mouse experiment was not the same as a proven treatment. The study did not establish that this approach was safe or effective in people. Scientists still need longer studies of unintended DNA changes, immune responses, and how precisely the system can target different tissues.

That evening, Emily returned to the animal results and examined the unstimulated areas. The discovery was not simply that the team had made a gene editor work. They had developed a way to keep it switched off and activate it at selected places and times, using light directly or light generated by focused ultrasound deep inside the body. The compact system could be delivered in one AAV particle, and mouse experiments showed that editing could be controlled in muscle, brain and liver tissue. Marcus imagined doctors guiding a gene-editing signal toward a particular tissue instead of activating it throughout the body. Emily reminded him that this remained a possibility to investigate, not a treatment ready for patients. The team would need to improve precision, study long-term safety and test reliability across tissues. As she closed her notebook, one thought stayed with her: if scientists could teach a molecular tool to wait for the right signal, what other powerful changes might one day be guided with sound or light?



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| By Dr. Avijit Das

63°C AND STILL GROWING: THE AMOEBA THAT CHALLENGED LIFE'S LIMITS

One quiet morning in California's Lassen Volcanic National Park, a team of scientists stood beside a steaming geothermal creek, wondering what kind of life could survive there. The water was warm enough to make ordinary living things struggle, and the ground released heat from deep beneath the Earth. "We know bacteria can survive incredible temperatures," said fictional researcher Elena Torres, peering into a sample bottle. "But what about creatures with more complex cells? Surely there must be a limit." Her colleague Mateo Ruiz smiled as he watched the water ripple over dark stones. They were searching for tiny organisms that lived in this unusual environment, where temperatures along the creek ranged from about 49°C to 65°C. They collected water, sediment and slippery material called biofilm from different places. Back in the laboratory, they prepared the samples and encouraged the microscopic life inside them to grow. Days passed, and then something unexpected appeared under the microscope: tiny, shape-changing creatures moving through the samples. They were amoebas, single-celled organisms often found in water and soil. But these were not ordinary amoebas. The scientists had discovered a creature that seemed comfortable in a world most other complex cells would find dangerously hot. What was its secret?

Elena and Mateo began carefully testing the mysterious amoeba, which the team eventually named Incendiamoeba cascadensis, meaning a "fire amoeba" connected to the Cascade mountain range where it was discovered. At first, the researchers needed to answer a simple but important question: was the creature merely surviving the heat, or could it actually grow and divide? Surviving and reproducing are not the same thing. A cell might remain alive for a short time under harsh conditions without being able to complete its life cycle. The team placed cultures at different temperatures and watched what happened over several days. At 42°C, the

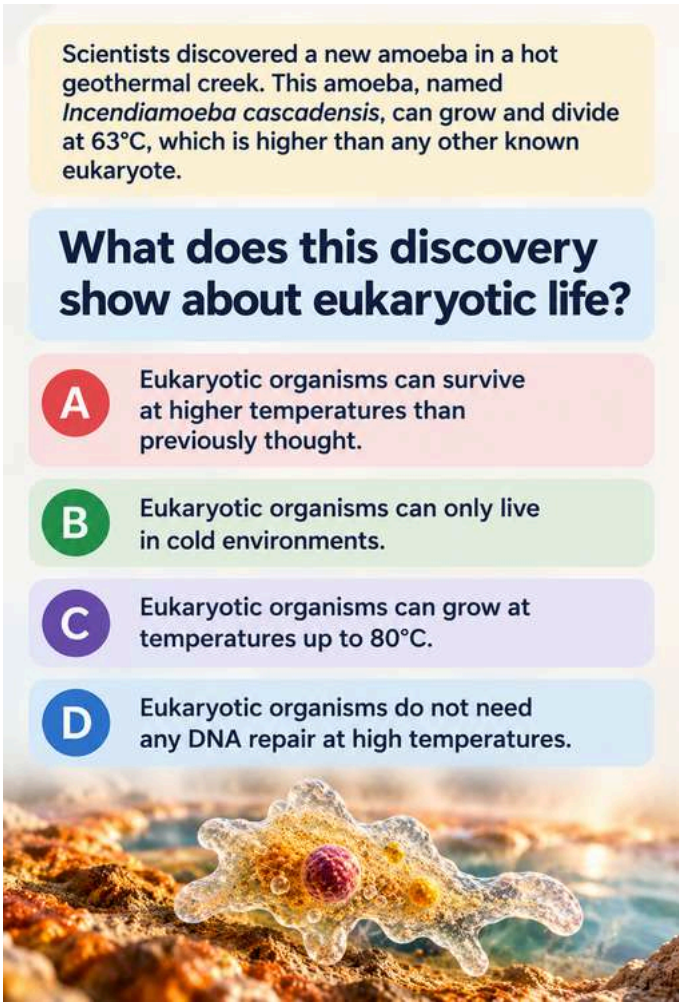


| By Dr. Avijit Das

amoeba could grow, but at 40°C or below, it showed no growth. Its best growth occurred between 55°C and 57°C. Then came the result that made the scientists look twice: the amoeba continued to reproduce at 63°C. At 64°C, it could no longer grow. To be certain that they were witnessing real cell division, rather than cells simply stretching or changing shape, the researchers used advanced microscopy to examine the dividing cells. They saw the structures involved in separating the cell's genetic material. The evidence showed that the amoeba was completing cellular reproduction at 63°C. Elena leaned back from the microscope. For decades, scientists had generally regarded 60°C as the upper growth limit for eukaryotes organisms whose cells contain a nucleus. This tiny creature had pushed that boundary higher.

But another mystery remained. How could a cell with delicate internal structures continue functioning in such extreme heat? High temperatures can cause proteins to lose their proper shapes, damage DNA and disturb the membranes that keep a cell's inner parts working together. Elena imagined the amoeba as a tiny factory operating beside a furnace. Every machine inside it had to keep working, even when the heat threatened to make the parts fail. To investigate, the researchers compared the amoeba's genetic activity at 48°C and 61°C. They studied which genes were more active at the higher temperature and looked for clues in the proteins the organism could make. Several protective systems stood out. The amoeba increased the activity of genes involved in managing proteins, including helpers that can prevent damaged proteins from clumping together or help them fold into the right shapes again. Genes linked to DNA repair and the maintenance of genetic information also became more active. Another important change involved membrane trafficking, the movement of materials between compartments inside the cell. Elena explained the finding to Mateo: "It is not just one defence. It looks as if several systems change together when the temperature rises." The team also found that many predicted proteins had chemical features that might help them remain stable under heat. In particular, their surfaces showed more positively charged building blocks, a pattern also seen in some heat-loving bacteria and archaea. The results offered clues, but the researchers knew that clues were not the same as proof of exactly how each protection worked.

Researchers discovered a remarkable heat-loving amoeba that challenges decades-old scientific assumptions. Near its preferred 57°C, the organism actively explores its geothermal creek environment by shifting between long, worm-like forms and shorter, irregular shapes. When temperatures exceed its growth limit, it enters a dormant state by forming protective cysts, allowing some cells to survive brief exposure up to 70°C before recovering. Genetic matches in New Zealand and Yellowstone suggest this creature belongs to a wider, poorly understood group of extreme heat-lovers. Crucially, the team proved a eukaryotic organism can complete cellular reproduction at 63°C, shattering previous biological limits. While Elena and her colleagues must still study its mysterious genes and potential biotechnology applications, this single microscopic discovery reminds scientists to never underestimate where hidden life might still thrive.



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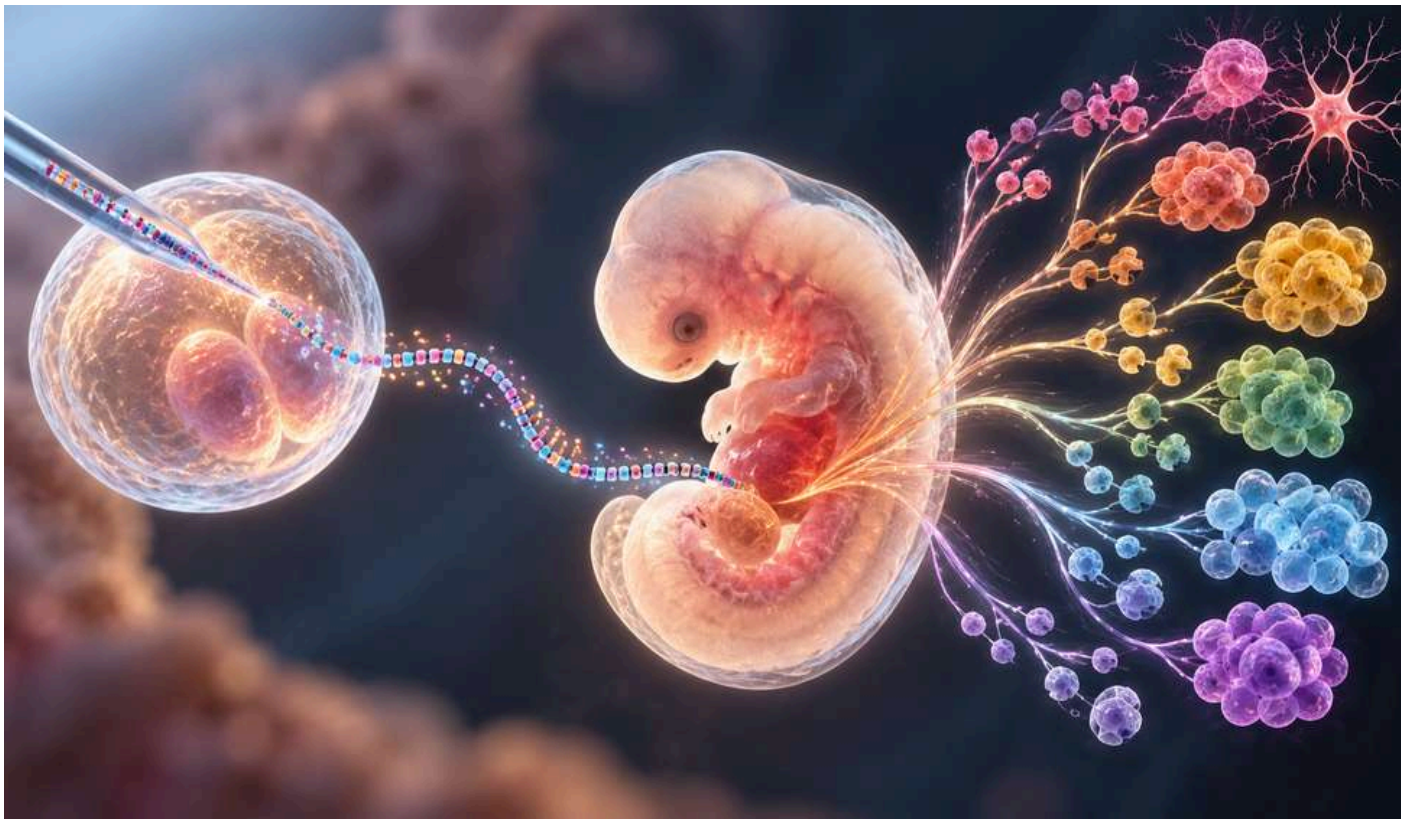
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| By Dr. Sourav Kumar

THE DNA TYPEWRITER: THE SECRET STORY OF A MOUSE WRITTEN IN ITS DNA

One quiet morning in a laboratory at the University of Washington in Seattle, geneticist Elena Brooks stared at a picture of a tiny mouse embryo on her computer screen. It looked like a small, ordinary collection of developing cells, but Elena had a question that would not leave her mind. "How could we ever know where every cell came from?" she asked her colleague, Marcus Reed. As a mouse grows, its cells divide again and again, forming the brain, heart, muscles, blood, and every other part of the body. Scientists can study these cells, but taking a cell out of an embryo is like opening a book and tearing out a page: they can see what the cell is doing now, but its earlier story is much harder to recover. Years ago, researchers had carefully mapped the development of a tiny transparent worm by watching each cell divide under a microscope. A mouse, however, was a far greater challenge. Its developing body was hidden from view, and its cells could not simply be watched from beginning to end. Elena wondered whether the cells themselves might hold clues to their past. What if scientists could build a recorder inside them one that kept writing as the embryo grew?

Marcus turned to a new technology called DNA Typewriter. "Imagine a notebook that writes itself," he explained. "Every time a cell divides, we want it to leave a mark that its descendants can inherit." DNA is the molecule that carries an organism's genetic instructions. The researchers designed a system that could add small, planned sequences of DNA to a special recording area, like typing symbols onto a strip of tape. As cells divided, these marks could accumulate in a particular order. Later, scientists could read the marks and use them to work out which cells were related. The team introduced the system into mouse embryos at the one-cell stage, when each embryo was still just a fertilized egg. But Elena knew that getting the recorder to work inside a living, developing animal would not be easy. Would the marks survive as cells multiplied? Would there be enough information to distinguish one branch of the family tree from another? To investigate, the researchers allowed the embryos to develop and then examined one embryo at a stage called E13.5, roughly halfway through pregnancy in a mouse. They collected its cell nuclei and used a method called single-nucleus RNA sequencing to study gene activity while also recovering the DNA records. It was like reading two kinds of information from the same tiny biological world: what each cell was doing and the marks it had inherited from its ancestors.

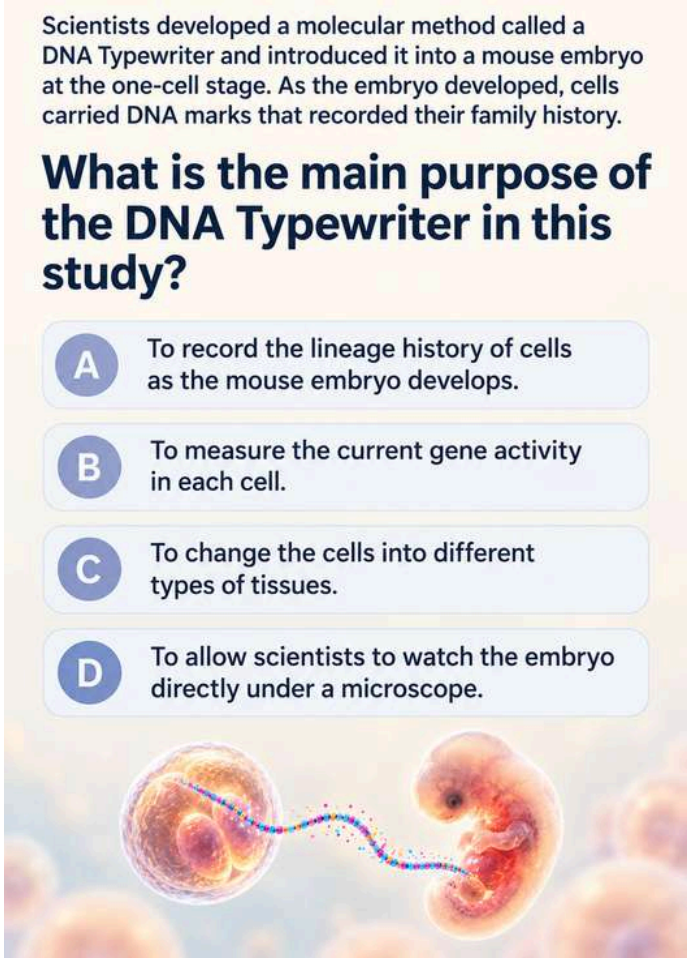


| By Dr. Sourav Kumar

The results began to reveal a remarkable history. The researchers obtained gene-activity profiles from more than 1.5 million nuclei, then used the DNA records to reconstruct relationships among the cells. One embryo became the focus of a detailed analysis. The team built a family tree containing 1,281,141 cells, tracing their relationships back toward the original fertilized egg. Elena leaned closer to the screen. Branches spread across the display, showing how cells were connected through earlier generations. The records even contained a striking clue from the embryo's earliest days: a burst of editing at the two-cell stage helped researchers distinguish the descendants of the embryo's first two cells. The team called these founding cells A and B. Their descendants contributed to many of the same kinds of tissues, although not in exactly equal numbers. As development continued, some groups of related cells became more numerous than others. The researchers also found that closely related cells often shared the same cell type more frequently than would be expected by chance. Some pairs of related cells had different identities, providing clues about how cells moved toward their final roles. "So the tree is not just a list of divisions," Marcus said. "It can help us investigate how development unfolds." Still, Elena knew the tree was not a perfect diary. Some DNA marks were missing, the recording rate changed over time, and parts of the reconstructed history were less certain than others. The team had built an extraordinary map, but some paths remained blurred.

As they studied the map, the researchers began asking deeper questions. Could the pattern of related cells help reveal when different cell types became linked during development? Their analyses identified groups of cell types that tended to appear together within branches of the tree. Many of these relationships matched familiar features of mouse development, including connections among cells that form particular tissues and organs. The team also explored the possible identities of ancestral cells whose own gene activity had not been directly measured. By comparing their descendants with a large atlas of developing mouse cells, the researchers inferred likely ancestral states for many internal branches. These inferred histories recovered several known developmental transitions, but they were predictions drawn from the data, not direct recordings of every cell's identity at every moment. Elena was excited, yet careful. The experiment involved one mouse embryo, and the tree represented only about ten percent of the embryo's estimated cells. The method also had technical limits: the recorder did not work at a constant speed, and the placement of some cells in the tree was uncertain. Further experiments in independent embryos would be needed to test how well the findings held up. Even so, the study showed that a molecular recorder could preserve enough inherited information to reconstruct a remarkably large cell-family tree inside a developing mammal.

That evening, Elena studied the DNA records, which revealed clues about each cell's ancestry and eventual role. Although the study did not capture the complete history of mouse development, it offered a new way to trace how cells acquire different identities. Future improvements could reveal more about these developmental journeys. Elena wondered: if DNA could uncover hidden histories in one developing mouse, what other secrets might living cells hold?



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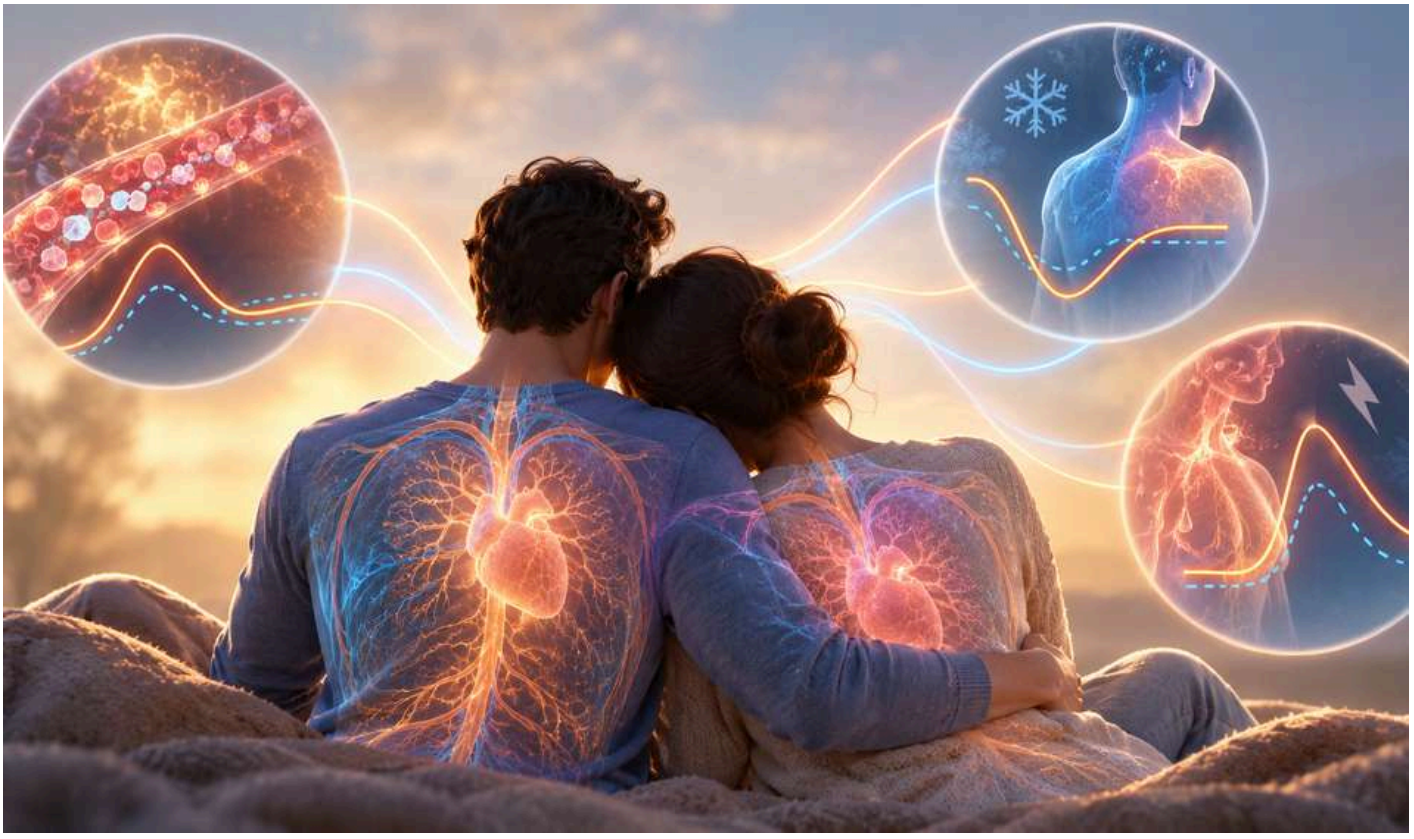
| By Dr. Sivan Friedman

THE HIDDEN POWER OF BEING TOGETHER: HOW OUR BODIES RESPOND TO THOSE WE LOVE

One quiet morning in Jerusalem, Yael sat beside her partner, Amir, in a university research laboratory. A simple question had brought the scientists there: could being close to someone change the way the human body works, even when we cannot feel the change? People often think of the body as a machine that works alone. The heart beats, the lungs breathe, and the body controls its temperature without asking anyone for help. But what if the presence of someone we trust could make some of these tasks easier? The research team at the Hebrew University of Jerusalem wanted to investigate this mystery. They called the idea Social Physiology the study of how the body may regulate itself more efficiently when another person is nearby.

Yael and Amir were not the real researchers, but imagine them as two volunteers taking part in the study. Their first challenge seemed almost too ordinary to reveal a scientific secret: eating bread. The researchers asked participants to eat a measured amount of white-wheat bread containing 50 grams of carbohydrates, a type of nutrient the body breaks down into sugar for energy. Then, over the next two hours, the team measured their blood glucose levels at several time points. Glucose is the sugar that travels through the blood,and the body must carefully control how much is present. This balancing act is called homeostasis, the process of keeping the body's internal conditions within a healthy range. Yael completed the test once alone and once with Amir nearby. The researchers repeated the same comparison with many participants, carefully measuring what happened instead of relying on how anyone felt.

The scientists had a prediction, but they needed evidence. After the bread challenge, glucose levels rose, as expected. Yet the measurements revealed a curious pattern: when participants were with their close partners, the rise was smaller and glucose levels returned toward their usual range more quickly. The team compared the body's overall response across time, not just a single reading. A smaller response that settled sooner suggested the body had met the same demand with less overall regulatory effort. The result was not simply a story about food. The researchers tested their idea in another way, too. Participants spent five minutes in a cold room, then returned to a warmer room while the team tracked skin temperature. Again, the body's temperature response was generally more efficient



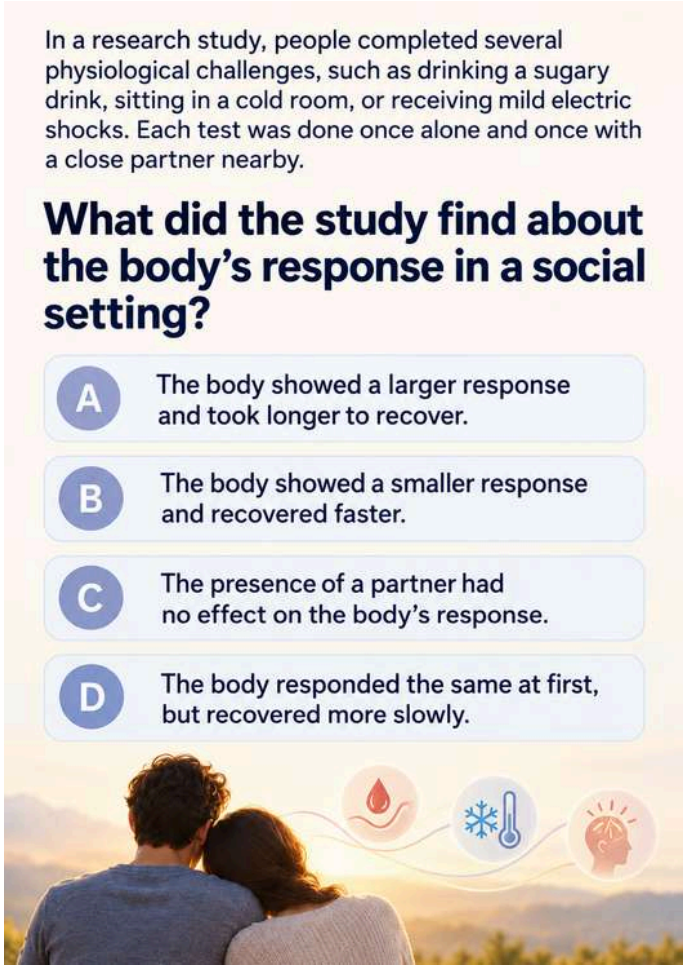
| By Dr. Sivan Friedman

when a close partner was present. Could the same quiet influence reach other parts of the body?

To find out, the team studied how adults responded to mild electric shocks used as a stress challenge. They measured changes in the skin linked to sweat-gland activity, which can reveal the body's level of arousal. They also examined infants during a brief, unpleasant sound, comparing their responses when their mothers were present with responses when they were not. Across these different tests, the researchers found evidence that physiological regulation was more efficient in the social condition. The pattern appeared in adults and infants, and it could not be explained simply by lower measured stress during the bread test. Touch also did not fully explain the results, although it may have contributed to temperature regulation. The findings supported a broader idea: the body does not always work as an isolated system. However, the scientists were careful not to claim that every person benefits in the same way, or that every social situation is helpful. Some participants showed smaller benefits, and a few showed the opposite pattern. The study revealed a real effect, while leaving its exact biological pathways for future research.

As the results came together, the laboratory's original question grew into something much larger. Perhaps close relationships offer more than comfort, cooperation, or protection; perhaps being near someone trusted can also help the body manage everyday demands with less effort. Over long periods, even small improvements might matter, but this study did not prove that companionship prevents disease or guarantees better long-term health. More research will be needed to understand why the effect occurs, how stable it is, and whether it applies to different relationships and situations. For now, the scientists had uncovered a subtle connection between social life and the body's inner balance. Yael looked at Amir and wondered how much of the body's work happened silently, beyond either of their awareness. Perhaps one of the body's quietest secrets is that, sometimes, being together changes more than we know.

The discovery invites us to look differently at ordinary moments: sitting beside a loved one, sharing a quiet meal, or simply enjoying each other's company after a long day. What often feels like a simple, routine gesture actually carries subtle physical significance beneath the surface. These shared experiences may do far more than bring fleeting happiness or emotional warmth; they may quietly influence how our bodies respond to everyday challenges, minor stressors, and sudden change. Even brief moments of familiar closeness seem to leave a measurable imprint on our physical state. Although many scientific questions remain unanswered regarding the exact physiological mechanisms at play, the findings remind us that human connections are deeply intertwined with our fundamental biology. Social warmth is not merely a psychological comfort or a cultural habit, but an active part of how we regulate ourselves from within. Perhaps the next time we sit beside someone we love, hold a familiar hand, or linger in unhurried conversation, we might remember that being together is not just emotionally comforting, but may also help our bodies maintain their delicate internal balance.



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| By Dr. Poulami Chakraborty

WHEN MONEY TELLS A HIDDEN STORY: UNCOVERING FINANCIAL ABUSE THROUGH BANK RECORDS

One rainy morning in London, Eleanor Whitmore stared at a computer screen and wondered whether money could tell a story that people were afraid to speak aloud. Outside, buses splashed through wet streets, and office workers hurried past shop windows. Inside a research office, rows of numbers filled her screen: payments, savings, loans, cash withdrawals and changes to bank accounts. Eleanor was part of a fictional research team investigating an important question: could ordinary banking records reveal the hidden signs of financial abuse? Financial abuse happens when someone controls another person's money, limits their access to it or uses debt to take away their independence. Unlike a physical injury, it may leave no visible mark. Someone can appear to be living an ordinary life while quietly losing control of every pound they earn. Eleanor knew that stories from survivors had already helped people understand this problem. But she wondered whether their financial records might reveal patterns that were difficult to see in interviews alone. If money could remember what people could not safely say, what might it reveal?

The question was serious, but finding an answer would not be easy. Financial difficulties can happen for many reasons. A person might lose a job, become ill, face unexpected bills or struggle with rising living costs. A missed payment alone could never prove that abuse had occurred. Eleanor and her colleagues needed a careful way to compare people whose experiences of financial abuse had been disclosed to a bank with people who had no known disclosure. The real study used anonymized records from a major UK retail bank, protecting customers' identities. Researchers examined 5,428 women who had disclosed experiences of financial abuse to the bank and compared their financial patterns with those of 15,602 similar individuals in a control group. The groups were matched using demographic and social and economic information from seven years before disclosure. The team studied 373 different financial measures, including savings, borrowing, spending, missed payments and account-management activity. Eleanor imagined each record as a small window into someone's daily life. Yet no single window could show the whole picture. To understand the pattern, the researchers would have to examine thousands of details across many years.

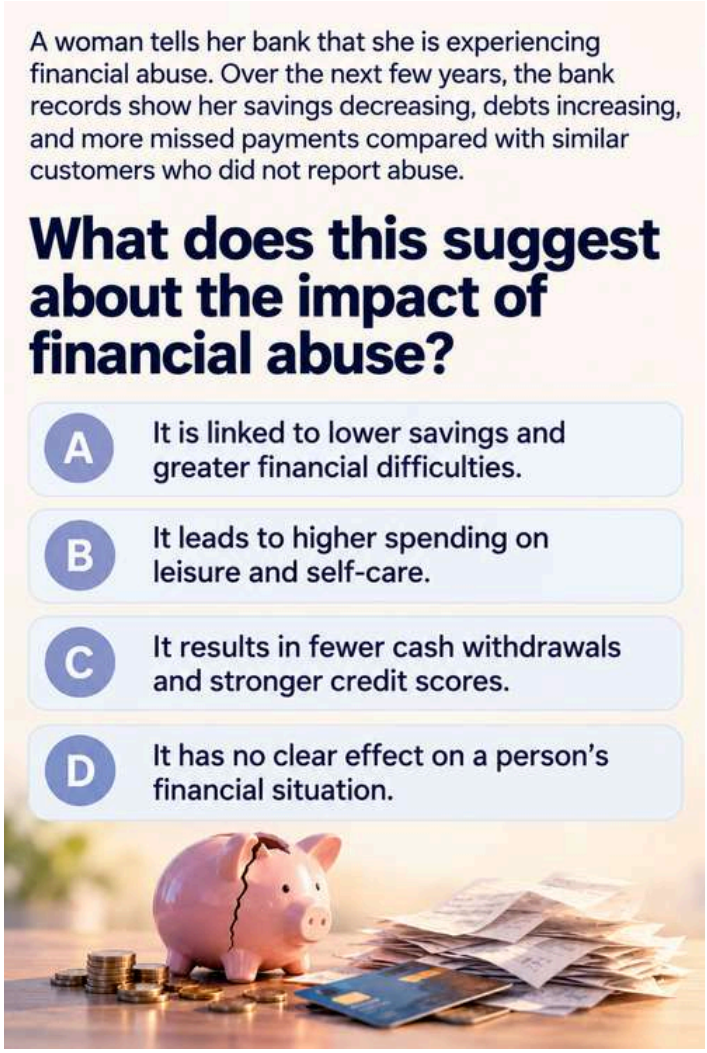


| By Dr. Poulami Chakraborty

As the analysis progressed, a troubling picture began to emerge. Compared with the matched control group, women who had disclosed financial abuse showed signs of growing financial pressure. Their savings were lower, while their debts and overdraft-related costs were higher. Missed automatic payments became more common, and credit scores declined. These were not merely numbers on a screen: missed payments can make borrowing more difficult, while damaged credit scores can create further barriers to financial recovery. The researchers also found differences beyond balances and debts. The women were less likely to spend money on some forms of self-care, including dental care and sport. They showed more activity involving cash withdrawals, taxi spending, password resets and address changes. Some also had higher legal expenses and were more likely to receive welfare benefits. Eleanor paused over the results. A password change might be routine for one customer, while for another it might be part of an effort to protect a bank account. A taxi journey could have many explanations, too. The meaning came not from one transaction, but from patterns across time and comparisons between groups. The study showed that banking data could reveal important signs associated with financial abuse, even when the abuse itself left no obvious physical evidence.

But Eleanor knew that an important discovery was not the same as a perfect answer. The researchers tested their findings using alternative comparison groups, including women experiencing similar levels of financial distress. Some differences remained, while others became smaller or no longer showed clear evidence of a difference. This mattered because financial hardship itself can affect spending, travel and everyday decisions. The study also had limits: it examined records from one bank, covered a maximum of seven years and relied on women who had disclosed their experiences. Some people experiencing abuse might never tell their bank, meaning the control group could include survivors whose experiences were unknown. And the analysis could not prove that financial abuse alone caused every observed financial difficulty. Eleanor understood that the numbers were clues, not verdicts. Still, the clues could help banks recognise when a customer might need support. With further research, carefully tested warning signs might help financial institutions identify vulnerability earlier, offer safer ways to manage accounts and connect people with appropriate services. Any such system would need to protect privacy and avoid treating a pattern as proof of abuse. The goal was not to judge customers, but to make it easier for people in danger to receive help.

That evening, Eleanor walked past London's glowing shop windows, reflecting on how easily financial abuse hides behind ordinary bank statements. Someone might buy groceries or pay bills while another person quietly controls their choices. The study exposed this hidden struggle, showing how financial records reveal depleted savings, rising debt, and changing behaviour. While data cannot identify every survivor or replace human support, everyday transactions might help institutions recognise unnoticed distress. Looking across the city, Eleanor wondered what other silent human struggles tomorrow's science might uncover within a simple set of numbers.



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| By Dr. Dhanashree Mundhe

WHEN AI TALKS, DO WE ACT? THE SURPRISING POWER OF A CONVERSATION

One rainy morning in London, a young researcher named Imogen Clarke opened her laptop and stared at a question that had troubled scientists for years. Could a conversation with artificial intelligence really change what a person did, or could it only change what they believed? Imogen was not one of the researchers conducting the study, but she imagined the question as a mystery waiting to be solved. People often said that AI could persuade them with clever arguments, facts, and friendly words. Yet agreeing with an idea was not the same as acting on it. A person might support protecting forests but never plant a tree, or worry about poverty but never donate to help a family in need. Scientists had already found that AI could influence people's opinions. What remained uncertain was whether those conversations could lead to real actions. Researchers working through institutions including the UK AI Security Institute and the University of Oxford's Oxford Internet Institute decided to investigate. Their challenge was simple to describe but difficult to answer: would people actually do something after talking to a machine?

The investigation began online, where thousands of adults living in the United Kingdom took part in two large experiments. Imagine a participant named Rhys Morgan, sitting at his kitchen table after work, opening a research survey on his computer. He was asked to discuss a real-world issue with an AI system. The topics varied, covering concerns such as nuclear disarmament, animal welfare, democratic reform, and protecting trees. In some conversations, the AI was instructed to persuade people to support a particular cause. Other participants chatted with AI about neutral subjects unrelated to politics. The researchers used several advanced AI models and recorded what happened afterward. Would Rhys sign a real petition? Would he choose to direct some available study money to the organisation behind a cause? The researchers measured people's opinions before and after the conversations, but they also looked beyond the screen's words. A person saying, “I agree,” was not counted as someone who had taken action. To count as signing, participants had to complete the actual petition process,



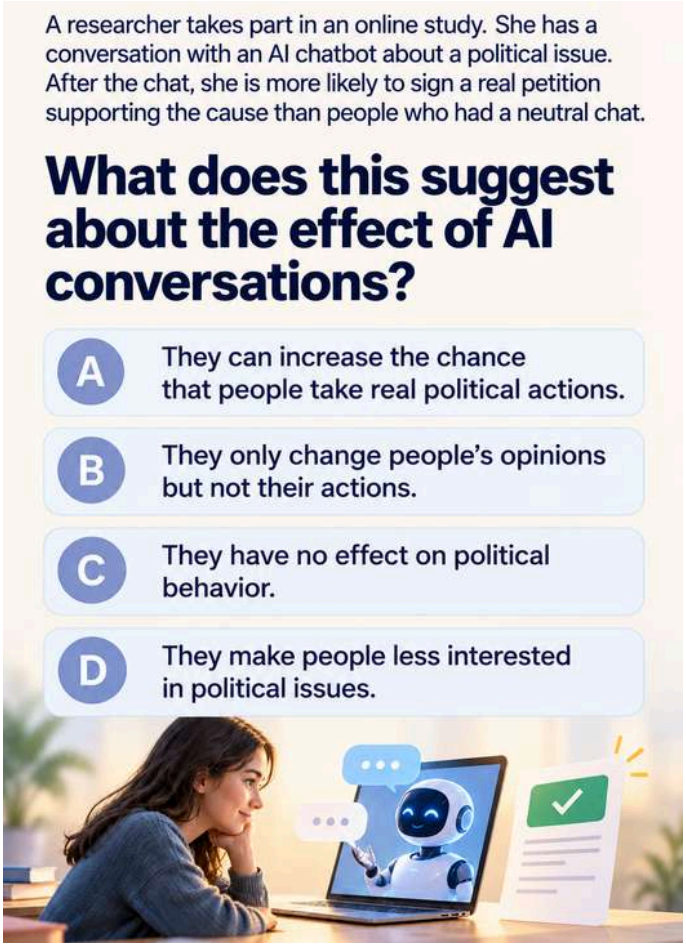
| By Dr. Dhanashree Mundhe

entering their details and confirming their signature. This distinction was at the heart of the mystery.

When the results arrived, the researchers discovered something striking. In both experiments, conversations with persuasive AI increased the likelihood that participants would sign petitions compared with the neutral-conversation group. In the second experiment, participants who had spoken with persuasive AI were 19.7 percentage points more likely to sign their assigned petition than those in the control group, after the researchers' statistical adjustment. The first experiment also found a meaningful increase. Some participants chose to direct more of their available study bonus to the organisation supporting the cause. The conversations were brief, lasting an average of about seven minutes in the first study. Yet they were followed by measurable differences in what people actually did. Rhys, in our imagined scene, might have closed his laptop believing that protecting trees mattered. But the scientists' real discovery was not simply that people could be convinced an issue was important. It was that a short AI conversation could also encourage a concrete action. The machine had not forced anyone to sign; participants could refuse or leave the process. Still, the pattern was clear enough to demand closer attention.

The next clue was even more surprising. The researchers compared changes in people's opinions with changes in their behaviour. They expected that the approaches that most strongly changed opinions might also be the approaches that best encouraged action. But the results did not show a reliable relationship between the two. Giving people more factual information often helped shift their attitudes, yet the information-focused strategy was not the strongest at encouraging petition signing. In the second experiment, the researchers tested eight approaches, including emotional appeals, making a clear action plan, reminding people of their identity, and combining several techniques. All eight increased petition signing compared with the control condition, and the combined approach produced the largest estimated effect. However, its advantage over the other strategies was modest. The findings suggested that changing someone's mind and helping them take action may be different challenges. A person can learn new facts and become more supportive without doing anything differently. Meanwhile, someone who already agrees with a cause may simply need a clear invitation to act. The study did not explain every reason people responded as they did, and the experiments took place in a paid online-survey setting, which may not reflect everyday conversations.

As researchers examined their results, the mystery deepened: if a brief AI conversation shapes real decisions, society must understand what people do afterward. While paid studies involving petitions or bonuses differ from high-stakes real-world choices, future research must determine when these effects occur and how to prevent unwanted influence. For Imogen, measuring agreement alone misses a vital nuance. AI can sound convincing without altering behavior, or spur action without shifting beliefs—a critical distinction for democracy and responsible technology. Even after the screen goes dark, the resulting choices linger, leaving us to wonder how much of our decision remains truly ours.



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| By Dr. Priyangana Deb

THE OCEAN THAT GREW QUIET: A HIDDEN WORLD LOSING ITS LIFE

One moonless night in the Gulf of Mexico, marine scientist Claire Bennett leaned over the side of a research vessel and stared into the black water. Somewhere beneath her, hundreds of metres below the waves, an enormous world was moving through the darkness. Tiny fish, shining creatures, shrimp-like animals and mysterious squid travelled through the deep ocean, hidden from sunlight and human eyes. Every night, many of these animals rose towards the surface to feed, then returned to deeper water as daylight approached. Claire had spent years studying this secret world, but a question now troubled her. What if the ocean's deepest living communities were changing in ways nobody had noticed? The Gulf was vast, and its deep waters seemed almost endless. Surely, she thought, such a huge ecosystem could withstand almost anything. Yet the latest samples were telling a different story. The nets were bringing fewer animals aboard, and the instruments were detecting something unexpected. The deep ocean was becoming quieter—not because the water had stopped moving, but because fewer living creatures seemed to be there.

To understand what was happening, Claire and her fellow researchers began comparing records from two periods. Their investigation focused on the deep-pelagic ecosystem of the Gulf of Mexico, the enormous region of open water below the surface. The team had collected thousands of samples, using research vessels, specialised nets and scientific equipment. An intensive survey in 2011 provided an important starting point. Further surveys were carried out between 2015 and 2023. The scientists used the same type of net and standard methods to make the comparisons as fair as possible. They also used an instrument called a scientific echosounder. It sent sound pulses into the water and recorded the echoes returning from animals below the ship. Stronger echoes could indicate more organisms, while weaker echoes could suggest fewer. It was like listening for a hidden crowd in a dark room without being able to see its members. The tea-

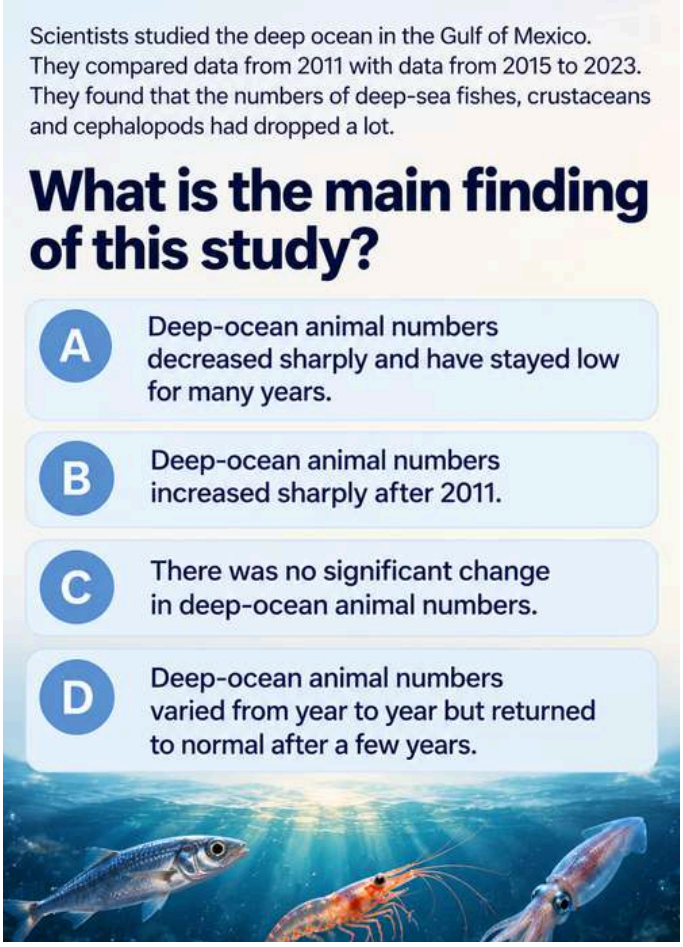


| By Dr. Priyangana Deb

m also examined genetic information from selected fish species to investigate whether the changes in animal numbers were accompanied by changes in genetic diversity —the variety of genetic differences within a population. Claire knew that one unusual sample could mislead them. But when different methods began pointing towards the same answer, she realised they might be uncovering a much larger problem.

The results were startling. Comparing the 2011 samples with those collected from 2015 to 2023, the researchers found that deep-pelagic animal populations had suffered severe declines. Fish abundance had fallen by about 63.5%, crustaceans by 62%, and small cephalopods, including squid relatives, by around 59.7%. Some especially important groups had declined even more. Krill-like animals, which provide food for many other creatures, had fallen by approximately 72.8%. Lanternfishes, small fish that serve as prey for larger predators, had declined by about 62.9%. The sound recordings supported the findings from the nets, giving the scientists independent evidence that the changes were real. Another discovery made the situation more worrying: large concentrations of prey, sometimes called “patches,” had become rare. These gatherings matter because predators may struggle to find enough food when animals are spread thinly across the ocean. Genetic analyses added another piece to the puzzle. Two of the three lanternfish species examined showed evidence of declining genetic diversity over parts of the study period, although their patterns differed. Claire looked at the results again. The ocean had not become empty, but an extraordinary amount of life had disappeared from the samples. And the decline had happened with astonishing speed.

The next question was the hardest: why had this happened? The researchers examined possible explanations, including changes in water temperature, oxygen levels, food supply and sampling methods. They found no natural environmental change that matched the scale and timing of the decline. The evidence instead pointed towards human activity. One event stood out: the Deepwater Horizon oil spill in 2010, which released millions of barrels of oil into the Gulf. The decline in deep-pelagic life began around 2011 and was clearly visible in later surveys. The researchers therefore identified the spill and its associated effects as the most plausible explanation, while recognising that the study could not prove every part of the causal chain directly. Oil-related contamination can harm marine animals, and traces of pollution have been found in deep-sea organisms years after the disaster. The consequences may extend beyond individual species. Deep-pelagic animals help move carbon from surface waters into the deep ocean as they feed and migrate. They are also an important source of food for larger fish, seabirds, whales and other predators. When their numbers fall, the effects can travel through the food web. Claire imagined a network of invisible threads connecting creatures across thousands of metres of water. If too many threads broke, the whole system could change. The ocean’s enormous size had not protected it as well as people once believed.



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| SCIENCE DESK |

Tiny Pores, Big Possibilities: Toward Intelligent Nanodevices



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| Scientific Profile |
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AREAS OF EXPENTISE
Electrohydrodynamics • Nano and Microfluidics • Interfacial flows • Bio-microfluidics



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AREAS OF EXPENTISE
Micro/nano-fluidics • Electrokinetic transport • Computational Fluid Dynamics • Nanoscale Energy harvesting

OUTLOOK

Can a tiny pore behave like an electronic switch without changing its physical structure? Could such microscopic channels help develop intelligent sensors and energy-efficient computers? In this article, Dr. Pramodt Srinivasula and Dr. Doyel Pandey explore the fascinating world of nanopores and explain how electric fields can control ion movement in unexpected ways. They discuss their research findings, potential applications and the challenges of turning these discoveries into practical technologies. Their insights raise an intriguing question: Could tiny pores become the building blocks of tomorrow's intelligent technologies?

Q *What are nanopores, and why is controlling the movement of ions through these tiny channels important in science and technology?*

A Nanopores are extremely tiny openings, often just a few nanometres wide, in thin membranes made from biological or synthetic materials. While conventional membranes are widely used to filter and separate substances, nanopores open up an entirely different world of possibilities. At such remarkably small dimensions, the movement of ions and molecules can be controlled in unusual and sometimes counterintuitive ways, revealing physical phenomena that are hardly noticeable at larger scales.

Understanding and harnessing these phenomena could enable technologies that once seemed futuristic. For example, nanopores and their clusters could serve as building blocks for brain-inspired computing systems that process information through the movement of ions rather than electrons, potentially offering more energy-efficient alternatives to conventional electronics which can be directly embedded in the physical and bio-physical systems. Other promising applications include harvesting electricity from saline water or wasted heat in the exhaust systems, by harnessing the differences in salt concentration or temperature across the membranes, respectively. Nanopores had also been an important pillar for developing highly sensitive biosensors capable of detecting individual DNA or protein molecules.

The exciting prospect is that nanopores could evolve from simple passages for transporting species into intelligent, controllable components of future technologies.

Q *How do electric fields influence the movement of ions through nanopores, and what makes this process challenging to understand?*

A Electric fields offer a powerful way to control ions i.e., electrically charged atoms or molecules. Within nanopores, these fields not only drive ions through tiny openings but also influence their distribution and interactions with the surrounding liquid and pore walls.

Interestingly, such electrical effects occur even in

everyday liquids containing dissolved salts. However, at larger scales, their influence is largely confined to extremely thin regions near surfaces. At the nanoscale, these regions become comparable to the pore dimensions, allowing previously surface-confined phenomena to govern the behaviour of the entire fluid, giving rise to unusual transport characteristics.

Understanding these phenomena presents two major challenges. First, strong electric fields and molecular interactions among ions, water and pore surfaces make their collective behaviour difficult to predict. Second, precisely fabricating nanopores and experimentally characterizing their transport behaviour requires sophisticated nanotechnology and a deep understanding of nanoscale fluid physics.

Q *Your research suggests that even a structurally uniform nanopore can behave differently in opposite directions. What causes this unusual behaviour?*

A Traditionally, directional ion transport in nanopores has been achieved by introducing asymmetry through cone-shaped geometries, patterned surface charges, or different salt concentrations across the pore. Such asymmetry enables diode-like behaviour, allowing ionic current to flow more readily in one direction than the other, a property valuable for future ionic circuits.

Our research explores an emerging alternative: voltage-gated nanopores, inspired by electronic transistors. An additional electrode, called a gate, surrounds the pore and controls its surface potential. While an axial electric field drives ions along the pore, the gate independently controls the electrical conditions across its width. Through mathematical modelling and simulations, we discovered that these electrical controls interact to create a nonuniform ion distribution along the pore, despite its uniform geometry and surface potential. Remarkably, adjusting the gate voltage can control directional ion transport and unusual fluid-flow patterns, opening possibilities for actively programmable nanopores.

Q *What does it mean when a nanopore selectively allows certain ions to pass or permits electrical current to flow more easily in one direction?*

A The distribution of ions within a nanopore, and how they respond to an applied electric field, can become asymmetric along its length due to either the pore's geometry or an externally controlled gate voltage. By manipulating this asymmetry, nanopores can act as extremely tiny, controllable filters, allowing certain ions to pass more readily than others. For example, a pore may favour positively charged ions over negatively charged ones. This property is known as ion selectivity. Even more interestingly, some nanopores allow electrical current to flow more easily in one direction than in the opposite direction, even when the applied voltage has the same magnitude. This phenomenon, called ionic current rectification, is similar to how an electronic diode works in conventional electrical circuits. Such behaviour in nanopores could serve as miniature ionic diodes, switches and other functional components for future technologies that process information or control molecular transport.

Q *What were the most important findings of your study, and how do they change our understanding of ion transport at the nanoscale?*

A Our study revealed two important insights into how electric fields govern ion and fluid transport through nanopores.

First, we identified a novel mechanism through which electric fields acting along and across a nanopore interact to create an uneven ion distribution, even in structurally uniform pores. This hidden electrical asymmetry gives rise to unusual phenomena, including selective ion transport, diode-like electrical conduction, directional fluid-flow preferences, and even tiny circulating flows called vortices within the pores.

Second, we developed a mathematical framework that characterizes these transport behaviours through a single measure of electrical asymmetry parameter. This provides a common basis for understanding and potentially comparing disparate asymmetry mechanisms in nanopores with different geometries, surface properties, or gate voltages.

Together, these findings advance our understanding from observing unusual nanoscale phenomena to explaining and predicting their underlying mechanisms, enabling the rational design of nanopores with tailored functions.

Q *Could these findings help develop better sensors, filtration membranes, or other nanotechnology-based devices? What practical applications do you*

foresee?

A Absolutely. One of the most exciting advantages of voltage-gated nanopores is their ability to be actively controlled through electrical signals, rather than having functions fixed by their physical structure. Our mechanistic understanding, combined with predictive mathematical models, opens a promising path towards what we envision as intelligent nanopores.

Imagine a nanopore that detects a molecule passing through it and instantly adjusts its electrical conditions to capture, release or examine it further. Integrating nanopores with artificial intelligence or machine-learning controllers could eventually enable such adaptive, real-time operations at sub-micron seconds.

These capabilities could transform highly sensitive biosensors for detecting individual DNA or protein molecules, and brain-inspired computing systems that process information using ions instead of electrons. Integration with conventional semiconductor electronics could further enable compact, energy-efficient devices combining ionic and electronic functions.

Although still emerging, these possibilities offer an exciting glimpse into how fundamental discoveries could shape tomorrow's intelligent technologies.

Q *What challenges remain in translating these theoretical findings into real-world technologies, and what are the next steps in your research?*

A One of the biggest challenges is bridging the gap between designing nanoscale fluid transport systems and emerging advances in nanofabrication. Although sophisticated nanofabrication techniques exist, integrating them with predictive physical models to develop practical, reliable, reproducible and economically viable technologies remains challenging.

Our research addresses this gap in two complementary directions. First, we are developing advanced mathematical models that connect



Figure 1. Nanopore-based DNA transcription and biosensing.

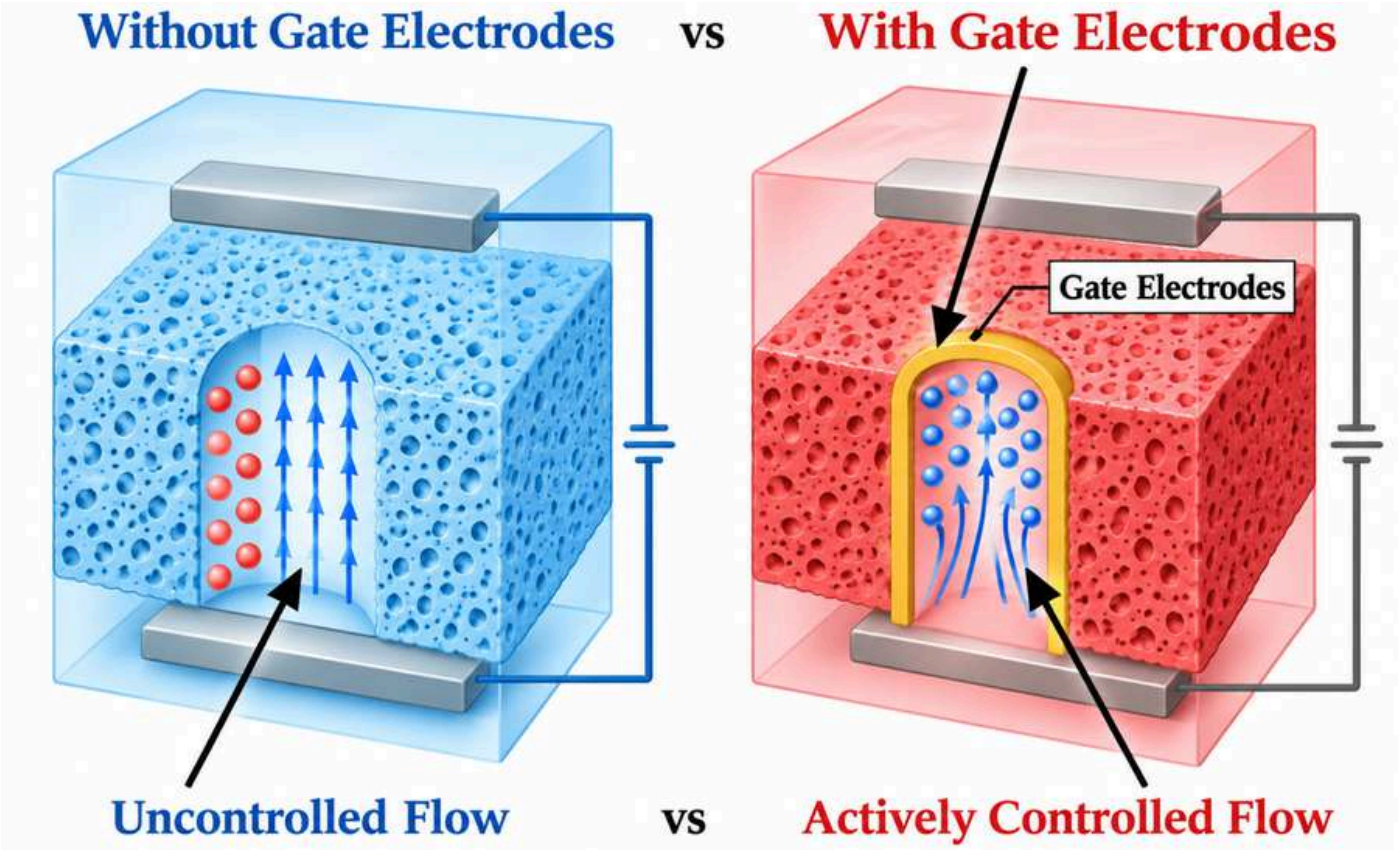


Figure 2. Graphical abstract comparing ion and fluid transport through a conventional nanopore and a voltage-gated nanopore.

molecular-scale interactions with the collective movement of ions and fluids at continuum scale. Incorporating the influence of water molecules and their interactions with ions and surfaces could significantly improve the reliability of nanofluidic device design. Second, we are exploring ways to integrate specialized nanofluidic device fabrication techniques with established semiconductor manufacturing processes, enabling affordable, large-scale production. What excites us most is the opportunity to combine fundamental scientific discovery with technological innovation. Beyond understanding the fascinating physics of the nanoscopic world, we aspire to translate these insights into practical technologies with the potential to transform the future.

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ABOUT THE AUTHORS

Dr. Pramodt Srinivasula is the Founder and Chief Technology Officer (CTO) of ElectroSoft Labs, Mumbai, India. His research focuses on how liquids and charged particles behave under electric fields. He uses mathematical models and computer simulations to explore applications in nanotechnology, energy systems and advanced devices. Dr. Doyel Pandey is an Assistant Professor at the Indian Institute of Technology (IIT) Mandi, India. Her research focuses on how liquids, charged particles and heat move through extremely small channels. She uses mathematical modelling, computer simulations and artificial intelligence to explore applications in energy generation, biosensors and nanotechnology. Together, their research aims to better understand the behaviour of fluids and ions at tiny scales and use this knowledge to develop smarter, more efficient technologies.

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SCIENCE DESK

Beach Plastics and the Hidden World of Antibiotic Resistance



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AREAS OF EXPERTISE
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AREAS OF EXPERTISE
Microbiology • biotechnology • antimicrobial resistance

OUTLOOK

What is living on the plastic washed up on our beaches? Could a discarded bottle offer clues to the spread of antibiotic resistance? In this article, Athira A. S. and Dr. Toms C. Joseph explore the hidden microbial communities on plastic debris from four Kochi beaches. They explain what DNA sequencing revealed, how these communities differ from those on natural materials, and why finding resistance genes raises questions without proving a direct threat to human health. Their work invites us to look beyond visible litter and consider what beach cleanups alone might miss.

Q *Most people see beach plastics as litter that harms marine animals. What led you to investigate the invisible communities of bacteria living on this waste?*

A Plastic pollution is usually discussed in terms of visible litter and its effects on marine animals. But plastic also remains in the environment long enough for microorganisms to attach to it and form biofilms. These communities are important because some bacteria can carry genes associated with antimicrobial resistance or traits linked to colonisation and disease. We wanted to understand whether beach macroplastic debris larger plastic items commonly found on shorelines support bacterial communities that differ from those on natural materials found in the same places. Macroplastics have received less attention than microplastics in this context, even though they can persist on shorelines and provide extensive surfaces for microbial growth.

Q *How do bacteria settle on plastic and form communities on its surface? What makes plastic a suitable habitat compared with natural materials such as driftwood, seaweed, and shells?*

A When plastic lies in seawater or on a beach, bacteria and other microorganisms can attach to its surface. They produce a surrounding matrix and form a biofilm a community of microbes living together on a surface. Plastic's durability, surface texture and water-repelling properties enable it to persist in the environment and provide a suitable surface for microbial colonisation. Most plastics in the environment break down slowly and can persist as stable surfaces. However, plastic is not automatically a better habitat for every bacterium. Our study found that natural materials such as driftwood, seaweed and shells supported richer and more evenly distributed bacterial communities overall, while plastic communities tended to be more dominated by particular groups.

Q *Your team studied four beaches along the Kochi coast. How did you collect the samples, and how did DNA sequencing help you discover which bacteria and genes were present?*

A We collected samples during the pre-monsoon season, from April to May 2024, at Fort Kochi, Cherai, Puthenthode and Puthuvypin. At each beach, we surveyed four 100 m × 50 m transects and collected plastic debris, including bottles, packaging

and fishing-related items. We also collected natural inanimate materials driftwood, seaweed and shells—from the same transects for comparison. Samples from the transects were combined by substrate type to make eight composite samples: four plastic-associated samples and four natural-substrate controls. We extracted DNA from the biofilm material and used shotgun metagenomic sequencing, which reads DNA from the mixed microbial community. This allowed us to identify the organisms represented and screen for genes associated with antimicrobial resistance, virulence-related functions and other biological processes. It gives a broad picture of genetic potential, rather than proving that every detected gene is active.

Q *What were the main differences between bacteria living on plastics and those on natural materials? Did beaches with more human activity show different patterns?*

A Across the samples, Pseudomonadota was the dominant bacterial phylum, followed by Bacillota, Actinomycetota and Bacteroidota. Plastic-associated communities were more strongly dominated by particular groups, including Vibrio, Alteromonas and Pseudoalteromonas. Natural substrates generally supported a more even mix of taxa, including groups such as Streptomyces and Marinobacter. Statistical analysis indicated that substrate type significantly influenced community composition, whereas differences between beach sites were not statistically significant in the beta-diversity analysis. We also observed broader antimicrobial-resistance gene profiles on plastics from the more urban-influenced beaches, Fort Kochi and Cherai, than at Puthenthode and Puthuvypin. These patterns are consistent with a possible influence of human activity, but the study was a limited, pre-monsoon comparison and does not establish that human activity alone caused the differences.

Q *You found genes linked to antibiotic resistance. What does this mean in simple terms, and why might their presence on beach plastics be a concern?*

A Antibiotics are medicines used to treat bacterial

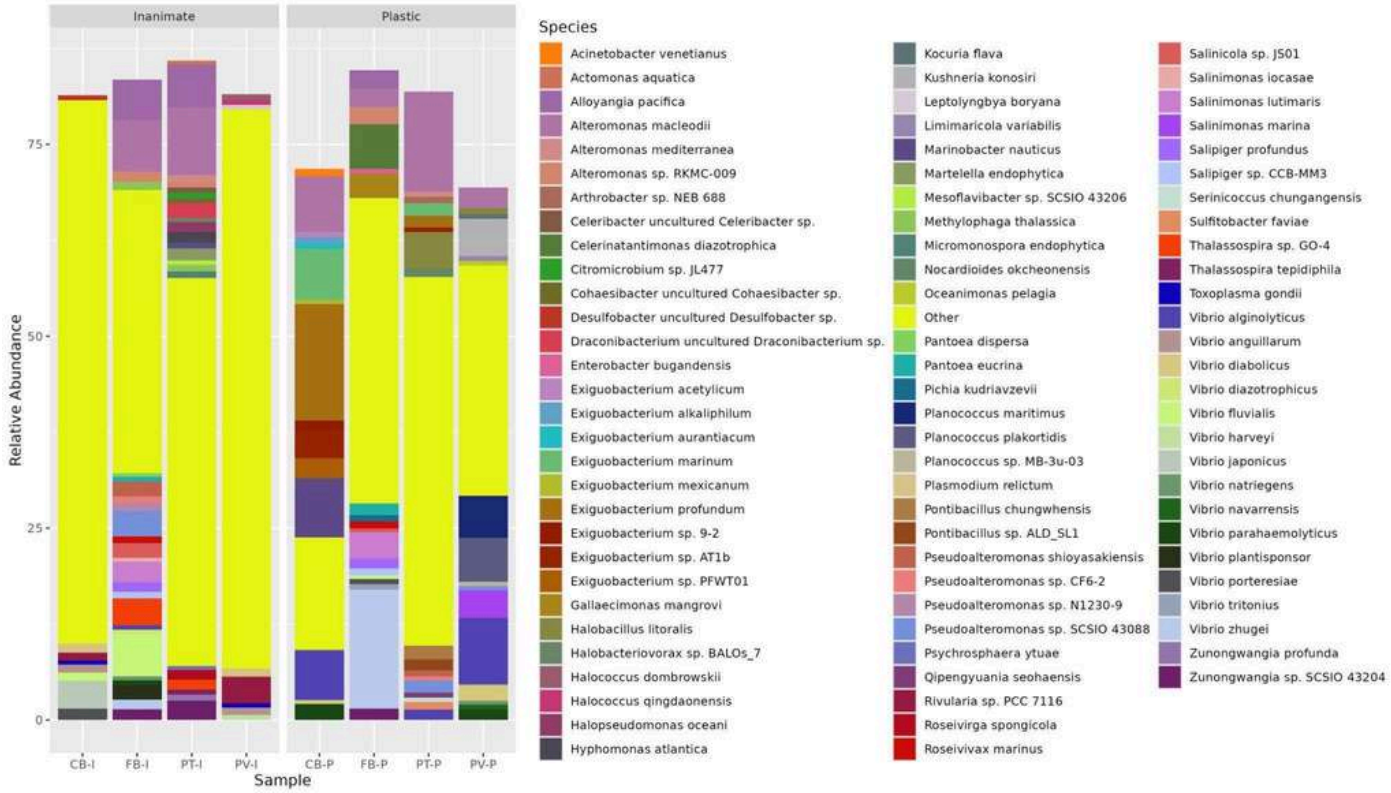


Figure 1. Relative abundance of bacterial communities associated with macroplastic (P) and natural inanimate (I) substrates collected from Fort Kochi, Cherai, Puthenthode and Puthuvypin, Kerala, India. The figure presents community composition at the phylum, class, genus and species levels, illustrating differences in bacterial community structure between plastic-associated biofilms and natural substrates. Abbreviations: FB, Fort Kochi Beach; CB, Cherai Beach; PT, Puthenthode Beach; PV, Puthuvypin Beach; P, macroplastic-associated sample; I, natural inanimate substrate sample. The y-axis represents relative abundance (%). Taxonomic names and classifications are provided in the figure legends.

infections. Antimicrobial resistance occurs when bacteria have genetic or other traits that allow them to withstand antibiotics that would otherwise inhibit or kill them. We detected 42 distinct antimicrobial resistance genes across the eight composite samples, representing eight antibiotic classes. Beta-lactam resistance genes accounted for approximately 42% of the detected resistance genes. Plastic-associated communities generally had broader resistance-gene profiles than natural substrates. In simple terms, plastic surfaces can provide a place where bacteria carrying these genes are present together. This raises an environmental concern because coastal water, waste and microbial communities are connected. However, detecting a resistance gene does not by itself demonstrate that it can move to a pathogen, that the bacterium is resistant in a clinical test, or that an infection will occur. Those possibilities need further investigation.

Q *Your study also detected genes associated with bacteria's ability to attach to surfaces or cause disease. What can these findings tell us about potential health risks, and what further evidence is needed before linking them to human infections?*

A The study identified 73 distinct virulence-associated genes, including genes linked to attachment, biofilm formation, secretion systems, siderophore production and toxin-related processes. Across samples, the number of virulence-related gene hits ranged from 1,264 to 2,046 per site, with higher counts in plastic-associated samples than in natural-substrate samples.

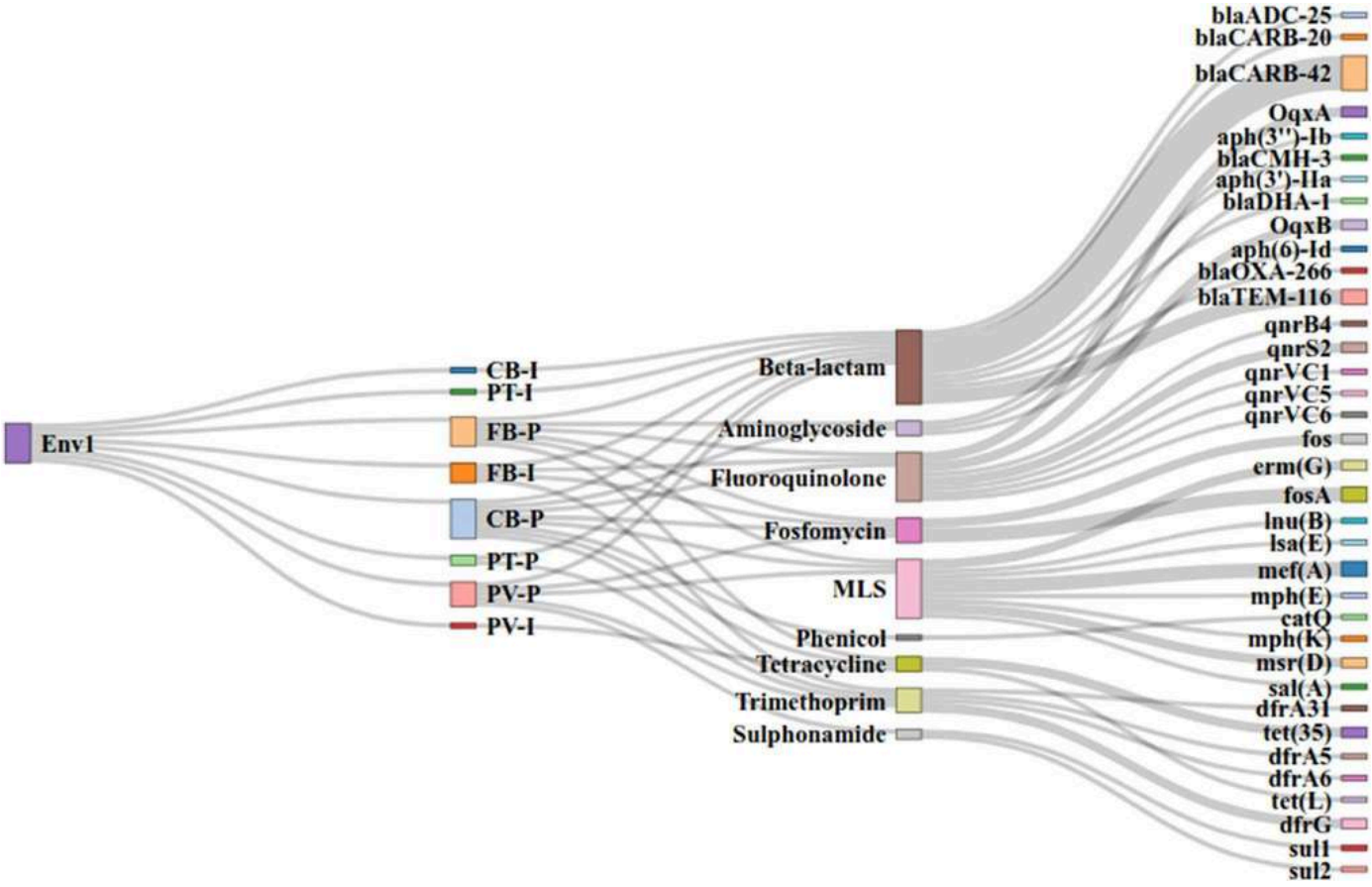


Figure 2. Distribution of antimicrobial resistance genes detected in macroplastic-associated and natural inanimate substrate samples collected from four beaches along the Kochi coast, Kerala, India. The Sankey diagram illustrates the detected resistance genes and their classification into antibiotic classes. The study identified 42 distinct antimicrobial resistance genes belonging to eight antibiotic classes, with broader resistance-gene profiles observed in plastic-associated communities. Abbreviations: Env1, environmental sample group as labelled in the original figure; FB, Fort Kochi Beach; CB, Cherai Beach; PT, Puthenthode Beach; PV, Puthuvypin Beach; P, macroplastic-associated sample; I, natural inanimate substrate sample; MLS, macrolide–lincosamide–streptogramin. ARG, antimicrobial resistance gene. Gene symbols (e.g., blaTEM-116, qnrS2, tet(35) and sul1) are shown as reported in the original analysis.

Such genes can help researchers identify microbial communities with traits that may be relevant to colonisation or interactions with hosts. They are indicators of potential, not proof that the organisms are causing disease. To connect these findings to human infections, further work would need to identify the host organisms carrying the genes, assess whether the genes are intact and expressed, test relevant bacterial isolates where appropriate, and investigate whether transmission pathways exist. Clinical or epidemiological evidence would also be needed before attributing infections to beach plastics.

Q *What should happen next? How could your findings inform beach cleanups, waste and sewage management, and future monitoring of antibiotic resistance along our coasts?*

A First, preventing plastic waste from entering coastal environments remains essential, alongside regular beach cleanups and better collection and disposal of fishing gear, packaging and other plastic items. Cleanups should be paired with effective sewage treatment and solid-waste management, because land-based waste and wastewater can introduce both plastics and microorganisms into coastal systems. Second, monitoring programmes could examine plastic and natural substrates together and track bacterial communities and resistance genes across seasons and locations. Larger studies with more independent samples, repeated sampling and complementary laboratory tests would help determine how stable these patterns are and whether detected genes are carried by viable bacteria. Finally, environmental data should be interpreted alongside public-health surveillance. Our findings support treating beach macroplastics as microbial habitats worth monitoring, while avoiding the conclusion that gene detection alone proves direct risk to people.

ABOUT THE AUTHORS

Dr. Toms C. Joseph studies microorganisms in seafood and aquatic environments at ICAR–Central Institute of Fisheries Technology, Kochi. His research explores antibiotic resistance, bacterial biofilms and food safety, alongside approaches to seafood preservation and sustainable packaging. His work connects the hidden microbial world with questions about environmental quality and human health. Athira A. S. is a PhD scholar at the same institute whose research focuses on microbial communities living on coastal plastic waste. Using DNA sequencing, she investigates how these communities differ from those on natural materials and examines the resistance-related genes they carry.

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| SCIENCE DESK |

Exploring Moringa as a Natural Approach to Osteoarthritis Management



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AREAS OF EXPERTISE
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OUTLOOK

Could the familiar drumstick tree offer clues to protecting ageing joints? And why might its pods deserve a closer look in osteoarthritis research? In this article, Dr. Snehal Ambadas Gojare explores how a Moringa pod extract influenced inflammation, movement and cartilage damage in a rat study. She explains what these findings suggest, which questions remain unanswered, and what scientists must establish before a promising plant extract can become a treatment for people.

Q *We hear a lot about managing arthritis pain. Why is it still so difficult to protect the joint itself?*

A Osteoarthritis (OA) is often called wear and tear, but the phrase undersells it. It is a disease of the whole joint: cartilage erodes, the bone beneath it remodels, osteophytes form and the synovial lining becomes inflamed. Global Burden of Disease estimates suggest that more than 600 million people are affected worldwide. That complexity is exactly what makes treatment difficult. Mechanical load, ageing, metabolic factors and persistent low-grade inflammation all feed the same process, and no single drug target captures them all.

What clinics can offer today is largely symptomatic. Paracetamol, oral non-steroidal anti-inflammatory drugs (NSAIDs) and intra-articular corticosteroids can ease pain and stiffness, but none has convincingly halted cartilage loss. Prolonged NSAID use carries gastrointestinal and cardiovascular risks, which matter most in older patients who often live with other conditions. By the time a joint replacement is discussed, the window for protecting cartilage has usually closed. This gap between symptom relief and genuine disease modification is why researchers keep looking at new candidates, including plants with long histories of traditional use. The aim is not to replace established care but to find safer options that could sit alongside it or, ideally, slow the disease itself.

Q *Moringa is something many readers know from their kitchens. How did it become the starting point for your research?*

A Moringa oleifera, known as the drumstick tree in English and shevga in Marathi, is familiar in Indian kitchens and village medicine alike. Leaves, flowers, seeds and pods are eaten, and preparations from the plant have been used traditionally for inflammatory complaints. Laboratory studies have reported antioxidants, anti-inflammatory and anti-arthritic activity, and several reports show that Moringa extracts can dampen NF-κB signaling, a central switch for inflammatory gene expression.

Yet most of this work has concentrated on leaves, flowers and seeds. The pod, which is widely consumed and easy to source, has received far less attention in the context of joint disease. Its low cost, wide availability and history as a food are attractive for a condition that is chronic, common and expensive to manage. That gap in literature was our starting point. We were also curious about whether a whole pod, hydroalcoholic extract, which is closer to how the plant is actually used than a purified compound, could show measurable effects on both symptoms and tissue structure.

Q *Once you began examining the pods, what did you find that helped you understand their potential?*

A Using phytochemical screening and high-performance thin-layer chromatography (HPTLC), we confirmed that our hydroalcoholic pod extract, which we abbreviate as HEMO, contains flavonoids

and phenolic acids. The fingerprint identified quercetin, kaempferol, gallic acid and chlorogenic acid.

Each of these has a plausible role in the joint. Quercetin and kaempferol are flavonoids known to scavenge free radicals and to restrain pro-inflammatory signaling. Gallic acid and chlorogenic acid are phenolic acids with antioxidants and anti-inflammatory properties reported in other disease models. Together they could act on two fronts: neutralizing reactive oxygen species before they damage chondrocytes and reducing the cytokine signals that push cartilage cells toward breaking down their own matrix. I should stress that this is a reasoned interpretation. We identified the compounds but did not test each one individually, so we cannot say which contributes most or whether they act together. Flavonoids and phenolic acids are not always efficiently absorbed after oral dosing, which is one reason why pharmacokinetic work matters so much later on.

Q *Before we get to your experiment, could you take us inside an arthritic joint? What is going wrong there, and where might an extract like this help?*

A Cartilage is a quiet tissue with little blood supply and limited capacity to repair itself, so it is vulnerable when the surrounding environment turns hostile. In OA, cytokines such as interleukin-1β (IL-1β) and tumor necrosis factor-α (TNF-α) prompt chondrocytes and synovial cells to produce matrix metalloproteinases, notably MMP-13, which cuts through type II collagen, the structural backbone of cartilage . Excess reactive oxygen species add to the damage by injuring chondrocytes directly and by amplifying the inflammatory signals [6].

This suggests a chain of events: oxidative stress and inflammation raise enzyme activity, enzyme activity degrades collagen, and collagen loss undermines the joint. Interrupting the chain at its early links, by supporting the body's antioxidant enzymes and lowering cytokine levels, could in principle slow the destruction downstream. This is the logic behind looking at plant-derived compounds that act on several links at once. It also explains why markers of inflammation, oxidative balance and cartilage breakdown are worth measuring together rather than in isolation: each tells us about a different step in the same story.

Q *How did you test whether Moringa pod extract could help, and what did the results reveal?*

A We induced OA in female Wistar rats with intra-articular papain, an enzyme that degrades cartilage and produces an OA-like picture. Animals were divided into five groups of six: normal control, untreated disease control, a glucosamine sulphate reference group, and two HEMO groups at 100 and 200 mg/kg given orally for 28 days. In a separate acute toxicity test following OECD Guideline 423, HEMO was well tolerated up to 2000 mg/kg with no deaths or signs of toxicity over 14 days.

Untreated arthritic animals lost weight, developed swollen knees, became stiff and moved less. Treatment reversed these changes in a dose-dependent way. At 200 mg/kg, HEMO significantly reduced knee diameter and joint stiffness, improved locomotor activity and helped restore body weight. The 100 mg/kg dose gave smaller, though still measurable, improvements. Radiographs and histology told a consistent story: the untreated joints showed narrowing of the joint space, osteophytes, inflammatory cell infiltration and disturbed cartilage matrix, whereas treated joints, particularly at the higher dose, looked considerably better preserved. It is worth being candid about the limits here: each group had only six animals, all were female, and the treatment period was short. The pattern was consistent across many independent measures, which gives me some confidence, but it needs replication before it can be treated as settled.

Q *Beyond the visible improvements, what did the blood tests tell you about how the extract might be helping and what remains uncertain?*

A The blood markers helped us understand why the joints looked better. In the disease control group, IL-1β averaged 61.8 and TNF-α 82.5 in the units reported, against 10.4 and 23.0 in normal animals. At 200 mg/kg, HEMO brought these down to 45.2 and 30.7. C-reactive protein and erythrocyte sedimentation rate, two general measures of inflammation, fell in parallel. Interestingly, the TNF-α value in the HEMO 200 mg/kg group was lower than in the glucosamine group, although glucosamine performed better on most other measures.

The antioxidant picture moved in the opposite direction. Superoxide dismutase and catalase, the enzymes that neutralize reactive oxygen species, were

depressed by papain and recovered with treatment, with the higher dose again doing more. Alkaline phosphatase, which reflects bone turnover and joint injury, was lowered as well.

The change in MMP-13 is perhaps the most telling. It roughly doubled in diseased animals (10.35 against 4.72 in normal controls) and dropped to 5.93 with HEMO 200 mg/kg. Since MMP-13 is the enzyme that dismantles cartilage collagen, this suggests that the extract does more than relieve swelling: it appears to act on a step that determines whether cartilage survives. Taken together, lower cytokines, restored antioxidant defenses and reduced MMP-13 fit with the improved histology. That said, these are associations measured in serum. We did not measure NF-κB or other signaling molecules directly, so the mechanism remains a hypothesis to be tested rather than a conclusion.

Q *These findings are promising. How close are we to knowing whether Moringa pod extract could help people with osteoarthritis, and what needs to happen next?*

A The results are encouraging, but a rat study is a first step, not a recommendation. Several things need to happen before anyone should consider Moringa pod preparations for people with OA.

First, the extract must be standardized. Plant chemistry varies with cultivar, soil, harvest time and extraction method, and the literature already points to differences between wild and cultivated Moringa [7]. A clinical product needs defined marker compounds, batch-to-batch consistency and quality control. Second, the safety work must go beyond a single acute test, to include repeated-dose and chronic toxicity studies, and an assessment of interactions with drugs commonly taken by OA patients, such as anticoagulants and antihypertensives. Third, pharmacokinetic studies are needed to learn which compounds are absorbed, at what levels, and whether they reach joint tissue.

On the science side, we should confirm efficacy in additional models, including surgically induced or mechanically driven OA, which may reflect human disease better than an enzyme-induced model, and in animals of both sexes and different ages. Mechanistic studies should test NF-κB and related pathways directly, and fractionation could identify the most active constituents. Our comparison with glucosamine sulfate is also worth handling carefully, since the clinical evidence for glucosamine itself is debated.

Only after this groundwork would well-designed, adequately powered, randomized controlled trials be justified, with outcomes that matter to patients, such as pain, function and imaging changes over time. Until then, Moringa pods are best viewed as a promising lead in the search for gentler, disease-modifying options, and people living with OA should continue to follow the advice of their physicians. Pod extracts are not a substitute for prescribed treatment, and self-medicating with concentrated preparations is not something these data support.

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Dr. Snehal Ambadas Gojare is an Assistant Professor in the Department of Pharmacology at Progressive Education Society's Modern College of Pharmacy, Nigdi, Pune, Maharashtra, India. Her research focuses on exploring the medicinal properties of natural products and their potential applications in treating human diseases. In one of her recent studies, she investigated the potential of Moringa oleifera pod extract in managing osteoarthritis, examining its effects on inflammation, oxidative stress, joint function and cartilage damage in experimental animals. Through her research and teaching, she is committed to advancing pharmacological knowledge, inspiring future pharmacy professionals and contributing to the development of safer and more effective therapeutic approaches.

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SCIENCE DESK

Awake Hand Surgery: Advancing Precision in Finger Tendon Repair



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Scientific Profile
Organization Link
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AREAS OF EXPERTISE
Hand Surgery • Microsurgery • Brachial plexus surgery • Reconstructive surgery

OUTLOOK

Can a patient help a surgeon test a repaired finger while the operation is still in progress? And could staying awake during surgery improve the chances of restoring normal hand movement? In this article, Dr. Madhusudhan N.C. explores an approach to finger tendon repair in which patients remain awake and actively move their fingers during surgery. Drawing on his clinical research, he explains how testing finger movement can help surgeons identify and correct problems before completing the operation. He also discusses the importance of patient participation, rehabilitation and the challenges of making this approach more widely available.

Q *A finger injury may seem minor, but damage to its tendons can seriously affect hand movement. What role do tendons play in finger function, and why are these injuries sometimes difficult to repair?*

A Tendons connect muscles to bones and transmit the force needed to move our fingers. The flexor tendons allow us to bend our fingers, grip objects, write, and perform everyday activities. Even a small injury can significantly affect hand function.

Repairing these tendons is particularly challenging in Zone II of the finger, often called the “no man's land” of tendon surgery. Here, the tendons travel through a narrow tunnel surrounded by pulleys that guide their movement.

The challenge is not simply to join the cut ends. The repair must be strong enough to withstand controlled movement while remaining smooth enough to glide through this confined space. A bulky repair or excessive scar tissue can restrict movement, while an inadequate repair may separate or rupture.

Successful treatment therefore requires both restoration of tendon continuity and preservation of smooth tendon gliding.

Q *Traditionally, many hand surgeries have been performed under general or regional anaesthesia. What challenges do surgeons face with these approaches, and what makes awake hand surgery different?*

A General and regional anaesthesia remain important options for hand surgery. However, depending on the anaesthetic technique, patients may be unable to actively move their fingers during the operation. This limits the surgeon's ability to assess tendon function under active movement before closing the wound.

A repair may appear satisfactory on visual inspection but develop gapping or mechanical obstruction when the patient moves the finger.

Wide-awake hand surgery offers an alternative for appropriately selected patients. By using local anaesthesia while preserving the patient's ability to cooperate and move the fingers, surgeons can assess the repair dynamically.

The key difference is the opportunity to evaluate not only how the repair looks, but also how it functions. This allows certain problems to be identified and corrected during the same operation rather than discovered later.

Q *Your research uses a technique called WALANT, which allows patients to remain awake during surgery. How does this technique work, and how can patients move their fingers without experiencing pain?*

A WALANT stands for Wide-Awake Local Anaesthesia No Tourniquet. It uses a local anaesthetic, commonly lignocaine, together with adrenaline (epinephrine). Lignocaine blocks pain signals, while adrenaline constricts small blood vessels and reduces bleeding, providing a chemical alternative to a tourniquet.

Once adequate anaesthesia has been established, the patient remains awake and can actively move the fingers when instructed. Because the technique does

not require the motor blockade associated with some regional anaesthetic approaches, active movement can be assessed during surgery.

Patients should not experience pain from the procedure when anaesthesia is adequate, although they may still perceive pressure or movement.

WALANT is more than an anaesthetic choice in tendon surgery. It creates an opportunity to assess the repaired tendon under active movement and explain the importance of rehabilitation directly to the patient.

Q *One of the key aspects of your work is assessing finger movement during surgery using a technique called iTAMe. How does this help surgeons identify and correct problems that might otherwise go unnoticed?*

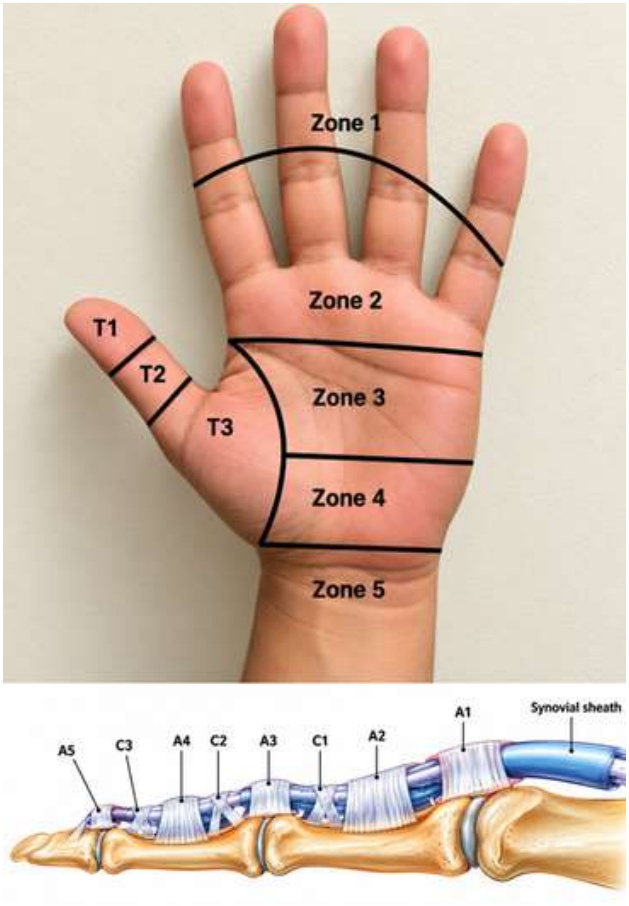


Figure 1. Illustration of the flexor tendon zones of the hand, including the thumb zones (T1–T3), alongside the digital flexor tendon pulley system and synovial sheath. The pulley system helps maintain the tendons close to the phalanges, enabling efficient tendon excursion and finger flexion. In Zone II, the close relationship between the flexor tendons and pulley system makes restoration of smooth tendon gliding particularly important during tendon repair.

A Intraoperative Total Active Movement examination, or iTAMe, is a structured assessment of tendon function during surgery. In our technique, the patient actively moves the finger while the surgeon evaluates repair integrity and tendon gliding.

The assessment includes checking for gapping at the repair site, observing smooth movement through the pulley system, and evaluating resistance during passive movement.

Gapping occurs when the repaired tendon ends separate under tension. Snapping or catching may indicate that the tendon is obstructed as it glides through the pulley system. Excessive resistance may also suggest tendon bunching or problems related to the repair.

Our protocol provides a systematic way to respond to these findings. Gapping can prompt additional suturing or re-repair, while pulley obstruction may require carefully judged partial pulley venting. Adjustments to the sutures may be needed if the repair is bulky.

The advantage is that the surgeon can identify and address these problems before wound closure, when correction is still possible.

Ultimately, the goal of hand surgery is functional restoration, not simply anatomical repair. In our work comparing functional outcomes in two-digit hands,2 we used objective measures of strength and hand function to evaluate the performance of different reconstructive configurations. This reflects a broader principle in hand surgery: surgical success should be judged by how well the reconstructed hand functions, alongside anatomical considerations.

Q *In your study, you describe your clinical experience involving 22 patients and 72 repaired tendons. What were the most important observations, and what do they suggest about the potential benefits of this approach?*

A Our published technical note describes preliminary experience with 22 patients undergoing Zone II flexor tendon repair using WALANT and iTAMe. A total of 72 tendons were repaired.

Intraoperative testing identified repair-site gapping in six tendons (8.3%) and pulley obstruction in 12 tendons (16.7%). These problems were addressed using the described troubleshooting approach.

During three months of follow-up, no tendon ruptures were recorded. Twenty of the 22 patients achieved full active finger motion. One surgical-site infection was

documented, and one patient was lost to follow-up.

These observations demonstrate the feasibility of combining wide-awake surgery with systematic functional assessment. They also illustrate how testing movement can reveal correctable problems that might not be apparent during static inspection.

However, this was a technique-focused report involving a small group of patients, and the findings were not statistically analysed. The results are encouraging but do not establish superiority over other approaches. Larger, controlled studies are needed to determine the long-term benefits and risks.

Q *Beyond improving surgical precision, what benefits could awake hand surgery offer patients? Could their active participation during surgery also help them better understand the recovery and rehabilitation process?*

A One important advantage is the opportunity for intraoperative patient education, which we refer to as iPE.3

Flexor tendon repair is only the beginning of recovery. Rehabilitation must balance controlled movement, which helps minimise stiffness and adhesions, against protecting the repair from excessive force that could cause rupture.

During awake surgery, the surgeon can explain the injury, demonstrate the repaired finger's movement, and discuss why the postoperative rehabilitation programme must be followed carefully. This can help patients understand that successful recovery depends on both the surgical repair and their participation afterwards.

When appropriate, involving a hand therapist can further reinforce rehabilitation instructions.

Nevertheless, being able to move the finger during surgery does not mean that unrestricted movement is safe after surgery. Patients must follow an individualised rehabilitation programme under the guidance of their surgical and therapy teams.

Q *Looking ahead, what challenges remain in making awake hand surgery more widely available, and what further research or technological advances could improve the treatment of finger tendon injuries?*

A Wider adoption requires appropriate training, careful patient selection, familiarity with WALANT techniques, and coordination between surgeons and rehabilitation teams. Patients also need clear explanations and reassurance about remaining awake during surgery.

WALANT should be viewed as an additional option rather than a universal replacement for general or regional anaesthesia. Its suitability depends on the patient, injury, procedure, and clinical circumstances.

Future research should include larger multicentre studies comparing outcomes across different anaesthetic and surgical approaches. Important measures include tendon rupture, adhesions, range of motion, complications, patient-reported function, and return to daily activities.

Our technical note also identifies ultrasound-assisted detection of tendon gaps and simulation-based training for iTAMe as promising areas for further development. These approaches could help improve assessment and standardise training, although their clinical value requires validation.

Ultimately, the goal is not merely to repair a tendon, but to restore useful movement and help patients return to their everyday activities. Combining sound surgical technique, real-time functional assessment, and informed patient participation offers a promising way to work towards that goal.



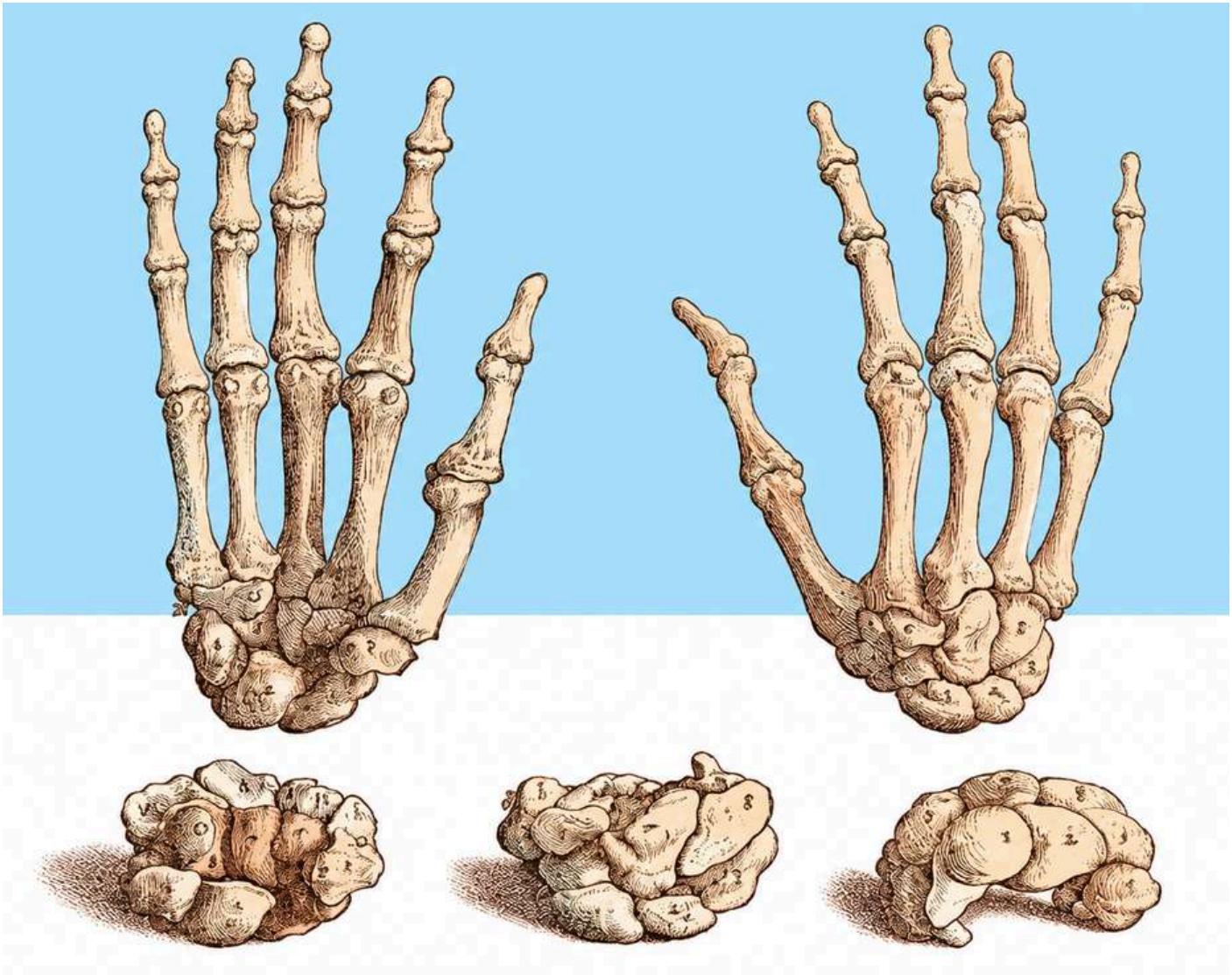
Figure 2. (A) A relatively small skin laceration over Zone II of the finger, with an external appearance that may underestimate the extent of the underlying injury. (B) Surgical exploration reveals multiple divided flexor tendons beneath the wound. (C) Intraoperative view following flexor tendon repair. This case highlights the importance of careful assessment and exploration of sharp lacerations in Zone II, as the size of the skin wound may not reflect the severity of the underlying tendon injury.

ABOUT THE AUTHORS

Dr. Madhusudhan N.C. is a Hand, Wrist and Microvascular Surgeon at Madhu Hand Surgery & Orthopaedic Centre, Bengaluru, India. His clinical and research interests include complex hand injuries, tendon repair, microsurgery and restoring hand function. His work focuses on improving surgical techniques, particularly awake hand surgery, where patients can actively participate during the procedure to help surgeons assess and improve treatment outcomes. He was selected as an ASSH International Traveling Fellow (USA) in 2026, representing the Indian Society for Surgery of the Hand. He also serves on the Editorial Board of the Journal of Hand Surgery (Asian-Pacific Volume) and has received several academic honours, including four gold medals.

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SCIENCE DESK

Brain Tuberculosis in Children: Why It Can Be Mistaken for Cancer



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Scientific Profile
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AREAS OF EXPERTISE
Neurooncology • Vascular neurosurgery • Neuroanatomy

OUTLOOK

Tuberculosis is commonly known as a lung disease, but it can also affect the brain, particularly in children. Sometimes, brain tuberculosis can look very similar to a brain tumor, making it difficult for doctors to identify the real cause. In this conversation, Dr. Nazmin Ahmed shares the case of a five-year-old child whose brain infection was initially suspected to be cancer. She explains how detailed laboratory testing helped doctors reach the correct diagnosis and provide appropriate treatment. The article highlights why early diagnosis, careful medical examination, and greater awareness of brain tuberculosis are important for protecting children's health and avoiding unnecessary cancer treatment.

Q *Tuberculosis is commonly known as a disease affecting the lungs. How can it also affect the brain, particularly in children, and what makes brain tuberculosis a serious medical concern?*

A Although TB is typically a lung disease, the bacteria can travel through the bloodstream to other organs such as the brain. In the central nervous system, infection can affect the meninges or result in a localized inflammatory mass known as a tuberculoma. A tuberculoma is not cancer, but rather an accumulation of immune cells and damaged tissue that occurs as a result of infection. However, it can be hazardous due to its location. The posterior fossa, which houses the cerebellum and brainstem, is particularly susceptible to the effects of increased volume as even a relatively small amount of increase can block the flow of CSF or compress structures that are critical for movement, consciousness, and breathing. When pressure increases in the skull, the level of consciousness and cognitive conditions of a child can deteriorate quickly. Early recognition is important, not only for infection control, but also to prevent neurological injury from hydrocephalus and mass effect.

Q *Your published case describes a five-year-old child whose brain lesion was initially suspected to be cancer. Could you briefly explain the child's symptoms, the initial findings, and what made this case particularly unusual?*

A We reported a previously healthy, immunocompetent 5-year-old boy from Kashmir who presented with a progressive increase in headache and irritability over a few weeks. He did not have any known TB contacts, fever, weight loss or night sweats, which would have been suspicious of TB. Brain magnetic resonance imaging showed a large lesion (45 × 38 mm) in the cerebellar vermis and left hemisphere. It compressed the fourth ventricle and surrounding brainstem structures, resulting in obstructive hydrocephalus. Imaging raised concern for a malignant posterior fossa tumor, such as atypical teratoid/rhabdoid tumor (AT/RT) or medulloblastoma. The unique feature was that an intraoperative crush biopsy also indicated an atypical rhabdoid tumor. It was only after the more extensive postoperative tissue examination that it was determined that this seemingly aggressive tumor was actually a tuberculoma.

Q *One of the most striking aspects of your report is that brain tuberculosis closely resembled an aggressive brain tumor. Why can these two conditions look so similar, and what makes it difficult for doctors to distinguish them?*

A Both a tuberculoma and a malignant tumor can fill space, produce swelling, deform normal anatomy, a-

nd obstruct the flow of cerebrospinal fluid. Both can thus cause headache, vomiting, imbalance or other symptoms of increased ICP. They may also have similar MRI appearances. Tuberculomas can appear as solid or ring-like pattern, with surrounding edema and significant mass effect, which are not specific to infection. In our patient, the lesion was mostly hypointense on T2/FLAIR imaging with a hyperintense rim and no diffusion restriction. These observations were useful but did not establish a diagnosis by themselves. Clinical context also makes interpretation difficult: a child can have isolated brain TB without the classic constitutional signs of pulmonary TB. Therefore, imaging should be used to help direct the differential diagnosis, and not as a definitive diagnosis of malignancy or tuberculosis.

Q *In this case, the initial examination of tissue suggested a malignant tumor, but further testing confirmed tuberculosis. What diagnostic methods helped establish the correct diagnosis, and why is detailed laboratory examination so important?*

A The first crush preparation made intraoperatively was suggestive of a rhabdoid tumor, which is a limitation of rapid tissue assessment: a small, distorted sample may not represent the lesion as a whole. However, multiple permanent histological sections revealed extensive necrosis, epithelioid granulomas, Langhans-type giant cells and macrophages. CD68-positive macrophages, negative epithelial membrane antigen (EMA) staining, and vimentin positivity in fibrotic tissue were demonstrated by immunohistochemistry. Importantly, Ziehl–Neelsen staining revealed acid-fast bacilli, which confirmed the diagnosis of mycobacterial infection in this histological setting. The published report also mentions that the treating institution did not have INI1 staining available when AT/RT was suspected. The lesson is that a preliminary diagnosis should be confirmed by the complete histological picture, appropriate special stains and, if available, molecular assays like Xpert MTB/RIF. This type of testing can avoid sending a child down the wrong path for cancer treatment.

Q *Once tuberculosis was confirmed, the child's treatment changed significantly. How was the condition managed, and what does the child's recovery tell us about the importance of early and accurate diagnosis?*

A The child initially needed a ventriculoperitoneal shunt for obstructive hydrocephalus and subsequently a left suboccipital craniectomy and decompression due to the size of the lesion and its pressure on critical structures. The definitive pathology confirmed tuberculoma and the treatment was changed from the expected oncological pathway to antitubercular therapy. The report shows a nine-month treatment period and a short three-day postoperative course of corticosteroid for edema. Follow-up MRI revealed significant reduction at 3 months and complete radiological resolution at 9 months, and neurological stability during follow-up. This is a positive result, but it does not mean that every child with brain TB should undergo the same surgery or treatment. Treatment is based on the site of the lesions, the presence of hydrocephalus, clinical stability, drug sensitivity and expert opinion. The overall message is that diagnosis is important and affects treatment and prognosis.

Q *Your report highlights that brain tuberculosis may occur even without typical symptoms such as fever, weight loss, or a known history of tuberculosis exposure. What should doctors and parents understand about recognizing this condition, especially in regions where tuberculosis is common?*

A The lack of fever, weight loss, night sweats, or history of exposure should not rule out CNS tuberculosis, especially in a geographical area where TB is common. Children who have persistent or progressive headache, unexplained irritability, vomiting, gait disturbance, or evidence of increased ICP should be evaluated urgently by a clinician. Tuberculosis should be considered in the differential diagnosis of a posterior fossa mass on imaging, in addition to neoplastic and other infectious diseases. A targeted TB assessment may involve a history of exposure, chest imaging, and immunological tests, but these tests are not sufficient to confirm or exclude a brain tuberculoma. Parents should be aware that these symptoms are not unique to TB or cancer, but are warning signs that need prompt medical attention. The purpose is not to cause anxiety, but to minimize unnecessary delays in the investigation of a potentially treatable condition.

Q *Based on your clinical experience and this case, what are the most important lessons for improving the diagnosis and management of brain tuberculosis in*

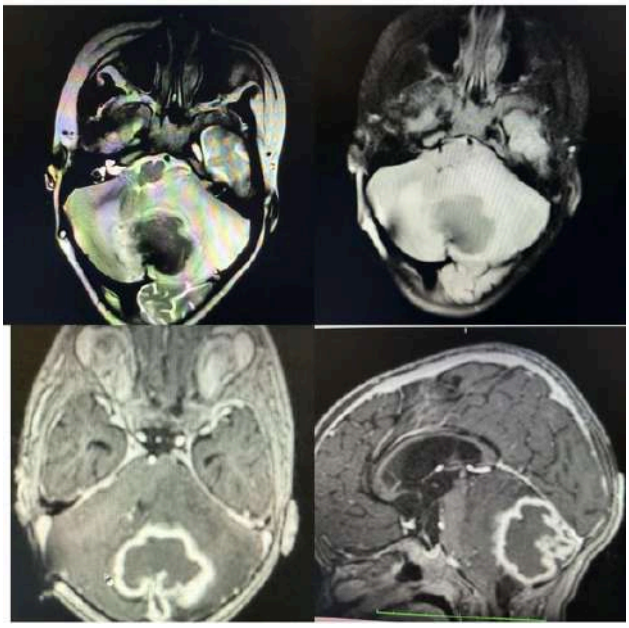


Figure 1. MRI of brain demonstrated a thick, irregular heterogeneous rim enhancing lesion, predominantly in the left cerebellar hemisphere, causing compression of cerebellar hemisphere and brainstem.

children? What further improvements in medical testing or clinical awareness would help prevent similar diagnostic challenges?

A There are three lessons to be learned from our case. First, a wide differential diagnosis should be considered when assessing posterior fossa masses in children, especially in TB-endemic areas. Second, preliminary intraoperative pathology should be interpreted with caution and permanent section histology, with the addition of immunohistochemistry if appropriate, and microbiological stains or molecular tests should be performed. Third, decisions must be made in concert by neurosurgeons, radiologists, pathologists, pediatricians and infectious-disease specialists, as the immediate threat from hydrocephalus may necessitate intervention before the underlying diagnosis is confirmed. Diagnostic uncertainty could be reduced with increased access to rapid molecular testing, appropriate tissue handling and specialist neuropathology. It is also important to teach that isolated CNS TB may be present without pulmonary symptoms. Our report is about one child and does not provide a screening protocol for TB, but does suggest a lower threshold for considering TB and appropriate investigations in children from endemic areas. In the end, diagnostic accuracy saves patients from under- and overtreatment of infection and presumed cancer.

It would be helpful to create multidisciplinary review pathways for atypical pediatric brain masses, including explicit reminders to think about infectious causes and to save tissue for microbiological evaluation. Families should be informed that an early radiological or intraoperative impression may be modified following final testing.

Follow-up imaging and neurological evaluation are also necessary to document response and complications. The aim is to make a careful and timely diagnosis, while not delaying emergency treatment of raised ICP.

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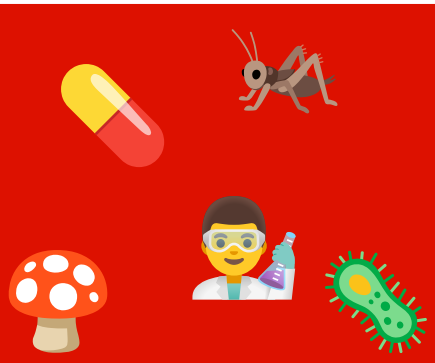
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Answers here – don't peek!





Q1

A plant is growing in poor soil. Which tiny helpers living near its roots could improve its growth?

A. Earthworms that eat the roots
B. Helpful microbes that make nutrients easier to obtain
C. Microbes that block sunlight
D. Bacteria that stop water absorption

Q2

Some plants have tiny bumps called nodules on their roots. What makes these bumps special?

A. They act like underground flowers
B. They store extra sunlight
C. They provide a home for bacteria that help supply nitrogen
D. They turn soil into seeds

Q3

Imagine a medicine designed to act on one particular target in a cell. Why might that be useful?

A. It can reduce unwanted effects on other targets
B. It makes all cells stop working
C. It removes the need to test medicines
D. It guarantees a cure

Q4

Our cells make RNA messages to guide protein production. What happens when some of these messages contain errors?

A. They always become useful proteins
B. They turn into new chromosomes
C. They remain in the cell forever
D. Cellular quality-control systems can identify and remove them

Q5

Some cancer cells survive chemotherapy by strengthening their internal defences. What could help make treatment more effective?

A. Giving the cancer cells more nutrients
B. Weakening the protective systems that help them resist treatment
C. Preventing medicines from reaching the tumour
D. Helping cancer cells multiply faster anyone

Q6

Could a blood sample offer clues about changes happening in the brain?

A. Yes, by revealing changes in certain molecules linked to metabolism
B. Yes, by showing the exact number of brain cells
C. No, blood contains no useful biological information
D. Yes, by predicting the exact day dementia will develop

Q7

A patient is receiving antibiotics, but a laboratory test suggests a different medicine would work better. What should the healthcare team do?

A. Ignore the laboratory result
B. Give every patient the same antibiotic
C. Review the treatment together and choose the most appropriate antibiotic
D. Stop communicating between departments

Q8

Why do some bacteria survive even when treated with certain antibiotics?

A. They become invisible
B. They turn into viruses
C. They stop needing nutrients
D. They produce enzymes that can break down the antibiotic

DISCOVERY HIGHLIGHTS

PHYSICS & ASTRONOMY



A STELLAR ENCOUNTER REVEALS TWO STAR CLUSTERS DRIFTING APART IN SPACE

Astronomers have discovered that a group of stars previously identified as a single cluster is actually two distinct star clusters that recently passed close to each other. Using precise measurements from the European Space Agency's Gaia spacecraft, researchers re-examined the stellar system UBC 63 and identified two populations with very different ages. The younger cluster, UBC 63A, is approximately 21 million years old, while UBC 63B is about 562 million years old, indicating that they formed at different times. By analysing the stars' positions and movements and conducting computer simulations, the researchers reconstructed the clusters' past interaction. Their findings suggest that the two clusters passed within approximately 23 light-years of each other around six million years ago. Despite this close encounter, the clusters are not gravitationally bound and are now moving apart. Simulations predict that their separation could increase substantially over the next 100 million years. The researchers also identified elongated stellar structures that may reflect gravitational disturbances caused by the encounter. The discovery provides new insights into how star clusters interact, influence one another and evolve within our galaxy.

Biswas S. et al., The Astronomical Journal, 2026.

ADAPTIVE QUANTUM SENSORS COULD MEASURE MAGNETIC FIELDS MORE ACCURATELY

Researchers have developed an adaptive approach that could improve the accuracy of quantum sensors used to measure magnetic fields under changing environmental noise. Quantum sensors can use entangled particles to achieve highly sensitive measurements, but their performance often declines when noise interferes with the quantum states. To address this challenge, the researchers developed a computer-based control system that automatically switches between two types of four-qubit quantum states depending on the measurement conditions. The system continuously evaluates recent measurements and selects the most suitable quantum state without requiring prior knowledge of the noise pattern. Using simulations across eight different noise environments, the adaptive method reduced measurement error by approximately 10% compared with a fixed-state strategy selected through validation. It performed better in seven of the eight tested environments, although its accuracy declined under consistently high noise. The findings demonstrate how adaptive control could make quantum sensing more reliable under changing conditions. While the approach has so far been evaluated through simulations rather than physical quantum hardware, it offers a promising direction for developing more robust quantum magnetometers and other precision measurement technologies.

Diwakar D. and Sambhaje V. S., Sensors, 2026.

CHEMISTRY & CHEMICAL SCIENCES



VISIBLE LIGHT OFFERS A GREENER WAY TO TURN CARBON DIOXIDE INTO USEFUL CHEMICALS

Researchers have developed a greener method for converting carbon dioxide (CO_2) into useful chemicals using visible light. The approach employs a specially designed organic photocatalyst called JS-2 to transform CO_2 and epoxides into cyclic carbonates, valuable compounds used in chemical manufacturing. Unlike conventional methods, the reaction requires no metal catalysts, halide add-

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itives or solvents. It relies on sequential two-photon activation, where the catalyst absorbs light energy in two steps to drive the transformation. The process operates at room temperature and atmospheric CO_2 pressure, requiring only a small amount of catalyst. It demonstrated high efficiency across various starting materials, while the catalyst remained reusable for five consecutive cycles. The findings highlight how light-driven chemistry could reduce chemical waste and support more sustainable manufacturing by converting carbon dioxide into valuable products.

SUNLIGHT AND SEAWATER OFFER A GREENER WAY TO PRODUCE HYDROGEN PEROXIDE

Researchers have developed innovative porous organic materials that use sunlight to produce hydrogen peroxide (H_2O_2), an important chemical used in disinfection, water treatment and industrial processes. The study introduces specially designed polymers that efficiently capture light and separate electrical charges to drive chemical reactions involving oxygen and water. Among the materials tested, IPM-402F demonstrated particularly high efficiency, producing hydrogen peroxide without conventional energy-intensive manufacturing processes. Remarkably, the material also generated hydrogen peroxide directly from seawater using sunlight and oxygen from the air, demonstrating its potential under practical conditions. By adjusting the chemical composition of these polymers, researchers improved their light-driven performance. The findings offer a promising approach to cleaner hydrogen peroxide production using abundant natural resources, potentially reducing the environmental impact of chemical manufacturing.

Dam G. K. et al., Materials Horizons, 2026.

MEDICINE AND HUMAN HEALTH



NEW CRISPR-BASED TEST OFFERS PROMISE FOR RAPID HEPATITIS DETECTION

Researchers have developed a CRISPR-based diagnostic method for detecting hepatitis B and C viruses, which cause serious liver diseases worldwide. The approach combines a rapid DNA amplification technique with the CRISPR/Cas13a system to identify viral genetic material through fluorescent signals. Unlike conventional molecular testing, the amplification process operates at relatively low temperatures, potentially reducing the need for sophisticated laboratory equipment. The researchers evaluated the method using 45 hepatitis B and 30 hepatitis C patient samples, demonstrating its ability to distinguish positive samples from healthy controls. By targeting conserved regions of the viral genomes, the method was designed to detect circulating viral variants in India. Although further validation is needed, this technology could support faster, more affordable hepatitis screening, particularly in rural and resource-limited healthcare settings.

Sata T. N. et al., Diagnostic Microbiology and Infectious Disease, 2026.

INDIAN STUDY REVEALS DISTINCT GENETIC FEATURES OF COLORECTAL CANCER

Researchers have identified distinctive genetic patterns in colorectal cancer among Indian patients, highlighting possible differences from internationally studied populations. The study combined DNA and gene-expression sequencing of 20 tumour samples and compared the findings with genomic data from 2,023 colorectal cancers worldwide. Researchers identified approximately 16,440 genetic variants and 814 genes showing altered activity. Several mutation patterns were detected that were absent from the comparison dataset, while commonly reported cancer-driving mutations in genes such as APC, TP53 and KRAS occurred less frequently. The study also identified specific genetic alterations in patients who did not survive, suggesting possible links to disease outcomes. These findings highlight the importance of studying cancer genetics across diverse populations to improve understanding of tumour biology and identify potential treatment targets. However, larger studies are needed to confirm these differences and their clinical significance.

Vashapaka A. et al., Neoplasia, 2026.

BIOLOGY AND LIFE SCIENCE

DISCOVERY HIGHLIGHTS



CHASING ELEPHANTS AWAY MAY WORSEN HUMAN–ELEPHANT CONFLICT IN WEST BENGAL

Researchers have found that chasing elephants away from human settlements in South West Bengal may provide temporary relief but fails to offer a lasting solution to human–elephant conflict. The study monitored elephant movements over 223 days, comparing natural movement with local chasing and organized hula drives. Elephants subjected to hula drives travelled an average of 9.43 kilometres daily, substantially farther than those experiencing local drives. Human attacks peaked on the day of organized drives, while crop damage increased afterward. Researchers also observed considerable community interference during these operations, reflecting the challenges of managing elephants in populated landscapes. The findings suggest that repeated chasing can disrupt elephant movement without preventing future conflict. The study highlights the need for sustainable, community-supported strategies that protect both elephants in populated landscapes. The findings suggest that repeated chasing can disrupt elephant movement without preventing future conflict. The study highlights the need for sustainable, community-supported strategies that protect both elephants and people.

Singh A. and Kumara H. N., iScience, 2026.

HABITAT FRAGMENTATION THREATENS THE SURVIVAL OF SLOTH BEARS IN NORTHERN INDIA

Researchers have investigated how habitat fragmentation threatens sloth bear populations in India's Central Terai landscape, highlighting the importance of maintaining connections between wildlife habitats. The study used genetic analysis to examine sloth bears living in a landscape increasingly divided by human activities. By analysing 209 non-invasively collected faecal samples, researchers identified 66 individual bears and examined 964 genetic markers to investigate population structure and connectivity. The research addresses concerns that isolated wildlife populations may experience reduced genetic diversity and increased inbreeding, potentially threatening their long-term survival. The findings underscore the importance of considering genetic connectivity when planning conservation measures in human-dominated landscapes. Protecting habitat corridors and reducing barriers to animal movement could help maintain healthier sloth bear populations and support their long-term conservation.

Rana D. et al., Heredity, 2026.

AGRICULTURE & FOOD SCIENCE



GENOME SEQUENCING REVEALS THE GENETIC SECRETS BEHIND KASHMIR'S AROMATIC RICE

Researchers have decoded the genome of Mushk Budji, a traditional aromatic rice variety from Kashmir, revealing genetic features responsible for its distinctive fragrance and cooking quality. Using whole-genome sequencing, the team assembled a 378-million-base-pair genome and identified more than 43,000 protein-coding genes. The analysis confirmed a characteristic mutation in the Badh2 gene associated with rice fragrance. Researchers also identified genetic variations in starch-related genes that may contribute to the rice's soft, cohesive texture after cooking. Evidence of historical selection suggested that farmers have helped shape desirable grain characteristics over generations. The findings provide a valuable genetic resource for conserving this heritage variety and developing improved rice varieties with desirable aroma, texture and adaptability. The study

DISCOVERY HIGHLIGHTS

highlights how modern genomics can help preserve traditional agricultural biodiversity while supporting future crop improvement.

Khan R. S. et al., Frontiers in Plant Science, 2026.

BENEFICIAL BACTERIA HELP RICE GROW IN SALTY SOILS WITH LESS CHEMICAL FERTILIZER

Researchers have developed a bacteria-based biofertilizer that improves rice growth and salt tolerance while reducing dependence on chemical fertilizers. The team screened 101 beneficial bacteria living inside plants and selected seven compatible strains capable of promoting growth under saline conditions. Genome sequencing revealed genes involved in nutrient availability, stress protection and plant growth promotion. These bacteria were combined into a powder-based biofertilizer and tested on rice plants exposed to different salinity levels. Remarkably, plants receiving the biofertilizer alongside a 75% reduced chemical fertilizer dose showed improved growth, nutrient uptake and stress tolerance. The treatment also enhanced soil nutrient availability while reducing sodium accumulation and oxidative stress. These findings highlight the potential of beneficial microorganisms to support sustainable rice cultivation in salt-affected agricultural regions, although field validation remains necessary.

Das G. et al., Microbiological Research, 2026.

ENVIRONMENT & CLIMATE SCIENCE



INDIAN RESEARCHERS IDENTIFY BACTERIA CAPABLE OF BREAKING DOWN MICROPLASTICS IN WASTEWATER

Researchers have identified a bacterial strain capable of degrading microplastics, offering a potential biological approach to plastic pollution management. The study examined industrial wastewater from Raipur, Chhattisgarh, and detected an average of 64 microplastic particles per litre. Polyethylene was the predominant plastic, alongside polypropylene, polystyrene and other polymers. Researchers subsequently isolated a bacterial strain, Bacillus paralicheniformis PWDS, from soil collected near a plastic dumping site. Laboratory experiments demonstrated approximately 8.4% microplastic degradation over 30 days under optimized conditions. Although the degradation efficiency remains modest, the findings highlight the potential of naturally occurring microorganisms to contribute to plastic waste treatment. Further research is needed to improve degradation efficiency and evaluate the bacterium's effectiveness under real-world wastewater treatment conditions.

Brijmohan N. and Vasanth D., Biodegradation, 2026.

DECADE-LONG STUDY REVEALS CHANGING AIR POLLUTION PATTERNS ACROSS BENGALURU

Researchers have analysed ten years of air pollution data from Bengaluru, revealing contrasting pollution trends across the rapidly growing city. The study examined air quality between 2016 and 2025 in Peenya, Majestic and Bellandur, using machine learning to reconstruct missing monitoring records. Majestic recorded higher traffic-related pollution, while Peenya showed elevated ammonia and ozone concentrations. Bellandur experienced greater fluctuations in particulate pollution, potentially linked to construction and urban expansion. Although fine particulate matter (PM2.5) declined in Peenya and nitrogen oxide pollution decreased in Majestic and Bellandur, larger particles (PM10) increased in Peenya and Bellandur. Pollution levels frequently exceeded recommended limits, particularly during winter and pre-monsoon periods. The findings highlight the need for neighbourhood-specific pollution control strategies and reliable monitoring to improve urban air quality.

Nisha P. G., Environmental Monitoring and Assessment, 2026.

BIODIVERSITY & CONSERVATION

CHASING ELEPHANTS AWAY MAY WORSEN HUMAN–WILDLIFE CONFLICT

Researchers have found that chasing elephants away from villages and farmland may provide temporary relief but could worsen human–wildlife conflict in the long term. The study monitored Asian elephant movements across 223 days in South Bengal, Ind-

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ia, comparing natural movement with local chasing and organized hula drives. Elephants subjected to hula drives travelled considerably longer distances, averaging 9.43 kilometres daily, compared with 5.20 kilometres during local drives. Human attacks peaked on drive days, while crop damage increased afterward. Researchers also observed mixed community responses, with local interference frequently disrupting operations. The findings suggest that repeatedly driving elephants away is stressful, resource-intensive and unlikely to provide lasting solutions. The study highlights the need for more sustainable, community-supported strategies that protect both elephants and people.

Singh A. and Kumara H. N., iScience, 2026.

GENOME SEQUENCING REVEALS THE EVOLUTIONARY HISTORY OF A CRITICALLY ENDANGERED TURTLE

Researchers have uncovered the evolutionary history of *Batagur baska*, a critically endangered river turtle facing severe population decline. Using advanced DNA sequencing, the team reconstructed eight complete mitochondrial genomes, each containing 37 genes. Genetic comparisons revealed a close evolutionary relationship with another endangered turtle, Batagur affinis. The analysis estimated that the lineage leading to B. baska diverged approximately 9.12 million years ago, during the Miocene epoch. Researchers also identified previously undocumented genetic variations, providing new insights into the species' evolutionary diversity. With no confirmed wild populations remaining, understanding its genetic characteristics is particularly important for conservation. The findings establish a valuable genomic resource that could support future captive-breeding programmes, population monitoring and potential reintroduction efforts aimed at preventing the extinction of this rare turtle.

Nawani S. et al., Genes, 2026.

EARTH & GEOLOGICAL SCIENCES

INDUSTRIAL LEAD POLLUTION FROM SOUTH AMERICA REACHES ANTARCTIC SNOW

Researchers have discovered evidence that industrial lead pollution from South America travels thousands of kilometres through the atmosphere before settling in Antarctica. The study analysed nine snow cores collected from three locations in coastal East Antarctica, using lead isotopes to trace pollution sources. Results revealed substantial human-derived lead contamination, despite the region's remoteness. Statistical modelling suggested that Argentina and Brazil together contributed approximately 72–84% of the deposited lead, with smaller contributions from Chile, Australia and local Antarctic sources. The findings demonstrate how atmospheric circulation can transport industrial pollutants across continents and oceans, reaching even the planet's most isolated environments. By establishing a baseline for modern lead contamination, the research highlights the importance of Antarctic snow records for tracking long-distance pollution and assessing the global environmental consequences of human activities.



Sundram S. et al., Environmental Pollution, 2026.

RISING SEAS AND DECLINING FRESHWATER THREATEN COASTAL GROUNDWATER PROTECTION

Researchers have found that rising sea levels and declining freshwater supplies can jointly intensify saltwater intrusion into coastal groundwater, threatening freshwater resources. Using computer simulations, the study evaluated two protective structures cutoff walls and subsurface

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dams under different groundwater conditions. Results showed that both barriers remained relatively effective when inland groundwater inflow was maintained, but became vulnerable under conditions controlled by groundwater levels. Subsurface dams exhibited a critical threshold beyond which their protective performance deteriorated rapidly, while cutoff walls provided more consistent protection. Importantly, the combined effects of sea-level rise and freshwater decline produced substantially greater saltwater intrusion than either factor alone. The findings highlight the importance of considering interacting climate and human-induced pressures when designing groundwater protection systems for vulnerable coastal regions.

Sadhasivam R. and Srinivasan V., Journal of Contaminant Hydrology, 2026.

OCEAN & MARINE SCIENCE

DEEP-SEA SURVEY REVEALS MARINE BIODIVERSITY BEFORE POTENTIAL MINING IN THE INDIAN OCEAN

Researchers have mapped zooplankton diversity across different ocean depths in the Central Indian Ocean Basin, establishing an important ecological baseline before potential deep-sea mining. Combining microscopic identification with DNA metabarcoding, the team examined zooplankton communities at three locations, collecting samples from depths reaching 5,000 metres. The analysis identified 115 taxa belonging to 81 genera,revealing substantial differences in species composition across locations and depths. Zooplankton diversity was generally highest near the ocean surface and declined with increasing depth, highlighting the importance of depth in shaping marine communities. The findings provide valuable reference information for assessing future environmental disturbances associated with deep-sea mineral exploration, including sediment plumes and contaminant exposure. This research could support biodiversity monitoring and more informed environmental management decisions in vulnerable deep-ocean ecosystems.



Ramadoss D. et al., Environmental Research, 2026.

BIODEGRADABLE AND CONVENTIONAL MICROPLASTICS FOUND TOGETHER IN MARINE FISH

Researchers have discovered that biodegradable and conventional microplastics can accumulate together in marine fish, raising concerns about seafood safety.

The study provides the first evidence from India of biodegradable microplastics in marine fish and their coexistence with conventional plastic particles. Approximately 11.2% of examined fish contained both types of microplastics in their digestive tracts, while their combined presence in edible tissues was detected only in S. indicus. The findings challenge assumptions that biodegradable plastics necessarily disappear harmlessly in marine environments, as incomplete degradation can generate smaller plastic particles. Estimates of dietary exposure suggested that children may face relatively higher microplastic intake through seafood consumption. Although direct health effects were not established, the research highlights the need for improved monitoring and food safety assessments.

Mukhopadhyay P. and Valsalan S. A., Environmental Pollution, 2026.

SPACE SCIENCE AND TECHNOLOGY

INDIA'S ADITYA-L1 REVEALS HOW MASSIVE SOLAR ERUPTIONS EXPAND UNEVENLY

Researchers using India's Aditya-L1 solar observatory have uncovered new details about how powerful eruptions from the Sun expand through its outer atmosphere. The study examined a coronal mass ejection observed on 5 August 2024, combining spectroscopic measurements from Aditya-L1 with images from NASA's Solar Dynamics Observatory. Researchers detected plasma moving at line-of-sight speeds reaching 218 kilometres per second, alongside a projected outward expansion speed of 1,135 kilometres per second.

Detailed analysis revealed that the eruption expanded unevenly rather than uniformly in all directions. A three-dimensional computer model helped explain the unusual spectral patterns observed during the event. These findings improve understanding of the early evolution of solar eruptions, which can trigger geomagnetic disturbances affecting satellites, comm-

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unication systems and power infrastructure. The research could ultimately contribute to more accurate space weather forecasting.

Tripathi S. et al., The Astrophysical Journal Letters, 2026.

NEW STUDY IMPROVES SATELLITE-BASED AIR POLLUTION ESTIMATES ACROSS INDIA

Researchers have developed an improved method for estimating sulfate air pollution across India by combining satellite-based atmospheric data with ground measurements. Sulfate particles contribute significantly to fine particulate pollution (PM2.5), posing risks to human health. The study analysed 2,583 observations from 167 monitoring sites across 37 Indian cities between 2017 and 2025.

Researchers found that NASA's MERRA-2 atmospheric dataset consistently overestimated ground-level sulfate concentrations, particularly during winter and post-monsoon seasons. By incorporating seasonal differences and city-specific conditions into a statistical model, the team reduced estimation errors by 38–42%. The improved analysis identified major sulfate pollution hotspots across the Indo-Gangetic Plain and parts of central and eastern India. These findings could support more accurate pollution monitoring and targeted emission-control strategies to improve air quality.

Tripathi A. et al., Environmental Pollution, 2026.

ENGINEERING & MANUFACTURING

NEW SILICON CHIP TECHNOLOGY COULD ENABLE FASTER AND MORE RELIABLE 6G COMMUNICATION

Researchers have demonstrated a new silicon-based photonic technology that could support faster and more reliable future 6G communication networks. The study introduces a specially engineered silicon crystal that allows terahertz electromagnetic waves to pass through certain barriers with minimal signal loss.

This unusual behaviour, known as photonic Klein tunnelling, enables efficient signal transmission through carefully designed pathways. Researchers demonstrated that the technology could preserve more than 98% of a key signal property across two barriers.

They also developed complex waveguides and signal-splitting devices capable of transmitting data at speeds reaching 100 gigabits per second. Importantly, the technology is compatible with established silicon chip manufacturing processes. The findings offer a promising foundation for developing compact, high-speed photonic circuits for next-generation wireless communication and data transmission systems.



Mulla S. et al., *Advanced Materials*, 2026.

NEW SMART GLASS TECHNOLOGY CAN SWITCH BETWEEN TRANSPARENT AND OPAQUE STATES

Researchers have developed an improved smart glass technology that can switch between transparent and opaque states, potentially offering an alternative to conventional window curtains. The system uses tiny liquid-filled channels within glass to control light transmission. By optimizing channel thickness and liquid viscosity, researchers reduced liquid consumption while improving switching performance. A channel thickness of just 100 micrometres, combined with a low-viscosity liquid, enabled stable transparency control and efficient drainage. In its opaque state, the glass transmitted approximately 16% of incoming light. The researchers also demonstrated customizable visual patterns, suggesting potential decorative and functional applications. The findings provide practical design principles for developing compact, energy-efficient

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dams under different groundwater conditions. Results showed that both barriers remained relatively effective when inland groundwater inflow was maintained, but became vulnerable under conditions controlled by groundwater levels. Subsurface dams exhibited a critical threshold beyond which their protective performance deteriorated rapidly, while cutoff walls provided more consistent protection. Importantly, the combined effects of sea-level rise and freshwater decline produced substantially greater saltwater intrusion than either factor alone. The findings highlight the importance of considering interacting climate and human-induced pressures when designing groundwater protection systems for vulnerable coastal regions.

Sadhasivam R. and Srinivasan V., Journal of Contaminant Hydrology, 2026.

COMPUTER SCIENCE & ARTIFICIAL INTELLIGENCE

INDIAN STUDY REVEALS HOW AI PERFORMANCE VARIES IN DIABETIC EYE DISEASE SCREENING

Researchers have evaluated three artificial intelligence (AI) systems for detecting diabetic retinopathy, a diabetes-related eye disease that can cause vision loss. Conducted at a primary healthcare centre in Punjab, India, the study analysed 272 retinal images from 136 participants using two different cameras. The findings revealed considerable differences in diagnostic accuracy across AI systems and imaging devices. One algorithm achieved sensitivity as high



as 97.5%, identifying most cases but producing more false-positive results. Another demonstrated a better balance between sensitivity and specificity, while the third showed moderate performance. Importantly, the same AI algorithm performed differently depending on the camera used. The findings highlight the need to validate AI screening tools under real-world healthcare conditions before widespread implementation, particularly in primary care settings where reliable early detection is essential.

Chauhan A. et al., Indian Journal of Ophthalmology, 2026.

ARTIFICIAL INTELLIGENCE COULD ACCELERATE DISCOVERY OF MATERIALS FOR NEXT-GENERATION BATTERIES

Researchers have proposed an artificial intelligence (AI)-driven framework to accelerate the discovery of solid electrolytes, essential materials for developing safer and more efficient next-generation batteries.

Unlike conventional liquid electrolytes, solid electrolytes offer potential advantages in battery safety and performance, but identifying suitable materials remains challenging. In this perspective article, scientists explain how advanced AI tools, including large language models and machine-learning-based simulations, could transform battery materials research. Their proposed approach integrates scientific literature analysis, material prediction, computer simulations and laboratory testing into a continuous, self-improving discovery process. Such systems could help researchers identify promising materials while reducing time-consuming experimental trials. However, challenges involving data quality, material interfaces and reproducibility remain. The framework offers a roadmap towards autonomous laboratories capable of accelerating solid-state battery innovation.

Cheng E. J. et al., Advanced Materials, 2026.

ROBOTICS & AUTOMATION

LOW-COST 3D-PRINTED ROBOTIC HAND USES MUSCLE SIGNALS AND AI TO CONTROL MOVEMENT

Researchers have developed a low-cost, 3D-printed robotic hand that uses muscle signals and artificial intelligence to control finger movements. The prototype, costing approximately $122–232 in components, offers a potentially affordable alternative to expensive commercial prosthetic systems. Using a sensor that detects electrical activity from muscles, the device translates signals into hand gestures through machine-learning algorithms. Researchers evaluated five AI models using experimental recordings from ten able-bodied participants. The Random Forest algorithm achieved the highest accuracy of 68.7% in identifying three gestures from previously unseen participants. The robotic hand responded within 285 milliseconds and successfully held objects weighing up to 200 grams. Although further testing with amputees

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is necessary, the study demonstrates a promising approach towards developing accessible, affordable and intelligent prosthetic technologies.

Shinde A. et al., Journal of Electrical Bioimpedance, 2026.

NEW AI FRAMEWORK COULD HELP AGRICULTURAL ROBOTS NAVIGATE CROP FIELDS MORE ACCURATELY

Researchers have developed an artificial intelligence (AI) framework designed to help autonomous agricultural robots navigate crop fields more accurately. Agricultural robots often struggle with changing light conditions, uneven soil surfaces and irregular crop arrangements, making reliable navigation challenging. The proposed system combines deep learning with a Temporal Dynamic Graph Neural Network to identify safe pathways between crop rows. Using annotated images of cornfields, researchers trained the framework to distinguish navigable areas from obstacles and extract stable navigation lines. The system achieved an overall accuracy of 98.01%, outperforming several existing approaches in the reported experimental comparisons. Although further validation under real-world field conditions is needed, the findings highlight the potential of advanced AI systems to improve robotic navigation, support precision agriculture and reduce dependence on manual field operations.

Kirubakaran S. et al., Pest Management Science, 2026.

ENERGY & CLEAN TECHNOLOGY

IIT BOMBAY RESEARCHERS DEVELOP MORE EFFICIENT AND SCALABLE PEROVSKITE SOLAR CELLS

Researchers at IIT Bombay have developed an improved approach to manufacturing larger, more efficient and stable perovskite solar cells, addressing a major challenge in next-generation solar technology. The team engineered an ultrathin molecular layer that improves the quality of light-absorbing perovskite films by reducing defects and enhancing uniformity. Smaller solar cells achieved a power conversion efficiency of 20.30%, while larger devices measuring 5.2 square centimetres maintained an impressive 18.88% efficiency. This represented only about a 7% relative efficiency reduction despite the substantial increase in device area. The optimized cells also demonstrated improved resistance to heat and moisture, retaining at least 75% of their initial performance for more than 680 hours under damp-heat testing. These findings offer a promising pathway towards commercially scalable, high-performance perovskite solar technologies.

Chityala V. G. et al., ACS Applied Materials & Interfaces, 2026.



SCIENTISTS TURN USED BATTERIES AND LEMON EXTRACT INTO MATERIAL FOR SOLAR DESALINATION

Researchers in India have developed an environmentally friendly approach to solar-powered desalination using discarded household batteries and natural lemon extract. The team recovered materials from spent zinc–carbon batteries and treated them with freshly squeezed lemon juice to create an efficient solar absorber. Under simulated sunlight, the recycled material achieved a water evaporation rate of approximately 4.02 kilograms per square metre per hour in saline water containing 3.5% salt. The material also performed effectively at higher salt concentrations and maintained its performance over repeated uses. Researchers found that lemon extract improved heat retention and evaporation efficiency more effectively than citric acid alone. By combining battery waste recycling with solar-driven water evaporation,efficiency more effectively than citric acid alone. By combining battery waste recycling wi-

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th solar-driven water evaporation, the study offers a promising approach to developing affordable desalination technologies while reducing environmental waste.

Ballav N. et al., ChemSusChem, 2026.

MATERIALS SCIENCE & NANOTECHNOLOGY

RESEARCHERS DEVELOP BRIGHTER AND MORE DURABLE INFRARED LEDs USING QUANTUM DOTS

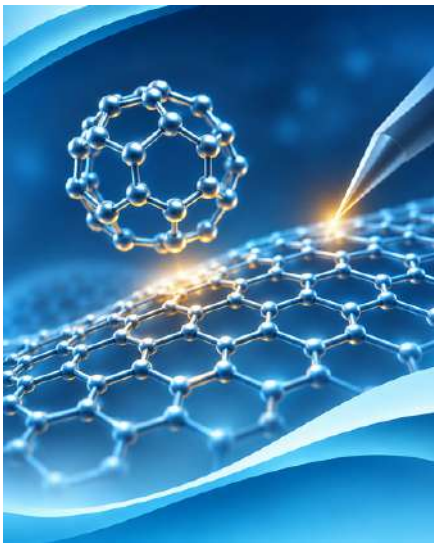
Researchers have developed an improved quantum dot technology that could enable brighter, more efficient and longer-lasting short-wave infrared light-emitting diodes (LEDs).

These devices are important for applications such as biomedical imaging and optical communication. The team engineered an extremely thin cadmium sulfide shell around lead sulfide quantum dots, improving their surface properties while maintaining efficient charge transfer. The optimized LEDs achieved an external quantum efficiency of 8.08% and a maximum radiance of 16.26 watts per steradian per square metre, representing improvements of 12% and 55%, respectively, over existing binary quantum dot designs.

Their operational stability also increased 3.5-fold compared with devices without protective shells.

The findings demonstrate a promising approach to manufacturing high-performance infrared light sources using solution-based processing techniques.

Mitra A. et al., ACS Applied Materials & Interfaces, 2026.



NEW THEORETICAL MODEL EXPLAINS HOW ELECTRIC FIELDS CAN CONTROL METAL–INSULATOR SWITCHING

A researcher has developed a theoretical framework explaining how certain materials can become trapped between metallic and insulating states, offering insights into future electronic memory technologies.

The study focuses on thin films of vanadium sesquioxide (V_2O_3), a material that undergoes a temperature-dependent transition between conducting and insulating states. Using mathematical modelling and simulations, the research shows how mechanical strain from the underlying substrate and structural disorder can prevent this transition from completing, leaving microscopic regions in different electronic states.

The model further predicts that an applied electric field can overcome these barriers and enable controlled switching between resistance levels.

Importantly, it distinguishes electric-field-driven switching from effects caused by heating. Although experimental validation is needed, the findings could guide the development of tunable electronic switches and multilevel memory devices.

Roy S., Journal of Physics: Condensed Matter, 2026.

BIOTECHNOLOGY & GENETIC ENGINEERING

CRISPR STUDY IDENTIFIES EFFECTIVE GENE-EDITING STRATEGY FOR PARKINSON'S DISEASE RESEARCH

Researchers have compared two CRISPR/Cas9 gene-editing strategies to develop cellular models for studying Parkinson's disease. The study targeted Park7, a gene associated with rare inherited forms of early-onset Parkinson's disease, using primary mouse embryonic fibroblasts. Scientists delivered CRISPR/Cas9 components directly as ribonucleoprotein complexes, avoiding plasmid DNA. A single-guide RNA approach achieved a higher overall editing frequency of 50.68%, compared with 24.87% using two guide RNAs. However, the dual-guide strategy generated larger DNA deletions and produced a substantially greater reduction in PARK7 protein levels, approximately 55%, compared with 12% using a single guide. These findings demonstrate that higher editing efficiency does not necessarily translate into stronger protein suppression. The approach could help researchers develop more reliable cellular models for investigating Parkinson's disease mechanisms.

Suryadevara L. et al., Molecular Biology Reports, 2026.

NEW CRISPR-BASED TEST DETECTS TICK-BORNE CATTLE INFECTION IN JUST 50 MINUTES

Researchers have developed a rapid CRISPR-based diagnostic test for detecting Theileria annulata, a tick-borne parasite responsible for tropical theileriosis in cattle. The disease causes substantial economic losses in livestock farming, making early detection essential. The new test combines recombinase polymerase amplification (RPA) with CRISPR/Cas12a technology to identify parasite DNA within 50 minutes. It detected as few as ten DNA

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copies per reaction without cross-reacting with other major bovine blood parasites. When evaluated using 206 cattle samples, the assay identified 163 positive cases, compared with 151 detected by conventional PCR and 116 by microscopy. Against PCR, it achieved 100% sensitivity and 78.18% specificity. The findings highlight its potential for rapid veterinary diagnosis, particularly in resource-limited settings, although further field validation is needed.

Mondal A. et al., Acta Tropica, 2026.

NEUROSCIENCE & BRAIN SCIENCE

BRAIN SIGNALS COULD HELP REHABILITATION DEVICES DETECT AND CORRECT MOVEMENT ERRORS

Researchers have demonstrated that brain activity can reveal movement errors during electrically assisted rehabilitation, potentially enabling smarter therapies for people with impaired motor function. The study investigated error-related brain signals generated when individuals observed or experienced movements that differed from expectations. Using electroencephalography (EEG), the researcher examined both virtual arm movements and movements produced through functional electrical stimulation, a technique that activates muscles using electrical impulses. A machine-learning system identified movement-related errors with an accuracy of 96% for discrete movements and 91% for continuous movements. Importantly, these signals were detectable even when errors originated from the stimulation device itself. The findings suggest that future rehabilitation systems could use brain signals to recognize movement errors and automatically adjust stimulation, potentially reducing dependence on additional physical sensors.

Bhagat N. A., npj Biomedical Innovations, 2026.

STUDY LINKS CHRONIC MICROPLASTIC EXPOSURE TO BRAIN DAMAGE AND METABOLIC DISRUPTION

Researchers have uncovered how prolonged exposure to polystyrene microplastics can disrupt brain metabolism and neurological function in fruit flies (Drosophila melanogaster). The study examined flies exposed to two concentrations of microplastics through their diet, revealing impaired movement, reduced climbing ability, altered feeding behaviour and disrupted daily activity rhythms. Detailed brain analysis identified widespread changes in amino acid metabolism, energy production and neurotransmitter regulation. Researchers also observed increased oxidative stress, mitochondrial dysfunction and neuronal damage. Activities of two important antioxidant enzymes, catalase and superoxide dismutase, declined by 46% and 40%, respectively. Reduced dopamine levels further suggested disruption of pathways involved in movement control. Although these findings cannot be directly extrapolated to humans, they provide important insights into the potential neurological risks associated with prolonged microplastic exposure.



Rathor P. et al., Neurotoxicology, 2026.

MATHEMATICS, STATISTICS & COMPUTATIONAL SCIENCE

AI IDENTIFIES SIX POTENTIAL BLOOD BIOMARKERS FOR EARLY DETECTION OF HEART, KIDNEY AND METABOLIC DISORDERS

Researchers have identified six potential molecular biomarkers that could help detect susceptibility to interconnected cardiovascular, kidney and metabolic disorders before significant organ damage occurs.Using an explainable artificial intelligence approach called Monoto-

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nic Additive XGBoost, the team analysed gene-expression data from cardiovascular disease, chronic kidney disease and type 2 diabetes. The analysis identified six genes—EEF1D, RPL27A, ERO1LB, JUN, POSTN and SERPINE2—associated with shared biological disturbances, including inflammation, vascular dysfunction, cellular stress and tissue fibrosis. These molecular signatures could potentially be measured through blood-based laboratory tests, offering a less invasive approach to early risk assessment. Although further clinical validation is required, the findings provide a promising foundation for developing integrated screening strategies that assess multiple interconnected chronic diseases rather than evaluating each condition separately.

Sharma Y. and Das A., Computational Biology and Chemistry, 2026.

NEW AI FRAMEWORK IMPROVES RIVER FLOW PREDICTION IN DAM-REGULATED BASINS

Researchers have developed an advanced machine-learning framework to improve river flow predictions in dam-regulated systems, where sudden discharge changes and extreme flows often challenge conventional forecasting models. Using daily river discharge records spanning 1972–2022, the team evaluated 17 model configurations and introduced 25 hydrological features to improve prediction accuracy. Their approach combined deep learning with specialized training strategies designed to capture high-flow events, particularly during monsoon conditions. The resulting ensemble model achieved a Nash–Sutcliffe eff-



iciency of 0.636 and a Kling–Gupta efficiency of 0.709, while reducing prediction bias by 63% compared with a baseline model. Importantly, the study found that hydrological feature engineering and training design contributed more to accuracy improvements than increasingly complex AI architectures, offering valuable insights for water-resource management and flood forecasting.

Dubey P. et al., Water Research, 2026.

SOCIAL & BEHAVIORAL SCIENCES

NEW MENTAL HEALTH SCREENING TOOL COULD STRENGTHEN PRIMARY HEALTHCARE IN INDIA

Researchers have developed and pilot-tested a simplified mental health screening and management workflow to help frontline healthcare workers identify and manage mental health and substance use disorders in India. The study involved 107 community health officers across six Indian states who received three days of classroom training and one day of supervised field practice. Following training, participants demonstrated significant improvements in mental health knowledge (12.8%) and practical skills (16.5%), alongside reduced negative attitudes. More than 89% successfully applied standard depression and anxie-



ty screening tools, while approximately 88% correctly identified mental health emergencies. The complete assessment took an average of 16.7 minutes. These findings suggest that structured training and simplified clinical guidance could strengthen mental healthcare delivery in underserved communities, although larger implementation studies are needed.

Dahiya N. et al., 2026.

STUDY CALLS FOR BETTER SCHOOL-BASED ALCOHOL EDUCATION TO PREVENT UNDERAGE DRINKING IN INDIA

Researchers identified critical gaps in school-based alcohol education across India through qualitative discussions with teachers, school counsellors, education officials, and students in Chandigarh and Delhi NCR. Existing programmes remain largely fragmented and inconsistent, hindered by limited teaching resources, inadequate specialised teacher training, and weak institutional support. Strong peer influence, family environments, and broader social norms also heavily shape adolescent attitudes. Consequently, the study recommends structured, age-appropriate prevention programmes that strengthen practical decision-making skills well beyond awareness of alcohol-related health risks.

Ghosh A. et al., Indian Journal of Psychological Medicine, 2026.

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SCIENCE IN FOCUS



NEW SATELLITE

India Launches New Satellite to Strengthen Its Navigation System

India has successfully launched a new navigation satellite, marking an important step towards strengthening its independent satellite navigation system, NavIC. The Indian Space Research Organisation (ISRO) launched NVS-03 aboard the GSLV-F18 rocket from Sriharikota on 30 October 2026. The rocket successfully placed the satellite into its planned transfer orbit. ISRO completed its first orbital manoeuvre on 31 October, with further adjustments planned to reach its designated orbit. NavIC is India's homegrown alternative to satellite navigation systems such as the United States' GPS. It provides location and timing services across India and approximately 1,500 kilometres beyond its borders. These services support transportation, aviation, shipping, agriculture, disaster management and telecommunications. NVS-03 is the third satellite in a planned series of five next-generation navigation satellites. Weighing approximately 2,250 kilograms, it carries navigation equipment operating across three frequency bands. It also includes an Indian-developed atomic clock that provides precise timing needed for accurate positioning. The satellite is designed to improve NavIC's reliability and reduce India's dependence on foreign navigation systems. Two additional satellites, NVS-04 and NVS-05, are planned to strengthen the network, supporting more reliable navigation services for civilian and strategic applications. Together, these developments represent an important opportunity to build more inclusive, affordable and locally relevant AI solutions for India's future.



DIGI YATRA TRIALS

India Begins Digi Yatra Trials for International Passengers at Seven Airports

India has begun testing Digi Yatra for international passengers at seven airports, marking a significant step towards making air travel faster and more convenient through digital technology. Digi Yatra is a digital identity system that allows passengers to move through airport checkpoints using facial recognition technology. Until now, the service has primarily supported domestic travel. The new trials, running from November to December 2026, cover airports in Delhi, Bengaluru, Hyderabad, Kochi, Mumbai, Chennai and Amritsar. Eligible Indian passengers holding e-passports can use the service on selected international flights operated by Air India and IndiGo. Passengers must create a digital identity credential through the Digi Yatra mobile application. This involves scanning their e-passport, reading its embedded electronic chip and verifying their identity through a selfie. The encrypted digital credential is securely stored on their personal smartphone for seamless verification at designated airport checkpoints. However, all passengers must still carry valid physical travel documents and complete standard immigration, customs, and other mandatory border checks. Currently, Digi Yatra already serves over 26.5 million registered users across 39 domestic airports, supporting more than 110 million contactless journeys. Operational feedback gathered from these ongoing international trials will guide a much wider rollout planned for 2027, potentially making cross-border travel smoother while expanding India's modern digital aviation infrastructure.

SCIENCE IN FOCUS



SUSTAINABLE FISH FARMING

India Launches Organic Fisheries Initiative in Sikkim to Promote Sustainable Fish Farming

India has taken a new step towards sustainable aquaculture by establishing its first organic fisheries cluster in Soreng district, Sikkim, under the Pradhan Mantri Matsya Sampada Yojana (PMMSY).The initiative aims to promote environmentally friendly fish farming while improving farmers' incomes and market opportunities. It builds on Sikkim's established organic farming practices. On 2 November 2026, the Indian government launched a Standard Operating Procedure (SOP) for organic fisheries certification in northeastern India. The framework is intended to support chemical-free fish production, improve product traceability and establish credible certification standards. The government also inaugurated fisheries projects worth ₹3.75 crore, including hatcheries, feed mills, cold storage facilities and advanced aquaculture technologies such as Biofloc and Recirculating Aquaculture Systems (RAS). The organic fisheries cluster will focus on species including Amur carp, Indian major carps and trout, encouraging production without harmful chemicals, antibiotics or pesticides. Sikkim has also signed an agreement with the Indo-Tibetan Border Police to explore regular procurement of locally farmed rainbow trout. Together, these targeted initiatives are expected to significantly strengthen sustainable fish production, improve direct market access, and create new income opportunities for local fish farmers, although their long-term environmental and economic benefits remain to be fully demonstrated.



LANGUAGES AND DIGITAL INNOVATION

India Launches Homegrown AI Models to Support Indian Languages and Digital Innovation

India has introduced three homegrown artificial intelligence (AI) models, marking an important step towards developing AI technologies suited to the country's languages and digital needs. Released on 3 November 2026 under the IndiaAI Mission, the models include EKA-1, developed by Soket Labs, and Dhīr 2B and Dhīr 5B, developed by ZenteiQ. EKA-1 contains 26.3 billion parameters and was trained on approximately 7.5 trillion tokens of data. It supports all 22 officially recognised Indian languages and English, with capabilities designed for mathematics, coding, reasoning and automated tasks. The smaller Dhīr models support English and 10 Indian languages. They are designed to operate on local devices, including smartphones, without continuous internet access. This could make AI services more accessible in remote areas while allowing sensitive information to remain on users' devices. The models were developed with government-supported computing infrastructure under the IndiaAI Mission, launched in 2024 to strengthen domestic AI research and innovation. These emerging technologies could effectively support critical everyday applications across education, healthcare, essential public government services, modern banking, and national cybersecurity. However, their wider long-term societal impact will ultimately depend on practical on-ground deployment, broad user accessibility, and reliable, consistent performance under demanding real-world conditions, particularly across India's diverse regional languages and varied digital environments.

SCIENCE IN FOCUS



NEW DIGITAL PLATFORM

India Launches New Digital Platform to Track Science and Technology Progress

India has launched a new digital platform to track scientific research, innovation and technological development across its states and union territories. Developed by NITI Aayog, the India Science and Technology (S&T) Scoreboard was launched on 3 November 2026 in New Delhi. It aims to bring together research and innovation data that were previously scattered across different sources. The interactive platform provides information on universities, research institutions, technology startups and innovation centres. It also tracks scientific publications, patents, research quality, impact and collaboration across academia, government laboratories and industry. Unlike traditional assessments that focus mainly on the number of publications or patents, the Scoreboard also considers research quality, collaboration and open access to scientific findings. Users can compare states and union territories, examine research trends over time and explore detailed profiles highlighting scientific strengths, policies and development priorities. The platform is intended to help governments identify research gaps, improve resource allocation and develop more effective science and technology policies. By making reliable scientific information much easier to access and compare, this initiative could significantly strengthen national research planning, encourage cross-institutional collaboration, and support more balanced regional technological development across India. Ultimately, its long-term impact will depend heavily on consistent data quality and sustained practical use.



ENERGY STORAGE

India Approves ₹14,500 Crore Plan to Expand Energy Storage and Support Renewable Power

India has approved a ₹14,500 crore programme to expand electricity storage, aiming to make renewable energy more reliable and strengthen the country's power supply. Solar and wind power depend on weather conditions, making electricity storage essential for supplying power when sunlight or wind is unavailable. Large-scale storage systems can save excess electricity and release it when demand increases. On 4 November 2026, the Union Cabinet approved a five-year funding scheme to support the development of 92 gigawatt-hours (GWh) of energy storage capacity by 2031. The proposed capacity includes 60 GWh from pumped hydropower, which stores energy by moving water between reservoirs, and 30 GWh from battery storage systems. Another 2 GWh will come from emerging storage technologies. The programme is expected to attract investments of approximately ₹97,600 crore. Battery storage projects must also meet a minimum 40% domestic content requirement to encourage Indian manufacturing and reduce import dependence. The scheme has been approved, but the proposed storage facilities are yet to be commissioned. Once developed, these systems could help balance electricity supply and demand, reduce dependence on conventional power generation and support India's transition towards cleaner, more reliable energy. This strategic investment could significantly accelerate clean renewable energy adoption while improving overall grid stability and national energy security.

SCIENCE IN FOCUS



LITHIUM AND NICKEL

India Approves ₹2,814 Crore Plan to Boost Lithium and Nickel Processing

India has approved a ₹2,814 crore programme to strengthen domestic processing of lithium and nickel, two important minerals used in batteries, electric vehicles and modern technologies. These minerals are essential for clean energy systems, electronics and defence equipment. However, India relies heavily on imported refined materials because its domestic processing infrastructure remains limited. On 4 November 2026, the Union Cabinet approved a five-year scheme covering 2026–2031 to support the establishment of mineral processing facilities. The programme aims to develop four plants: two lithium processing facilities, each with a minimum capacity of 30,000 tonnes, and two nickel processing facilities, each with at least 50,000 tonnes. Cobalt may also be recovered during nickel processing. Under the scheme, eligible projects can receive subsidies covering 30% of their investment costs, subject to specified limits. Companies will be selected through technical assessments and competitive bidding. Although the funding scheme has been approved, the proposed facilities have not yet been established. Once operational, these plants could reduce dependence on imported refined minerals, strengthen domestic battery supply chains and support India's growing electric vehicle and renewable energy industries. Their success will depend on investment, technology availability and implementation. The initiative could also encourage technological innovation and create skilled employment opportunities in mineral processing. Developing domestic expertise will be crucial for building a competitive and sustainable critical minerals industry.



NATIONAL PARKS

India Introduces New Guidelines to Protect Biodiversity Beyond National Parks

India has introduced new conservation guidelines to protect biodiversity in areas outside traditional national parks and wildlife sanctuaries. Many important ecosystems, including sacred groves, wetlands, coastal habitats and community-managed landscapes, support wildlife but lack formal protected-area status. Recognising their conservation value could help protect more of India's natural heritage. On 3 November 2026, India released its 2026 guidelines for Other Effective Area-Based Conservation Measures (OECMs) at the United Nations biodiversity conference in Armenia. The guidelines establish a framework for identifying and recognising areas that provide long-term biodiversity conservation without changing their ownership or legal status. Eligible sites may include biodiversity parks, community-managed water bodies, seagrass beds and seasonal fishing restriction zones. Recognised areas will undergo periodic monitoring to assess conservation outcomes. Alongside the guidelines, India has initiated a six-year conservation project covering six landscapes and seascapes, including Odisha, Uttarakhand and Lakshadweep. The ambitious new project aims to establish 50,000 hectares of vital terrestrial conservation areas, restore 5,000 hectares of severely degraded land, and directly benefit 50,000 local people across the region. Together, these targeted ecological initiatives could significantly strengthen active community participation in long-term biodiversity conservation efforts and effectively support India's broader global commitment to conserving 30% of its national land and marine areas by 2030.

SCIENCE IN FOCUS



STERILE MEDICINES

India Proposes Stricter Microbial Safety Standards for Sterile Medicines

India has proposed new safety standards to strengthen microbial contamination monitoring in pharmaceutical manufacturing, aiming to improve the quality and safety of sterile medicines.

Sterile medicines, including injections and intravenous fluids, must be manufactured under carefully controlled conditions to prevent contamination by microorganisms. Even small amounts of microbial contamination can pose serious risks to patients. On 4 November 2026, the Union Health Ministry announced proposed amendments to Schedule M of the Drugs Rules, 1945, to align India's manufacturing requirements with World Health Organization (WHO) guidelines. The proposed changes focus on Grade A clean areas, where sterile medicines, containers and components are exposed during manufacturing. Under the revised requirements, any microbial growth detected in these highly controlled areas would trigger an investigation. This approach aims to identify possible contamination sources and strengthen quality control. The amendments are intended to bring Indian pharmaceutical manufacturing standards closer to internationally recognised practices. Importantly, these changes have only been proposed and are not yet final. The government has invited public comments and suggestions before proceeding. If effectively implemented, the revised regulatory standards could improve microbial contamination monitoring, strengthen pharmaceutical quality assurance, and enhance global confidence in the safety of sterile medicines manufactured across India.



TARGETS 2047

Odisha Sets Ambitious Millet Cultivation Targets for 2047

Odisha is planning a major expansion of millet cultivation to strengthen food security, improve nutrition and support climate-resilient agriculture. Millets are nutritious crops that can grow under challenging conditions, making them increasingly important as farmers face changing rainfall patterns and rising temperatures. At a national event on agro-biodiversity conservation and sustainable food systems held in Bhubaneswar on November 10, 2026, a long-term vision was outlined to expand millet cultivation in Odisha from 1.79 lakh hectares to 5 lakh hectares by 2047, with a production target of 8 lakh metric tonnes. The state has already made progress through its Shree Anna Abhiyan initiative. During 2024–25, Odisha procured 7.5 lakh quintals of ragi, or finger millet. The state has also documented 163 traditional finger millet landraces, highlighting its valuable agricultural diversity. Future priorities include improving cultivation practices, promoting lesser-known millets such as suan and kangu, developing affordable processing machinery and strengthening farmer organisations and women's self-help groups. A dedicated Centre of Excellence on Millets at Odisha University of Agriculture and Technology has also been proposed. These initiatives could help conserve traditional crop diversity while creating new opportunities for farmers, food businesses and sustainable agriculture. Expanding millet cultivation could also strengthen rural livelihoods and encourage healthier dietary choices. Traditional farming knowledge with modern agricultural research will be essential for achieving ambitious goals.

SCIENCE IN FOCUS



DIGITAL INITIATIVE

India Opens National Research Facilities to Startups Through New Digital Initiative

Developing new technologies often requires expensive laboratory equipment, testing facilities and specialised research infrastructure. For many startups, accessing these resources remains a major challenge, slowing innovation and increasing development costs. To address this gap, India launched a digital integration between the Startup India and I-STEM portals on November 6, 2026, making it easier for government-recognised startups to discover and request access to research facilities across the country. The initiative connects startups with scientific equipment and testing infrastructure available at universities and research institutions. As of November 6, the I-STEM platform listed 31,540 equipment items across 4,044 registered institutions. The new system enables automated verification of startup recognition and simplifies the process of finding suitable facilities. However, access requests will still require approval from the institutions managing the equipment. Future plans include introducing a single sign-on system to make access more convenient. The initiative could particularly benefit startups working in biotechnology, advanced materials, electronics and other emerging technologies by reducing the need to purchase costly equipment. By directly connecting emerging startups with existing national research infrastructure, India aims to significantly strengthen collaboration between academia and industry, accelerate commercial product development, and make far better use of publicly funded scientific resources.



RESEARCH PROGRAMME

India Moves Closer to Joining Europe's Major Research and Innovation Programme

India and the European Union (EU) have taken a major step towards strengthening international scientific cooperation by completing negotiations for India's participation in Horizon Europe, one of the world's largest research and innovation funding programmes. Announced on November 7, 2026, the development builds on existing scientific partnerships between India and the EU. Discussions began following the India–EU Summit in January 2026, with formal negotiations starting in July. Once the association is formally completed, Indian universities, research institutions and industries will be able to participate in eligible Horizon Europe funding opportunities alongside European partners. The programme supports research across important fields, including healthcare, biotechnology, digital technologies, space, climate change, clean energy, agriculture and sustainable food systems. Participation could help Indian scientists access advanced research facilities, collaborate with international experts and develop new technologies. It may also create opportunities for researcher mobility and joint innovation projects. The agreement could be particularly valuable for addressing shared challenges such as climate change, emerging diseases, food security and sustainable development. Although negotiations have concluded, the announcement does not confirm that India's association has formally taken effect. Further steps will be needed before researchers can benefit from the new arrangements.

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 BIOACTIVE HYDROGEL THAT COULD HELP DIABETIC WOUNDS HEAL FASTER

Healing a wound can be particularly difficult for people living with diabetes. Even minor injuries may take longer to heal, increasing the risk of infection and other complications. Although conventional wound dressings can protect damaged tissue and maintain moisture, they do not always address the cellular problems responsible for delayed healing. A patented invention proposes a bioactive hydrogel designed not only to cover diabetic wounds but also to support the natural repair processes of skin cells.

The technology combines gelatin and chitosan, two materials used in biomedical applications, with an enzyme called neuraminidase. The enzyme targets the glycocalyx, a sugar-rich coating surrounding cells. In diabetes, changes in this coating can interfere with the movement and activity of fibroblasts, the cells responsible for producing collagen and helping repair damaged skin. By modifying this layer, the hydrogel aims to improve fibroblast movement, multiplication and tissue regeneration.

Laboratory experiments using human diabetic skin cells showed improved cell migration and approximately 20% greater cell proliferation in the presence of the enzyme. Further testing in diabetic rats showed encouraging wound-healing results, including increased collagen formation, development of new blood vessels and regeneration of the skin surface. After 14 days, wounds treated with two enzyme-loaded hydrogel formulations had remaining wound areas of approximately 5.81% and 4.36%, respectively.

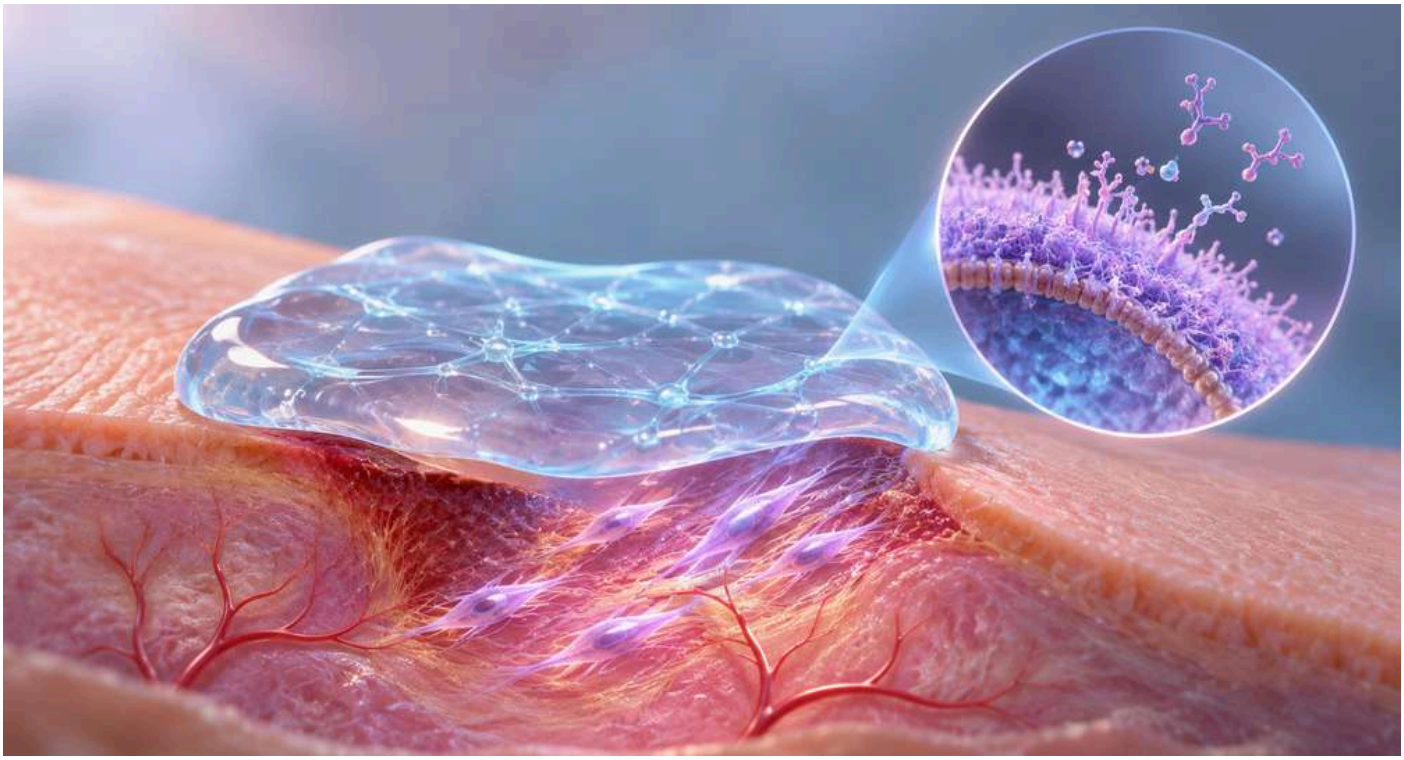
The invention's significance lies in combining a protective wound dressing with an active ingredient that addresses a biological mechanism associated with poor wound healing in diabetes. Unlike conventional dressings that primarily provide a protective environment, this approach seeks to improve the behaviour of the cells involved in tissue repair. Although the laboratory and animal findings are promising, clinical studies will be necessary to establish its safety and effectiveness in patients. The invention highlights how biomaterials and cell biology could contribute to more effective wound-care technologies.

INNOVATION

Sen, S. R., Ganesan, V., & Jahan, I. (2026). Hydrogel for diabetic wound protection. Indian Patent Application No. 202621008967, Patent No. 608410. Indian Patent Office.

By

Indian Institute of Technology Bombay.



| By Dr. Priyanka

TURNING AGRICULTURAL WASTE INTO HIGH-VALUE SILICON CARBIDE

Agricultural waste is a growing environmental concern, particularly in farming regions where large quantities of crop residues are burned or discarded after harvesting. Materials such as rice husks, wheat straw and sugarcane bagasse are often treated as waste, despite containing valuable chemical components. Meanwhile, industries depend on silicon carbide, an exceptionally hard and heat-resistant material used in electronics, electric vehicles, cutting tools and high-temperature equipment. Conventional silicon carbide production requires substantial energy and often relies on fossil-derived carbon sources. A new patented invention proposes a more sustainable approach by converting agricultural residues into high-purity silicon carbide.

The technology takes advantage of two naturally occurring components of agricultural waste: silica and carbon-rich organic matter. The process begins by treating dried crop residues with acid and alkaline solutions to extract silica and lignin, a natural substance found in plant cell walls. These components are then recovered together to form a finely mixed precursor material.

After drying and grinding, the material undergoes controlled heating at high temperatures, allowing silica and carbon to react and form silicon carbide. Additional treatment removes unwanted impurities to obtain a purified powder.

According to the patent description, the process can produce silicon carbide with a reported purity of 90–98%, depending on the agricultural material and processing conditions. The resulting material is described as having high hardness, thermal stability and semiconductor properties, making it potentially suitable for electric vehicle power electronics, renewable energy systems, industrial cutting tools and heat-resistant components.

The invention's significance lies in transforming low-value agricultural residues into a technologically important industrial material. Unlike conventional production methods that depend heavily on mined silica and fossil-derived carbon, this approach uses renewable biomass as a starting resource. It could also create opportunities to reduce agricultural waste burning while generating value from materials that are otherwise discarded.

INNOVATION

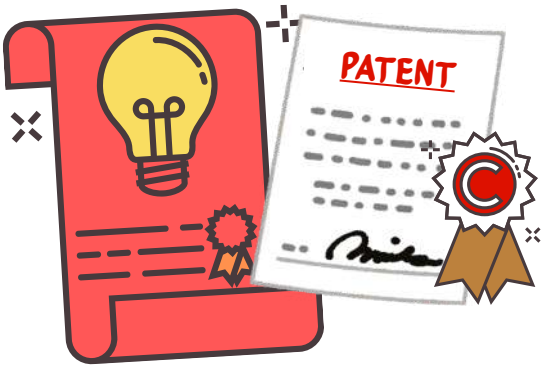
Gupta, N. (2026). A sustainable process for the preparation of highly pure silicon carbide (SiC) from agricultural waste. Indian Patent No. 608395

By

Agrosil Private Limited.



Dark by Design, Cool by Function: Defect-Engineered Spinel Pigments for Solar Heat Management





Dr. Sheik Muhammadhu Aboobakar Shibli
University of Kerala, India
| Scientific Profile |
| Organization Link |
| Factors Press |

AREAS OF EXPERTISE
Protective coatings • Electrocatalysts • Electrodes • Photocatalytic Hydrogen Generation



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| Factors Press |

AREAS OF EXPERTISE
Sustainable and Functional coatings • Advanced material characterization • Surface and Interface Engineering • Hydrogen Generation

THE INNOVATION EDGE

Can dark-coloured buildings and vehicles stay cool under the sun? Prof. Sheik Muhammadhu Aboobakar Shibli and Dr. Saithathul Fathima Sameera of the University of Kerala have developed a patented technology challenging the idea that dark surfaces must absorb more heat. Their specially engineered pigments retain dark colours while reflecting significant solar infrared radiation. By precisely modifying crystal structures, these pigments offer a promising solution for cooler roofs, buildings, and vehicles, potentially reducing cooling energy demand and supporting sustainable, heat-resilient cities without compromising appearance.

Have you observed that wearing a black shirt on a hot summer day makes you feel hotter, whereas a white shirt helps keep you cooler? We've all learned the simple rule that dark colours absorb sunlight and trap heat, while light colours reflect it. But what if a surface appears pitch black or deep brown to our eyes, yet behaves like a shiny mirror reflecting the sun's heat away?

Looking Beyond What the Eye Can See

Let's look at sunlight. The light hitting a surface isn't just the visible colours we that see; but a major part of the sun's energy arrives as invisible near-infrared (NIR) radiation, which carries pure heat, particularly around 1100 nm. Pigments are coloured substances that give paints, inks, and other materials their colour by selectiv-



Figure 1. Comparative Analysis of Conventional and Advanced Near-Infrared (NIR) Reflective Cool Roof Performance. Comparison of performance of conventional and advanced roofs under solar radiation. Left: A Conventional low-reflectance roof (R% 10-20, high heat absorption, high building temperature). Right: A High-reflectance IR cool roof (R% 61 using a new dark-colored pigment; reflects heat, lowering building temperature).

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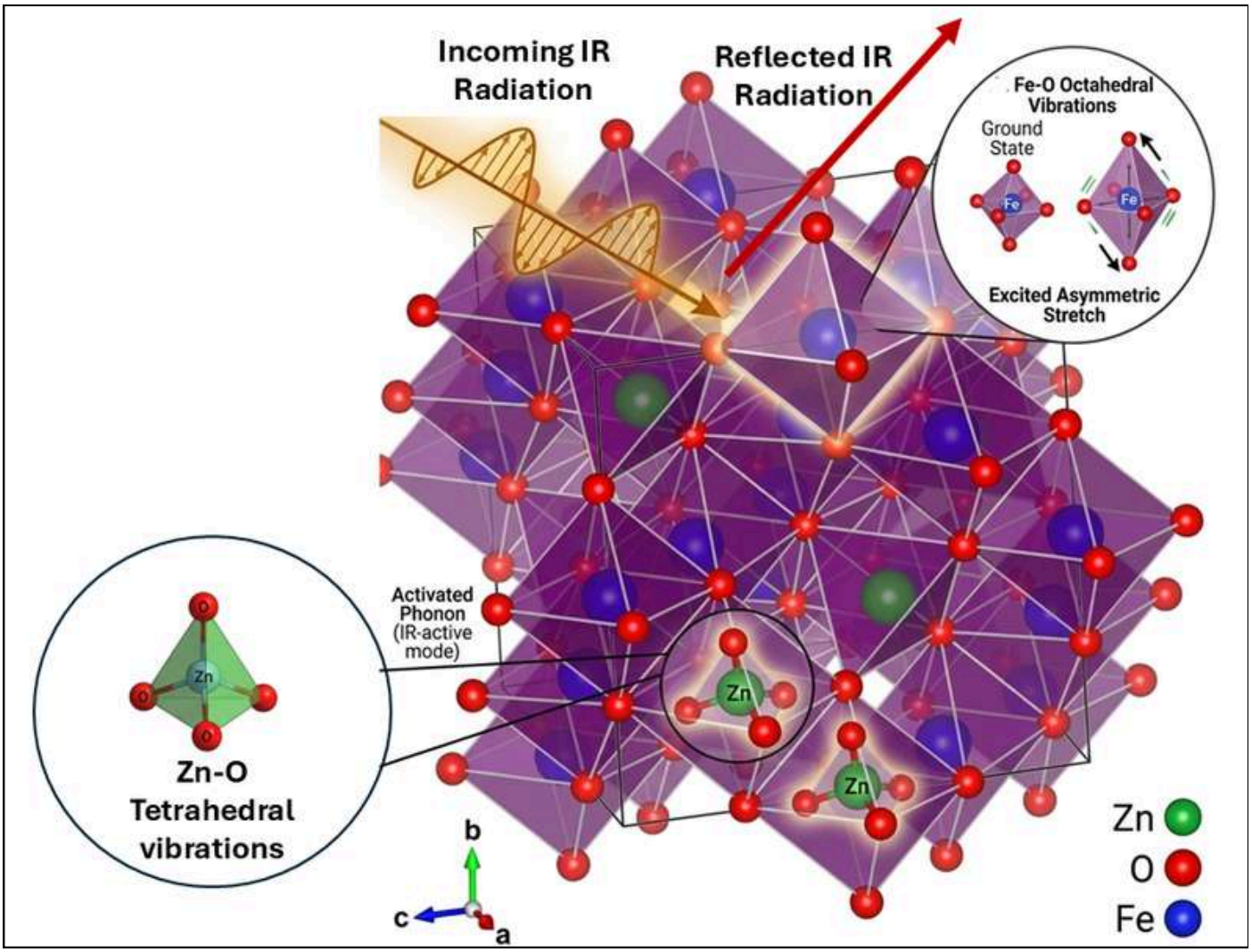


Figure 2. Infrared (IR) Reflection in a Spinel Lattice. Illustration of the interaction of incoming near-infrared (NIR) radiation with a complex spinel-type oxide crystal lattice. The lattice is composed of zinc (Zn, green spheres), iron (Fe, blue spheres), and oxygen (O, red spheres). The phonon excitations within iron-centered Fe-O octahedra; and a Zn-O tetrahedron are shown.

ely absorbing and reflecting light. Pigments are used in paints, printing inks, plastics, textiles, cosmetics, ceramics, paper, construction materials, and art. Inorganic pigments are more stable under common environmental conditions than their organic counterparts. White pigments have high light-reflecting properties, which can produce excessive brightness or glare. This may cause visual discomfort, especially under strong lighting or sunlight. Hence, dark-shaded pigments are preferred and also for their aesthetic appeal. But in terms of functionality, commercial dark pigments often absorb both visible and near-infrared radiation, which limits aesthetic applications. Hence, buildings, pavement and automotive surfaces painted with conventional dark colours can become substantially hotter under intense sunlight. This creates a challenge for modern infrastructure: people require dark, attractive colours, but dark surfaces are often linked with greater heat absorption. This challenge becomes increasingly important as cities experience rising temperatures, increasing energy demand for cooling, and more recurring extreme-heat events. Concrete jungles act as thermal sponges, exacerbating the “urban heat-island effect” documented in the cities worldwide. Buildings account for approximately 30% of the worldwide energy demand. Thus, buildings, both residential and commercial, and infrastructure need to become not only energy-efficient but also more resilient to solar heat. Many materials have been developed for their heat reflective properties. Numerous approaches have been explored to control solar heating, including reflective coatings, cool roofs, and passive radiative cooling technologies. However, the challenge lies in achieving a dark aesthetic while maintaining high solar-reflective efficiency.(Fig.1)

The present approach tackles this problem at the level of the pigment material itself.

Engineering Colour and Heat Reflection

In the present work, we focus on engineering ceramic oxide materials, specifically transition metals. Instead of accepting the usual trade-off between dark colors and heat absorption, we precisely tweak the crystal lattice at the atomic level via controlled substitution of metal ions, resulting in a targeted crystal defect. By carefully replacing selected metal ions and controlling the defects in the crystal lattice, we can tune how the pigment interacts with sunlight; absorbing visible light for a rich dark colour while reflecting much of the heat-carrying NIR radiation out. Particle size tuning effectively optimizes Mie scattering specifically for NIR photons.

This process is unique in that it allows the pigment to selectively absorb light in the visible region, producing vibrant dark hues while remaining aesthetically striking. This is the mechanism of the present patented technology. (Fig.2)

The innovation is highly suitable for industrial scalability. The developed colourants can provide efficient total solar reflectance, which is the fraction of incoming sunlight reflected by a surface, while retaining visually attractive dark shades. Importantly, the concept is not restricted to a single colour. It can be meticulously extended across a wider palette of dark shades, including brown tones, creating opportunities for applications where aesthetics is as important as thermal performance.

The pigments are primarily crystallographically designed so as to be heavy-metal-free and can be incorporated into a wide range of conventional coating formulations. Validated at TRL-4, the developed pigments easily blend into industrial acrylic and polyurethane coatings.

Thus, without requiring significant infrastructure expenditures, the present cool coatings offer an affordable, scalable urban climate adaptation technique that can greatly improve air quality, lowers peak electricity use, and increases community resilience to climate change.

The current market of infrared-reflective coatings enters a phase change of structural expansion across the construction, automotive, and defense sectors. Due to the adoption of automotive LiDAR and ADAS, industrial automation, and construction activities, the Asia-Pacific region is the largest and fastest-growing regional market. With growing demand for energy-efficient buildings and heat-resilient infrastructure, the present pigments can offer an exciting opportunity to bring dark, aesthetically appealing surfaces for the next generation of cool coatings. For industries, the present material offers a feasible path to delivering "dark by design, cool by function" solutions that could satisfy both consumer aesthetic demands and the rigorous energy mandates of the next decade.

The next stage is the transition from laboratory validation to larger-scale coating demonstrations, weather-accelerated testing, durability assessment, and optimization for different substrates and climates. Integration with building-envelope technologies and smart material design could further expand the impact. By employing low-cost raw materials and a scalable synthesis approach, this high-performance IR-reflective pigment provides an economically viable, energy-saving alternative to the current expensive commercial cool pigments.

Ultimately, the objective is straightforward: A roof does not need to be white to be cool. A vehicle does not need to sacrifice its aesthetic dark colour to manage heat. And a building does not need to choose between aesthetics and energy performance.

The present patented technology offers a pathway towards the development of a new generation of materials in which appearance and thermal function are designed together—dark by design, cool by function.

All cool surfaces may therefore need not to be white in the next generation. It may be black, brown or any colour that the end users' prefers.

Memory, Ageing, Alzheimer's Disease and Biotech Innovation



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AREAS OF EXPERTISE
Alzheimer's disease | Memory reconstruction | Ageing | Mitochondrial dysfunction | Synaptic plasticity | Translational biotechnology

SNAPSHOT

Moving from academic research to biotechnology requires identifying practical opportunities and building collaborations to turn discoveries into useful technologies. In this conversation, Dr. Mordhwaj Singh Parihar, Founder and CEO of Bioexons LLC, shares his journey from neuroscience to entrepreneurship. Drawing on his work in ageing, memory, and Alzheimer's disease, he discusses startup challenges, funding, intellectual property, and the skills researchers need beyond academia, offering practical insights for scientists interested in turning laboratory discoveries into real-world applications.

Q *What first drew you to ageing, brain health and mitochondrial biology?*

A I was fascinated by a simple puzzle: why does a brain that works well for decades slowly lose its edge? Ageing is the largest risk factor for neurodegenerative disease, yet it is often treated as background rather than biology. My work led me to mitochondria, which power every cell. Neurons are especially energy-hungry, and when mitochondria falter, calcium balance, oxidative stress and synaptic strength all suffer. Three questions drive me: what makes a brain resilient, what changes first with age, and can we intervene early enough to matter?

Over three decades, my research has examined how oxidative stress and mitochondrial damage build up in the ageing brain, and how that stress can impair the connections between neurons. This led me to see memory loss as the end of a long chain of small failures in energy, repair and communication. Understanding that chain, not only its final stage, has shaped everything I have worked on since.

Q *What happens when we remember, and why does it matter for Alzheimer's?*

A We tend to imagine memory as a filing cabinet. The evidence suggests otherwise. Each time we remember, the brain rebuilds the memory from distributed pieces and then stabilizes it again, a process called reconsolidation. Remembering is closer to performing music than playing a recording.

If memory were a static archive, Alzheimer's would simply be lost files. If memory is active reconstruction, the disease can be seen as progressive failure of the machinery that rebuilds and restabilizes memories, which is a different research target.

Our review in Ageing Research Reviews (Parihar et al., 2027) adds a further step: a rebuilt memory becomes useful only when it is brought into conscious awareness and woven into our sense of self, place and time, which we call conscious integration. In Alzheimer's, both stages may falter, so a person loses not only facts but the felt continuity between past and present. This remains a testable idea.

Q *What evidence led you to see Alzheimer's as a disruption of memory rebuilding?*

A Two observations. People with early Alzheimer's disease often show uneven memory, accessible one day and not the next, which fits a rebuilding problem better than clean loss; and laboratory studies show that retrieval makes memories temporarily fragile, with re-stabilization depending on synaptic plasticity, protein synthesis and energy supply, systems stressed in Alzheimer's disease.

Other findings point the same way. In animals, blocking protein

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synthesis shortly after retrieval can weaken a memory, while in Alzheimer's mouse models some apparently lost memories can be recovered by stimulating the neurons that hold them, suggesting the trace is sometimes intact but hard to retrieve. Mitochondrial dysfunction, which I have studied for years, also limits the energy that synaptic remodeling needs.

In our article in Ageing Research Reviews, with Vihaan Goplani and Garima Sharma, we brought this evidence together and were candid about limits. Direct evidence of reconsolidation failure in patients remains thin, and inflammation, vascular factors and protein misfolding clearly contribute. It is a framework to test, not a replacement.

Q *How are memory and the brain's sleep rhythms connected?*

A During deep sleep, slow waves, spindles, and hippocampal sharp-wave ripples occur in tightly timed sequence, letting the hippocampus replay recent experiences to the cortex for long-term integration. Sleep is the brain's overnight editing session.

In people at risk of Alzheimer's, these rhythms are often disrupted. That matters twice: altered rhythms could be an early signal before obvious memory loss, and poor sleep may feed the disease by impairing memory reconstruction and waste clearance. Sleep measures are non-invasive and relatively inexpensive, making them attractive candidates for early detection.

Q *Why do amyloid-lowering treatments give only modest benefit, and what else should we investigate?*

A Removing amyloid is a real achievement and confirms it is part of the story. But plaques are one visible product of a long process; by the time they are cleared, circuits, energy supply and synaptic health may already be compromised.

The next wave should include protecting mitochondrial function and metabolic resilience, restoring healthy sleep and network rhythms, supporting synaptic plasticity, addressing inflammation, and intervening earlier. Combination strategies matched to a person's biology are likely to outperform any single approach.

Q *How could this view change diagnosis and treatment evaluation, and what evidence is missing?*

A Diagnostics could ask not only whether someone remembers, but how well they reconstruct and update memories, combining such tasks with sleep electrophysiology and standard biomarkers. Trials could add measures of memory dynamics and network function to broad cognitive scales.

In practice, this could mean a short battery of memory-updating tasks at routine check-ups, paired with a home sleep recording, to flag people for further testing. In drug trials, it would show whether a therapy restores memory rebuilding itself, not only whether plaques fall. These measures should be tested alongside existing biomarkers to show what they add.

We still need long-term studies tracking memory reconstruction, sleep rhythms and biomarkers together, direct evidence of reconsolidation changes in patients, and proof that any new measure predicts real-world outcomes. Until then, this is a promising hypothesis, not a clinical tool.

Q *How did Bioexons LLC begin, and what need was it created to address?*

A I founded Bioexons LLC in Washington State in 2018. After more than three decades in research, academic leadership and administration, I saw that many promising laboratory discoveries never progress toward products or solutions. The gap is often not innovation itself but translation: limited interdisciplinary collaboration, weak development strategy, and poor links between researchers and industry.

Bioexons LLC is a platform for life-science research and research-based technologies. As Founder and CEO, I provide scientific vision and strategy, evaluate opportunities, develop project concepts, explore collaborations, and keep our work rigorous and practical.

Q *What does Bioexons LLC do, and what are its priorities?*

A Bioexons LLC is a life-sciences research and development company that helps translate scientific ideas into potential real-world applications. Our current interests fall into three areas.

First, neuroscience, memory, and Alzheimer's: how memories are processed and reconstructed, and how this fails in ageing, with attention to synapses, mitochondria, and network dynamics. Second, artificial intelligence and integrative research: combining computational models with neuroscience to generate testable hypotheses. Third, translational biotechnology: evaluating research concepts and building

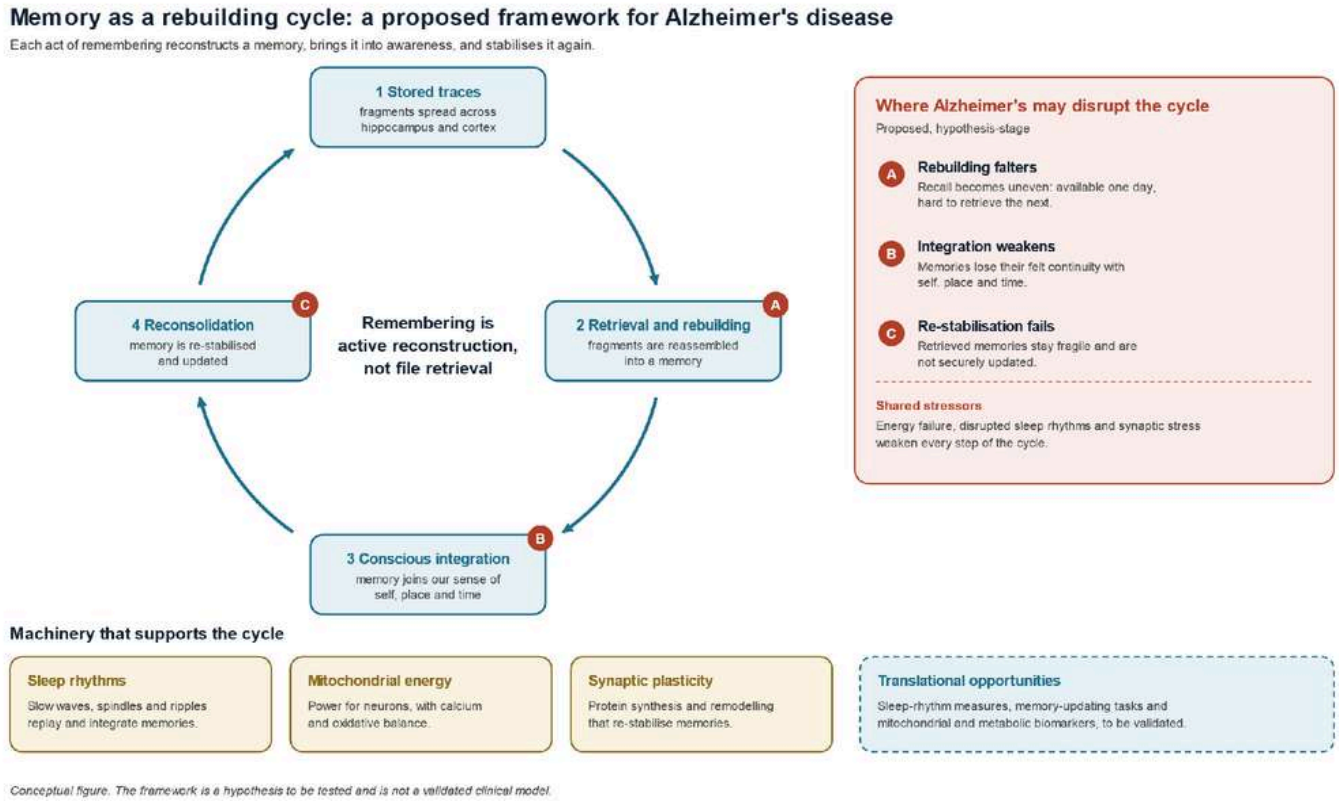


Figure 1. Memory as a rebuilding cycle: a proposed framework for Alzheimer's disease. Cycle (left): four steps run in a loop: stored traces, retrieval and rebuilding, conscious integration, and reconsolidation. The centre label reads "Remembering is active reconstruction, not file retrieval". Alzheimer's panel (right): three red markers show where the cycle may break. A is rebuilding that falters, B is integration that weakens, and C is re-stabilization that fails. A short "Shared stressors" note covers energy failure, disrupted sleep rhythms and synaptic stress. Bottom band: sleep rhythms, mitochondrial energy and synaptic plasticity appear as the machinery supporting the cycle. A dashed box lists translational opportunities, marked "to be validated".

collaborations toward practical applications. These are early-stage directions, not established products or demonstrated clinical benefits.

Q *How does your mitochondrial research connect to Bioexons LLC?*

A Directly. Mitochondria govern neuronal energy, calcium regulation and redox balance, and when they fail, neurons become vulnerable to oxidative stress and synaptic dysfunction. Through Bioexons LLC I hope to develop three areas: biomarkers of mitochondrial and metabolic dysfunction; the link between mitochondrial health, synaptic resilience and the brain's capacity to reconstruct memories; and AI-assisted analysis of how metabolic stress, network disruption and cognitive decline relate. These remain areas for investigation. I would not describe them as validated diagnostics or proven treatments.

Q *How do you decide which ideas to pursue, and what lesson stands out?*

A I ask four questions. Is the biology sound and reproducible? Does it address a genuine unmet need? Can it be tested realistically? Can it be protected and advanced with the resources available? An idea that fails may still be interesting, but it needs more academic work before it belongs in a company.

A key milestone was founding Bioexons LLC, which gave me a platform to combine neuroscience, molecular biology, and research leadership, and sharpened my focus on one connected theme: mitochondrial dysfunction, synaptic impairment, and brain ageing.

The main lesson: a good research finding is not necessarily a good product.

It must first survive independent validation and a feasibility check, so I advance in stages and commercialize only when the evidence justifies it.

Q *What challenges have you faced, and how have funding, collaboration and intellectual property shaped your decisions?*

A Biotechnology is slow, capital-intensive, and uncertain. Funding determines which questions you can test and how

fast, so I prioritize by scientific importance, feasibility, and translational value rather than chasing many ideas at once. No small organization has every skill needed, so I rely on collaborations across neuroscience, computation, engineering, and clinical research.

Intellectual property forces clarity about what is truly new, and I prefer to consider it early while keeping appropriate scientific transparency. The hardest shift for an academic is that publication ends a university project but is only the beginning in a company.

Q *What would meaningful progress look like, and what advice would you give scientists moving beyond the laboratory?*

A For Alzheimer's research: earlier detection, treatments that preserve function and quality of life, and a deeper grasp of how memories are formed, reconstructed, and lost. For Bioexons LLC: advancing work on mitochondrial and synaptic resilience toward biomarkers and intervention strategies, and developing AI-enabled research tools. I would measure success by reproducible evidence, not project counts.

To fellow scientists: maintain rigor and never present a hypothesis as an established result; build interdisciplinary collaborations; learn about intellectual property, funding and regulation early; and stay connected to your purpose, which is to understand important questions and ultimately improve lives.

ABOUT THE AUTHORS

Dr. Parihar has spent more than three decades studying ageing, mitochondrial biology and neurodegeneration, with research and faculty appointments at Vikram University, India; Southern Illinois University School of Medicine, USA; and Ohio State University College of Medicine, USA. His 2026 article in Ageing Research Reviews, co-authored with Vihaan Goplani and Garima Sharma, reframes Alzheimer's disease as a progressive failure of dynamic memory reconstruction and conscious integration. As Founder and CEO of Bioexons LLC, he is exploring how this perspective could inform early biomarkers and the path from discovery to application.



| OBITUARY |

Prof. P. V. Joseph

A LIFE DEDICATED TO UNDERSTANDING THE MONSOON

29 December 1932
–
6 November 2026



India's scientific community has lost a distinguished atmospheric scientist with the passing of Professor P. V. Joseph, whose research advanced understanding of the Indian monsoon. He passed away on 6 November 2026, aged 94. Throughout his career, he investigated the winds, rainfall patterns and ocean–atmosphere interactions that shape one of the country's most important natural systems. His work connected fundamental questions about atmospheric circulation with a subject of immediate public importance: the seasonal rains that sustain agriculture, replenish water supplies and influence the lives of millions.

Professor Joseph joined the India Meteorological Department in 1957 and served as Director of its Meteorological Training School from 1979 to 1989. He later continued his research as an Emeritus Professor at Cochin University of Science and Technology (CUSAT). These appointments brought together two important responsibilities: investigating the atmosphere and helping others develop the knowledge needed to understand it. His career extended across operational meteorology, academic research and scientific training, reflecting the close relationship between observing weather, explaining its behaviour and preparing future researchers.

At the centre of his scientific work was a question with wide practical significance: how do winds carry the moisture that becomes monsoon rainfall? The monsoon involves much more than rain clouds gathering over land. It depends on a vast circulation connecting the Indian Ocean, the atmosphere and the Asian continent. Within this system, narrow regions of particularly strong winds transport moisture over long distances. Understanding where these winds travel, how strongly they blow and why their pathways change is essential to explaining the behaviour of the rainy season. These questions formed a continuing thread through Prof. Joseph's research.

One of his important early contributions came through research with P. L. Raman, published in 1966. Using five years of upper-air wind observations, they established the existence of a low-level westerly jet stream over peninsular India during July. Its strongest winds occurred approximately 1.5 kilometres above sea level. For a general reader, a jet stream can be understood as a concentrated current of fast-moving air. Their work helped identify an important feature of the monsoon circulation and demonstrated how careful examination of observations could reveal an organised atmospheric structure within a seemingly complex pattern of winds.

The importance of this current lies partly in its role as a pathway for moisture. Water evaporating from the ocean must be carried towards regions where atmospheric conditions allow clouds and rainfall to develop. The low-level monsoon jet helps provide that transport. Its behaviour therefore matters far beyond wind measurements alone. A change in its position can alter where moisture travels and where rain-producing conditions develop. Prof. Joseph's investigations helped connect the movement of air over the ocean with rainfall over land, bringing attention to the physical processes behind a seasonal event familiar to every Indian household.

His later research examined how this circulation changes within a single monsoon season. The rainy months do not bring an uninterrupted supply of rainfall. Instead, the monsoon moves through active periods and weaker intervals, commonly described as breaks. Research by Prof Joseph and Dr. S. Sijikumar examined the changing position of the low-level jet during these phases. During active conditions, its core passes through peninsular India; during breaks, it can move south and bypass the peninsula. This work offered a physical explanation for an important aspect of monsoon variability: a seasonal wind system can remain present while its changing pathway alters rainfall over India.

Prof. Joseph also investigated whether these patterns were changing over longer periods. In work with Anu Simon published in 2005, he examined a weakening trend in the southwest monsoon current through peninsular India. The research drew attention to increasing weak monsoon spells

OBITUARY

and changes in the routes followed by moisture-bearing winds. Its wider significance was clear: seasonal rainfall totals cannot fully describe the experience of a monsoon. Two seasons with similar totals may distribute their rain differently, with very different consequences for crops, soil moisture and water storage. His research encouraged closer attention to the timing and continuity of rainfall.

Another important research direction concerned the arrival of the monsoon over Kerala. The first substantial showers do not necessarily mark the establishment of the seasonal circulation. Distinguishing a temporary spell of rain from the developing monsoon requires examining conditions over a much wider region. A 2006 paper by Prof Joseph, K. P. Sooraj and C. K. Rajan investigated the onset process over South Asia and presented an objective method for determining the onset date over Kerala. Their analysis linked the development and northward movement of deep atmospheric convection with the strengthening low-level jet, treating onset as an evolving physical process. His contribution extended beyond publications. During approximately 15 years as an Emeritus Professor in CUSAT's Department of Atmospheric Sciences,Prof. Joseph collaborated with research students investigating atmospheric and ocean systems. He also held visiting academic appointments at universities in Colorado and Hawaii. His professional associations included Fellowship of the Indian Meteorological Society and Emeritus membership of the American Meteorological Society. These connections reflected a career sustained through teaching, collaboration and participation in a wider scientific community. His writings on the monsoon and climate change provided another avenue through which his knowledge reached readers beyond individual research projects.

His achievements received recognition through the National Award in Atmospheric Science and Technology in 2016 and the Sir Gilbert Walker Gold Medal of the Indian Meteorological Society. These honours acknowledged sustained contributions to atmospheric science. Yet the significance of his work also lies in the questions it helped clarify. Understanding how moisture reaches India, why rainfall weakens during a season and how the monsoon becomes established provides a foundation for further research. Such knowledge develops through years of observation, comparison and interpretation, often requiring scientists to revisit familiar phenomena with increasingly precise questions.

Remembering Professor Joseph means recognising the patient investigation behind our understanding of the rains. His career showed how a question about winds above the peninsula could open into a larger understanding of seasonal rainfall and its variability.

For young scientists, his work offers an example of the value of careful observation and sustained attention to a problem of national importance. Science Factors extends its heartfelt condolences to his family, colleagues, students and the scientific community. We honour a life devoted to atmospheric research, scientific learning and a deeper understanding of the monsoon that sustains so much of India's life.



By
Rosalind Franklin
Council of Scientific Research
(**RFCSR**)

SCIENCE NEWS & OPPORTUNITIES

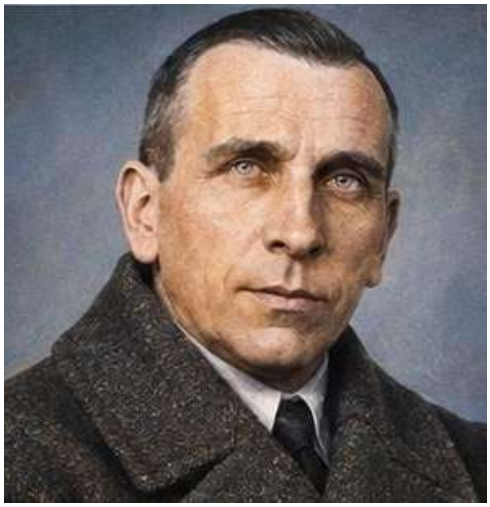
"Science News & Opportunities" keeps you updated with the latest scientific breakthroughs and opens doors to exciting careers, scholarships, and research programs.



1 NOVEMBER 1880 — Alfred Wegener

01

Alfred Wegener was a German scientist who transformed our understanding of Earth's geological history by proposing the theory of continental drift. In 1912, he suggested that today's continents were once joined together in a giant landmass called Pangaea before gradually separating. Wegener supported his theory using similarities in fossils, rock formations and geological structures across distant continents. Although many scientists initially rejected his ideas because he could not explain the driving mechanism, later discoveries in seafloor spreading and plate tectonics confirmed continental movement. His pioneering work laid the foundation for modern geology, fundamentally changing how scientists understand Earth's dynamic surface today.



7 NOVEMBER 1867 — Marie Curie

02

Marie Curie was a pioneering physicist and chemist whose discoveries transformed scientific understanding of radioactivity. Working alongside Pierre Curie, she discovered the radioactive elements polonium and radium in 1898. Her groundbreaking research earned her the Nobel Prize in Physics in 1903 and the Nobel Prize in Chemistry in 1911, making her the first person to receive two Nobel Prizes. Curie's investigations helped establish the scientific foundations for radiation-based medical technologies, including cancer treatment. During the First World War, she also promoted mobile X-ray units to assist wounded soldiers. Her achievements continue to inspire scientists, particularly women pursuing careers in research worldwide.



7 NOVEMBER 1888 — C. V. Raman

03

Chandrasekhara Venkata Raman was an Indian physicist whose discovery transformed our understanding of how light interacts with matter. In 1928, he demonstrated that light changes its wavelength when scattered by molecules, a phenomenon now known as the Raman effect. This discovery earned him the 1930 Nobel Prize in Physics, making him the first Asian scientist to receive a Nobel Prize in the sciences. His work established the foundation for Raman spectroscopy, widely used to identify chemical compounds and investigate molecular structures. Today, Raman spectroscopy supports research in medicine, pharmaceuticals, materials science and environmental monitoring, demonstrating the lasting importance of his discovery.



8 NOVEMBER 1656 — Edmond Halley

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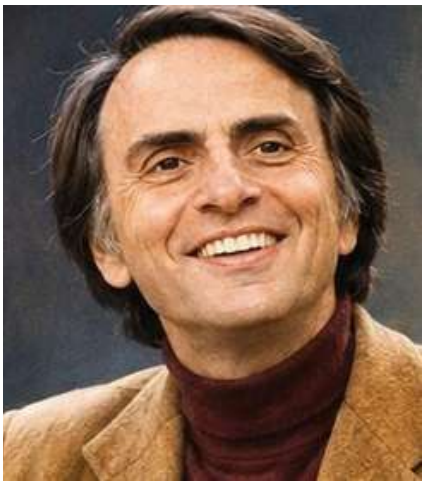
Edmond Halley was an English astronomer and mathematician who demonstrated that comets follow predictable paths through space. By examining historical observations and applying Newton's laws of motion, he recognised that comets observed in 1531, 1607 and 1682 were appearances of the same celestial object. He predicted its return around 1758, a prediction confirmed after his death. The comet was subsequently named Halley's Comet in his honour. Halley also investigated Earth's magnetic field, stellar movements and astronomical phenomena. His contributions strengthened the scientific understanding of celestial mechanics and demonstrated how mathematical principles could accurately predict events occurring across the Solar System.



9 NOVEMBER 1934 —Carl Sagan

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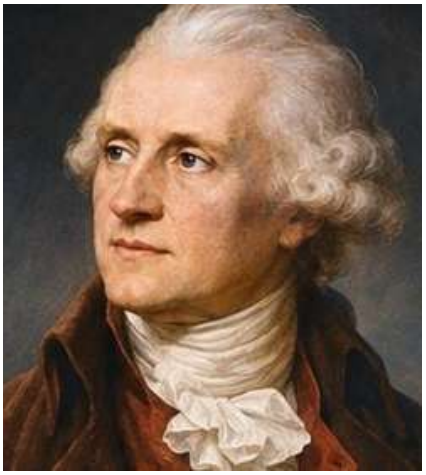
Carl Sagan was an American astronomer, planetary scientist and science communicator who inspired millions to explore the universe. His research contributed to understanding planetary atmospheres, particularly the extreme greenhouse effect on Venus and environmental conditions on Mars. Sagan also investigated the possibility of extraterrestrial life and participated in NASA's planetary exploration programmes. He helped develop the messages carried aboard the Voyager spacecraft, representing humanity to potential extraterrestrial civilisations. His television series Cosmos, first broadcast in 1980, introduced astronomy and scientific thinking to audiences worldwide. Through research, books and public communication, Sagan made complex scientific ideas accessible and inspired curiosity about space.



15 NOVEMBER 1738 — William Herschel

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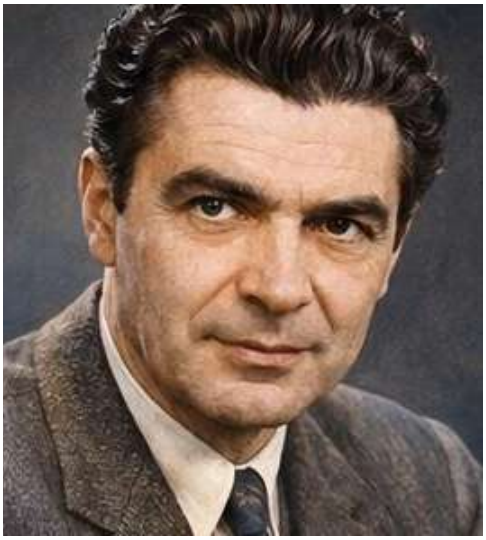
William Herschel was a German-born British astronomer whose discoveries expanded humanity's understanding of the universe. In 1781, he discovered Uranus, the first planet identified using a telescope in modern history. This discovery extended the known boundaries of the Solar System and transformed observational astronomy. Herschel constructed powerful telescopes and systematically studied stars, nebulae and celestial structures. Working with his sister Caroline, he catalogued thousands of astronomical objects and investigated the distribution of stars within the Milky Way. In 1800, he also discovered infrared radiation, revealing invisible energy beyond red light. His contributions helped establish the foundations of modern observational astronomy.



19 NOVEMBER 1912 — George Emil Palade

07

George Emil Palade was a Romanian-born American cell biologist whose discoveries transformed our understanding of cellular organisation and protein production. Using electron microscopy, he investigated the internal structures of cells and identified the importance of ribosomes in protein synthesis. His research also clarified how proteins move through the endoplasmic reticulum and Golgi apparatus before being transported or secreted. These findings established fundamental principles of modern cell biology. In 1974, Palade shared the Nobel Prize in Physiology or Medicine with Albert Claude and Christian de Duve. His discoveries continue to influence molecular biology, biotechnology and biomedical research into cellular function.



20 NOVEMBER 1889 — Edwin Hubble

08

Edwin Hubble was an American astronomer whose observations transformed humanity's understanding of the universe. During the 1920s, he identified Cepheid variable stars in the Andromeda nebula, demonstrating that Andromeda was a separate galaxy located far beyond the Milky Way. This discovery established that the universe contains countless galaxies beyond our own. Hubble subsequently investigated the relationship between galactic distances and recession velocities, providing important observational evidence for cosmic expansion. His findings helped establish modern cosmology and influenced theories about the universe's origin and evolution. The Hubble Space Telescope, launched in 1990, honours his contributions to astronomy and cosmic exploration.



25 NOVEMBER 1844 — Karl Benz

09

Karl Benz was a German engineer and inventor whose innovations helped establish the modern automobile industry. In 1885, he developed the Benz Patent-Motorwagen, widely recognised as the first practical automobile designed around an internal combustion engine. The vehicle received a German patent in 1886, marking a significant milestone in transportation history. Unlike earlier motorised carriages, Benz designed an integrated vehicle incorporating an engine, chassis, steering and transmission. His wife, Bertha Benz, demonstrated its practical potential through a pioneering long-distance journey in 1888. His engineering achievements transformed personal mobility and contributed to the emergence of an industry that continues shaping transportation worldwide today.



26 NOVEMBER 1876 — Willis Haviland Carrier

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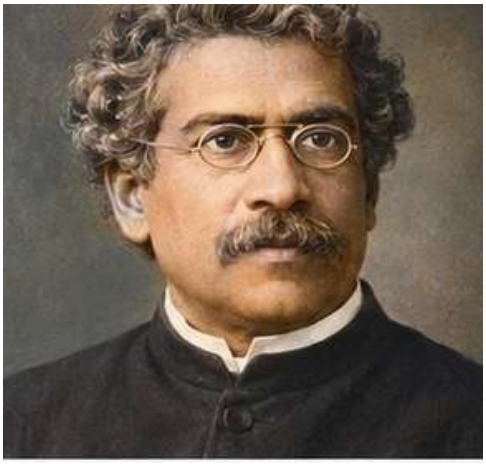
Willis Haviland Carrier was an American engineer whose invention of modern electrical air conditioning transformed industry and everyday life. In 1902, he designed a system to regulate temperature and humidity at a printing plant in Brooklyn, where changing atmospheric conditions affected printing quality. His innovation established important principles of modern climate-control technology. Carrier subsequently developed systems that enabled precise indoor environmental regulation, supporting industries such as textiles, pharmaceuticals and food processing. Air conditioning later became essential in hospitals, laboratories, offices and homes. His achievements demonstrate how solving a specific engineering problem can generate technological advances with lasting benefits for society worldwide.



30 NOVEMBER 1858 — Jagadish Chandra Bose

11

Jagadish Chandra Bose was an Indian physicist and plant physiologist whose pioneering experiments contributed to radio science and biological research. During the 1890s, he investigated electromagnetic waves and developed instruments capable of generating and detecting millimetre-wave radiation. His experiments demonstrated important properties of electromagnetic waves, advancing early wireless research. Bose later investigated plant physiology, designing highly sensitive instruments, including the crescograph, to measure minute changes in plant growth and responses to environmental stimuli. His research revealed how plants respond to light, temperature, chemicals and mechanical stimulation. His interdisciplinary achievements established an enduring legacy in Indian physics and plant science.





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.

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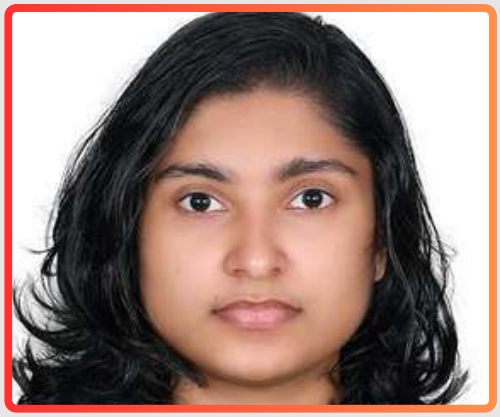
Evolution of proteins: a stride between stability and flexibility



Prof. N. Prakash Prabhu
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| Factors Press |

AREAS OF EXPERTISE
Protein Biophysics



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AREAS OF EXPERTISE
Protein Biophysics

WHY IT MATTERS

Can extreme cold damage proteins just as heat does? And how do living organisms survive in freezing conditions while keeping their proteins working? In this article, Soorya K. P. and Prof. N. Prakash Prabhu explore how proteins maintain a delicate balance between stability and flexibility to function at different temperatures. They explain why proteins sometimes lose their structure in extreme cold and how certain protective compounds may help preserve them. Could understanding these changes lead to better ways of storing vaccines, medicines, and other biological materials? The article offers an interesting look at how studying proteins in extreme conditions could improve biological preservation and open new possibilities for biotechnology in the future.

The evolution of living forms from RNA molecules capable of performing functions and carrying information to more complex, refined systems is a journey of billions of years. Over the course of evolution, DNA evolved as a stable archive for genetic information, and RNA became a molecular courier and an orchestrator to guide the synthesis of biological machinery that builds, maintains, and drives life - the protein. Across the evolutionary landscape, from the extremes of heat to the depths of cold, organisms are shaped by evolutionary pressure to adapt to their environments. Thermophiles, mesophiles, and psychrophiles reflect how life thrives under different conditions and how organisms adapt to their thermal niches. In particular, protein structure, dynamics, surface hydration, and interactions are driven by the surrounding environment.

Molecular interactions are essential for organisms to communicate and coordinate different functions. This necessitates that molecules be flexible and dynamic, whereas unrestrained flexibility will compromise the specificity of interactions. Thus, the molecules need to maintain certain rigidity and retain structural constraints on their dynamics. Higher temperatures might facilitate flexibility but collapse the structure, whereas lower temperatures might provide structural rigidity but reduce the flexibility. Balancing these two factors across the temperature range is challenging and evolutionarily optimized.

Harmony between stability and flexibility in proteins

Proteins have adapted to diverse environments and can function under conditions ranging from freezing polar regions to hot-spring

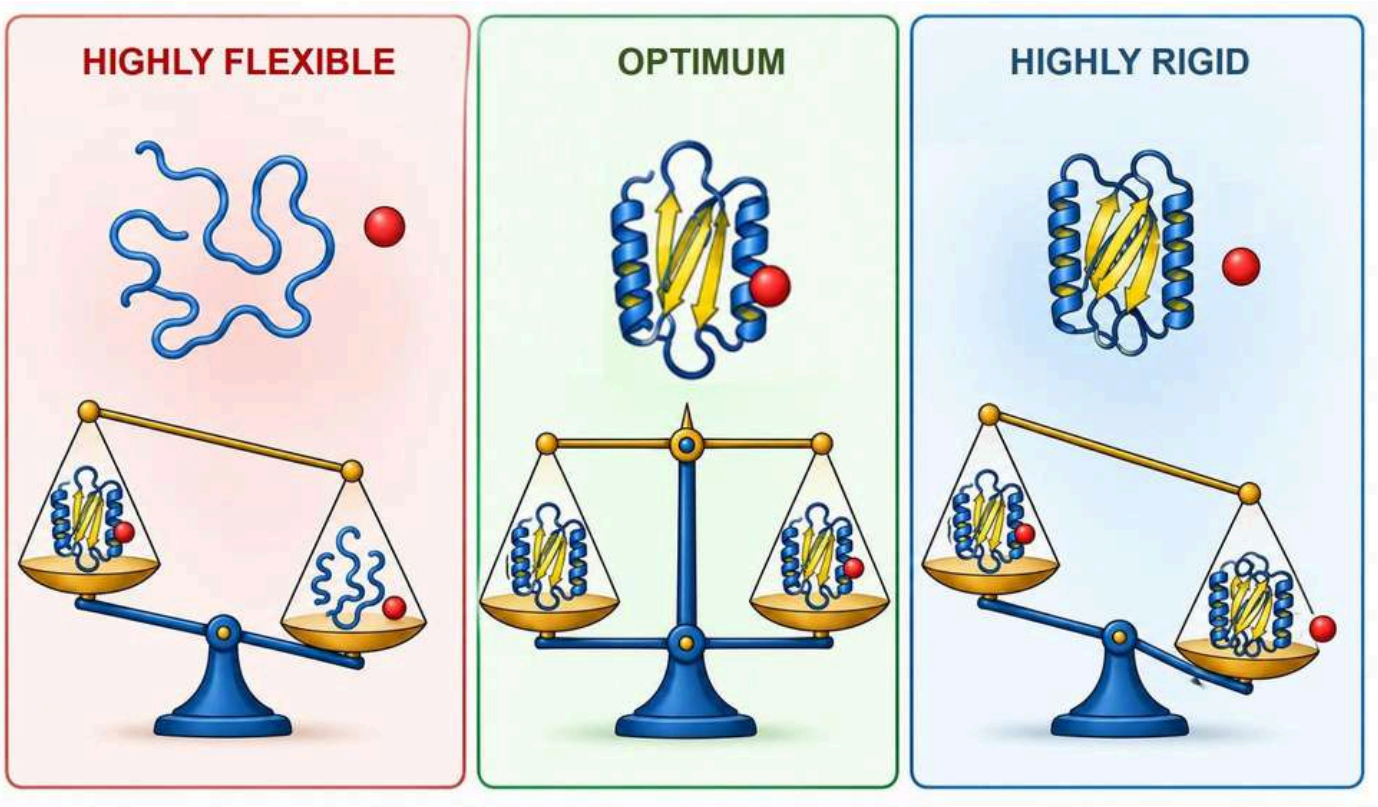


Figure 1. Fine-tuning of flexibility and stability in molecular interactions.

hydrothermal vents. The three-dimensional structure provides a foundation for their function. While a protein structurally adapts to various temperatures, the regions responsible for performing its function are carefully maintained with enough flexibility to interact with other molecules. However, other parts of the protein provide a more rigid or flexible scaffold depending on the environmental condition, whether it is hot or cold, respectively. Altogether, this allows the protein to protect its structural integrity while unyielding its essential dynamics to function under different conditions.

For example, IscU, an essential protein involved in synthesizing iron–sulfur (Fe-S) clusters across several organisms, requires larger flexibility to accommodate Fe-S clusters having a volume of ~70 Å3 (compared to ~11.5 Å3 for a water molecule). IscU adapts to various thermal niches and has a conserved flexible region common among thermophiles, mesophiles, and psychrophiles. However, to stabilize its global structure in thermophiles, the regions around the Fe-S binding site have become more compact than the corresponding regions in mesophiles and psychrophiles. PEPCK (phosphoenolpyruvate carboxykinase) is a protein that plays pivotal roles in carbon dioxide fixation in microorganisms and plants and in gluconeogenesis in animals, and is widely adapted to different temperatures. In thermophiles, the protein exhibits strong interactions and a compact overall structure; in mesophiles and psychrophiles, loose intramolecular interactions allow more flexible structures. This phenomenon of "corresponding states", adaptation of flexibility with respect to the survival temperature, has been observed in many other proteins as well.

Extreme heat and cold challenge the stability of proteins

Proteins function under the environmental conditions to which they adapt. Any temperature beyond this limit can disrupt their structure and eventually cause a loss of function. When temperature increases, it enhances molecular motion and disrupts the interacting forces that provide structure, leading to protein unfolding. At the same time, a decrease in temperature can also disrupt the molecular interactions, leading to protein denaturation. Protein denaturation at higher temperatures is widely studied. Due to the higher stability of globular proteins at sub-zero temperatures, cold denaturation studies are less explored. Hardly, cold denaturation has been experim-

entally observed only for a dozen of proteins so far. This may be due to the challenges in attaining and maintaining such low, sub-zero temperatures that can unfold globular proteins.

This practically limits the cold-denaturation studies.

Temperature-induced changes are primarily investigated using circular dichroism (CD), fluorescence spectroscopy, and NMR. CD assesses global structural changes across temperature ranges; fluorescence spectroscopy reveals whether the compact packing region is exposed to solvent by monitoring intrinsic fluorescence changes of the protein. NMR spectroscopy captures changes in the structure and dynamics of different regions of the protein, revealing alterations at the individual-residue level. Thus, combining optical and magnetic resonance spectroscopic methods can provide a comprehensive view of the pathways and intermediates involved in cold-induced denaturation.

The alternative pathways of cold and heat denaturation

Protein structure may be categorized into a core region and flexible regions. The core region is packed with amino acids that interact with substrate molecules to carry out their activity. This region is mostly surrounded by hydrophobic (water-hating) amino acid residues, whereas the flexible region is primarily composed of hydrophilic (water-loving) amino acid residues that are exposed to the solvent, water. The core region is mostly shielded by the flexible region to keep the region away from the surrounding water. Stability and overall compactness are governed by interactions among the hydrophilic residues and with water (hydrogen bonding and electrostatic). The hydrophobic residues pack themselves to minimize their exposure to water (hydrophobic interactions), which also significantly contributes to protein stability. Loss of either of these interactions can lead to protein unfolding.

At sub-zero temperatures, water can penetrate the core region, possibly due to favorable interactions between water and hydrophobic surfaces. This phenomenon is called hydrophobic hydration. Increased water-core interaction weakens the overall compactness, and eventually the protein starts to unfold. The amino acids in the flexible region and solvent-exposed amino acids in the core region may respond to low temperature first, followed by the other residues. Nevertheless, denaturation at high temperatures follows a different pathway. At high temperatures, increased molecular motion reduces the interactions between hydrophilic residues. The unfolding process begins with solvent-exposed residues in flexible regions that lose their native conformation. As the temperature increases, the core region is affected, which eventually results in disruption of the overall three-dimensional structure. Therefore, the intermediates formed during these two processes differ markedly in structure and in their interactions with water. Generally, the unfolded state formed by cold denaturation is compact and may partially retain some of the structural features, whereas the heat-induced unfolded state is more of a random coil structure.

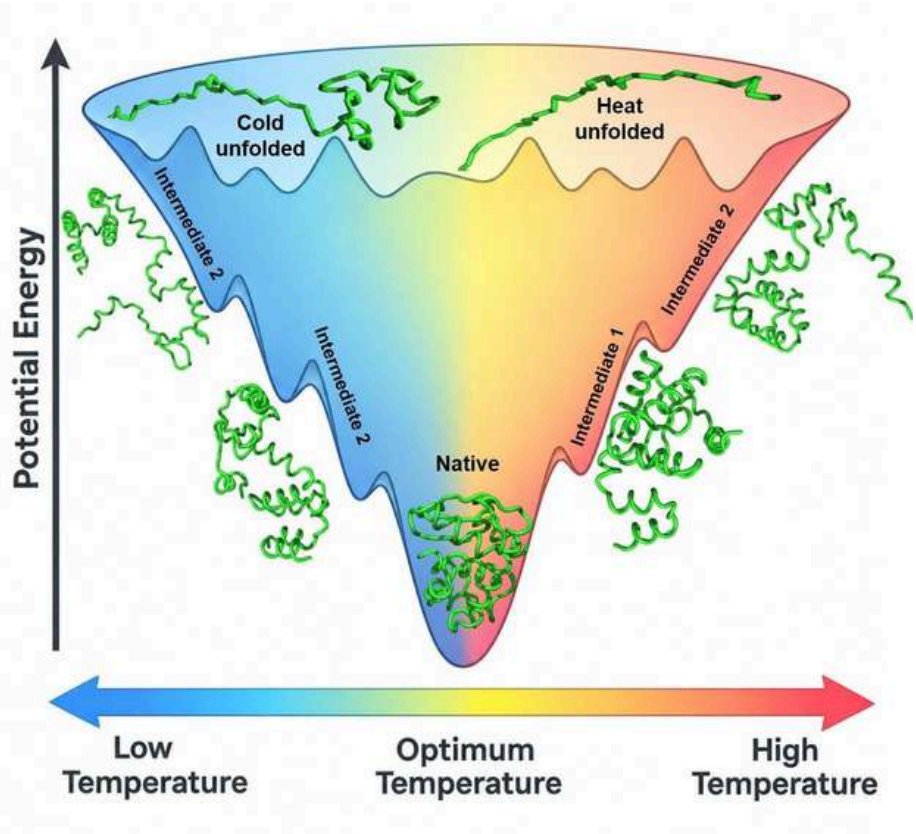


Figure 2. Energy of different states of a protein

Cold as a protector: Implications of cold denaturation

Cold conditions are useful for storage and preservation. Reduced molecular motion in cold temperatures slows down undesirable chemical reactions, substrate activities, and microbial growth. This can increase the stability and shelf life of the materials. Refrigeration is a common method for preserving temperature-sensitive biological samples, pharmaceuticals, vaccines, enzymes, and food materials. Controlled temperatures can help preserve sensitive ingredients such as peptides, proteins, vitamins, and antioxidants by maintaining their properties and functions in drugs, cosmetics, and other products. For long-term storage of cells, tissues, and other biological materials, cryopreservation with additives is very important. Additives protect biological materials from the damaging effects caused by freezing. Compounds such as glycerol, dimethyl sulfoxide (DMSO), and trehalose are the most commonly used additives that help in storage by lowering the freezing point of solvents.

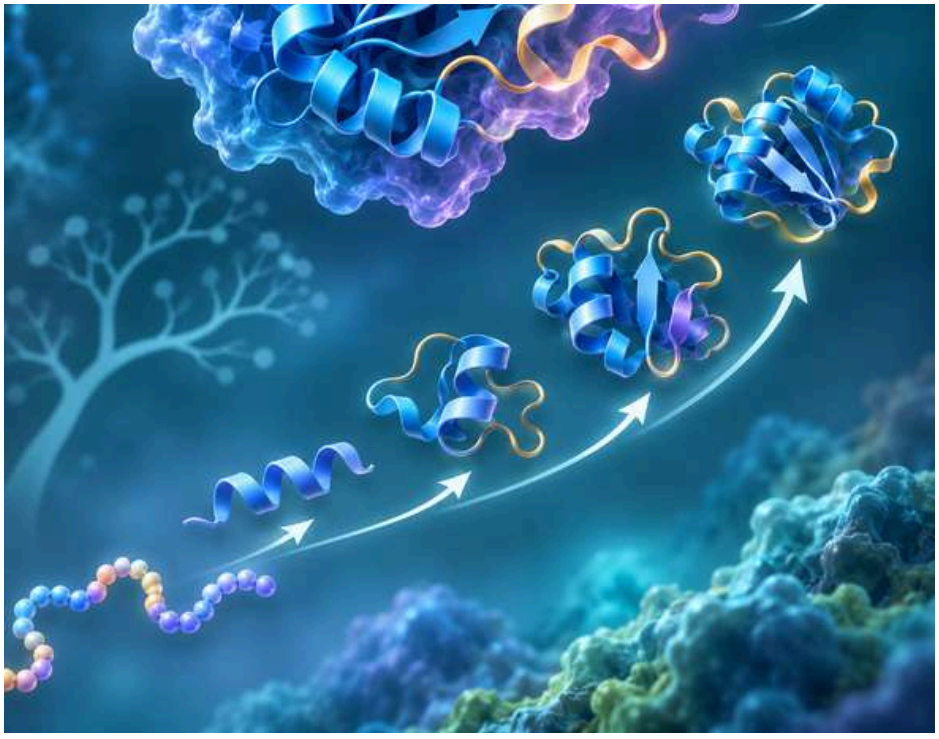
However, the effects of additives on the structure and stability of biological molecules, particularly proteins, under low-temperature conditions are not fully understood. Emerging studies reveal that additives might exert an asymmetric effect on protein stability, stabilizing proteins at low temperatures but promoting denaturation at higher temperatures, or vice versa. Such effects of various classes of additives on DNA and other biological macromolecules have yet to be investigated. This emphasizes that the experimental landscape of cold denaturation studies requires further exploration. Future experiments must not only explain the theoretical framework for the effects of cold on the stability of proteins and other biological molecules, but also elucidate the effects of various additives, thereby benefiting research labs and the biological industry.

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ABOUT THE AUTHORS

Prof. N. Prakash Prabhu is a faculty member in the Department of Biotechnology and Bioinformatics at the University of Hyderabad, India. His research focuses on understanding how proteins maintain their structure, stability, and function under different conditions. His work explores how temperature, natural compounds, and the surrounding environment affect protein behaviour. Through his research, he aims to improve our understanding of protein stability, with potential applications in biotechnology, medicine, and biological preservation. Soorya K. P. is a research student in the same department at the University of Hyderabad, working in the field of protein biophysics. Together, they explore how proteins respond to extreme temperatures and how this knowledge could help improve the storage and preservation of important biological materials.



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EMERGING INSIGHT

Turning Sunlight into a Tool for Drug Discovery



Dr. Subrata Das

Associate Professor & Former Head
Founder-cum-Director, PhotonicR Private Limited, Dept. of Chemical Science & Technology, National Institute of Technology Patna, India

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AREAS OF EXPERTISE

Organic Synthesis & Photochemistry • Metal–Pyrimidine Complexes • Functional Graphene Materials

WHY IT MATTERS

Could sunlight become a powerful tool for discovering new medicines while reducing chemical waste? In this article, Dr. Subrata Das explores how sunlight-driven chemistry could offer cleaner and more sustainable ways to develop promising drug molecules. He explains how light can drive chemical reactions and how specially designed photoreactors could make these processes more efficient. Could combining sunlight, advanced technologies, and artificial intelligence transform future drug discovery? The article explores how these approaches could open new possibilities for greener pharmaceutical research.

Turning Sunlight into a Tool for Drug Discovery

Drug discovery often begins with the traditional knowledge of Indigenous peoples, long before medicinal compounds are scientifically validated, developed, and commercialized in the market. For generations, people in villages have used sunlight to prepare natural remedies and preserve medicinal plants. Researchers first need to make diverse molecules, identify promising biological activity and then refine selectivity, safety and performance through repeated testing. How these molecules are made matters because it affects energy and material consumption, rigorous conventional synthetic routes, waste production, process safety, and the variety of molecules researchers can develop and study.

Could sunlight become a practical tool in this discovery?

Yes, sunlight offers an intriguing opportunity not as a universal replacement for conventional synthesis, but as an additional tool for constructing molecular interfaces. Sunlight-mediated studies involve chemical reactions and physical changes that occur when atoms or molecules absorb ultraviolet (100–400 nm), visible (400–750 nm), or infrared (750–2500 nm) radiation from the sun. Light absorption can promote a substrate or catalyst to an electronically excited state, changing its redox properties and enabling reaction methodologies that sometimes may not be possible under conventional conditions . Photochemical transformation comprises several mechanistic routes, including direct photoexcitation, photoredox catalysis, energy transfer, oxidative or reductive quenching, photoinduced charge-transfer interactions, single-electron transfer (SET), hydrogen-atom transfer (HAT) and excitation of electron-donor-acceptor (EDA) complexes. These methodologies proceed through radical or ionic intermediates under mild, selective conditions for carbon-carbon and carbon-heteroatom bond formation . So light-driven transformation and synthesis considered here demonstrate several routes to increasing structural diversity around bioactive molecule frameworks. Light can therefore be used not only as an alternative energy source but also to control reaction selectivity, intermediate formation, and bond construction.

A long-standing idea with growing relevance

The idea of using sunlight to carry out useful synthesis is not new. From 1889 to 1921, Prof. G. Ciamician pioneered sunlight-driven chemical reactions using a simple outdoor laboratory on the roof of the Chemistry building in University of Bologna, Italy.



Figure 1: From Genomic Variation to Therapeutic Hypothesis

His pioneering work demonstrated the potential of sunlight to drive chemical transformations and laid the foundation for modern photochemistry and sustainable solar-driven synthesis. Another important outcome in 2009, "The sunny side of chemistry: green synthesis by solar light," by Stefano Protti and Maurizio Fagnoni surveyed examples showing that sunlight could drive a wide variety of organic transformations. Their review covered photochemical processes such as cycloadditions and cyclizations, rearrangements and isomerizations, arylation and halogenation, oxygenation reactions, and the synthesis of organometallic or other specialised compounds. The breadth of these examples established an important principle: solar radiation can be a genuine source of photochemical activation, rather than merely a source of heat.

From molecular diversity to drug molecules

Some reports in the literature describe using direct sunlight to design and synthesize drug molecules. A study by Matsumoto and Takahashi demonstrated the synthesis of pyrrolo[2,3-d]pyrimidine-2,4-diones through the sunlight-induced cyclisation of suitably functionalised uracil derivatives. The method achieved 84–96% yields for the reported products, with reaction times ranging from 40 minutes to 5 hours. These fused heterocyclic scaffolds are particularly interesting because related compounds have reported antibacterial, anticancer, and antiviral activities. The approach highlights sunlight's potential to drive efficient molecular transformations without metal catalysts or additional oxidising agents for the cyclisation step.

Another study demonstrated the sunlight-induced trifluoromethylation of (hetero)aromatic compounds and electron-deficient olefins using decatungstate photocatalysis and an inexpensive trifluoromethylating reagent. The method enabled the introduction of CF_3 groups into medicinally relevant molecular scaffolds, including caffeine and theophylline derivatives. Such modifications can influence important molecular properties, including lipophilicity, metabolic stability and biological activity.

A recent study demonstrated the solar-assisted synthesis of 3,4-dihydropyrimidin-2(1H)-one, achieving a 64% yield in 4 hours using aluminium-pillared montmorillonite as a reusable heterogeneous catalyst . This approach highlights the potential of solar irradiation to support sustaina-

ble synthesis while reducing reliance on conventional processing methods.

Our recent work illustrates how sunlight chemistry may contribute to this goal. This study described sunlight-mediated multicomponent synthesis of fused pyridopyrimidines from uracil derivatives, aldehydes, and cyanoacetic acid; however, without light, we observed only the bis-pyrimidine derivatives. The proposed pathway involves an EDA assembly formed from reaction-derived components; sunlight/visible-light absorption can activate this assembly and promote radical chemistry followed by ring formation. Under the reported conditions, the method did not require an added photocatalyst or an additional reaction-promoting additive. Selected products showed good preliminary bioactivity against Escherichia coli in the reported screening assay. This shows that photochemical synthesis can provide access to molecular scaffolds worth further investigation, and that synthesis, mechanistic evidence, and biological evaluation must remain distinct steps.

Sunlight is renewable but not automatically reproducible

Sunlight is attractive because it is widely available and renewable, yet its intensity and spectral distribution change with weather, location, season and time of day. A reaction that works on a clear afternoon may proceed more slowly under cloud cover or give a different result in another laboratory. Reliable solar synthesis therefore requires careful reporting of the location and conditions, exposure time, reactor geometry, illuminated area and temperature; where possible, solar irradiance or incident photon flux should also be measured. Dark controls and other suitable experiments are needed to confirm that the transformation is genuinely light-driven.

Is the reactor can determine the result?

Light is absorbed as it travels through a reaction mixture, so material deeper inside a large vessel may receive fewer photons than material near the illuminated surface. Simply increasing the size of a flask can therefore reduce efficiency and alter product distributions. Thin-film and flow photoreactors address this challenge by spreading the liquid into a shallower layer or moving it through a defined illuminated region, helping to manage photon delivery, heat transfer and mass transfer.

A falling-film looping photoreactor developed by our team with collaborators provides one example of this engineering approach. For more detail, see our own developed photoreactor company (photonicr.com). We evaluated this platform using benchmark photoreactions and different reactor modules, focusing on the photonic characteristics relevant to scale-up. It provides a practical framework for testing whether a reaction first observed at milligram scale can be translated to larger quantities while maintaining control over irradiation, as well as BASTR or CSTR mode [12].

What should happen next? Solar photoreactor

A hybrid solar-LED falling-film photoreactor, rather than a solar-only reactor, is an alternative solution. Use direct sunlight for experiments when conditions permit and photovoltaic-charged batteries to operate the LEDs when consistent illumination is required. Keep the two irradiation modes independently measurable so their performance can be compared scientifically. Over the next five to ten years, progress will depend on connecting molecular discovery with rigorous measurement and reactor design. Machine learning may help identify promising conditions, but only if datasets record details such as wavelength, light intensity, reactor dimensions and reaction volume.

Sunlight is a practical tool, not a magic solution

The future is likely to be a design and initial synthetic reactions can proceed under direct sunlight, and optimisation may then continue on controlled wavelengths with suitable photoreactors if needed. The most useful advances will combine selective photochemistry with reproducible photon management, accessible equipment, safer materials and meaningful biological evaluation. From a drug discovery point of view, selectivity and mild reaction conditions are very important in synthetic drug discovery, as production of side products and unwanted byproducts under conventional methods can cause additional disadvantages with detrimental effects on both the environment and human health. Sunlight will not solve every challenge in drug discovery, and some reactions will remain unsuitable for outdoor operation or industrial production. Yet solar photochemistry can broaden the ways chemists build and explore biologically relevant molecules. By bringing mechanistic chemistry, reactor engineering and biological validation together from the outset, we can turn sunlight from a symbol of green chemistry into a practical means of discovering which molecul-

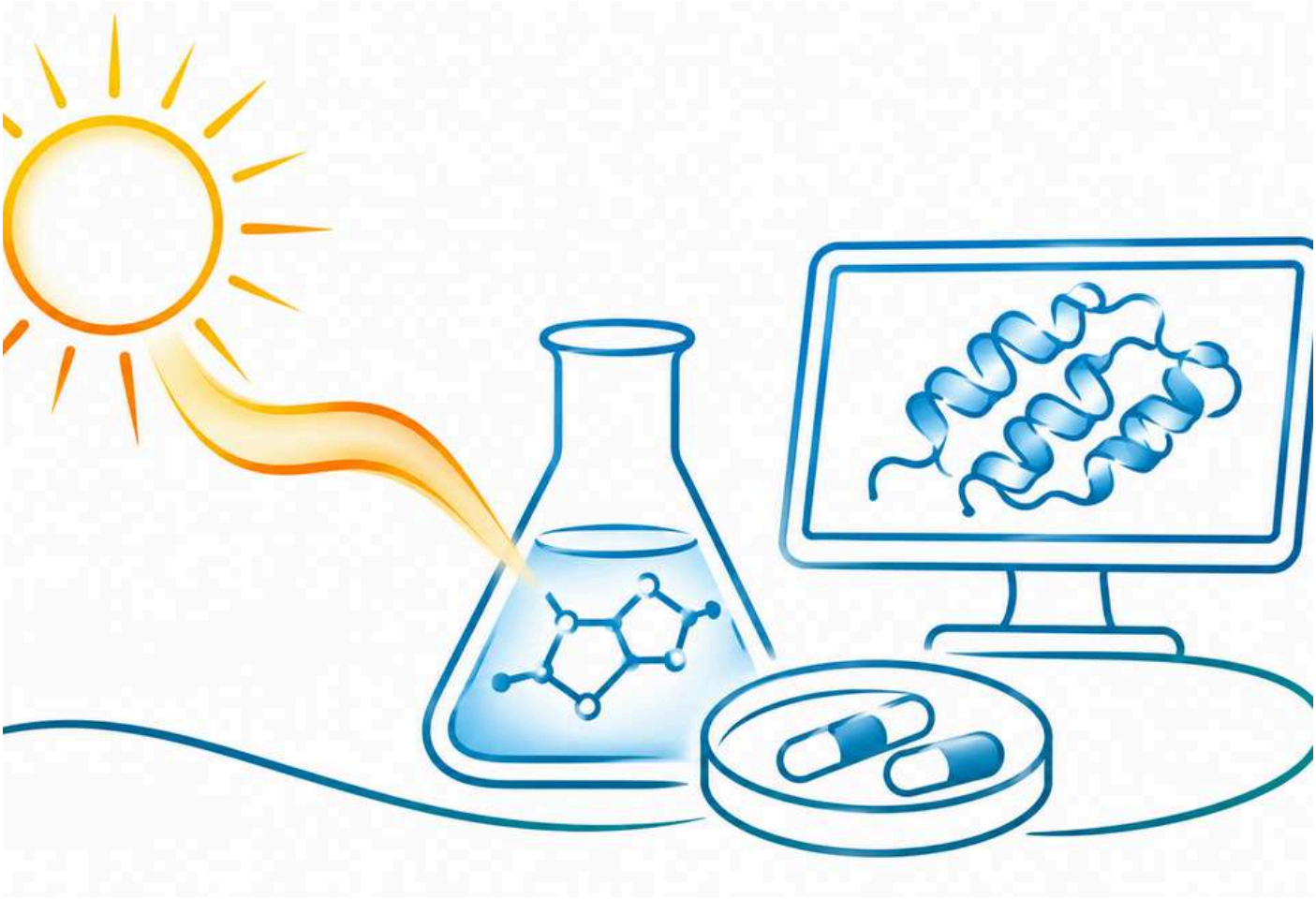
es are possible and which deserve closer study.

ABOUT THE AUTHORS

Dr. Subrata Das is an Associate Professor and Former Head of the Department of Chemical Science and Technology at the National Institute of Technology Patna, India. Alongside his academic role, he is also the Founder and Director of PhotonicR Private Limited. His multidisciplinary research focuses on developing innovative chemical reactions, harnessing visible light to synthesize valuable organic compounds, and exploring novel functional materials. Over the years, he has extensively worked on advanced photochemical technologies that use light to make chemical transformations significantly faster, more energy-efficient, and scalable for larger-scale industrial manufacturing. Ultimately, his research aims to develop cleaner, greener, and more practical methods for sustainable chemical production, offering wide-ranging potential applications in pharmaceuticals, medicine, and modern industry.

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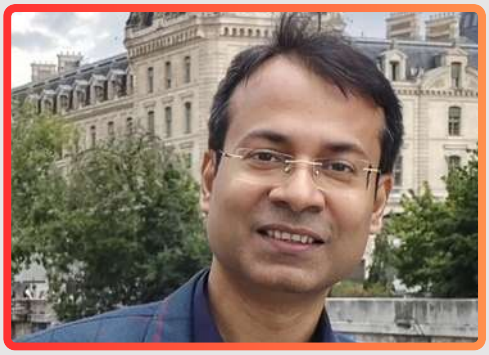


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SCIENCE FACTORS!

EMERGING INSIGHT

Cancer Therapy with Light: Engineering Intelligent Iridium Drugs for Precision Medicine



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AREAS OF EXPERTISE
Bioorganometallic Chemistry • Medicinal Chemistry • Metal-Based Anticancer Agents • Cancer Therapy



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AREAS OF EXPERTISE
Bioorganometallic Chemistry • Medicinal Chemistry • Ir(III)-Based Anticancer Agents • Photodynamic Cancer Therapy

WHY IT MATTERS

Light could offer a way to control where and when a cancer treatment becomes active. In this article, Dr. Priyankar Paira and Ms. Sreejani Ghosh explore how compounds containing the metal iridium could combine light-triggered treatment with imaging to track their location in cells. They discuss emerging strategies to reach deeper tumours, work in low-oxygen conditions and tackle treatment resistance, while highlighting the safety testing and practical challenges that must be addressed before these experimental approaches can benefit patients.

Iridium Compounds for Precision Phototherapy

The next step in photodynamic cancer therapy is to move beyond simply designing more powerful photosensitizers. The real goal is to develop "intelligent" photosensitizers that can decide when, where, and how to act. Iridium (III) complexes are particularly attractive for this purpose because their photophysical properties can be tuned through ligand design. They can also produce reactive oxygen species (ROS), target specific cellular organelles, and, importantly, possess intrinsic luminescence that can be used for imaging. Future systems are therefore likely to combine several functions within one molecular platform. An Ir(III) complex could, for example, recognize a tumour-associated feature, remain relatively inactive in healthy tissues, become activated by conditions such as acidic pH or elevated glutathione, and then generate ROS after exposure to light. At the same time, its luminescence could provide information about its cellular localisation. This represents a shift from photodynamic therapy to precision phototherapy, where the objective is not simply to kill cancer cells, but to control the location and timing of therapeutic activity.

Understanding What Happens Inside Cancer Cells

Perhaps the biggest question is how much control we actually have over the biological outcome of phototherapy. We know that ROS can damage DNA, proteins, membranes, and organelles. But the consequences of that damage are not always predictable. Depending on where ROS are produced and how much oxidative stress is generated, a cell may undergo apoptosis, ferroptosis, pyroptosis, necroptosis, or other forms of programmed cell death. This raises a fascinating possibility: can we design a molecule to determine not only whether a cancer cell dies,

but how it dies?

There are other fundamental questions too. How does an Ir (III) complex behave after entering a living organism? Does it remain intact? Which proteins bind to it? Where does it accumulate? How is it metabolized and eventually eliminated? And what happens after repeated exposure?

These questions are still much less understood than the photochemistry of these compounds, yet they could ultimately determine whether an otherwise promising molecule can become a useful therapeutic agent.

Reaching Deeper Tumours and Overcoming Low Oxygen

The most important breakthroughs may not come from chemistry alone. Better light delivery, biological modelling, and quantitative dosimetry are equally important. At present, many laboratory studies use carefully controlled irradiation conditions that are difficult to reproduce across different experiments. Wavelength, light intensity, exposure time, and delivered energy can all influence the biological outcome. Establishing more consistent approaches to light dosimetry would make results easier to compare and could help bridge the gap between laboratory experiments and clinical applications. Technology must also solve the problem of delivering light to tumours located deep inside the body. This creates an opportunity for red/NIR excitation, multiphoton approaches, and other strategies capable of extending the effective treatment depth.

At the molecular level, another important breakthrough will be the development of reliable oxygen-independent photochemical pathways. If therapeutic ROS can be generated efficiently even under hypoxic conditions, one of the fundamental limitations of conventional PDT could be addressed.

Combining Light, Targeted Treatment and Immune Defence

One of the most interesting trends is the convergence of phototherapy and cancer immunology.

For a long time, the objective of PDT was viewed mainly as direct destruc-

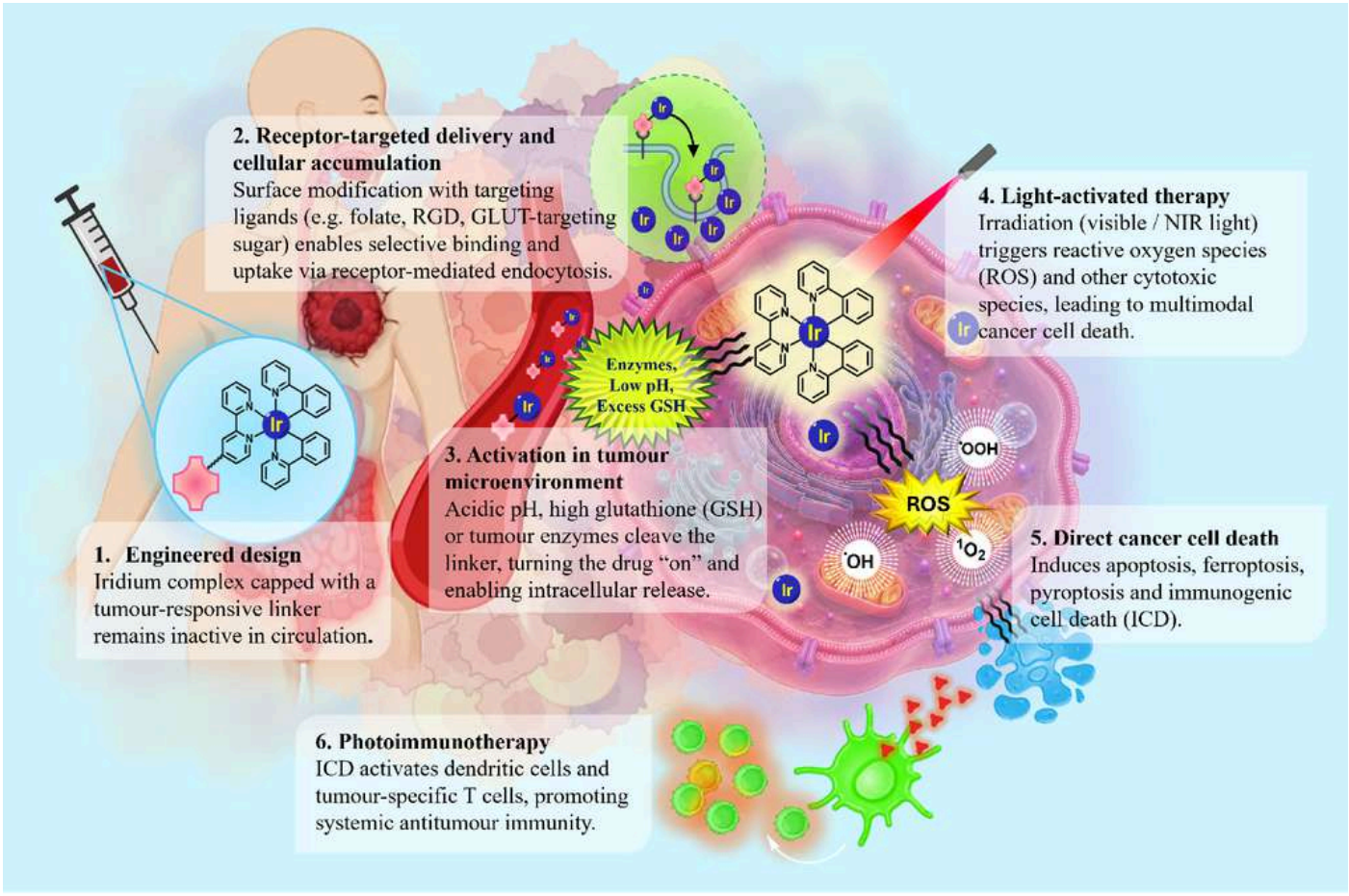


Figure 1: Schematic representation of a stimuli-responsive cyclometalated Ir(III) photosensitizer for precision phototherapy: tumour targeting, receptor-mediated accumulation, light activation, ROS generation, cancer-cell death, and immune response.

tion of tumour cells. We now know that certain forms of treatment-induced cell death can release danger signals and tumour-associated material that influence the immune system. This creates the possibility of using phototherapy not only to destroy a tumour locally, but also to help stimulate an antitumour immune response. Another important development is the increasing interest in combination therapy. Instead of expecting one molecule to solve every problem, researchers are exploring combinations of photodynamic therapy with chemotherapy, drug delivery systems, and immunotherapy.

At the molecular level, organelle targeting is also becoming increasingly sophisticated. Directing a photosensitizer specifically toward mitochondria, lysosomes, endoplasmic reticulum or other vulnerable compartments provides a way of controlling where oxidative damage begins.

The most promising systems may therefore be those that combine spatial control, multiple therapeutic mechanisms, and biological selectivity.

Building a Complete Picture of Treatment Performance

We think the field will gradually move away from evaluating photosensitizers primarily through parameters such as phototoxicity, IC_{50} values, or ROS production, and toward a much more complete picture of therapeutic performance.

A future study may need to answer a sequence of questions: Where does the molecule go? How long does it remain there? What activates it? What type of ROS does it produce? Which biomolecules are damaged? Which signaling pathways are affected? What type of cell death follows? And what happens to the compound after treatment?

This will require closer collaboration between synthetic chemistry, photophysics, cell biology, pharmacology, imaging, and materials science.

We also expect the field to become more selective about complexity. Multifunctional nanoparticles and sophisticated delivery platforms can produce impressive results, but every additional component introduces questions of reproducibility, manufacturing, characterisation, and regulation. Consequently, the next decade may favour designs that achieve sophisticated biological behaviour while remaining chemically well-defined and practically manufacturable.

From Laboratory Molecules to Future Cancer Medicines

Several developments will fundamentally reshape the field in the future. Firstly, deeper light penetration through red/NIR and multiphoton activation could expand phototherapy to tumours that are difficult to reach with conventional visible light. Secondly, the development of hypoxia-tolerant photosensitizers and oxygen-independent photochemical pathways could help overcome one of the major limitations of conventional PDT. Thirdly, the integration of therapy with diagnosis could enable Ir(III) complexes to simultaneously treat tumours and provide information about their localization and behaviour through their intrinsic luminescence. Fourthly, a deeper understanding of alternative cell-death pathways, including ferroptosis, pyroptosis, necroptosis, and immunogenic cell death, could open new strategies against treatment-resistant tumours. Finally, perhaps the most important development will be the transition from elegant molecules to clinically realistic medicines. Demonstrating predictable activity, distribution, safety, and scalable manufacturing will be essential for moving Ir(III)-based phototherapy beyond the laboratory.

The future may therefore be less about finding a single “perfect” photosensitizer and more about engineering adaptive, multifunctional molecular systems that can dynamically sense, respond, treat, and report within the complex biological environment of a tumour. Achieving this vision will require sustained interdisciplinary collaboration across synthetic chemistry, photophysics, targeted drug delivery, and clinical oncology, ultimately bridging innovative laboratory design with practical, personalized cancer therapies that safely and reliably improve long-term patient outcomes.

ABOUT THE AUTHORS

Dr. Priyankar Paira and Ms. Sreejani Ghosh work in the Department of Chemistry at Vellore Institute of Technology, Tamil Nadu, India. Their current research explores novel metal-containing compounds as potential cancer treatments, particularly light-activated iridium compounds. They study how these specialized molecules target specific cancer cell organelles and emit bright light for real-time tracking, aiming to develop safer, more precise cancer therapies.

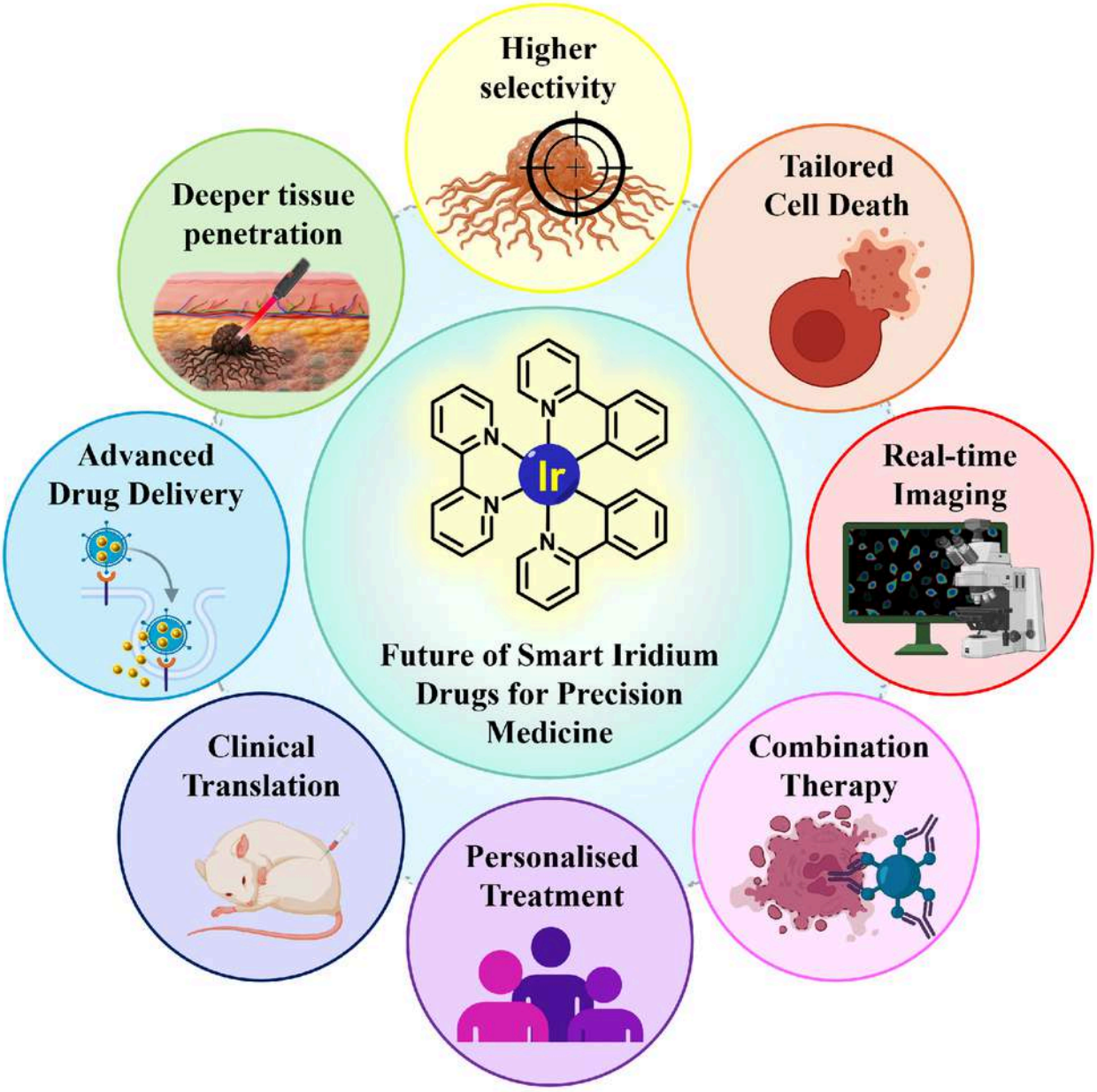


Figure 2: Future directions for intelligent Ir(III) phototherapy, including NIR activation, hypoxia tolerance, combination therapy, theranostics, and clinical translation.

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SCIENCE FACTORS!

EMERGING INSIGHT

Molecular Biomarkers and the Future of Bladder Cancer Assessment

WHY IT MATTERS

Bladder cancer can behave differently in different patients, making early detection, monitoring and treatment decisions challenging. In this article, Prof. Minakshi Vashist, Anuradha Sharma and Rohit Kaushik explore how molecular biomarkers could help improve bladder cancer diagnosis and assessment. They explain how genetic changes, blood-based proteins such as YKL-40, and liquid biopsy approaches may provide useful information about cancer risk and progression. The article highlights how combining molecular markers with existing clinical methods could support more accurate diagnosis, better disease monitoring and personalised treatment, while emphasising the need for further clinical validation before routine use.



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AREAS OF EXPERTISE
Human genetics • Cancer Biomarkers • Genetic Polymorphism



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AREAS OF EXPERTISE
Clinical Genetics

Molecular Biomarkers and the Future of Bladder Cancer Assessment

Bladder cancer does not behave in the same way in every patient. Even when clinical and pathological features appear similar, patients may differ considerably in recurrence, disease progression and response to treatment. Cystoscopy, imaging and histopathological examination therefore remain central to diagnosis and follow-up. At the same time, advances in molecular biology are providing additional information about the biological differences that exist between tumours.

Molecular biomarkers are of interest because they can capture changes that may not be evident from conventional clinical assessment alone. Genetic variants, tumour-associated molecular alterations, circulating proteins and tumour-derived DNA are all being investigated for their possible roles in detection, risk assessment, disease monitoring and treatment selection. The important question, however, is not simply whether a biomarker is associated with bladder cancer. Its real value depends on whether the finding can be reproduced and whether it adds useful information to clinical decision-making.

Understanding Bladder Cancer Through Molecular Biomarkers

Bladder cancer develops through a combination of genetic and biological events. Alterations in cell growth, inflammation, tissue remodelling and angiogenesis can all contribute to the development and progression of the disease. Because several processes operate simultaneously, it is unlikely that one biomarker will adequately describe the complete biological behaviour of bladder cancer.

Vascular endothelial growth factor A (VEGFA) is one molecular factor that has received considerable attention. It plays an important role in angiogenesis, the process through which new blood vessels are formed. Changes in tumour growth and in the

surrounding microenvironment can influence the demand for blood supply, making angiogenic pathways relevant to cancer progression.

Another molecule of interest is YKL-40, also known as chitinase-3-like protein 1 (CHI3L1). YKL-40 is a circulating protein associated with inflammation and tissue remodelling. Its possible role in bladder cancer has been investigated previously. In a case-control study, serum YKL-40 concentrations were reported to be higher in patients with bladder cancer than in healthy controls, while urinary YKL-40 was also associated with invasive disease.

Our recent study examined YKL-40 in relation to genetic variation in VEGFA. The study included 120 patients with bladder cancer and 120 age- and sex-matched controls. We investigated the VEGFA rs833061 (-460T>C) promoter polymorphism together with serum YKL-40 concentrations. Differences in VEGFA genotype distribution were observed between patients and controls. Serum YKL-40 was also higher among patients, and its concentration varied according to VEGFA genotype.

The significance of these observations lies partly in the fact that the two markers provide different types of biological information. A genetic polymorphism reflects inherited variation, whereas a circulating protein can provide an indication of biological activity occurring in the disease setting. Considering these measurements together may therefore provide a more informative picture than examining either marker independently.

The Promise of Liquid Biopsy

Liquid biopsy has become an important area of investigation in molecular oncology. Tumours can release DNA and other biological material into body fluids, allowing researchers to examine molecular features without relying exclusively on tissue obtained through an invasive procedure.

Circulating tumour DNA (ctDNA) is particularly interesting because it can contain molecular information originating from tumour cells. Studies are exploring its potential for assessing tumour burden, identifying molecular alterations and following molecular changes during treatment.

Bladder cancer has a particular advantage in this area because urine is directly associated with the urinary tract. Urinary DNA, RNA, proteins and other molecular components can therefore be investigated as potential sources of disease-related information. Blood and urine can also be collected repeatedly, which creates an opportunity to monitor molecular changes over time.

There are nevertheless important limitations. The amount of tumour-derived material present in a sample may differ between patients and may also depend on disease stage. Sample collection and storage, laboratory processing and the analytical platform used can affect the final result. For this reason, promising liquid-biopsy markers still require careful analytical and clinical validation before they can be incorporated into routine practice.

Recent recommendations from the International Bladder Cancer Group have emphasized the growing role of biomarkers while also stressing the importance of prospective validation, standardized testing and demonstrated clinical utility. The recommendations also point to opportunities for ctDNA-based testing and molecular assessment of actionable alterations, including FGFR3, in suitable clinical settings.

From Discovery to Clinical Application

One of the major difficulties in molecular oncology is moving a promising biomarker from the research laboratory into clinical practice.

A statistically significant association is an important starting point, but it does not by itself establish that a biomarker is ready for clinical use. Findings need to be reproduced in independent patient populations, and the performance of the test should remain acceptable under different clinical and laboratory conditions.

Clinical relevance is equally important. A biomarker becomes more useful when its result can contribute to a specific clinical decision. In bladder cancer, this could involve improving risk assessment, helping to monitor disease or identifying patients who may be suitable for a particular treatment.

YKL-40 illustrates this distinction well. Increased YKL-40 concentrations among patients with bladder cancer support its biological and diagnostic interest. However, additional studies are required to establish how consistently the marker performs across different populations and disease stages. It is also important to determine whether YKL-40 provides information beyond that already obtained from established clinical and pathological characteristics.

Genetic biomarkers face a similar challenge. An association between a genetic variant and cancer risk does not necessarily demonstrate a causal relationship, nor does it automatica-

lly establish clinical usefulness. Replication in independent populations, functional investigation and prospective evaluation are needed before such findings can be translated into routine clinical testing.

Toward Integrated Molecular Assessment

The direction of bladder cancer research is increasingly moving toward the combined interpretation of multiple molecular features. Rather than expecting one biomarker to provide a complete assessment, future approaches may bring together several types of information.

A potential molecular profile could include inherited genetic variants, tumour-associated mutations, circulating proteins, ctDNA, urinary biomarkers and conventional clinical information. Such an approach may help explain why patients with apparently similar clinical characteristics can nevertheless have different disease courses.

Computational biology may also contribute to this process. Large molecular datasets contain relationships that can be difficult to recognize when individual biomarkers are examined separately. With appropriate validation, computational approaches may help identify combinations of molecular features that are associated with clinically meaningful outcomes.

At the same time, adding more biomarkers does not automatically produce a better diagnostic or prognostic tool. A useful panel needs to be reproducible and clinically interpretable. It should also be practical to perform, and the additional cost and complexity should be justified by the information obtained.

For this reason, molecular biomarkers are more likely to complement established clinical methods than replace them. Histopathology, imaging, cystoscopy and clinical assessment will continue to have important roles in bladder cancer management. Molecular testing can provide another layer of information, particularly when the aim is to understand biological differences between tumours or identify patients with different levels of risk.

Looking Ahead

The next phase of bladder cancer biomarker research will depend on how effectively molecular findings can be connected with clinical needs. Our observations involving VEGFA and YKL-40 provide one example of this approach. Examining a genetic polymorphism alongside a circulating biomarker allows researchers to consider both genetic variation and disease-associated biological activity. However, these findings need confirmation in larger and multicentre populations before their broader clinical relevance can be established.

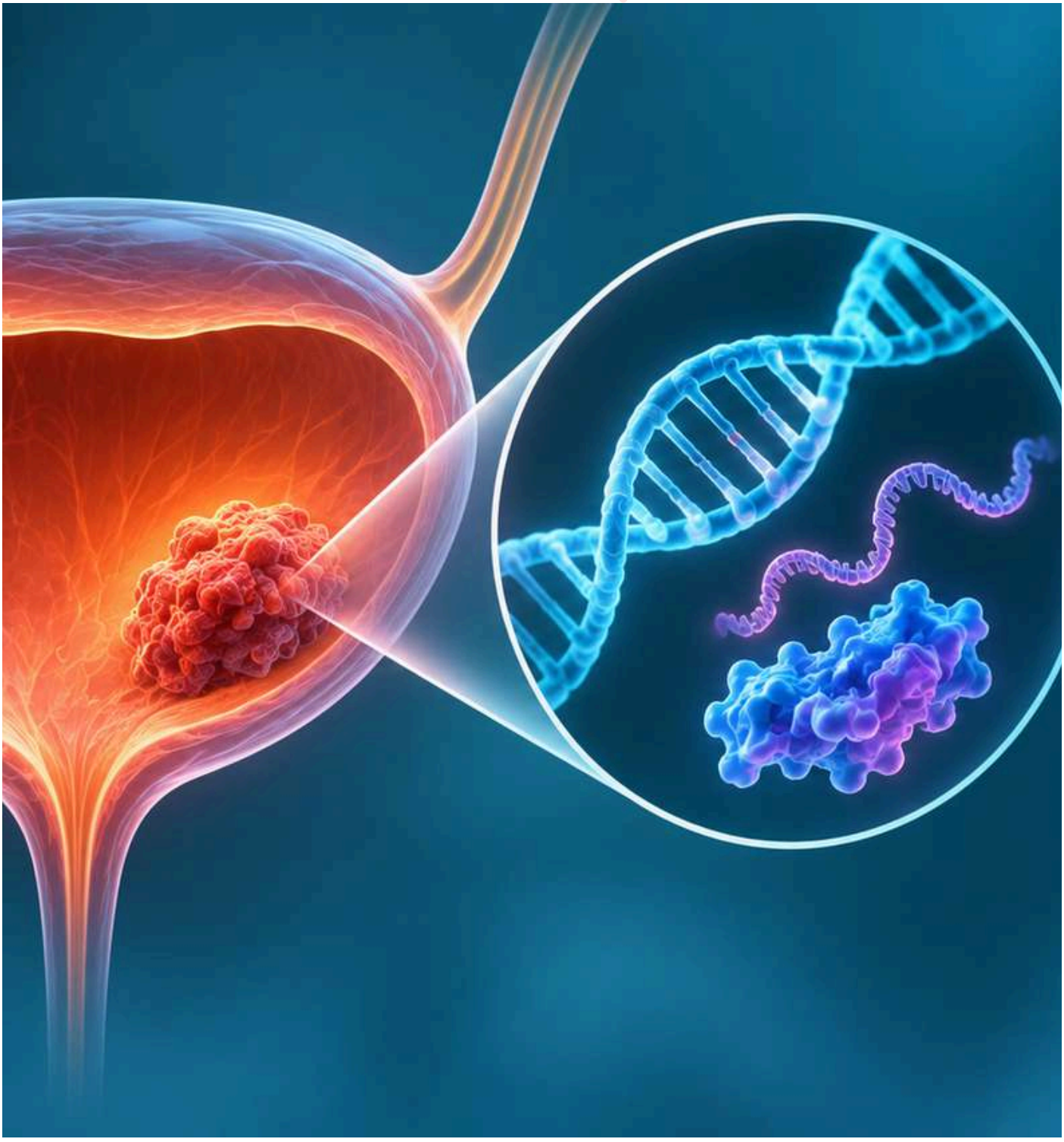
Reproducibility, standardization and clinical utility should therefore remain major priorities. Prospective studies and appropriately designed clinical trials will be necessary to determine which molecular markers can make the transition from experimental research to practical clinical application.

It is unlikely that the future of bladder cancer assessment will be based on a single molecular marker. A more realistic direction is the integration of several biological signals with clinical and pathological information. Advances in genomics, liquid biopsy, molecular pathology and computational analysis are making such integrated approaches increasingly possible.

The central challenge is now to translate the growing volume of molecular information into results that are reliable and useful in clinical practice. Biomarkers will have their greatest impact when promising biological observations are supported by rigorous validation and ultimately converted into practical tools that can assist clinicians and improve patient care. Achieving this goal will require close collaboration among laboratory scientists, clinicians, and healthcare systems to ensure equitable, real-world clinical adoption.

ABOUT THE AUTHORS

Prof. Minakshi Vashist is faculty in the Department of Genetics at Maharshi Dayanand University, Rohtak, Haryana, India. Her research focuses on human genetics, cancer biomarkers, and genetic variations associated with diseases, with the aim of improving cancer diagnosis and patient care. Dr. Anuradha Sharma is a genetic counsellor associated with the same department, with expertise in clinical genetics and an interest in understanding the role of genetics in human health. Dr. Rohit Kaushik is a researcher whose work includes studying genetic variations and molecular biomarkers associated with bladder cancer. Together, the authors combine their knowledge and research experience to explore how advances in genetics and molecular biology could support early cancer detection, better disease monitoring, and more personalised treatment, ultimately contributing to improved patient care.



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SCIENCE FACTORS!

EMERGING INSIGHT

Double Diabetes: When Type 1 Diabetes Meets Insulin Resistance



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AREAS OF EXPERTISE
Functional genomics • Diabetes • Insulin resistance

WHY IT MATTERS

Can someone with type 1 diabetes also develop insulin resistance? Why does this combination, known as double diabetes, make treatment more difficult for children? Dr. Satyajeet Khare explores why insulin resistance remains difficult to measure in type 1 diabetes. Drawing on research involving young people in India, he explains how blood-cell counts may offer clues about insulin sensitivity. Could these findings improve diagnosis and treatment? The article highlights the need for better diagnostic methods, deeper biological understanding and effective treatments to protect young people from long-term complications.

A child with type 1 diabetes (T1D) whose insulin dose keeps rising while glucose control does not improve may have a second problem: insulin resistance. This combination is called double diabetes, and it matters because it is associated with a higher risk of diabetic complications. Two gaps hold back progress: we cannot reliably measure insulin resistance in T1D, and we have little evidence on how to treat it in young people.

Diabetes mellitus is characterised by persistently high blood glucose. Long-standing diabetes raises the risk of kidney, nerve, eye, and cardiovascular complications, with cardiovascular disease the leading cause of death. Diabetes is common and rising in India. T1D, the insulin-dependent form, is characterised by insufficient insulin production by the pancreatic islets. Globally, T1D accounts for a minority of cases (roughly 5–10%), while type 2 diabetes (T2D) accounts for over 90%. In most people, T1D follows autoimmune destruction of the insulin-producing beta cells and is therefore treated with exogenous insulin. T1D typically begins in childhood but can start at any age. T2D is driven largely by insulin resistance, in which tissues respond poorly to insulin. Unlike T1D, T2D is often treated with oral drugs, such as metformin, that improve insulin sensitivity (Magliano & Boyko, 2021).

Some children and adults with T1D develop insulin resistance, often first noticed as a rising insulin dose needed to keep glucose in range. However, current evidence does not support use of Metformin in T1D adolescents to improve HbA1c. Therefore, treatment of double diabetes in children remains an unmet clinical need (Figure 1). Measurement is the other problem. Though higher insulin requirement indicates insulin resistance, it is also influenced by diet, physical exercise, puberty, and other factors.

Why insulin resistance is hard to measure in T1D

Clinicians look for signs such as acanthosis nigricans, a velvety darkening of the skin. The reference method is the hyperinsulinaemic-euglycaemic clamp (HEC). However, acanthosis nigricans is not specific, and HEC is too laborious for small clinics. As a result, alternative equations have been developed based on routinely measured clinical parameters. One such equation, the homeostasis model assessment of insulin resistance (HOMA-IR), is widely used in T2D. However, HOMA-IR relies on fasting insulin, which is typically raised in T2D but often very low or undetectable in T1D. It is therefore unsuitable for T1D.

In a systematic review of how insulin resistance and metabolic syndrome are assessed in T1D, we identified three equations (Khandagale et al., 2024). These combine waist circumf-

erence or waist-to-hip ratio, HbA1c, triglycerides or HDL-cholesterol, and blood pressure. However, few studies have tested whether they predict clinical outcomes. More importantly, the equations agree poorly with one another, so the choice of equation can change who is classified as insulin resistant.

What the biology of double diabetes may tell us

As noted above, drugs used for insulin resistance in T2D have limited use in young people with T1D. This is the second unmet need. New treatments need a better understanding of the underlying biology. We recently examined blood-cell correlates of insulin sensitivity in 343 children and youth with T1D in western India. Insulin sensitivity was estimated using the equation from the Coronary Artery Calcification in Type 1 Diabetes (CACTI) study (Duca et al., 2016). In our cohort, most participants had a normal-to-low BMI yet low estimated insulin sensitivity. Eosinophil counts were positively associated, and neutrophil, lymphocyte and platelet counts negatively associated, with insulin sensitivity. Most effects were modest, and they varied by age, sex and BMI (Figure 2). These associations differed from those reported in adults without T1D (Khandagale et al., 2026). These findings hint that double diabetes may differ biologically from insulin resistance in T2D. A single retrospective study cannot show this, so replication is essential.

Where this leaves clinicians and researchers

Although T1D is a minority of diabetes, it affects children who will live with its consequences for decades, and it deserves dedicated attention. Inconsistent measurement methods and scarce data linking double diabetes to complications make interventions hard to design. Few biological studies also slow the search for new treatments, especially in children. In light of the above, three priorities can be set: (1) validating a T1D-specific insulin resistance index against the clamp in Indian youth; (2) multicentre paediatric T1D cohorts with standardised measurement and follow-up for complications; and (3) safety and efficacy trials of insulin sensitisers in younger children. We cannot treat what we cannot measure, and in young people with double diabetes we can do neither well yet.

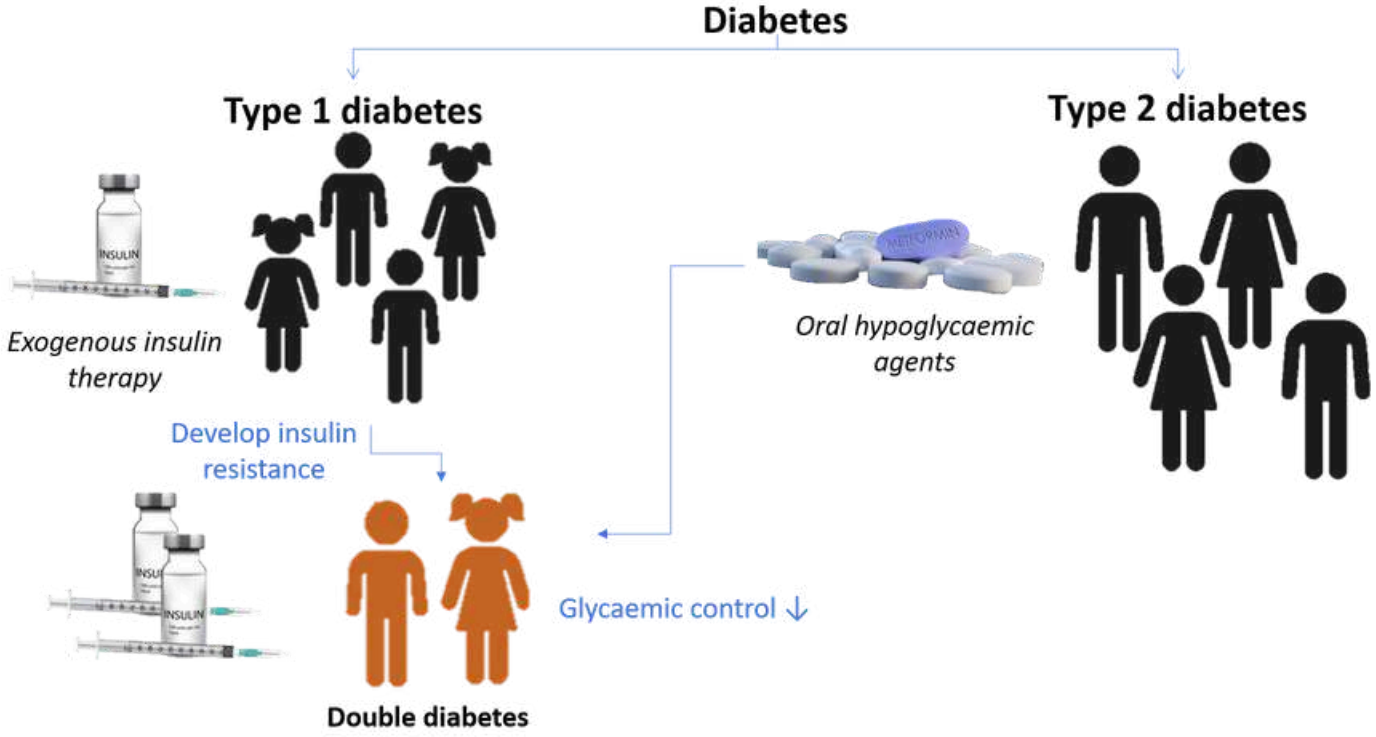


Figure 1. Double diabetes: insulin resistance developing in people with type 1 diabetes (T1D).

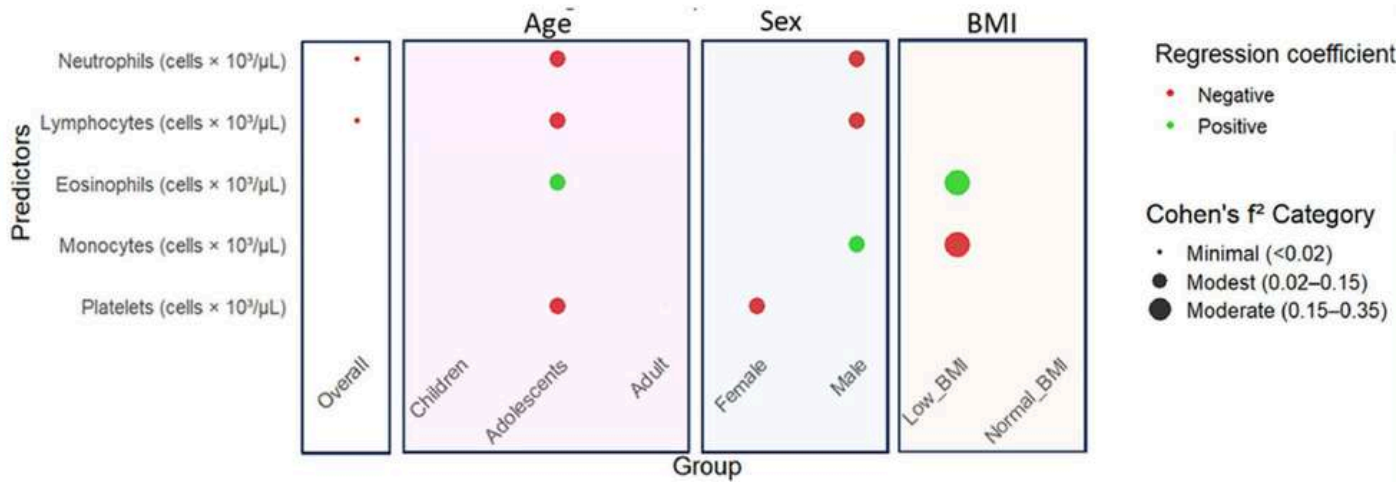


Figure 2. Association between estimated insulin sensitivity and blood-cell counts (haemogram) in 343 children and youth with T1D, by multiple regression. Red: negative association; green: positive. Dot size shows effect size (Cohen's f²). Only significant associations are shown. Adapted from (Khandagale et al., 2026).

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Dr. Satyajeet Khare is a functional genomics researcher at the Symbiosis School of Biological Sciences, Symbiosis International (Deemed University), Pune, India. His research focuses on bioinformatics, genomics, proteomics and data science, particularly in understanding diabetes, insulin resistance and other complex human diseases. He collaborates with clinicians, mathematicians and data scientists to combine genomic, clinical and computational approaches to address important biomedical questions. His work also covers gene expression analysis, metabolic disorders, cancer and psychiatric diseases, with the aim of improving our understanding of disease mechanisms and supporting better diagnosis and treatment.

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SCIENCE FACTORS!

EMERGING INSIGHT

Unlocking Natural Tick Resistance in Indigenous Cattle for Sustainable Livestock Farming



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| Scientific Profile |
| Organization Link |
| Factors Press |

AREAS OF EXPERTISE
Animal Breeding • Genomics • Transcriptomics • Biostatistics



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AREAS OF EXPERTISE
Acaricide Resistance • Haemoprotozoology • Molecular Parasitology

WHY IT MATTERS

Ticks and tick-borne diseases are a major challenge for dairy farmers, affecting animal health, milk production and farmers' livelihoods. In this article, Dr. Jay Prakash Gupta and Dr. Shyma K.P. explore how India's indigenous cattle, particularly the Kankrej breed, possess natural resistance to tick infestation. They explain how stronger skin immune responses and genetic differences may help these animals resist parasites. The article highlights how understanding and using this natural resistance in cattle breeding could reduce dependence on chemical treatments, improve livestock health and support more sustainable dairy farming.

Ticks and tick-borne diseases are among the major challenges affecting milk production in India, causing considerable economic losses to dairy farmers. In addition to the merely visible presence of parasites on the animals, their impact goes far beyond. Ticks act as vectors of important haemoprotozoan and bacterial diseases; besides this, tick infestation can cause irritation, skin damage, blood loss, and poor body condition. The resulting compromise of animal health and productivity can cause substantial economic losses for livestock farmers.

Chemical acaricides have been the major method of tick control for decades. However, repeated application of chemical treatment is not an appropriate long-term solution. Problems associated with arising resistance, high treatment costs, contamination of environment and the need for repeated application for tick control highlight the importance of complementary approaches. One such promising approach is to explore the cattle breeds possessing natural resistance. Our recent work on Kankrej and crossbred cattle provides an important example in this regard. A study involving 116 naturally exposed cattle, 27 Kankrej and 89 Holstein Friesian (HF) crossbreds revealed that HF crossbreds carried significantly higher tick burdens than Kankrej cattle under field conditions. The study also investigated the biological basis of this difference through examination of skin immune responses and candidate immune genes. This study can further be viewed together with transcriptomic evidence generated from indigenous and crossbred cattle exposed to Theileria infection. The RNA-Seq study identified substantial differences in gene expression and immune-related pathways between infected and non-infected cattle and

between indigenous and crossbred animals. The combined evidence points towards a broader concept that indigenous cattle may possess biological mechanisms that enable them to respond more effectively to important tropical disease and parasite challenges.

Ticks: Concern to animal health, production and livelihood

Ticks are not merely external parasites. Their feeding causes local tissue damage and irritation, while heavy infestation can adversely affect the overall health and productivity of cattle and can transmit several pathogens responsible for economically important diseases. The consequences can be particularly serious for majority small and marginal farmers of India, for whom these animals represent an important source of income and household security.

The problem in tropical countries like, India remains greater where cattle are exposed to combinations of heat stress, nutritional limitations, parasites and infectious diseases. Thus, exploring animals that can tolerate these environmental and biological challenges is increasingly important for sustainable livestock production. The Kankrej is one such cattle on which study provides direct evidence differential ticks burden between breeds. HF crossbred cattle showed significantly greater tick loads than Kankrej cattle, demonstrating that the host animal itself is an important component of tick-control biology. The adaptive characteristics of these animals, including their resilience to diseases and parasites, represent valuable genetic resources for future livestock improvement. Our recent study on Kankrej cattle revealed three important features that may contribute to their natural resistance to tick infestation: lower tick burden, stronger cutaneous immune responses, and breed-associated differences in candidate immune genes. These findings highlight the potential of indigenous cattle as valuable genetic resources for improving disease resistance and supporting sustainable livestock production.

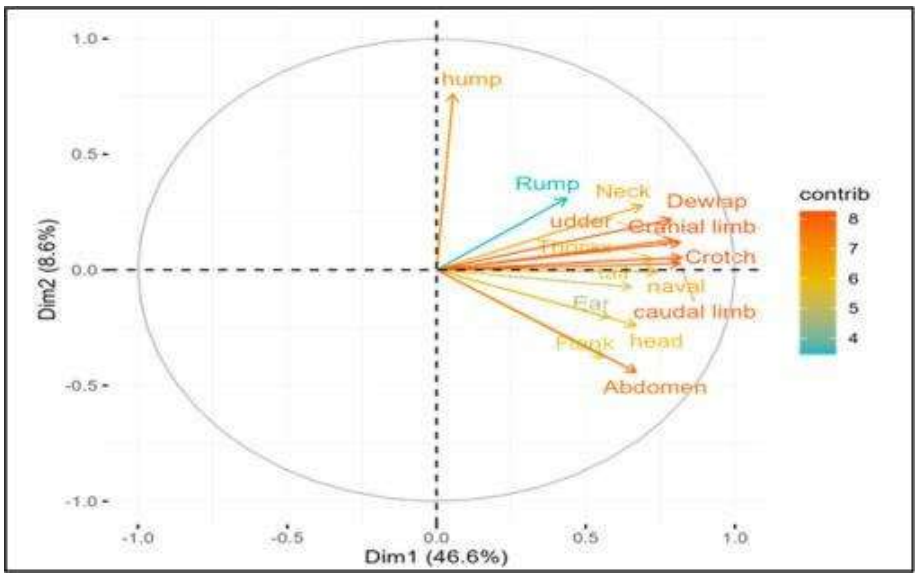


Figure 1: Principal component analysis (PCA) loading plot showing the contribution of different anatomical regions to tick infestation patterns in cattle. PC1 and PC2 explained 46.59% and 8.57% of the total variation, respectively. The dewlap, cranial limb, udder, and crotch regions showed the highest positive loadings on PC1.

Kankrej breed of cattle carried significantly fewer ticks than HF crossbreds under similar management conditions in the field. Further, histopathological examination showed greater mast-cell infiltration in these cattle, not only this, even non-infested Kankrej animals had a comparatively higher baseline mast-cell population than HF crossbreds. Mast cells participate in local inflammatory reactions and release mediators that can influence the response of skin tissue to invading organisms and ectoparasites. Therefore, the higher baseline mast-cell population observed in Kankrej cattle provides a credible biological explanation for their stronger local response to tick attachment.

The candidate immune-related genes CD209 studied was found to be polymorphic in HF crossbreds but monomorphic in the Kankrej population. A significant association was observed for CD209, with the AA genotype showing a substantially higher odds of tick infestation than the AB genotype. However, tick resistance is a complex trait, and the candidate-gene study itself does not establish that CD209 alone determines resistance. Rather, it identifies a potentially useful genetic marker that warrants validation in larger populations.

Lower Tick Burden, Stronger Immunity

The most interesting interpretation from the discussed research is that when a tick attaches to cattle skin,

the host does not remain biologically passive. The attachment site initiates local tissue and immune responses. There is marked mast-cell infiltration at tick attachment sites in Kankrej cattle associated with a stronger response than in HF crossbreds. This suggests that Kankrej cattle may be better primed to recognise and respond to tick attack. A faster or stronger local response could make the host environment less favourable for successful tick feeding and persistence.

The additional RNA-Seq information strengthens the broader immunological interpretation. CD14 is involved in inflammatory and innate immune signalling, while CLEC4D is associated with innate immune responses. CD59 is related to the complement system. These findings indicate that infection induces coordinated changes in innate immune-related genes in indigenous cattle. The pathway analysis indicated that In indigenous infected cattle, upregulated genes were enriched in pathways including MAPK, NF-κB, Toll-like receptor, Ras and chemokine signalling, all these are important components of cellular and immune responses. Thus, study provide valuable evidence that the indigenous host has a distinctive capacity to activate immune and inflammatory pathways.

Indigenous Vs. crossbred cattle

The transcriptomic comparison indicated that the upregulated genes in indigenous cattle were associated with functions including phagocytosis, cytokine production and scavenger receptor activity. Several immune-related genes were prominent in this response, including DYSF, SLC11A1,

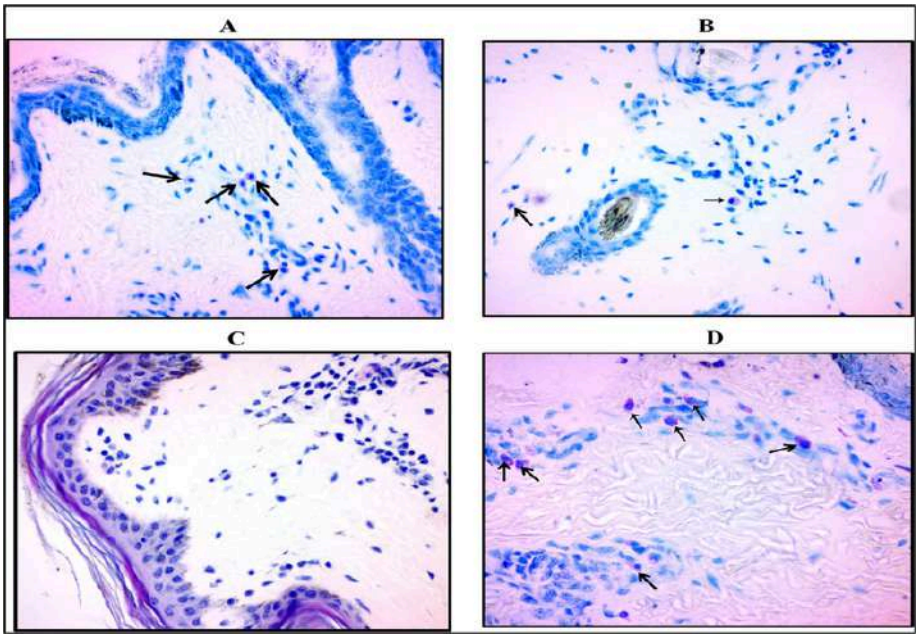


Figure 2: Representative micrographs of skin sections from non-infested and tick-infested cattle, illustrating mononuclear cell infiltration (with a focus on mast cells): (A) Toluidine blue stained (400 ×) skin section from non-infested Kankrej cattle, showing moderate mast cell infiltration. (B) Toluidine blue stained (400 ×) skin section from non-infested HF crossbred cattle, showing minimal or rare mast cell infiltration. (C) Haematoxylin and Eosin stained (400 ×) skin section from tick-infested HF crossbred cattle, showing extensive infiltration of mononuclear cells, though mast cells are not easily distinguishable. (D) Toluidine blue stained (400 ×) skin section from tick-infested Kankrej cattle, showing marked mast cell infiltration.

CD300LF, TREM1, EREG, NFIL3, CD14 and CTSH. It is also to be noted that the crossbred cattle also showed enrichment of immune pathways including NOD-like receptor, JAK-STAT, MAPK, NF-κB and Toll-like receptor signalling. Therefore, the correct interpretation is that breed differences may occur in the nature, magnitude, timing or regulation of host responses. Interestingly, when infected indigenous and crossbred animals were directly compared, MAPK, PI3K-Akt and AGE-RAGE signalling pathways were among those enriched in the comparison. Thus, the combined evidence suggests that host resilience is biologically complex and involves multiple genes, pathways and cellular responses.

Ticks predilection sites

The distribution of ticks across the body is not random, study identified the crotch, udder, dewlap and limbs as important predilection sites. These regions can provide favourable conditions for tick attachment because of differences in skin characteristics, hair density, moisture, temperature, local microclimate and accessibility. Skin folds and relatively protected regions may also provide favourable conditions for the parasite to remain attached. The finding also has implications that if tick counts are to be used as a measure of resistance, researchers should standardise the anatomical regions examined and

consider the effect of season and environmental exposure.

Natural resistance can be harvested

Natural tick resistance is a complex, potentially polygenic adaptive trait, rather than a single-gene characteristic. The Kankrej study provides several possible indicators: actual tick burden, anatomical distribution, skin immune response and genetic variation.The candidate-gene study identified CD209 as particularly interesting because the AA genotype showed 12.89-fold higher odds of tick infestation than the AB genotype. The transcriptomic data provide that no common DEG was identified across all three major comparisons, demonstrating the complexity of the host response.

In practical breeding programmes, animals could first be evaluated for repeated tick burden under standardised conditions. Animals consistently showing lower infestation could then be evaluated for immune and genomic characteristics. Validated markers could eventually be incorporated into breeding programmes along with milk production, fertility, longevity, disease resistance and climate adaptation.

Low dependence on chemical for tick-control

Natural resistance is not at all replacement for veterinary treatment. Instead, it may be one of the components of integrated tick management. If cattle with naturally lower tick burdens can be identified and selectively bred, the overall parasite pressure in a herd may potentially be reduced. Combined with pasture and housing management, regular inspection and appropriate acaricide use, when necessary, this could reduce unnecessary chemical exposure.The Kankrej study specifically highlights the potential of indigenous breeds in sustainable tick-control strategies. The broader transcriptomic findings reinforce the scientific rationale for studying indigenous cattle as reservoirs of adaptive immune variation.

Message for Indian livestock breeding

Many years, cattle improvement programmes have understandably focused heavily on production traits such as milk yield. However, the challenges for livestock production in India is broader. Animals must cope simultaneously with heat, parasites, infectious diseases, variable feed availability and diverse production environments. Indigenous cattle have evolved within these conditions and therefore represent an important reservoir of adaptive genetic diversity.

The Kankrej cattle showed lower tick infestation and a stronger cutaneous mast-cell response than HF crossbreds.

Conclusion

India's indigenous cattle are more than a heritage resource. They may also represent a valuable biological reservoir of parasite resistance, immune responsiveness and environmental adaptability. Research in Kankrej cattle has demonstrated significantly lower tick burdens than in HF crossbreds and has linked this phenotype with a stronger cutaneous mast-cell response. Candidate-gene analysis has identified potentially useful genetic variation, particularly involving CD209. The ultimate opportunity is therefore to combine phenotypic tick resistance, skin immunology, transcriptomics and genomics to identify animals that are naturally better adapted to parasite and disease challenges.

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Dr. Jay Prakash Gupta is an Associate Professor in the Department of Animal Genetics and Breeding at Bihar Animal Sciences University, Patna, India. His research focuses on animal breeding, genomics, genetic diversity, and sustainable livestock improvement. He studies economically important traits such as disease resistance, heat tolerance, milk production, and reproductive performance in indigenous cattle and other livestock species. His recent work on Kankrej cattle explores natural resistance to tick infestation, localized skin immune responses, and associated genetic factors. Ultimately, his research aims to effectively use valuable native genetic resources for improving livestock health, reducing dependence on chemical treatments, and supporting long-term sustainable animal production.

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SCIENCE FACTORS!

EMERGING INSIGHT

Teaching an Old Flavonoid New Tricks: What's Next for Diabetic Wound Therapeutics



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AREAS OF EXPERTISE
Drug Repurposing • Formulation Development of Complex Generics • Novel Drug Delivery Systems • Pharmacology and Regulatory Toxicology



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AREAS OF EXPERTISE
Diabetic wound • bioinformatics • machine learning • network pharmacology

WHY IT MATTERS

Could a natural compound found in everyday plants help treat wounds that struggle to heal in people with diabetes? In this article, Shricharan Pandey and Dr. Suhani Sinha explore the potential of luteolin, a plant-derived compound that has shown promising effects on wound healing in laboratory studies. By combining bioinformatics, machine learning, and cell-based experiments, their research identifies a possible molecular pathway that could support the development of new treatments. But can these early findings lead to effective wound dressings for patients? The article explores the challenges that remain and how better experimental validation and innovative drug-delivery technologies could help turn this promising discovery into affordable treatments for diabetic wounds in the future

India now has more than 77 million adults living with diabetes, and somewhere between 5% and 14% of these people will develop a foot ulcer that won't heal on its own. Stalled healing is more than one problem. It's the simultaneous presence of chronic inflammation, impaired blood vessel growth, oxidative damage, and faulty tissue remodelling. This is precisely why a single-target drug so often doesn't suffice. In a recent study, we combined transcriptomic data mining and wet-lab cell biology to ask whether a flavonoid that is already part of our everyday diet, luteolin, which can be found in Martynia annua, celery, parsley, thyme, and many other plants, might actually work the way the problem does: on several fronts at the same time.

Using three independent datasets of diabetic wound gene expression, we distilled hundreds of dysregulated genes into a small, convergent list. Four completely different analytical approaches statistical differential expression, an independent public database, a machine-learning feature-selection algorithm, and chemical-target prediction for luteolin itself all converged on the same gene: PIK3R1, a regulatory subunit of the PI3K/AKT pathway. Then we tested luteolin directly on human skin fibroblasts under high-glucose stress. It improved cell viability, cut oxidative stress dramatically, accelerated wound closure in a scratch assay by about 40%, and nudged the PI3K/AKT/NRF2 signalling machinery in the direction you would want for healing: more survival signal, less apoptosis, and more antioxidant defence.

The convergence looks satisfying on a page. It is also, we think, a useful case study in where phytochemical wound-healing research needs to go next, because for every question this kind of study answers, it raises two more.

The biggest unanswered question is also the most basic one: does luteolin really bind PIK3R1 inside a living cell, or are we looking at a well-correlated bystander? Docking and molecular dynamics can tell you that a ligand could sit comfortably in a binding pocket; they cannot tell you that it does in the crowded, competitive environment of a real cell. To close this gap, we would need direct evidence of target engagement, which we have not yet obtained, or surface plasmon resonance, isothermal titration calorimetry, cellular thermal shift assays, or PIK3R1 knockdown-and-rescue. Until then, "luteolin targets PIK3R1" is a good hypothesis, not an established mechanism, and the field would do well to treat that distinction more carefully than it sometimes does.

The real breakthrough we need is not a new pathway or a new natural compound. There is no shortage of either. It is cheaper, faster, and more routine access to tools for target engagement and functional validation, so that computational hits no longer die quietly at the hypothesis stage. Today, a lab can generate a confident protein-protein interaction network and a strong docking score in a week, and then spend a year, if it spends the time at all, trying to prove that the interaction is real and functionally load-bearing. Democratising that second step, through shared CETSA or SPR facilities, cheaper knockdown reagents, or better computational proxies for binding, will do more for natural-product drug discovery than almost any single new molecular finding.

The trend we expect to dominate the next few years is the one our own study relied on: combining multiple independent lines of evidence, differential expression, public repositories, machine learning, and compound-target prediction, and trusting only what survives the intersection of all of them. It is statistically crude, but it is a good filter against the single-method false positive that has quietly populated the phytochemical literature over the last two decades. We expect this type of multi-method consensus approach to become a near-minimum standard for target-identification papers, much like power calculations have become standard for clinical trials.

We think the field is moving toward delivery over the next five to 10 years, not just mechanisms. Other groups have already formulated luteolin itself into nanovesicle gels, hydrogels, and dissolving microneedle patches, each addressing a different aspect of the problem: sustained release, biocompatibility, and painless application directly to the wound bed. The real-world approach to a clinic is not a luteolin pill, but a topical formulation, possibly in combination with a second agent hitting a complementary target such as a growth factor or an anti-inflammatory peptide, delivered through one of these platforms, tested first in an actual diabetic animal wound model, and eventually in a trial measuring real wound closure, rather than a signaling marker on a Western blot.

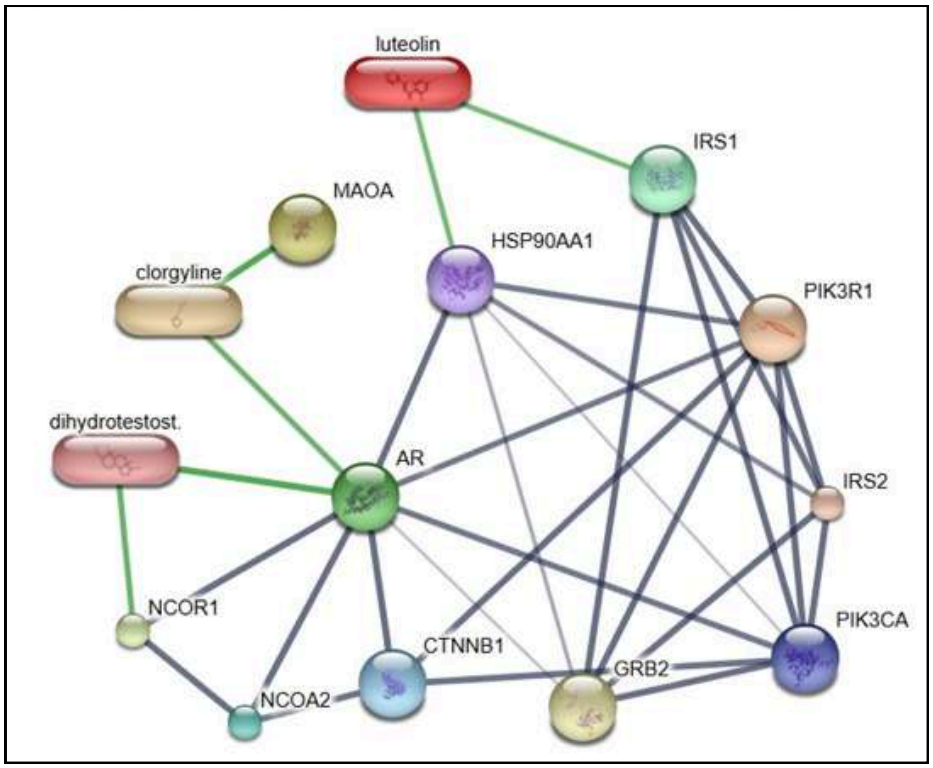


Figure 1: Protein-protein interaction network showing PIK3R1 as a highly connected node linking luteolin to the PI3K/AKT signaling machinery (HSP90AA1, PIK3CA, IRS1, IRS2) in diabetic wound-associated dermal fibroblasts.

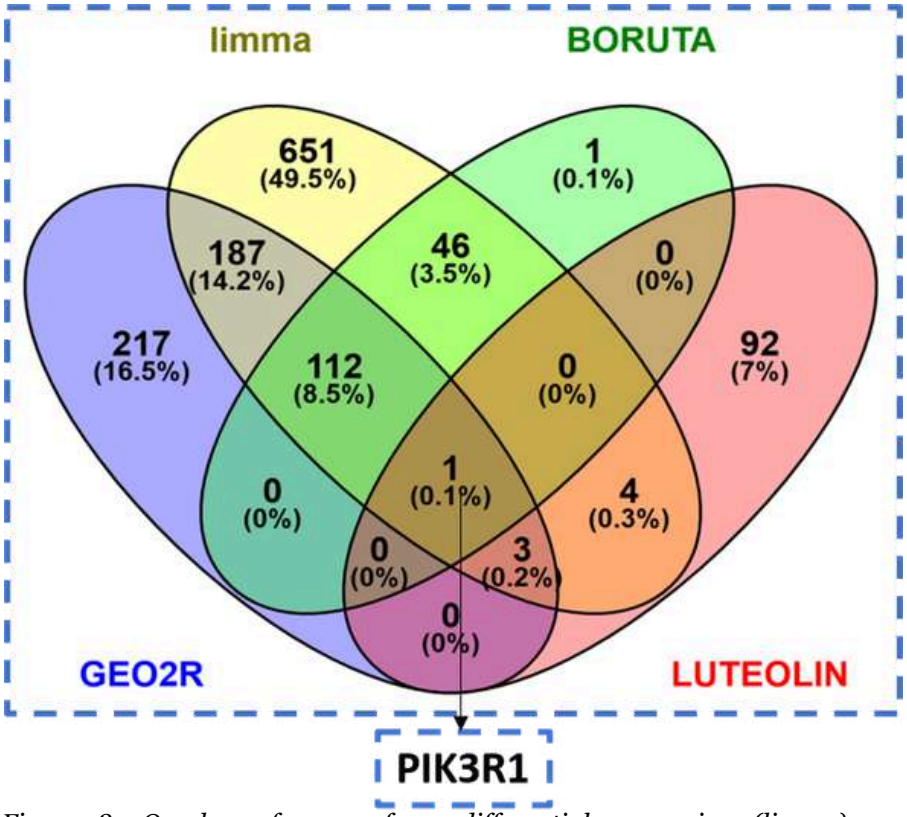


Figure 2: Overlap of genes from differential expression (limma), an independent database (GEO2R), machine-learning selection (BORUTA), and luteolin's predicted targets, with PIK3R1 converging across all four.

There is a uniquely Indian opportunity worth mentioning here, as the burden of disease is overwhelmingly ours. India has the largest diabetic population in the world, projected to be 134 million by 2045. Plant-derived flavonoids like luteolin will easily meet the supply chain limitations. A validated, well-made luteolin-based wound dressing would be a truly low-cost intervention for the health system most in need. We believe the institutional capacity to translate findings like ours from a 96-well plate into a validated dressing, shared docking and simulation compute, affordable target-validation cores, and GMP-grade phytochemical standardisation is as important a "next step" for the field as any single molecular target.

There are three limitations in particular; firstly, the translation of the findings to pre-clinical and clinical studies is missing. Whether anyone runs it or not, we're included. Second, a cell line does not completely simulate a human wound itself, although it provides a valuable proof of concept. Third, we do not yet have a joint statistical analysis to determine whether the metabolic signals we found in addition to the protein data—changes in an amino acid (leucine) and a membrane lipid (sphingomyelin) that are known to interact with PI3K/AKT signaling—are downstream effects that we might want to target in their own right, or just correlated noise. Furthermore, whether PIK3R1-centered approaches generalize beyond fibroblasts to the keratinocytes, macrophages, and endothelial cells that a real wound actually depends on, since healing is not a single-cell-type process, and our cell line model was never meant to pretend otherwise. None of this is to be a criticism of the state of natural-compound wound-healing research today. That's a pretty good description of science doing what it's supposed to do: a limited, clearly labeled hypothesis. The honest answer to "what's next" isn't a bigger claim, but a narrower. more validated claim.

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Dr. Suhani Sinha is an Associate Professor in the Department of Pharmacy at GD Goenka University, Gurugram, India. With experience across academia and the pharmaceutical industry, her research focuses on drug development, novel drug delivery methods, and repurposing existing medicines to develop better treatments for diseases like diabetes and cancer. Shricharan Pandey is a PhD scholar at NIPER-Hajipur, Bihar, India, focusing on diabetic wound healing, bioinformatics, and machine learning.

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SCIENCE FACTORS!

EMERGING INSIGHT

Can Mathematics Turn Doubt into a Decision?



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AREAS OF EXPERTISE

mathematics • mathematical modelling • decision methods • uncertainty analysis • fuzzy mathematics

WHY IT MATTERS

Can a difference of just one mark decide whether a medical student becomes a doctor? And is it fair to judge someone's ability using a single pass or fail score? In this article, Dr. Yogeesh N explores how mathematics could help make such important decisions fairer and more transparent. By combining fuzzy logic and Bayesian reasoning, he explains how examiners can better understand uncertain results and decide when more evidence is needed. But could this approach change how we assess future doctors and other professionals? The article offers an interesting look at how mathematics could transform examinations, reduce uncertainty, and support more reliable decisions without replacing human judgment.

TWO MEDICAL STUDENTS walk out of the same final practical examination. The pass mark is 60 per cent. One scores 60 and, within months, will be caring for patients. The other scores 59 and must repeat the year. Ask the examiners whether a single mark truly separates a safe doctor from an unsafe one, and most would hesitate.

That hesitation is what this article is about. Every year, examiners meet candidates whose performance sits right on the edge: not clearly competent, not clearly incompetent. Traditionally, the system settles that doubt by ignoring it. A line is drawn, and everyone lands on one side of it. Mathematics offers a better option: describe the doubt honestly, measure it, and reduce it step by step until a fair decision is possible. The numbers here are illustrative; the dilemma is real.

When evidence points in different directions

Clinical examinations usually take the form of a circuit of short stations. At each one, a candidate might take a patient's history, examine a patient, explain a diagnosis or carry out a procedure while an examiner watches. For most candidates, the picture is consistent. For a borderline candidate, it rarely is: confident communication at one station, a hesitant examination at the next, a nearly correct procedure at a third.

Examiners feel this uncertainty too. Research on high-stakes clinical examinations reports that examiners give 'borderline' grades precisely when they lack enough information for a clear pass or fail, that they feel less confident failing a student than passing one, and that their judgments can drift over a long examination day. (3)

A fixed cut-off hides all of this. It treats 59 and 60 as worlds apart, yet treats 60 and 95 as the same. It also hides how sure we are: a 60 built from consistent performance and a 60 assembled from wildly mixed observations receive the same verdict. The problem is not careless examiners. It is that a single number throws away exactly the information we need most in the hardest cases (Figure 1).

Two ideas that take doubt seriously

Two branches of mathematics, born two centuries apart, both begin by admitting uncertainty rather than ignoring it.

The first is fuzzy logic, which grew from the theory of fuzzy sets that Lotfi Zadeh introduced in 1965.2 Ordinary logic insists that a statement is either true or false; fuzzy logic allows degrees of truth. Is a temperature of 37.6 °C a fever?Is dusk day or night? Our natural answer, 'partly', is exactly what fuzzy logic puts into numbers. Instead of labelling performance at a station simply 'pass' or 'fail', it can be described as mostly competent with some gaps: a degree between 0 and 1.

Clinical competence, like dusk, comes in shades.

The second is Bayesian reasoning, named after the eighteenth-century minister and mathematician Thomas Bayes. It describes how a belief should change as new evidence arrives. Doctors already reason this way: symptoms suggest several possible diagnoses, and each test result makes some more likely and others less so. Bayesian reasoning attaches numbers to that process, so each observation shifts our confidence in proportion to how informative it is.

Each idea solves half the problem. Fuzzy logic captures the nuance in every observation but does not say how confident we should be overall. Bayesian reasoning combines evidence powerfully but needs it in a usable form. Together they make a natural partnership: fuzzy logic can translate what examiners see into graded evidence, and Bayesian reasoning can combine that evidence into an overall probability that a candidate is genuinely competent, with an honest sense of how certain that probability is. My colleagues and I recently brought the two together in a hybrid approach to standard setting, the process of deciding where an examination's pass standard should lie.(1)

Reaching a decision step by step

Return to our 59-per-cent candidate; call her Meera. Under a fixed cut-off, her story ends in one line. In a Bayesian–fuzzy framework, it unfolds in four steps (Figure 2).

1. *Gather*. Observations from every station, including checklist scores and examiners' overall judgments, are kept rather than collapsed into one total.
2. *Grade*. Fuzzy logic converts each observation into a degree of competence. Meera's communication is strongly competent; her physical examination is only partly so.
3. *Update*. Starting from a neutral position, the framework revises its confidence after every station. Clear evidence moves the needle a lot; ambiguous evidence moves it a little.
4. *Decide*. If the evidence clearly points to competence, the candidate passes; if it clearly points the other way, she does not. If it remains genuinely mixed, the framework says so and recommends gathering more evidence first.

For Meera, six stations leave the evidence genuinely mixed. Instead of forcing a verdict, the framework recommends one extra station focused on physical examination. She performs it well, and her result moves firmly into the pass zone. Had that station revealed a real weakness, the framework would have supported a fail with the same confidence and equally clear reasons.

That third option, 'not sure yet', is the heart of the approach. A fixed cut

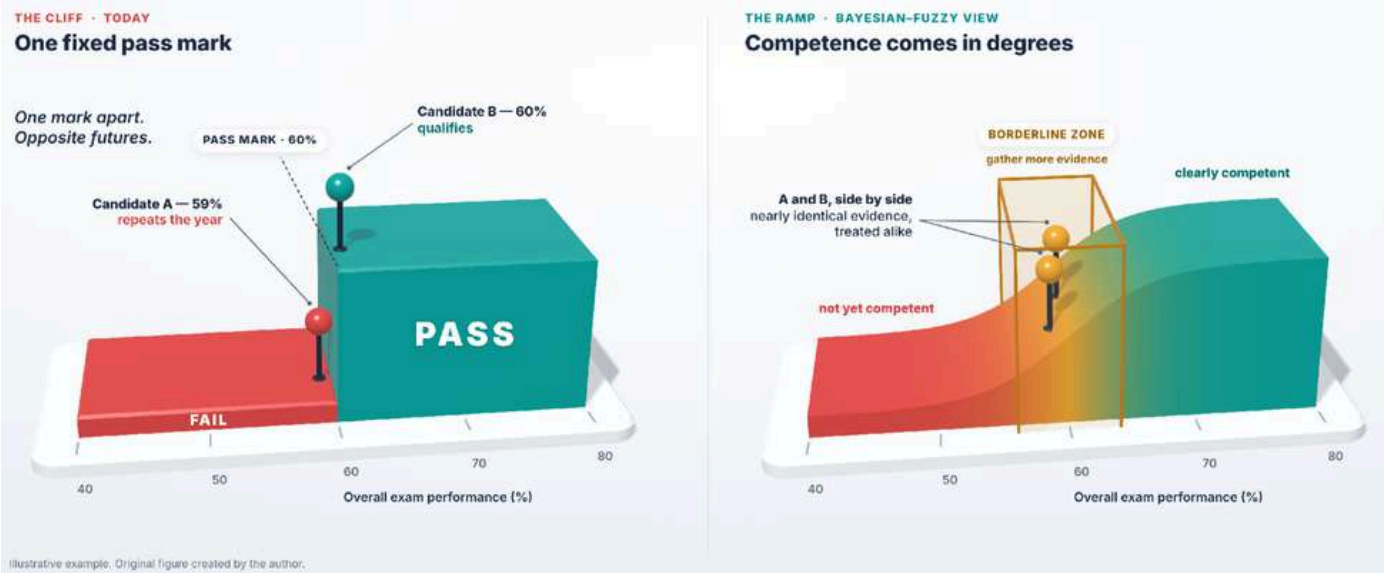


Figure 1: The cliff and the ramp. Left: under a fixed pass mark, two candidates one mark apart receive opposite outcomes. Right: a Bayesian–fuzzy view describes performance as a degree of competence. Candidates inside the amber borderline zone are treated alike and flagged for more evidence, rather than being forced onto one side of the line. Illustrative values. Original figure created by the author.



Figure 2: Top: the four steps of a Bayesian–fuzzy assessment. Bottom: an illustrative 3D decision dial for a borderline candidate. After six stations, mixed evidence keeps her result in the uncertain zone; one targeted extra station supplies clear evidence and moves the needle to a confident, explainable decision. Original figure created by the author.

off must push every candidate onto one side of the line, even when the evidence supports neither. The framework turns doubt into a structured next step instead, and every decision comes with its reasons: which observations counted, by how much, and why. A decision that can be explained is a decision that can be defended, to the candidate, to the institution and, ultimately, to patients.

Keeping human judgment in the process

No formula should decide a person's future on its own, and this framework is not designed to. Its role is to support examiners by making their collective judgment more consistent, transparent and fair, not to replace them. The fuzzy grades encode what experienced clinicians regard as competent, and people still make the final call on borderline cases.

Real challenges remain. The framework is only as good as the observations fed into it, so examiner training and well-designed stations still matter. Institutions must agree in advance how much certainty a pass requires, which is a value judgment rather than a mathematical one. And the approach must be tested across medical schools, countries and examination formats before it can be widely trusted.

The opportunity reaches well beyond medicine. The same logic applies wherever people are judged against a standard using imperfect evidence: nursing and pharmacy licensing, professional certification, even recruitment. Wherever a single cut-off is asked to carry more weight than it can bear, an honest mathematics of doubt can help.

THE TAKEAWAY

Medicine has long accepted that uncertainty is unavoidable; good doctors manage it rather than pretend it away. We ask future doctors to weigh evidence carefully, revise their thinking as new results arrive, and know when to seek a second opinion. It is only fair that we judge them the same way. Mathematics cannot remove doubt from that judgment, but it can make doubt visible, measurable and, finally, something we can act on wisely.

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SCIENCE FACTORS!

EMERGING INSIGHT

Staying Ahead of Designer Drugs: New Technologies for Faster and More Reliable Forensic Detection



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AREAS OF EXPERTISE

WHY IT MATTERS

What happens when a new designer drug appears that even modern laboratories cannot identify? As new drugs continue to emerge, existing testing methods often struggle to detect them. In this article, Prof. Astha Pandey and Anirudha Dixit explain how modern technologies, including advanced chemical testing and artificial intelligence, can help scientists identify unknown drugs faster and more accurately. They also highlight why sharing information between laboratories around the world is important for detecting new drug threats. Could these technologies help us identify dangerous drugs before they become a major public health problem? The article explores how future advances in forensic science could make drug detection faster, more reliable, and better prepared for new challenges.



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AREAS OF EXPERTISE

A forensic laboratory can generate excellent analytical data and still fail to identify a substance. The instrument detects a chemical signal, but the compound does not match any entry in the available reference libraries. A small structural modification to a known drug may be enough to create a substance that routine screening methods cannot confidently recognize. This is a growing challenge in the analysis of novel psychoactive substances (NPS), commonly called designer drugs. These compounds can mimic the effects of established drugs while presenting new analytical and regulatory challenges.

In August 2026, the United Nations Office on Drugs and Crime (UNODC) reported 1,525 NPS from 155 countries and territories through its monitoring system. A further 110 substances were reported for the first time during the 2025/26 reporting period, although the most recent figures remain preliminary [1]. For forensic laboratories, the challenge is no longer simply to detect known drugs. It is to investigate substances for which reference standards, toxicological information and validated methods may not yet exist.

Why Conventional Testing Is Not Enough

Traditional drug analysis relies on comparison with known compounds. Analysts examine characteristic signals, retention times and mass spectra, often using certified reference materials to support identification. These approaches remain reliable for established substances when appropriate validated methods are available. Problems arise when an unfamiliar c-

ompound enters the sample. Structural changes can alter fragmentation patterns and chromatographic behaviour, preventing a match with existing library entries. Complex mixtures, low analyte concentrations and the presence of adulterants further complicate interpretation. In biological specimens, the parent drug may also decline before collection, leaving metabolites as the principal evidence of exposure. Non-targeted analysis offers a complementary approach. Rather than examining only a predefined list of compounds, analysts investigate a broader range of detectable chemical features. This does not guarantee identification of every unknown, but it increases the likelihood of recognising unexpected substances and generating useful leads.

High-Resolution Mass Spectrometry: Beyond Targeted Screening

High-resolution mass spectrometry (HRMS) has become an important tool for investigating unfamiliar drugs. It measures mass-to-charge ratios with high accuracy, helping analysts determine candidate molecular formulas and interpret fragmentation patterns. Combined with chromatography, it can provide detailed information about substances within complex mixtures. One of its greatest advantages is retrospective analysis. Consider a seized sample examined before its active ingredient is known. Months later, another laboratory identifies a new drug and publishes its characteristic spectral data. If the original HRMS acquisition captured the relevant signals, analysts may be able to search the stored data for evidence of that substance without reanalysing the physical sample.

This capability is particularly valuable because emerging drugs can spread faster than laboratories can develop reference materials and confirmatory methods. HRMS research has increasingly explored retrospective screening, broad-spectrum wastewater analysis and computational approaches to interpreting unfamiliar compounds [2]. However, accurate mass alone rarely establishes a unique molecular structure. Closely related compounds can share molecular formulas and produce similar fragmentation patterns. Depending on the case, additional evidence, an orthogonal analytical technique or an authentic reference standard may be necessary for confirmation.

Additional Dimensions: Ion Mobility and Artificial Intelligence

Ion mobility spectrometry can complement HRMS by separating gas-phase ions according to their movement through a gas under an electric field. This behaviour depends partly on an ion's size and shape. Certain isomers compounds with the same molecular formula but different structures can therefore exhibit different mobility characteristics. Collision cross section (CCS), a parameter describing an ion's interaction with the surrounding gas, provides another measurement for comparison. Although ion mobility can help distinguish some isomers, it cannot resolve every structural ambiguity. CCS should be interpreted alongside other analytical evidence rather than treated as a unique identifier.

Artificial intelligence (AI) offers another way to manage the growing complexity of chemical data. Machine-learning models can suggest structural families, predict

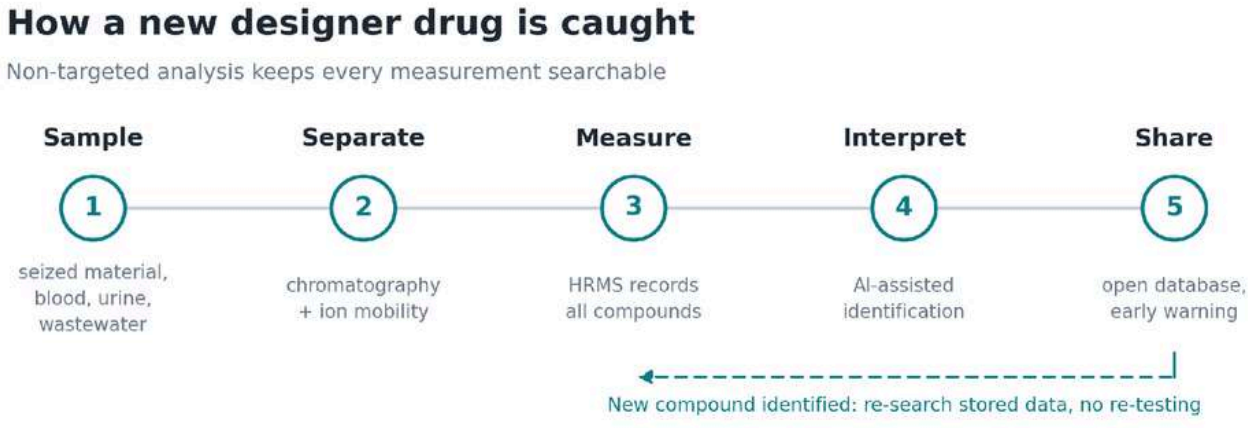


Figure 1: Non-targeted analysis turns every measurement into a searchable record

candidate fragmentation spectra and prioritise signals for further investigation. Such tools may help analysts narrow the possibilities when conventional library searches return no satisfactory match. Their reliability, however, depends on the quality and diversity of training data.A model trained primarily on familiar compounds may perform poorly on genuinely new chemical classes or data collected using different instruments. Before adoption in forensic casework, these systems require independent validation, testing on unfamiliar compounds and realistic mixtures, and transparent reporting of uncertainty. A computational prediction is not a confirmed identification. The most defensible role for AI is to support expert interpretation, not replace it.

Building a Global Early-Warning Network

Analytical innovation is only part of the solution. When a laboratory identifies a new substance, that information must reach other laboratories quickly enough to influence their testing strategies. Shared spectral libraries and quality-controlled databases can help laboratories compare findings, update suspect lists and develop appropriate methods. Consistent data formats, reporting standards and transparent identification criteria are essential for meaningful international collaboration. Wastewater analysis provides another complementary source of intelligence. HRMS can help researchers investigate chemical residues and metabolites in wastewater to identify patterns that may indicate changing substance use. Such findings can support population-level surveillance without directly identifying individual users. Nevertheless, a detected chemical signal does not automatically establish the prevalence of use, and environmental findings require careful interpretation.

Together, evidence from seized materials, biological specimens and wastewater could strengthen early-warning systems. Their effectiveness will depend on reliable analytical data, appropriate interpretation and timely communication between forensic laboratories and public-health authorities.

What the Next Decade Could Bring

Over the next five to ten years, progress is likely to depend on integrating existing technologies rather than relying on a single breakthrough. In the near term, wider adoption of retrospective HRMS analysis could allow laboratories to extract more value from previously collected data. Machine-learning tools may subsequently become useful decision-support systems as their performance is independently validated. Computational predictions of drug metabolism could also help researchers prioritise potential biomarkers for experimental investigation. A longer-term ambition is a connected network in which an unfamiliar spectrum can be compared against international datasets and used to generate candidate structures, likely metabolites and suggested analytical targets. Such a system could reduce delays between a substance's first detection and its recognition elsewhere, although expert interpretation and confirmatory testing would remain essential.

Achieving this vision requires investment in instrumentation, reference materials, specialist training and accessible data infrastructure. International cooperation is equally important, particularly for laboratories with limited analytical resources.

From Reaction to Anticipation

Forensic drug analysis has traditionally responded after a new substance enters circulation. A compound appears, investigators identify it, and laboratories develop methods to detect it. HRMS, ion mobility, computational tools and shared databases offer opportunities to shorten this process. The objective is not to predict every new drug before it appears. It is to ensure that unfamiliar substances can be investigated efficiently, analytical uncertainty is communicated honestly, and reliable findings reach the wider scientific community without unnecessary delay. The chemistry of designer drugs will continue to evolve. Forensic science must respond not only with better instruments, but also with stronger validation, skilled analysts and a willingness to share knowledge. These are the foundations of a more anticipatory approach to emerging drug threats.

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Prof. Astha Pandey is a Professor at the School of Forensic Sciences, National Forensic Sciences University (NFSU), India, and Head of the Centre of Excellence for Research and Analysis of Narcotic Drugs and Psychotropic Substances. With over 20 years of experience, she has led several research projects focused on forensic drug analysis, emerging designer drugs, and new methods for detecting illegal substances. Her work aims to improve drug identification and address emerging challenges in forensic science. Anirudha Dixit is a Research Scholar at NFSU, India, working in the field of forensic science.Together, they highlight how modern technologies can improve the detection of emerging drugs and help protect public health.



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SCIENCE FACTORS!

EMERGING INSIGHT

The Invisible Allies of Green Restoration: Harnessing Plant Microbiomes Against Heavy Metal Pollution



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AREAS OF EXPERTISE
Environmental microbiology • Metagenomics • Phytoremediation • Green chemistry • Abiotic stress

WHY IT MATTERS

Could the solution to cleaning polluted soil be hiding inside plants themselves? As heavy metal pollution increases, finding sustainable ways to restore contaminated land is becoming important. In this article, Dr. Soumya V. explores how tiny bacteria and fungi living inside plants may help them survive in polluted environments. Drawing on research involving *Catharanthus roseus*, the article explains how pollution changes these microbial communities and their potential role in environmental restoration. Could future technologies help scientists use these beneficial microorganisms to clean polluted land naturally? The article explores how plant microbiomes, genetic sequencing, and biotechnology could contribute to a cleaner and greener future.

Beneath the visible architecture of every plant lies an intricate biological world, an assemblage of microscopic fungi and bacteria that can profoundly influence its ability to survive environmental adversity. These microorganisms, known as endophytes, inhabit internal plant tissues without necessarily causing disease. Increasingly, they are being recognised as essential contributors to plant resilience, nutrient acquisition, stress adaptation and environmental detoxification.

Their significance becomes particularly compelling in ecosystems burdened by heavy metals released through industrial activity, mining and urbanisation. Unlike many organic pollutants, metals such as cadmium, lead and chromium cannot be biologically degraded into harmless elements. They persist in soils, disrupt cellular metabolism, compromise plant growth and may enter food chains, threatening ecological integrity and human health.

Conventional remediation can be expensive, disruptive and difficult to implement across extensive contaminated landscapes. Phytoremediation, the use of plants to remove, immobilise or manage pollutants, offers a more ecologically compatible alternative. Yet its effectiveness depends not only on the plant itself, but also on the microbial partners operating within its tissues. Understanding this hidden microbiome could redefine how science approaches pollution control and ecosystem restoration.

When Pollution Reshapes the Invisible Ecosystem

My recent research published in the International Journal of Phytoremediation in October 2026, offers important insights into this emerging field. Investigating *Catharanthus roseus*, a medicinally significant plant, my colleagues and I examined fungal and bacterial endophytes in plants cultivated for 12 months in industrially contaminated soil from Hindustan Shipyard Limited, Visakhapatnam, and in comparatively uncontaminated garden soil.

Using Oxford Nanopore sequencing to profile fungal and bacterial genetic markers, the study revealed pronounced differences in microbial community composition between contaminated and control environments. Root tissues generally supported greater microbial diversity than leaves, while contaminated con-

ditions were associated with substantial community restructuring and selective enrichment of microorganisms potentially adapted to metal stress.

These observations suggest that pollution acts as an ecological filter. Rather than affecting every microorganism equally, environmental stress changes the competitive landscape, favouring certain microbial lineages while diminishing others.

The implications extend beyond identifying which organisms survive. They invite a deeper question: can plants recruit, retain or benefit from microbial partners whose biological capabilities help them withstand hostile environments?

From Microbial Diversity to Functional Resilience

The study identified several bacterial groups in contaminated-site samples, including *Pseudomonas, Bacillus, Rhizobium, Variovorax* and *Sphingomonas*. Distinctive fungal taxa were also detected, including members of *Cortinarius, Inocybe* and *Coprinopsis*.

Previous studies have associated members of these microbial groups with diverse functions, including metal binding, nutrient mobilisation, stress tolerance, and the transformation of environmental contaminants. Some microorganisms can produce siderophores, molecules that bind iron and influence metal availability, while others may contribute to antioxidant defence, organic acid secretion or the sequestration of toxic elements.

Such capabilities could support plants through complementary mechanisms. Microorganisms may immobilise metals, reducing their availability for uptake; alternatively, they may facilitate metal mobilisation and transport into harvestable plant tissues. The appropriate outcome depends on the contaminant, plant species and restoration objective.

A crucial distinction remains: the sequencing study demonstrates changes in microbial composition, not direct proof that every enriched organism performs a particular remediation function. Establishing these relationships requires functional experiments, chemical measurements and controlled plant–microbe trials.

Nevertheless, the findings strengthen an important conceptual advance: plant resilience should be understood through the interacting biological system formed by the plant and its associated microbiome, rather than through plant physiology alone.

New Tools for Discovering Hidden Biological Potential

The emergence of high-throughput sequencing has transformed the study of plant-associated microorganisms. Traditional cultivation methods reveal only organisms that grow under selected laboratory conditions, overlooking much of the microbial diversity present in nature.

By combining fungal internal transcribed spacer sequencing with bacterial 16S ribosomal RNA gene profiling, the study examined two major microbial groups within the same experimental framework. Nanopore sequencing also offers the practical advantage of generating long genetic reads, supporting rapid and increasingly accessible microbial characterisation.

The next scientific frontier lies in connecting microbial identity with biological function. Metagenomics can investigate the collective genetic potential of microbial communities; transcriptomics can reveal which genes are active; and metabolomics can identify the small molecules produced during plant–microbe interactions.

Emerging research is also exploring machine learning and integrated multi-omics approaches to identify promising microbial combinations and predict their performance under different environmental conditions. Recent studies and reviews have highlighted microbiome engineering, microbial consortia and precision-guided remediation as important directions for improving biological treatment of metal-contaminated soils.

Together, these developments could move environmental restoration from trial-and-error inoculation towards evidence-based selection of microbial partners suited to particular pollutants, soils and plant hosts.

Current Challenges and Emerging Opportunities

Despite its promise, microbiome-assisted phytoremediation faces substantial scientific and practical constraints. Microbial performance in controlled experiments may not persist in heterogeneous field environments, where soil acidity, moisture, nutrient availability, competing microorganisms and mixed contaminants influence community behaviour.

Taxonomic enrichment alone cannot establish remediation efficiency. Researchers must determine whether candidate microorganisms survive over time, improve plant growth, alter metal bioavailability or increase safe metal removal. The dis-

tinction between immobilisation and extraction is particularly important: reducing metal mobility may limit immediate exposure, whereas extracting metals requires their transfer into plant biomass and subsequent safe disposal or recovery. Biosafety also deserves attention. Introducing non-native or genetically modified microorganisms may create ecological risks, while indiscriminate mobilisation of metals could increase their movement into groundwater or food webs. Medicinal plants present an additional concern because contamination may affect the safety and chemical composition of harvested material.

The opportunity, therefore, is not simply to introduce more microorganisms. It is to identify stable, functionally complementary and environmentally appropriate microbial communities, prioritising native endophytes where feasible and validating their performance under realistic field conditions.

Future Perspective: Engineering Restoration Through Living Systems

Tomorrow's environmental biotechnology may combine native microbial resources, advanced sequencing, soil chemistry and predictive modelling to design site-specific restoration strategies. In this framework, microbial communities would be selected according to the dominant contaminants, the ecological characteristics of the site and the desired remediation outcome. For *Catharanthus roseus*, the microbial patterns identified in contaminated soil provide a starting point for isolating candidate endophytes and testing their effects on metal tolerance, plant growth, metal accumulation and medicinally relevant phytochemicals. Similar approaches could be investigated in other plant species suited to industrial wastelands, mine tailings and degraded agricultural soils.

Long-term field trials will be essential to establish whether microbial benefits persist across seasons and changing environmental conditions. Future studies should also integrate microbial function with metal speciation, plant physiology, soil recovery and ecological risk assessments. Ultimately, restoration success must be measured not merely by plant survival, but by demonstrable reductions in exposure and improvements in ecosystem function.

Conclusion: Seeing Beyond the Plant

The hidden microbiome represents an underexplored resource in the search for sustainable solutions to environmental pollution. The evidence from Catharanthus roseus illustrates how heavy-metal stress can reorganise the microbial communities living within plants, creating opportunities to investigate biological mechanisms of resilience and restoration.

Science tomorrow must move beyond observing which organisms survive contamination to understanding what they do, how they interact and whether their capabilities can be harnessed safely. By integrating microbial ecology, molecular technologies and field-based environmental science, researchers can develop more precise and ecologically sensitive approaches to restoring polluted landscapes.

The future of phytoremediation may therefore depend not on plants alone, but on the invisible partnerships that enable them to endure, and potentially help repair, a damaged environment.

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SCIENCE FACTORS!

EMERGING INSIGHT

E-Waste to Strategic Resources: India's Emerging Leadership in Rare-Earth Recycling



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AREAS OF EXPERTISE
E-waste Recycling • Heterogeneous catalysis • Energy conversion • Environmental Sustainability

WHY IT MATTERS

The growing demand for electric vehicles, renewable energy and advanced electronics is increasing the world's dependence on rare-earth elements, while millions of tonnes of electronic waste are discarded every year. In this article, Dr. Sriram Mansingh, Dr. Smruti Prakash Barik and Mr. G. Prabaharan from Attero Recycling explore how recovering valuable materials from discarded electronics could reduce environmental pollution, conserve natural resources and strengthen supply chains. They highlight India's emerging opportunities in rare-earth recycling, supported by scientific innovation, government initiatives and industrial investment. Their perspective shows how electronic waste could become a valuable resource for building a cleaner, more sustainable and technologically self-reliant future.

The Hidden Wealth in Electronic Waste

What if tomorrow's electric vehicles, wind turbines, and advanced electronics could be manufactured using valuable materials recovered from yesterday's discarded devices?

As the world accelerates towards clean energy, electric mobility, and digital technologies, demand for critical minerals and rare-earth elements (REEs) is increasing rapidly. Elements such as neodymium, praseodymium, dysprosium, and terbium are essential for manufacturing high-performance permanent magnets used in electric vehicles, wind turbines, robotics, aerospace, and defence technologies. However, geographically concentrated supply chains and geopolitical uncertainties threaten their long-term availability.





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AREAS OF EXPERTISE
electronic waste recycling • metal recovery/refining • secondary resource utilization • sustainable waste management

Meanwhile, discarded electronics, electric motors, and permanent magnets represent an overlooked reservoir of valuable materials. According to the Global E-waste Monitor 2024, approximately 62 million tonnes of electronic waste were generated globally in 2022, yet only 22.3% was formally collected and recycled. This figure could reach 82 million tonnes by 2030. With recycled materials currently supplying only a small fraction of global rare-earth demand, efficient recovery offers significant opportunities for resource security and environmental sustainability. For India, transforming electronic waste into strategic resources could strengthen industrial self-reliance while accelerating the transition towards a circular economy.

India's Policy Push: Securing Critical Minerals

India is increasingly recognising critical-mineral recycling as a strategic priority rather than merely a waste-management activity. The E-Waste (Management) Rules, 2022, implemented in April 2023, strengthened Extended Producer Responsibility, establishing recycling obligations for manufacturers and producers. A major milestone followed in January 2025 with the approval of the National Critical Mineral Mission (NCMM), involving a government outlay of ₹16,300 crore and anticipated additional investments of ₹18,000 crore. The mission supports mineral exploration, processing, research, technological development, and recovery from secondary resources. Further momentum came through the Rare Earth Permanent Magnet Manufacturing Scheme, approved in November 2025 with an allocation of ₹7,280 crore. It aims to establish 6,000 tonnes annually of integrated domestic permanent-magnet manufacturing capacity. The Union Budget 2026–27 also announced Rare Earth Corridors across Odisha, Kerala, Andhra Pradesh, and Tamil Nadu, creating opportunities to integrate mineral processing, scientific research, recycling infrastructure, and advanced manufacturing. Together, these initiatives represent India's evolving ambition to establish a technologically independent and resilient critical-mineral ecosystem.

The Global Race for Rare-Earth Independence

Rare-earth elements are increasingly influencing international industrial strategies. China currently dominates several critical stages of rare-earth separation, refining, and permanent-magnet manufacturing, creating supply-chain vulnerabilities for other economies. To address these concerns, the European Union's Critical Raw Materials Act establishes a 2030 recycling benchmark of 25% of annual strategic raw-material consumption. The United States is investing in rare-earth recovery through national laboratories, universities, and industrial partnerships. Japan continues developing magnet-recycling technologies, while South Korea is leveraging its electronics and automotive industries to strengthen resource resilience. These developments highlight an important reality: future industrial competitiveness will depend not only on access to mineral deposits but also on advanced separation technologies, recycling infrastructure, and manufacturing capabilities. India's opportunity lies in integrating indigenous scientific innovation with industrial-scale recovery and downstream production.

Attero Recycling: Translating Research into Industry



Figure 1: Represents the year-wise advancement and development of Attero towards E-waste recycling

An emerging example of India's technology-driven recycling sector is Attero Recycling, established in 2008. The company operates in electronic-waste and end-of-life lithium-ion battery recycling, illustrating the potential of recovering commercially valuable materials from discarded products. Attero patented technologies, i.e., 46 globally recognized patents enable the extraction of 22 green metals with 99.9% purity and achieve greater than 98% extraction efficiency from Lithium-ion battery recycling, and e-waste sources. In February 2026, Attero announced plans to invest approximately ₹7,000 crore over five years in advanced refining and processing facilities. Its proposed expansion includes rare-earth recycling alongside the recovery of lithium, cobalt, nickel, graphite, and other critical materials. The company has also announced ambitions to increase rare-earth magnet recycling capacity from approximately one tonne daily to multi-fold in coming years, although these remain planned targets. Another development was the operationalization of its Research and Development Centre of Excellence in Greater Noida in September 2026. Recognized by the Department of Scientific and Industrial Research as an in-house industrial R&D center, the facility reflects growing emphasis on indigenous engineering and process development. Reported technological initiatives include robotics-assisted battery cutting, advanced discharge systems, energy-efficient roasting, automated handling, filtration, and improved processing infrastructure. Such advancements could improve operational safety, resource recovery and industrial efficiency. Attero's expanding research and manufacturing ambitions demonstrate how private-sector investment can complement national critical-mineral policies. Nevertheless, long-term success will depend on verified recovery efficiency, product purity, environmental performance, and commercial scalability. Below figure 1 shows the year-wise advancement of Attero in the direction of e-waste recycling.

The Science Behind Rare-Earth Recovery

Recovering rare-earth elements from electronic waste and magnets requires sophisticated chemical engineering because these elements frequently coexist with other metals. Hydrometallurgy employs controlled leaching, solvent extraction, ion exchange, and precipitation to separate valuable metals. Pyrometallurgy use elevated temperatures to transform or separate materials, although energy requirements and environmental emissions remain important considerations. Emerging electrochemical technologies offer controlled metal recovery, while advanced membranes and selective adsorbents could improve separation efficiency. Researchers are also exploring recyclable solvents, environmentally compatible extraction systems, and energy-efficient purification strategies. However, achieving high recovery efficiency alone is insufficient. Recovered materials must satisfy stringent purity requirements for industrial applications, particularly permanent-magnet manufacturing. The challenge is therefore to develop technologies that combine chemical selectivity, economic feasibility, and environmental sustainability.

Challenges Between Laboratory and Industry

Despite growing opportunities, several obstacles continue to restrict large-scale rare-earth recycling. Rare-earth-containing components are distributed across diverse products, complicating collection and identification. Informal recycling networks and inconsistent waste streams further limit reliable feedstock availability. Complex separation chemistry creates additional difficulties because rare-earth elements exhibit similar chemical properties. Economic competitiveness depends on capital investment, reagent consumption, energy costs, fluctuating material prices, and stable demand. Environmental sustainability also requires efficient water management, reagent recovery, emissions control, and responsible residue disposal. Importantly, recovering rare-earth concentrates represents only one stage of the value chain. Further purification, alloy production, and material qualification are necessary before recovered elements can re-enter advanced manufacturing. Addressing these challenges requires coordinated scientific research, industrial investment, regulatory support, and transparent performance assessment.

Artificial Intelligence and the Future of Urban Mining

Artificial intelligence could accelerate the transformation of electronic waste into valuable industrial resources. AI may support automated waste identification, pre-



Figure 2: An over-view of Attero towards sustainable e-waste recycling and Rare earth recovery.

diction of optimal separation conditions, process monitoring, and improved product-quality control. Combined with advanced analytical techniques, robotics, and electrochemical processing, these approaches could enhance recovery efficiency while reducing operational costs. India's proposed Rare Earth Corridors could provide a platform for integrating such innovations through partnerships among universities, national laboratories, recycling companies, and manufacturing industries. For Odisha and other participating states, these initiatives may stimulate specialized research facilities, pilot-scale recycling infrastructure, skilled employment, and advanced materials industries. Nevertheless, successful implementation will require reliable experimental validation, sustained investment, and effective coordination between research institutions and industrial stakeholders.

The Mines of Tomorrow May Already Be Around Us

Rare-earth recycling represents more than an environmental solution; it offers a pathway towards technological independence, industrial competitiveness, and sustainable economic growth. India's National Critical Mineral Mission, permanent-magnet manufacturing initiatives, and proposed Rare Earth Corridors provide a foundation for developing an integrated circular-resource economy. Meanwhile, industrial developments such as Attero Recycling's expansion plans demonstrate growing interest in translating scientific innovation into commercial capabilities. The next challenge is converting these ambitions into measurable achievements. By connecting government policy, fundamental research, advanced engineering, and industrial innovation, India can emerge in global rare-earth economy. Figure 2 depicts an over-view of Attero activities in the domain of e-waste recycling.

ABOUT THE AUTHORS

Dr. Sriram Mansingh is an Associate Manager at Attero Recycling Pvt. Ltd.'s R&D Technology Center in Greater Noida, India. His research focuses on nanomaterials, photocatalysis, electrocatalysis, clean energy, and environmental remediation, with publications on advanced materials for sustainable applications. Dr. Smruti Prakash Barik, Chief Technology Officer (CTO) at Attero Recycling Pvt. Ltd., specializes in hydrometallurgy, metal recovery, lithium-ion battery recycling, and patented technologies for recovering valuable metals from waste. Mr. G. Prabaharan is Director of Attero's R&D Technology Center, specializing in electronic waste recycling and metal recovery. Together, their work highlights how scientific innovation transforms electronic waste into valuable resources, supporting sustainable manufacturing and resource security.

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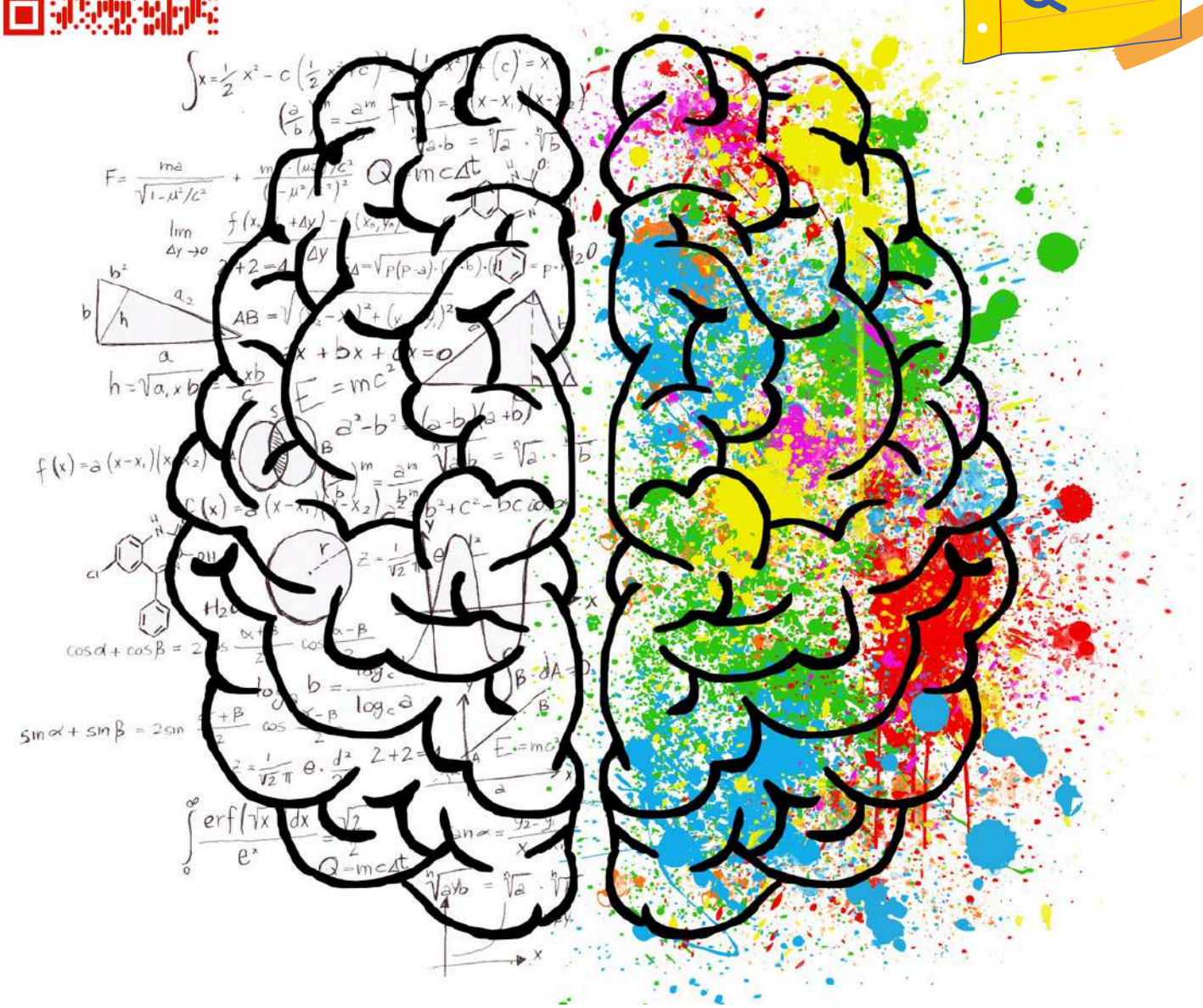
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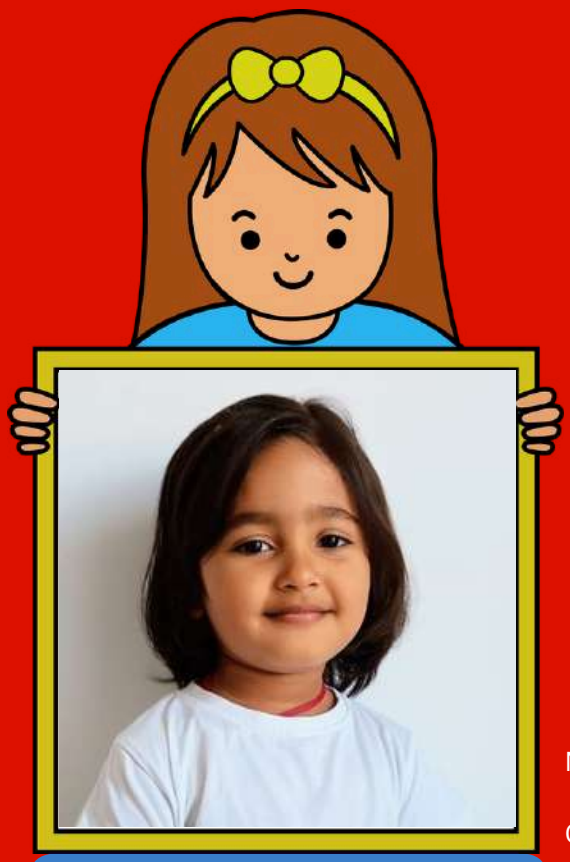


RESEARCHERS LIFELINE RESEARCH HEALTH





back to school





NAME: **Ayukta Das**

Grade: **KGII**

SCHOOL: **The Mother's International Institute Of Education, West Bengal, India**

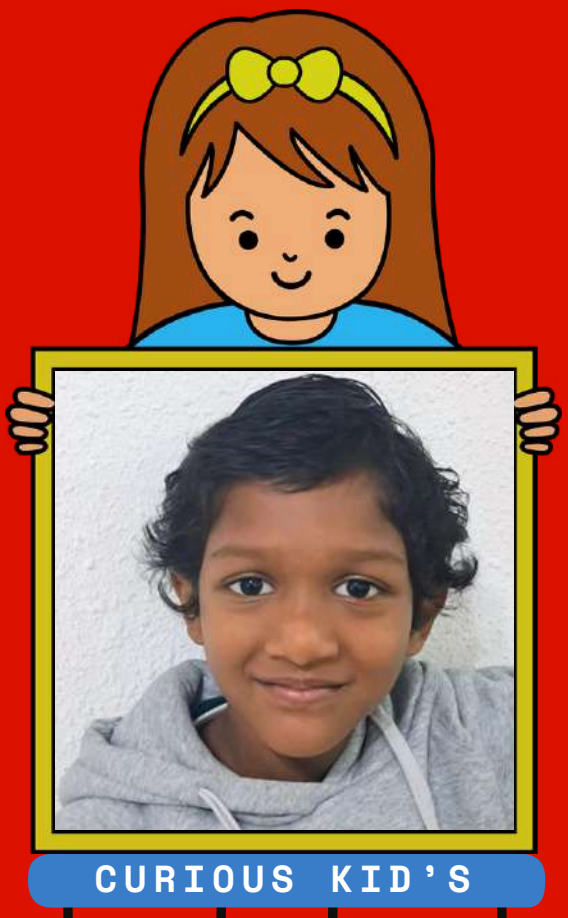
A Butterfly's Secret Clue!

Can you spot the butterflies in the picture? What do you think they're looking for?
Some flowers have patterns on their petals that many butterflies can see but we can't. The patterns can guide a butterfly to nectar, a sweet liquid inside the flower. A butterfly has a long, curly tube that works like a straw. When it lands on a flower, it unrolls the tube and takes a sip. While it drinks, tiny grains called pollen can stick to its body. The butterfly may carry some pollen to the next flower it visits. This can help the plant make seeds.

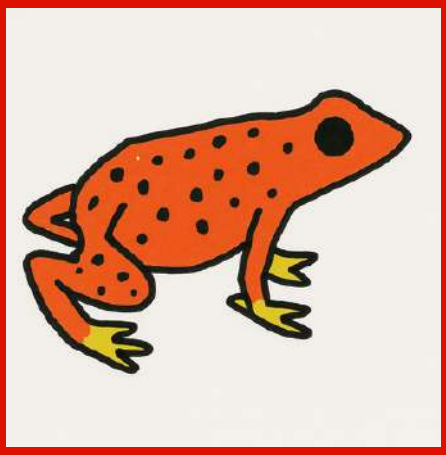


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back to school







NAME: **Shai Sri Rakshan**

Age: **6 Years**

SCHOOL: **Moshe Smilansky School Rehovot, Israel**

FOCUS:

Look but Don't Touch!

These frogs are very bright and colorful. Their colors work like a warning sign. They are saying, "Do not touch me!" Poison dart frogs have poison in their skin. If another animal touches or bites them, it can feel pain and become very sick. So predators learn to stay away.Long ago, people used a little bit of this frog's poison on arrows for hunting. That is why they are called poison dart frogs.



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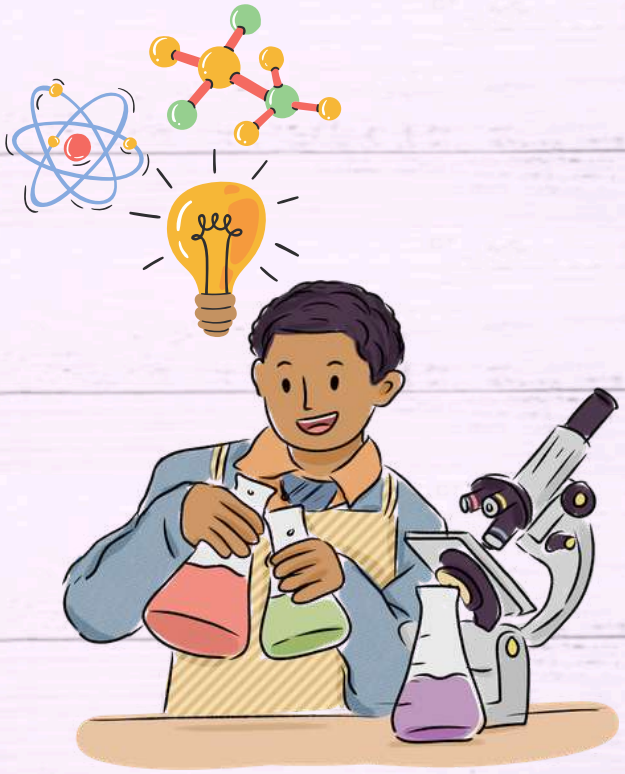
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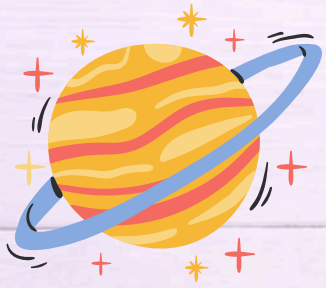
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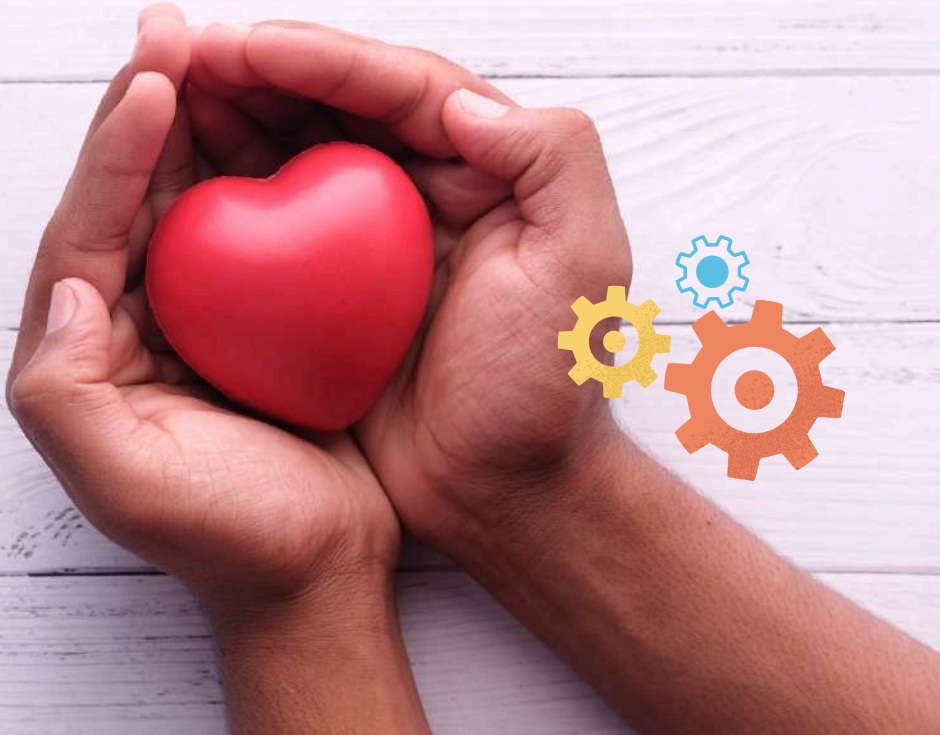
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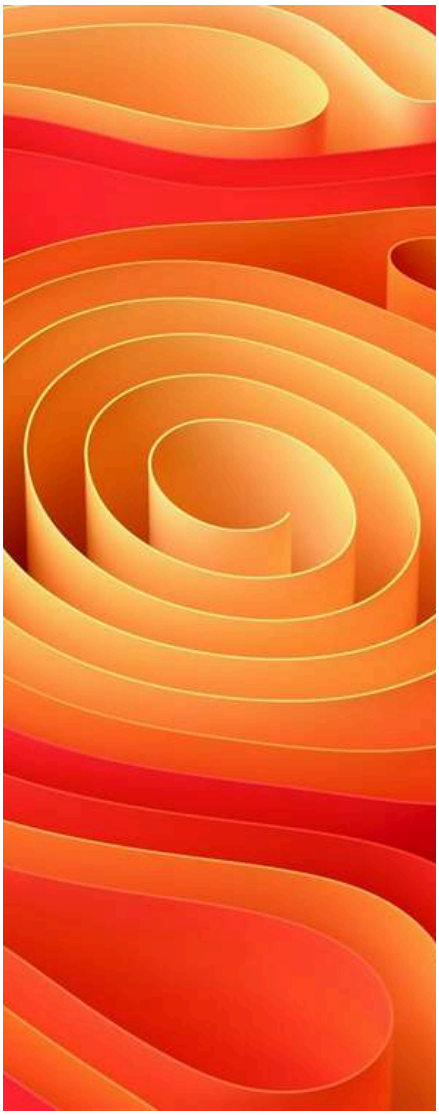














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