



SCIENCE FOR AGRICULTURE AND ALLIED SECTOR

VOLUME 8 ISSUE 9

Sept. 2026



**A Monthly
Magazine**

Online ISSN 2582-368X

www.agriallis.com

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AL04543

DECIPHERING THE MECHANISMS OF HYPERPARASITISM: *Ampelomyces quisqualis*- MEDIATED SUPPRESSION OF POWDERY MILDEW

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Powdery mildew diseases pose a persistent challenge to crop production because of their wide host range, rapid epidemic development, and increasing difficulties associated with fungicide resistance and host resistance. In this context, hyperparasitism offers a distinctive biological control strategy in which one fungus directly recognises, penetrates and exploits another pathogenic fungus. *Ampelomyces quisqualis*, a naturally occurring intracellular mycoparasite of powdery mildew, exemplifies this specialised interaction. Its hyperparasitic process involves a coordinated sequence of host recognition, conidial germination, directed germ-tube growth, attachment, penetration and intracellular colonisation. Following invasion, hydrolytic enzymes such as β -1,3-glucanases, chitinolytic enzymes and proteases contribute to weakening host structures and facilitate progressive cellular degradation. The interaction subsequently shifts from relatively biotrophic colonisation towards destructive phases, resulting in the degeneration of powdery mildew hyphae and conidiophores. Importantly, *Ampelomyces* also targets reproductive structures, including conidiophores, developing conidia and immature chasmothecia, thereby reducing both asexual sporulation and sexual propagule formation. These effects can diminish secondary inoculum and interfere with successive disease cycles. However, the effectiveness of hyperparasitism is influenced by humidity, temperature, pathogen developmental stage, application timing, strain characteristics and formulation properties. Understanding these interconnected mechanisms provides a basis for improving the consistency of *Ampelomyces*-based biocontrol and integrating it with resistant cultivars, cultural practices, disease forecasting and judicious fungicide use. Thus, deciphering the biology of this intimate fungal interaction is essential for translating a naturally occurring hyperparasitic relationship into a more predictable and sustainable component of powdery mildew management.

Powdery mildew diseases are among the most widespread and recognisable fungal diseases of plants, affecting nearly 10,000 angiosperm species, including economically important cereals, fruits, vegetables, ornamentals and other high-value crops. Caused by obligate biotrophic fungi of the order Erysiphales, powdery mildews form conspicuous superficial colonies on aerial plant tissues, impairing photosynthesis and plant vigour, interfering with flowering and fruit development and ultimately reducing crop yield and quality. Crops such as wheat, barley, grapevine, cucumber and strawberry are particularly vulnerable, as favourable weather conditions can support rapid epidemic development through successive cycles of airborne conidia. Management largely depends on resistant cultivars and fungicides; however, the emergence of pathogen populations that overcome host resistance or develop reduced sensitivity to fungicides, together with the selection pressure imposed by repeated chemical applications, highlights the need for complementary and environmentally compatible approaches. Hyperparasitism, in which one organism parasitizes another parasite, represents an intriguing mechanism of biological control because fungal hyperparasites can directly recognise, penetrate and exploit pathogenic fungi rather than relying solely on competition or antibiosis. Among the best-known examples are *Ampelomyces* species, naturally occurring intracellular mycoparasites of powdery mildew fungi. Historically referred to mainly as *Ampelomyces quisqualis*, these mycoparasites colonise powdery mildew hyphae and reproductive structures, grow intracellularly within infected tissues and eventually produce pycnidia. This intimate interaction can suppress mildew development and reduce the production of conidia and overwintering inoculum, thereby disrupting subsequent disease cycles. The interaction involves several mechanisms, including the activity of hydrolytic enzymes such as exo- β -1,3-glucanase, which contributes to degradation of fungal cell-wall components during mycoparasitism. Understanding the molecular, cellular and ecological mechanisms by which *A. quisqualis* recognises, penetrates and exploits powdery mildew can therefore provide valuable insights into fungal hyperparasitism and support the development of more reliable, sustainable and environmentally compatible strategies for powdery mildew management.

Sequential Mechanism of Hyperparasitism by *Ampelomyces quisqualis*

The hyperparasitic action of *Ampelomyces quisqualis* against powdery mildew follows a well-organised sequence of events involving host recognition, conidial germination, directed germ-tube growth, attachment, penetration, intracellular colonisation, enzymatic degradation and eventual destruction of the pathogen. Upon recognising suitable powdery mildew

structures, *A. quisqualis* germinates and produces germ tubes that grow towards the host, attach to its surface and penetrate the fungal cell wall. The hyperparasite then proliferates within the pathogen, where hydrolytic enzymes facilitate the breakdown of structural components, leading to progressive cellular disorganisation and death. Colonisation of conidiophores and sexual reproductive structures further interferes with sporulation and reproductive development, thereby reducing the production of secondary inoculum and ultimately restricting the progression and spread of powdery mildew.

Host Recognition and Targeting

The interaction between *Ampelomyces quisqualis* and powdery mildew begins with the germination of *Ampelomyces* conidia on the plant surface, followed by the directed growth of germ tubes towards susceptible powdery mildew structures. This early stage is strongly influenced by the presence of the mycohost, suggesting that host-derived signals play an important role in recognition. Studies have shown that extracts from powdery mildew conidia can stimulate *Ampelomyces* germination, indicating the involvement of water-soluble chemical compounds released by the host. Consequently, the presence of living powdery mildew can enhance conidial germination compared with conditions where the host is absent. After germination, the emerging germ tubes grow preferentially towards nearby powdery mildew hyphae rather than randomly across the leaf surface, indicating that *Ampelomyces* can perceive and respond to physical and/or chemical cues associated with its host. Once contact is established, the hyperparasite forms a close association with the powdery mildew structure and develops at the site of penetration, marking the transition from host recognition to active colonisation.

The interaction is not limited to the vegetative hyphae of powdery mildew; *Ampelomyces* can recognise and colonise various developmental structures, including hyphae, conidiophores, conidia and immature sexual structures. At the point of host contact, appressorium-like structures may develop, indicating that the germ tube undergoes specialised differentiation to facilitate firm attachment and penetration. Entry into the host appears to involve both mechanical and enzymatic processes, with physical force assisting penetration and extracellular hydrolytic enzymes, particularly β -1,3-glucanase and other cell-wall-degrading enzymes, contributing to the weakening and degradation of the powdery mildew cell wall. Thus, host targeting occurs through a coordinated sequence of events involving chemical stimulation of conidial germination, directed germ-tube growth, physical contact and

attachment, followed by localised penetration. These processes provide the foundation for the subsequent intracellular growth and colonisation of *Ampelomyces* within the powdery mildew mycelium.

Penetration and Intracellular Colonization

Once *Ampelomyces quisqualis* establishes contact with a powdery mildew colony, its germ tube attaches to and penetrates the pathogen's intact hyphae through a combination of mechanical pressure and enzymatic activity. Appressorium-like structures may form at penetration sites, indicating localised differentiation of the germ tube, while extracellular lytic enzymes, particularly exo- β -1,3-glucanase and other cell-wall-degrading enzymes, contribute to weakening the powdery mildew cell wall. Following penetration, *Ampelomyces* hyphae enter the host cytoplasm and grow intracellularly, extending from one cell to another through septal pores. The interaction initially appears relatively biotrophic, but as the hyperparasite proliferates, progressive degeneration of the host cytoplasm occurs, eventually leading to the atrophy and destruction of invaded hyphae and conidiophores. With continued colonisation, *Ampelomyces* forms intracellular pycnidia within powdery mildew hyphae, conidiophores and immature sexual structures. These pycnidia subsequently mature and produce numerous conidia, completing the hyperparasitic cycle while simultaneously impairing the pathogen's vegetative growth and reproductive capacity. Thus, *A. quisqualis* does more than compete with powdery mildew on the plant surface; it directly invades the pathogen and exploits its cells as an intracellular niche, making penetration, intracellular colonisation and destruction central features of this specialised mycoparasitic interaction.

Enzymatic Degradation

A critical component of *Ampelomyces quisqualis* hyperparasitism is its ability to produce a diverse range of cell-wall-degrading and hydrolytic enzymes that support penetration and destruction of the powdery mildew host. Studies have demonstrated extracellular activities of β -1,3-glucanases, β -glucosidases, β -N-acetylglucosaminidase/chitinolytic enzymes and proteases, indicating that *A. quisqualis* possesses a versatile enzymatic arsenal capable of targeting different components of the fungal host. Among these, the *exgA* gene-encoded exo- β -1,3-glucanase is expressed during mycoparasitism, and enzyme-containing culture filtrates have been shown to degrade powdery mildew hyphal walls, providing evidence for its role in host cell-wall disruption. β -1,3-glucanases break down glucan polymers, chitinolytic enzymes target chitin-containing components and proteases degrade host proteins, collectively

weakening the fungal structure and facilitating access to the host interior. These enzymes are likely to act together rather than independently, with their complementary and potentially synergistic activities progressively compromising the powdery mildew cell wall and cellular integrity. Differences in the activities of chitinases, proteases and β -1,3-glucanases among *Ampelomyces* strains have also been associated with variations in mycoparasitic performance, suggesting that the coordinated action of multiple hydrolytic enzymes is an important factor determining the efficiency of pathogen penetration, intracellular colonisation and destruction.

Cellular Disruption and Pathogen Death

Ampelomyces progressively disrupts the structure and functioning of invaded powdery mildew cells, transforming an initially compatible, apparently biotrophic association into a destructive interaction. During the early stages of mycoparasitism, *Ampelomyces* hyphae grow intracellularly within the host without immediately causing complete loss of cellular integrity. However, as the hyperparasite continues to proliferate, the powdery mildew cytoplasm undergoes progressive disorganisation and eventual disintegration, impairing the physiological functions of the host and contributing to the cessation of conidiophore development and sporulation. With advancing colonisation, the interaction shifts towards a more necrotrophic phase, in which *Ampelomyces* exploits and destroys the increasingly weakened host cells. Parasitised powdery mildew structures subsequently show atrophy, severe cytoplasmic disruption and eventual collapse of hyphae and conidiophores. The formation of intracellular *Ampelomyces* pycnidia further damages reproductive structures and prevents the successful production of powdery mildew propagules. Thus, host death appears to result not primarily from a secreted toxin, for which convincing evidence is lacking, but from the combined effects of intracellular invasion, nutrient exploitation, progressive cellular degeneration and physical destruction. This transition from relatively biotrophic colonisation to necrotrophic destruction is a defining feature of *Ampelomyces* hyperparasitism and underpins its ability to suppress both the growth and reproductive capacity of powdery mildew fungi.

Reproductive Suppression

One of the most important outcomes of *Ampelomyces* hyperparasitism is the disruption of powdery mildew reproduction, as the hyperparasite targets not only vegetative hyphae but also the pathogen's reproductive structures. *Ampelomyces* can colonise conidiophores and developing conidia, forming intracellular pycnidia within these tissues and interfering with their normal development, maturation and sporulation. Its effects can also extend to the sexual

phase, where invasion of immature chasmothecia (formerly cleistothecia) may disrupt their development and reduce the formation of viable sexual propagules. This reproductive interference is particularly significant because powdery mildew epidemics depend largely on continuous production of airborne conidia for secondary spread. At the same time, sexual spores formed within chasmothecia contribute to pathogen survival and subsequent disease initiation. Consequently, *Ampelomyces* infection can reduce conidial production, impair chasmothecia development and compromise overwintering success. By simultaneously suppressing both asexual and sexual reproduction, the hyperparasite reduces the inoculum available for dispersal, limits successive infection cycles and ultimately slows disease progression. Thus, even when powdery mildew colonies continue to develop temporarily after colonisation, their reproductive capacity can be substantially weakened, highlighting reproductive interference as a key component of the biocontrol potential of *Ampelomyces*.

Harnessing Hyperparasitism for Disease Management

The effectiveness of *Ampelomyces quisqualis* as a biological control agent depends strongly on weather conditions, the developmental stage of powdery mildew and the timing of application. Adequate moisture is particularly important because conidial germination, germ-tube growth, penetration and intracellular colonisation are favoured by high relative humidity and actively developing mildew colonies. Temperature also influences its development, while rainfall and prolonged leaf wetness can facilitate conidial movement within the crop canopy. Therefore, *Ampelomyces* is generally more effective when applied during the early stages of disease development, before extensive sporulation and epidemic build-up. Once dense colonies are established and producing abundant secondary inoculum, the relatively slower development of the hyperparasite may result in only partial disease suppression. Field performance can consequently vary with environmental conditions, inoculum density, host–pathogen combinations and formulation characteristics. Protective polymers, oils and suitable adjuvants have therefore been investigated to improve conidial survival and minimise the effects of low humidity, temperature fluctuations and ultraviolet radiation.

The greatest potential of *A. quisqualis* lies not in completely replacing conventional fungicides, but in its integration into sustainable disease-management programmes. By directly attacking powdery mildew and reducing both pathogen growth and reproductive inoculum, *Ampelomyces* can complement resistant cultivars, cultural practices and judicious fungicide use, particularly where reduced chemical inputs are desirable. However, variable field efficacy,

dependence on favourable humidity, relatively slow development, strain variation and challenges in mass production and formulation remain important constraints. Future progress will depend on identifying highly effective strains, improving formulation and delivery systems, synchronising applications with pathogen development and environmental conditions, and clarifying the molecular basis of host recognition, penetration and intracellular colonisation. Integrating these insights with disease forecasting, precision application and compatible integrated disease-management programmes could make *Ampelomyces* a more reliable and durable component of sustainable powdery mildew management rather than simply an alternative to conventional fungicides.

Conclusion

The hyperparasitic interaction between *Ampelomyces quisqualis* and powdery mildew represents a highly specialized sequence of biological events, beginning with recognition of the pathogen and conidial germination, followed by directed germ-tube growth, attachment and penetration, intracellular colonization, enzymatic degradation, and progressive destruction of invaded fungal cells. Importantly, *A. quisqualis* also colonizes conidiophores and other reproductive structures, reducing conidium formation and interfering with sexual development, thereby decreasing secondary inoculum and restricting disease progression. This direct and targeted mode of action highlights its potential as a precise and sustainable biocontrol agent within integrated disease management. However, variable environmental conditions, strain-specific performance and formulation constraints remain important challenges. Future research integrating molecular, genomic, physiological and formulation-based approaches could facilitate the selection of highly effective *Ampelomyces* strains, improve application strategies and elucidate the mechanisms governing host recognition, penetration and intracellular destruction, ultimately enabling more predictable and mechanism-based hyperparasite-mediated management of powdery mildew diseases.

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Article Id
AL04544

FISH PASSAGE AND RIVER CONNECTIVITY

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The role of rivers in transporting water from its source to destination is simplistic. They are longitudinally connected systems, where organisms and their movements, along with sediments, nutrients, and energy transfers, provide a mechanism of sustaining ecological processes. However, dams and other barriers interfere with such continuity by fragmenting habitat and obstructing the routes of migration for certain fish species for reproduction, feeding and completion of their life cycle. The impact of the dams on the water bodies in terms of changes in the hydrology, trapping of sediments and alteration of thermal regime is well researched and documented. Yet, the biological impact resulting from disconnection is understated during decision making regarding river management and dams construction. In this paper we will explore how dams prevent fish migration and connectivity in rivers, the impacts of such a disruption in an ecological and socioeconomic manner and different methods being employed to facilitate fish migration and re-establish connectivity in the form of fish passages and dams removal.

Rivers act as continuous corridors of ecology longitudinal from source to mouth, lateral from channel to floodplain, and vertical from surface to groundwater level. In doing so, they make it possible for migratory and non migratory fish species to reach their breeding grounds, nursery areas, and feeding grounds during all seasons. The construction of dams for irrigation, electricity generation, flood management, and water supply disrupts such a continuum. Currently, over 60% of the world's long rivers are not free flowing, making river fragmentation a major cause of extinction of fresh water species besides fishing and pollution.

How Dams Disrupt River Connectivity?

Dams create physical barriers that stop anadromous and potamodromous fish like hilsa, mahseer, or salmon from reaching their spawning grounds. What used to be a single open route

for migration turns into a broken-up series of river sections. Fish can only go as far as the first dam they hit. Even if they aren't killed trying to get past, the effort drains them, and repeated failures can mess up their timing. Sometimes, they miss the crucial window for spawning, and that means fewer offspring even if migration isn't completely blocked.

Controlled river flows change things too. Natural rivers pulse with seasonal floods, and these floods trigger spawning or help larvae drift downstream. But once there's a dam, flow becomes steady flattened by human control for things like irrigation or power generation. Fish that evolved to time their spawning to specific cues like rising water, warmer temperatures, or cloudy, sediment-laden pulses lose their signals. So, spawning can end up off schedule, weaker, or just doesn't happen, even if the total annual water released seems about right.

Dams also trap sediment. Normally, sediment moves downstream, delivering nutrients and building up deltas and riverbanks. Without that sediment, spawning gravel gets worse, and deltas and coasts start to erode. River channels downstream can even cut down deeper over time, leaving them further disconnected from their floodplains. Temperature and water quality take a hit too. Dams often release water from deep in a reservoir, and this water is colder and has less oxygen compared to what fish are used to. Cold releases at the wrong time can block spawning cues linked to seasonal warmth. At the same time, water from the oxygen-starved bottom layer can create dead zones downstream, especially in the dry season when there's less water to dilute it. For fish and invertebrates, these shifts can be deadly. All this creates fragmented habitats. Populations get split into smaller, isolated groups that are more likely to suffer from disease or climate swings. Genetic mixing drops, which ramps up the risk of inbreeding and lowers genetic diversity a big problem, especially for migratory fish like Himalayan mahseer, which are already threatened. Isolated populations are also on thin ice: just one pollution disaster or disease outbreak can wipe out a whole group, since there's no nearby population to help repopulate the area.

Dams also cut off rivers from their floodplains and wetlands. Seasonal floods used to spread water, nutrients, and fish across the landscape, giving young fish places to feed and grow. Without these flood pulses, even fish that manage to migrate up and downriver can lose their best nursery grounds. And it's not just fish feeling the impact. Dams break up migrations for all sorts of river life freshwater prawns, mollusks, and invertebrates many of which need to move between rivers, estuaries, or even the sea to complete their life cycles. The fallout ripples through the food web, hurting the species that depend on them.

Ecological and Socioeconomic Consequences

When rivers get broken up by dams and barriers, migratory fisheries crash and millions of people feel the loss. Just look at hilsa in the Ganga-Padma system, their numbers have dropped sharply upstream of the barrages. It's the same story for mahseer caught downstream from Himalayan hydropower dams. There's more at stake than just fish, though.

When sediment can't travel downstream, whole deltas become less stable and coastal fish farming struggles. Blocked nutrients mean less productivity in the water, changing food webs and hurting the communities that count on them.

Restoring Connectivity: Fish Passage Solutions

Fish ladders or fishways work like staircases for fish, letting them get past barriers by swimming or jumping up a series of steps or pools. Each pool breaks up the water's energy, giving fish a chance to rest before taking on the next stage. But the design really matters. A steep, fast, salmon-style ladder won't help weaker swimmers like Indian carps or catfish they need a gentler slope, slower water, and lots of nearby resting spots. All too often, people build generic ladders that look good on paper but barely get used because they don't fit local species. You end up with an expensive structure that offers little ecological benefit. Fish lifts and elevators are more high-tech. These are for really tall dams where a ladder just isn't practical. The idea is simple: fish get herded into a chamber, then the machine lifts them over the dam and releases them upstream. It does move lots of fish over big barriers, but the system isn't cheap or set it and forget it you need staff to run it, continuous maintenance, and electricity. That makes fish lifts more common on big hydropower projects, not the thousands of small dams and checks splitting up most rivers. And honestly, a lift only works if fish can actually find the entrance among all the wild currents near the dam face, so the collection design is just as important as the lifting mechanism.

Nature like fishways take a different approach you get a bypass channel that looks and acts like a natural stream, with real rocks, mixed currents, and plants along the edges. Instead of mechanical pools or boxes, these channels feel like mini rivers, which means not just more fish get through, but so do juveniles, weaker swimmers, and even crayfish or insects. Because it mimics real habitat, you sometimes get extra benefits, fish don't just pass through, they might stay to spawn or grow, making these bypasses more than simple corridors.

Environmental flow releases shift the focus to water management, not just physical structures. Here, dam managers release water downstream at certain times to mimic the natural signals fish use for migration or spawning like a pulse of rising water, a drop in temperature, or some murky flow that stirs up the urge to move. Fish don't follow calendars, so these flows have to be based on their natural life cycles rather than some basic rule about minimum flows. If the timing is off, the release doesn't trigger migration, even if there's plenty of water. Getting this right helps keep connections open not just for upstream swimming but for allowing fish, larvae, and food to move into floodplain habitats.

Dam removal goes straight to the root of the problem. In places like the US and Europe, where you find old or unsafe dams that don't really serve a purpose anymore, tearing a dam down can instantly reconnect miles of river that fish haven't seen in decades. After Washington's Elwha River dams came out, salmon started swimming up and recolonizing their old spawning grounds within just a few years, and the river mouth began rebuilding itself with sediment that had been trapped behind the dam for ages. Of course, you can't remove every dam many still supply water or power but in the right cases, it's the most direct fix. Sediment bypass systems often get less attention but matter just as much. These channels or tunnels send sand and gravel around a reservoir instead of letting it pile up behind the dam. That way, sediment still flows downstream, keeping riverbeds healthy, gravel clean for fish eggs, and river deltas stable. Without sediment, even if fish can swim past the dam, they might find the spawning grounds downstream aren't usable anymore. So, sediment bypass helps restore a river's full function, not just the fish pathway.

When it comes to tackling barriers, mapping and prioritization tools are helping managers figure out where to make the most impact. There are thousands of tiny barriers out there old weirs, small check dams, culverts and they often fragment rivers more than the big dams. Careful mapping helps spot exactly which barrier, if removed or modified, will open up the most river for the least cost. Sometimes, upgrading a forgotten roadside culvert creates more new habitat than building a fancy fish ladder on a big dam. Finally, for hydropower dams that are here to stay, smarter turbines and better intake screens are essential, especially for young fish heading downstream. Downstream mortality is easy to miss people focus on helping fish go up, but forget countless juveniles get chopped or stranded on their way out to sea. Upgrading turbines and adding good screens makes a real difference for survival and helps keep populations stable in fragmented river systems.

Policy and Management Implications

If we want to really fix river connectivity, we have to design for fish passage right from the start not wait until we've already seen the damage and then try to patch things up. That means environmental impact assessments need to dig deeper. Instead of just checking boxes for things like minimum downstream flow, we should look at how dams and barriers break up rivers, both along their length and across their width. And it's not enough to focus on just one type of fish or barrier. Planners need to consider the needs of all local species, what happens when there are several barriers on the same river, and both upstream and downstream movements. Downstream migration, for example, gets ignored a lot, even though fish getting killed by turbines can wipe out whole populations just as badly as a blocked upstream route. In India, some positive shifts are happening there's the National Mission for Clean Ganga and state fisheries departments starting to include fish passage in new hydropower projects. The problem is, enforcement is spotty, and the designs often don't fit local fish. Most fishways in the region are borrowed from northern salmon runs, but local species like major carps aren't built for leaping; the current setups just don't work for them. More research focused on native species, making it mandatory to check if fishways actually work after they're built (not just building them and walking away), and getting departments like irrigation, power, and fisheries to share information and work together right now, they're all over the place, with different goals and not enough data sharing.

Looking at other places helps. The European Union's Water Framework Directive set real targets for bringing rivers back together, which pushed governments to remove barriers and build better fishways. It's worked well enough to offer some ideas for how things could work elsewhere. And lately, people have realized it's the little barriers culverts, check dams, and low weirs that together do more harm than the big name dams, just because there are so many of them and they're rarely regulated. So, policy can't just focus on the big hydropower projects it has to cover all these smaller, everyday structures too. Planning at the watershed scale makes a lot more sense than just looking at one dam at a time. If you map where all the breaks are in a river network, you can figure out which barriers, if you fixed or removed them, would open up the most habitat for the least cost. This way, you can judge new projects not just by themselves but by how much they'll add to an already chopped-up river system.

At the moment, funds set aside for river restoration are pretty rare, and schemes like mitigation banking in which developers fund connectivity projects elsewhere are even rarer,

especially for rivers. International conservation spending is still skewed towards oceans and forests, leaving freshwater systems underfunded. One more thing real progress means listening to local people. Fishing communities often know more about fish migration patterns and river changes than official reports ever will. Their knowledge is priceless for figuring out when and where to help fish move, but policymakers often leave them out of the loop. If we start bringing that knowledge into the planning process, everyone benefits, including the rivers.

Conclusion

Dams don't just change a stretch of river where they rebuilt they break the flow between a river's source and where it meets the sea. This ripple effect hits hard: migratory fish populations dwindle, sediment stops moving like it used to, nutrients end up in the wrong places, and floodplains lose the regular cycles that kept them full of life. Zoom out, and the numbers start to look even bleaker. More than half of the world's long rivers don't flow freely anymore. We've built tens of thousands of big dams, not to mention millions of smaller barriers. Losing this kind of river connectivity is quietly driving freshwater wildlife into serious decline and most people hardly talk about it. No single fix gets us out of this mess. Sure, there are fish ladders, lifts, or "nature-like" detours that help fish get around some dams. These tools can reconnect parts of a river, especially where taking out a dam isn't an option. But they're really hit or miss. Sometimes they work for a few species at certain spots, but often they look good on paper while the river stays broken for most species. When it's possible especially for old, outdated, or low value dams removing the dam is still hands down the best way to actually heal the river. The speed of ecological bounce back after certain removals proves this point. Still, lots of dams aren't going anywhere. They're too important for water supplies, electricity, or flood control. For these, there are other ways to chip away at the problem: tweak the water release schedules, redesign turbines to let fish through, add systems to shuffle sediment, or rank which barriers matter most at a basin scale. These options can help, even if they can't fix everything.

The first step is treating river connectivity as a real priority, just like water and energy. It's the only way to keep healthy rivers delivering fish, clean water, and livelihoods to people who depend on them. That means putting money into research that doesn't just focus on well studied temperate rivers and salmon, but also learns from tropical rivers and the Global South which have been largely ignored. Regulations need to catch up, setting clear standards for connectivity in dam planning. Long-term monitoring has to become the norm, not the

exception, so we know our fixes actually work and don't just check a box. In the end, keeping rivers connected is about more than conservation it's about securing the food, jobs, and life giving benefits only free flowing rivers can offer millions of people.

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Article Id
AL04545

THE FUTURE OF FISH FARMING: HOW AI, GENOMICS AND PRECISION AQUACULTURE ARE TRANSFORMING THE BLUE REVOLUTION

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Fish is one of the world's most nutritious and sustainable sources of animal protein, supplying essential amino acids, omega-3 fatty acids, vitamins and minerals. As the global population is expected to approach 10 billion by 2050, the demand for safe and nutritious seafood will continue to increase. However, capture fisheries have reached their biological limits, making aquaculture the fastest-growing food production sector in the world. Today, aquaculture supplies more than half of the aquatic foods consumed globally, highlighting the crucial role of aquaculture in ensuring future food and nutritional security (FAO, 2024).

Aquaculture faces major challenges, including disease outbreaks, rising feed costs, declining water quality and climate change. Traditional farming practices, largely based on routine management and experience, are no longer sufficient to meet these challenges. A new era, Aquaculture 4.0 is therefore emerging, integrating Artificial Intelligence (AI), genomics and precision aquaculture to make fish farming smarter, more productive and environmentally sustainable (Joffre et al., 2022).

Artificial Intelligence: The Digital Brain of Fish Farming

Artificial Intelligence (AI) enables computers to analyse vast amounts of data, identify patterns and support management decisions. In aquaculture, AI is improving feeding, health management and water quality monitoring. Smart feeding systems equipped with cameras and computer vision estimate fish appetite and deliver feed only when required, reducing feed wastage and improving feed conversion efficiency. Since feed accounts for nearly 50–70% of production costs, even small improvements significantly increase farm profitability (Føre et al., 2018).

AI is also becoming an effective tool for disease surveillance. Machine-learning algorithms analyse fish behaviour and identify subtle changes in swimming activity or feeding response that often occur before visible disease symptoms appear. Early detection enables timely intervention, reducing mortality and limiting the use of antibiotics (Li et al., 2023).

Networks of sensors continuously monitor temperature, dissolved oxygen, pH and ammonia, while AI analyses these data and recommends immediate corrective actions. Such systems reduce production losses while conserving water and energy. Rather than replacing farmers, AI serves as a reliable digital assistant that supports faster and more informed decision-making (Kumar et al., 2023).

Genomics: Building Better Fish for Tomorrow

The reasons for fish growth, disease resistance and higher feed utilisation lie in their genes. Genomics, the study of an organism's complete genetic makeup, is transforming aquaculture by enabling scientists to develop superior fish and shrimp with improved productivity and resilience (Houston et al., 2020).

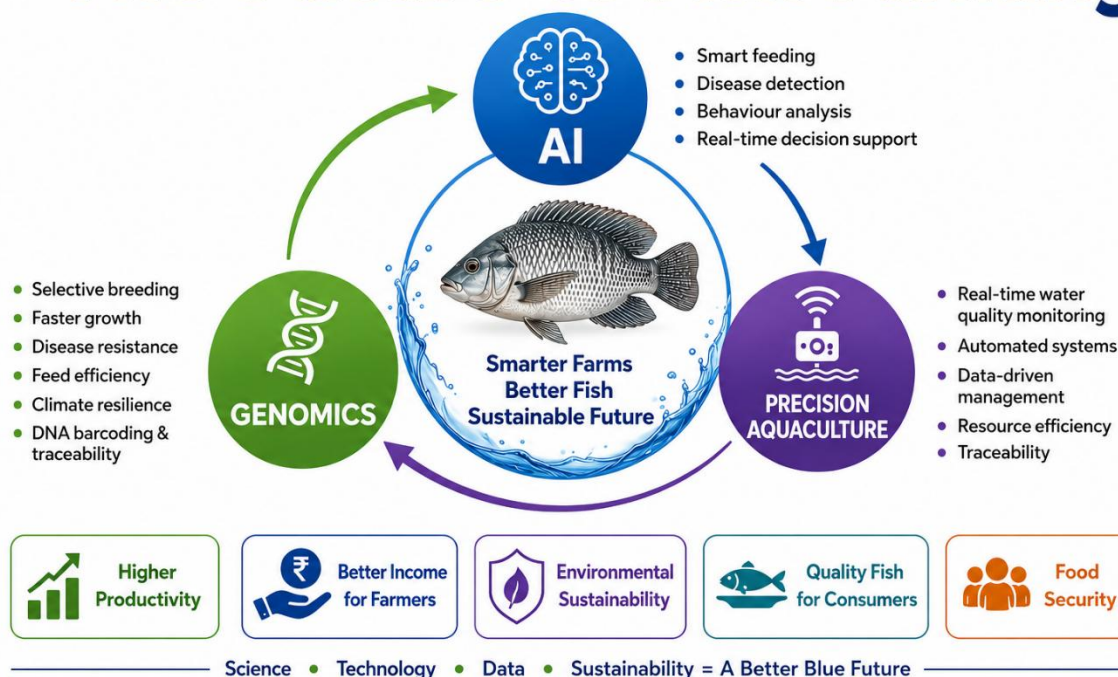
Genomics has already contributed to the development of faster-growing and disease-resistant strains of Atlantic salmon, Nile tilapia and Pacific white shrimp. Improved genetic stocks not only enhance production but also reduce dependence on antibiotics and other chemical treatments, contributing to more sustainable aquaculture (Gjedrem & Rye, 2018).

Beyond breeding, genomic tools such as DNA barcoding support accurate species identification, biodiversity conservation and traceability of seafood products. As sequencing technologies become increasingly affordable, genomics is expected to play a central role in developing climate-resilient strains of aquaculture species capable of meeting future food demands (Yue, 2023).

Precision Aquaculture: Farming with Data

Modern fish farming is increasingly shifting from experience-based management to data-driven decision-making. Precision aquaculture combines digital sensors, automation and cloud computing to monitor production continuously and respond to changing farm conditions in real time (Føre et al., 2018).

The Future of Fish Farming



Production records on growth, feed efficiency and survival help farmers improve planning, reduce waste and increase profitability. When integrated with AI and genomics, precision aquaculture provides a comprehensive management system capable of enhancing productivity while minimising environmental impacts (Joffre et al., 2022). Ultimately, precision aquaculture empowers farmers to make informed decisions based on scientific evidence rather than guesswork, paving the way for a more efficient and sustainable aquaculture industry.

India's Opportunity in the Digital Blue Revolution

India, the world's second-largest fish producer, relies on aquaculture for food security, livelihoods and export earnings. However, increasing disease outbreaks, rising production costs and climate-related challenges demand a shift from conventional farming to technology-driven aquaculture.

Increasing smartphone penetration and internet connectivity offers new opportunities for adopting AI and precision aquaculture even in small and medium-scale farms. Affordable sensors, automated feeders and mobile applications can help farmers monitor water quality, optimise feeding and receive real-time technical guidance. Similarly, genomic breeding programmes can accelerate the development of fast-growing, disease-resistant and climate-

resilient strains of commercially important species such as Indian major carps, tilapia and shrimp. By integrating research, digital technologies and effective extension services, India is well positioned to lead the next phase of the Blue Revolution.

Conclusion

The future of aquaculture lies in producing more fish with fewer resources while ensuring environmental sustainability. Artificial Intelligence, genomics and precision aquaculture are no longer futuristic concepts but practical tools that are already improving fish health, feed efficiency, farm management and profitability across the world. Together, these technologies enable farmers to make informed decisions based on real-time data rather than intuition.

Although challenges such as investment costs, technical expertise and infrastructure remain, rapid technological advances are making these innovations increasingly affordable and accessible. With continued research, capacity building and farmer-friendly technologies, Aquaculture 4.0 has the potential to transform fish farming into a smarter, more efficient and environmentally sustainable enterprise. The next Blue Revolution will therefore be driven not only by better farming practices but also by the intelligent application of science and technology.

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Article Id
AL04546

WASTE TO WHEELS: TRANSFORMING ANIMAL FATS INTO BIODIESEL

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The growing demand for energy, depletion of fossil fuels and increasing environmental concerns have intensified the search for renewable fuels. Biodiesel, produced from biological oils and fats, is a promising alternative to conventional diesel.

Edible vegetable oils are widely used for biodiesel production, but their use for fuel raises concerns about food security, land use and food–fuel competition. This has increased interest in non-edible and waste-derived feedstocks, including animal fats.

Animal fat generated during slaughtering and meat processing is rich in triglycerides that can be converted into fatty acid methyl esters (FAME), the major components of biodiesel. Its recovery can therefore convert an underutilized slaughterhouse by-product into renewable fuel while supporting sustainable waste management.

Why Animal Fat?

Animal fats obtained from slaughterhouses and meat-processing industries include beef tallow, poultry fat and other rendered fats. Their use as biodiesel feedstocks offers several advantages:

- **Low-cost feedstock:** Animal fat can be less expensive than refined edible oils.
- **Waste utilization:** It provides a productive use for slaughterhouse by-products.
- **Reduced food competition:** It avoids diverting edible oils towards fuel production.
- **Energy recovery:** Lipid-rich animal fat can be converted into renewable fuel.
- **Resource recovery:** Waste material is transformed into a value-added product.
- **Circular bioeconomy:** It connects livestock production with renewable energy generation (Binhweel *et al.*, 2023).

From Fat to Fuel

Biodiesel production from animal fat generally involves fat recovery, purification, pretreatment and conversion into fatty acid methyl esters.

Fat Recovery and Pretreatment

Animal fat collected from slaughterhouses may contain water, proteins, tissue particles and other impurities. Rendering, filtration and moisture removal are therefore important for obtaining a suitable lipid fraction.

The free fatty acid (FFA) content is particularly important. Animal fats with high FFA levels may require pretreatment before alkaline transesterification because FFAs can react with alkaline catalysts and form soaps, reducing biodiesel recovery.

Transesterification

Transesterification is one of the most commonly used methods for biodiesel production. During this process, triglycerides present in animal fat react with an alcohol, generally methanol, in the presence of a catalyst.

The main products are:

- Fatty acid methyl esters (biodiesel)
- Glycerol

The efficiency of conversion depends on several factors:

- Alcohol-to-fat ratio
- Catalyst concentration
- Reaction temperature
- Reaction time
- Moisture content
- Free fatty acid concentration

Other approaches, including dilution, micro-emulsification and advanced conversion technologies, have also been investigated for improving the utilization of waste oils and animal fats (Xie *et al.*, 2026).

Role of Catalysts

Catalysts play an important role in improving the efficiency of biodiesel production. Several catalytic systems have been investigated for animal-fat feedstocks.

Homogeneous catalysts: Sodium hydroxide (NaOH) and potassium hydroxide (KOH) are commonly used because of their effective catalytic activity. However, high FFA and moisture contents can promote soap formation and complicate product separation.

Heterogeneous catalysts: Solid catalysts such as calcium oxide and modified metal oxides can be separated from the reaction mixture and may offer opportunities for catalyst recovery and reuse.

Enzymatic catalysts: Lipases can catalyse biodiesel production under relatively mild conditions and can reduce some unwanted side reactions. However, enzyme cost and operational requirements remain important considerations (Aslam *et al.*, 2026).

What Makes Animal-Fat Biodiesel Promising?

Animal-fat biodiesel possesses several characteristics that make it attractive as a renewable fuel:

- **High cetane number:** Supports favourable ignition characteristics.
- **Good oxidative stability:** Higher saturated fatty acid content can improve resistance to oxidation.
- **High energy content:** Animal fats are energy-dense lipid sources.
- **Waste reduction:** Conversion into fuel reduces the quantity of fat requiring disposal.
- **Renewable origin:** The feedstock is obtained from biological sources.

Biodiesel production from waste oils and animal fats can simultaneously address energy requirements and waste-management concerns. It also provides an opportunity to reduce dependence on fossil fuels while recovering value from materials generated by the food and livestock industries (Singh *et al.*, 2026).

Challenges in Animal-Fat Biodiesel Production

However, several factors can limit the large-scale production and use of animal-fat biodiesel:

- **High FFA content:** May require additional pretreatment before transesterification.

- **Moisture and impurities:** Can interfere with the conversion process.
- **Feedstock variability:** Fat composition can differ according to animal species, tissue source and processing conditions.
- **Cold-flow limitations:** High saturated fatty acid content can increase the melting point of biodiesel.
- **Processing cost:** Collection, rendering, pretreatment and purification can increase overall production costs.
- **Fuel quality:** Maintaining consistent biodiesel quality requires proper processing and effective quality control.

Efficient feedstock management and economical processing technologies are therefore essential for successful large-scale production.

Opportunities for Sustainable Production

The future development of animal-fat biodiesel can focus on improving processing efficiency, reducing costs and integrating biodiesel production with broader waste-management systems.

Improved Pretreatment: Efficient pretreatment methods can reduce moisture, impurities and free fatty acids, allowing low-quality animal fats to be used more effectively.

Low-Cost Catalysts: The development of reusable, efficient and waste-derived catalysts can reduce production costs while improving the sustainability of the process.

Integrated Waste Management

An integrated approach to slaughterhouse waste management can maximize the value of different by-products through applications such as:

- Biodiesel production
- Biogas generation
- Fertilizer production
- Protein recovery
- Other value-added products

Sustainable Supply Chains

Efficient collection, transportation, processing and distribution systems are important for maintaining a reliable supply of animal fat. Supply-chain optimization can improve economic performance and help manage uncertainties related to feedstock availability, processing capacity and market demand (Sarkar *et al.*, 2025).

Conclusion

Animal fat generated from slaughterhouses represents a valuable resource for sustainable biodiesel production. Its utilization can reduce waste-disposal problems, minimize dependence on edible oils and support renewable energy generation. Although feedstock quality, pretreatment and production costs remain important challenges, advances in catalysts, processing technologies and supply-chain management are improving its potential. Converting animal fat into biodiesel can therefore provide a practical link between livestock production, waste valorization and the circular bioeconomy.

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Article Id
AL04547

TRADITIONAL MEDICINAL PLANTS OF NORTHEAST INDIA: NEW OPPORTUNITIES FOR DRUG DISCOVERY THROUGH MOLECULAR DATABASES

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Northeast India is rich in biodiversity and traditional medicinal knowledge. The region, comprising eight states, supports a wide variety of medicinal plants because of its diverse climate, forests and agroecological conditions. For generations, indigenous communities and rural households have used local plants to manage fever, digestive disorders, skin diseases, wounds and other health problems.

Traditional knowledge offers valuable clues for modern scientific research. Many medicinal plants contain bioactive compounds, known as phytochemicals, that may interact with proteins, enzymes and other biological components of the human body. Studying these compounds can help researchers identify potential candidates for developing new medicines.

However, traditional use does not necessarily prove that a plant can cure a disease. Its chemical composition, effectiveness, dosage and safety must be scientifically investigated before it can be considered for medical applications.

An important development in this field is the North East India Medicinal Plants Database (NEI-MPDB), developed by researchers associated with the CSIR–North East Institute of Science and Technology. The database brings together information about medicinal plants, their traditional uses and their reported chemical constituents, supporting research into natural-product drug discovery.

Medicinal Plant Diversity of Northeast India

The medicinal plants of Northeast India are closely associated with the traditional practices of indigenous communities. Different plant parts, including leaves, roots, bark, rhizomes, flowers, seeds and fruits, are used in traditional preparations.

The NEI-MPDB publication reported 561 unique medicinal plant species and 9,225 phytochemicals. This collection provides a valuable starting point for researchers interested in investigating plant-derived compounds and their possible biological activities.

The database helps connect three important areas of research: traditional knowledge about medicinal plants, information about their chemical constituents, and biological targets associated with diseases.

Important Medicinal Plants for Drug Discovery

Several medicinal plants associated with Northeast India deserve scientific attention because of their reported chemical constituents and biological activities.

1. Kalmegh (*Andrographis paniculata*)

Kalmegh is an important medicinal herb found in several parts of Northeast India. It has been traditionally used for conditions such as fever and digestive disorders. Its major reported constituents include andrographolide and related compounds.

Andrographolide has attracted scientific interest because of its reported anti-inflammatory and other biological activities. Researchers can investigate whether this compound interacts with proteins involved in inflammatory diseases, cancer-related pathways or infectious diseases.

For malaria research, scientists must establish whether a compound can inhibit the parasite at concentrations that are safe for human cells. Computational screening can help identify candidates, but laboratory experiments are necessary to confirm their effectiveness.

2. Guduchi (*Tinospora cordifolia*)

Guduchi, also known as Giloy, is used in several Indian traditional healthcare systems. Its chemical constituents include alkaloids, diterpenoids and other compounds that have attracted scientific interest.

Researchers may investigate individual compounds for their potential effects on inflammatory signalling and metabolic pathways. Molecular databases can help identify suitable candidates for further studies.

However, the safety of Guduchi preparations requires careful consideration, as liver injury has been associated with some products. Its traditional use should not be taken as proof of effectiveness or safety for every condition.

3. Saptaparni (*Alstonia scholaris*)

Saptaparni is a medicinal tree documented in ethnobotanical literature from Northeast India. Its bark and other plant parts have been used in traditional practices. The plant contains indole alkaloids, a group of compounds known for their diverse biological activities.

Researchers can investigate whether specific alkaloids interact with proteins essential for the survival of malaria parasites or other pathogens. Such studies may help identify new molecular candidates for antimicrobial research.

Any promising findings must be confirmed through appropriate laboratory testing and toxicity assessment.

4. Mishmi Teeta (*Coptis teeta*)

Mishmi teeta is associated particularly with Arunachal Pradesh and the traditional knowledge of communities in the eastern Himalayan region. Its rhizome contains alkaloids, including berberine.

Berberine has been studied for various biological activities, although its effectiveness and safety depend on the condition, preparation and dose. Researchers can use molecular databases to investigate the interactions of berberine and other compounds with selected disease-related proteins.

5. Nayantara (*Catharanthus roseus*)

Nayantara, also known as Madagascar periwinkle, is widely cultivated as an ornamental plant in India. It is an important example of how medicinal plant research can contribute to modern medicine.

The plant produces vincristine and vinblastine, compounds used in certain cancer treatments. These medicines demonstrate the potential of natural products to provide valuable starting points for pharmaceutical development.

6. Tulsi (*Ocimum tenuiflorum*)

Tulsi is widely cultivated in household gardens and has a long history of use in traditional Indian medicine. Its leaves contain compounds such as eugenol and other phenolic and terpene constituents.

Some of these compounds have demonstrated biological activities in experimental studies. Researchers may investigate their interactions with selected proteins associated with inflammation, oxidative stress and infectious diseases.

The chemical composition of Tulsi can vary with the plant variety, growing conditions and harvesting methods. Therefore, standardised chemical analysis is important for reliable research.

Molecular Databases and Modern Drug Discovery

Molecular databases are valuable tools for connecting traditional medicinal knowledge with modern biotechnology. They allow researchers to examine plant-derived compounds, retrieve chemical structures and investigate possible interactions with disease-related proteins.

In addition to NEI-MPDB, researchers can use several complementary resources:

- IMPPAT: <https://cb.imsc.res.in/imppat/> — provides information on Indian medicinal plants, phytochemicals and their reported associations.
- PubChem: <https://pubchem.ncbi.nlm.nih.gov/> — provides chemical structures, identifiers and molecular properties.
- Protein Data Bank: <https://www.rcsb.org/> — provides three-dimensional structures of proteins and other biological molecules.

Using these databases together can help researchers verify compound identities, identify potential molecular targets and prepare candidates for computational screening.

How Molecular Docking Helps

Molecular docking is a computer-based technique used to estimate how a small molecule may interact with a protein. It is widely applied during the early stages of drug discovery.

For example, a researcher investigating malaria may identify phytochemicals from plants traditionally used for fever. The researcher can then select a validated protein target of the malaria parasite and use docking software to examine whether any of the compounds may interact with it.

The results can help prioritise compounds for further investigation. However, a favourable docking score does not prove that a compound can treat malaria or any other disease.

Promising candidates must undergo laboratory testing to determine their biological activity, selectivity and toxicity.

Researchers may also use computational methods to predict absorption, distribution, metabolism, excretion and toxicity. These predictions can help identify potential limitations before expensive experiments are conducted.

Potential Applications in Serious Diseases

Malaria

Malaria is an important area for medicinal plant research in Northeast India. Ethnobotanical studies have documented numerous plant species traditionally used to manage malaria and associated symptoms.

Researchers can combine these records with phytochemical databases to identify candidate compounds for investigation against Plasmodium parasites. The strongest candidates must be tested in appropriate laboratory assays to establish whether they can inhibit the parasite without causing unacceptable harm to human cells.

Traditional remedies must not replace diagnostic testing or proven antimalarial medicines.

Cancer

Cancer research is another important area for natural-product drug discovery. Researchers can investigate whether plant-derived compounds influence proteins associated with tumour growth, cell division or programmed cell death.

The discovery of vincristine and vinblastine from *Catharanthus roseus* demonstrates the contribution of plant-derived molecules to cancer treatment.

Nevertheless, most compounds identified through computational screening will require extensive investigation before their suitability for medical use can be established.

Diabetes and Metabolic Disorders

Certain plant-derived compounds are being investigated for their potential effects on enzymes and pathways involved in glucose metabolism. Molecular databases can help researchers identify compounds for further study.

However, predicted interactions with metabolic enzymes do not establish that a plant can control diabetes. Laboratory studies, safety assessments and appropriate clinical research are required before therapeutic claims can be made.

Antimicrobial Resistance

The increasing resistance of some pathogens to existing medicines has created a need to explore new chemical structures. Medicinal plants may provide useful starting points for investigating compounds that inhibit microbial growth or affect essential microbial proteins.

Researchers must confirm these effects through laboratory experiments and determine whether the compounds are safe and effective against relevant pathogens.

From Computational Screening to Laboratory Validation

Successful drug discovery requires several stages of investigation. First, researchers must identify the plant correctly and verify its reported chemical constituents. Next, suitable compounds are selected for computational screening against disease-related targets.

Promising candidates may then undergo additional modelling, chemical analysis and laboratory experiments. These studies establish whether the predicted interactions translate into measurable biological activity.

Further research may include toxicity testing, pharmacokinetic studies and preclinical investigations. Only candidates supported by sufficient evidence can proceed towards clinical trials and possible pharmaceutical development.

This step-by-step approach helps researchers use limited resources more efficiently while reducing the risk of drawing conclusions from computational predictions alone.

Opportunities for Agriculture and Rural Livelihoods

Medicinal plant research also offers opportunities for agricultural development and rural entrepreneurship. If a plant or its compounds become important for scientific or commercial applications, farmers may benefit from the development of suitable cultivation practices and reliable supply chains.

Agricultural research can support the selection of suitable varieties, propagation techniques, soil and nutrient management, harvesting methods and post-harvest processing. These interventions can improve plant quality and help maintain consistent levels of important phytochemicals.

Farmer producer organisations, rural entrepreneurs and community institutions may also explore medicinal plant nurseries, cultivation, authenticated raw material production and quality-controlled processing, subject to actual market demand and applicable regulations.

At the same time, conservation must remain a priority. Unsustainable harvesting of roots, bark or whole plants can damage natural populations. Cultivation and responsible collection practices can help reduce pressure on wild resources.

Commercial opportunities should be developed only after assessing market demand, production costs, environmental impacts and the requirements of potential buyers.

Protecting Traditional Knowledge and Biodiversity

The medicinal plant wealth of Northeast India is closely connected with indigenous knowledge preserved over generations. Research and commercial development must respect the communities that maintain this knowledge.

Researchers should obtain appropriate consent before documenting community-held knowledge, follow applicable biodiversity regulations and establish fair benefit-sharing arrangements where required.

They should also acknowledge knowledge holders, protect culturally sensitive information and avoid practices that threaten vulnerable plant species.

Ethical research can help ensure that scientific progress benefits not only researchers and commercial organisations but also the communities whose knowledge contributes to discovery.

Conclusion

Northeast India possesses an exceptional combination of medicinal plant diversity, traditional knowledge and opportunities for modern scientific research. Resources such as NEI-MPDB can help researchers connect ethnobotanical information with chemical structures and computational drug discovery.

By combining traditional knowledge with molecular docking, bioinformatics, laboratory testing and agricultural research, scientists can identify promising natural compounds for further investigation into malaria, cancer, metabolic disorders and infectious diseases. However, the identification of a potential compound is only the beginning of drug discovery. Its effectiveness, safety and suitability for human use must be established through rigorous scientific research.

For the agricultural sector, medicinal plant research can also encourage sustainable cultivation, biodiversity conservation and new livelihood opportunities. Collaboration among farmers, indigenous communities, agricultural institutions, chemists and medical researchers will be essential to realise this potential.

Traditional knowledge can guide scientific discovery, molecular databases can help identify promising candidates, and experimental evidence must determine whether those candidates can become safe and effective medicines.

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