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COVER STORY

The Asian koel (*Eudynamys scolopaceus*), commonly known as කොවුලා/කොහා (Kowla/Koha) in Sinhalese, is considered a symbol of the Sinhalese and Hindu New Year in Sri Lanka. The call is often heard during the breeding season around March-June, which aligns with the Sinhala/Tamil New Year, therefore it is called the "New Year Bird". The size of the bird is about 39-46 cm and the male bird has a metallic black tinged blue, long tail, and red eyes. Females are black to brown with white spots and barred underparts.

Common nesting sites are found in home gardens, cultivated and other wooded areas, avoiding dense forests from lowland to hilly areas. It eats almost entirely fruit, including berries of some ornamental garden plants. Because this bird is a nest parasite, it lays its eggs in the nests of other birds such as crows (Jungle crow and House crow) and sometimes in Bablers. Newborn chicks grow up with foster parents.

Photograph by Dr. Praneeth Ratnayake

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IOBSL NEWS AND EVENTS

Sri Lankan Biology Olympiad | 2023

We are delighted to announce the successful conclusion of the Sri Lankan Biology Olympiad 2023. This prestigious competition witnessed the participation of talented young minds eager to showcase their prowess in the field of biology. A total of seventeen exceptional students have emerged victorious, securing their positions in the second round of the International Biology Olympiad (IBO) selection training program. This accomplishment stands as a testament to their dedication, hard work, and passion for the biological sciences.

Looking ahead, the journey continues for these aspiring biologists as they prepare for the next stage of the competition. Four outstanding students will be chosen to represent Sri Lanka at the 35th IBO, scheduled to take place in Astana, Kazakhstan, from July 7 to 14, 2024. This global platform promises to be a remarkable opportunity for these bright minds to showcase their skills on an international stage.

We extend our heartiest congratulations to all the medal winners of the Sri Lankan Biology Olympiad 2023. Your achievements serve as an inspiration to budding scientists across the nation, and we eagerly anticipate witnessing your continued success in the world of biology.

For more information and updates on the IBO, please visit http://www.iobsl.org/

For more than fifteen years, the IOBSL has been instrumental in conducting the Sri Lanka Biology Olympiad examination and training talented candidates for the IBO. With the expert guidance and mentorship of university academics linked with the IOBSL, students undergo thorough training and preparation for the challenges ahead.

Register Now for the
Inter-University Biology Quiz Competition | 2024

Calling all undergraduate biology enthusiasts! The IOBSL is thrilled to announce the commencement of registration for the Inter-University Biology Quiz Competition 2024. This esteemed competition, now in its seventh consecutive year, is designed exclusively for undergraduates from state universities and UGC-approved Universities in Sri Lanka.

The primary objective of this event is to offer undergraduates a unique educational experience while igniting and nurturing their passion for biology. Through engaging quiz rounds, participants will not only test their knowledge but also delve deeper into the fascinating world of biological sciences.

Moreover, the competition serves as an exceptional platform for fostering collaboration and inspiration among students, academics, and universities nationwide. It is an opportunity to showcase your skills, network with peers, and explore new avenues of learning.

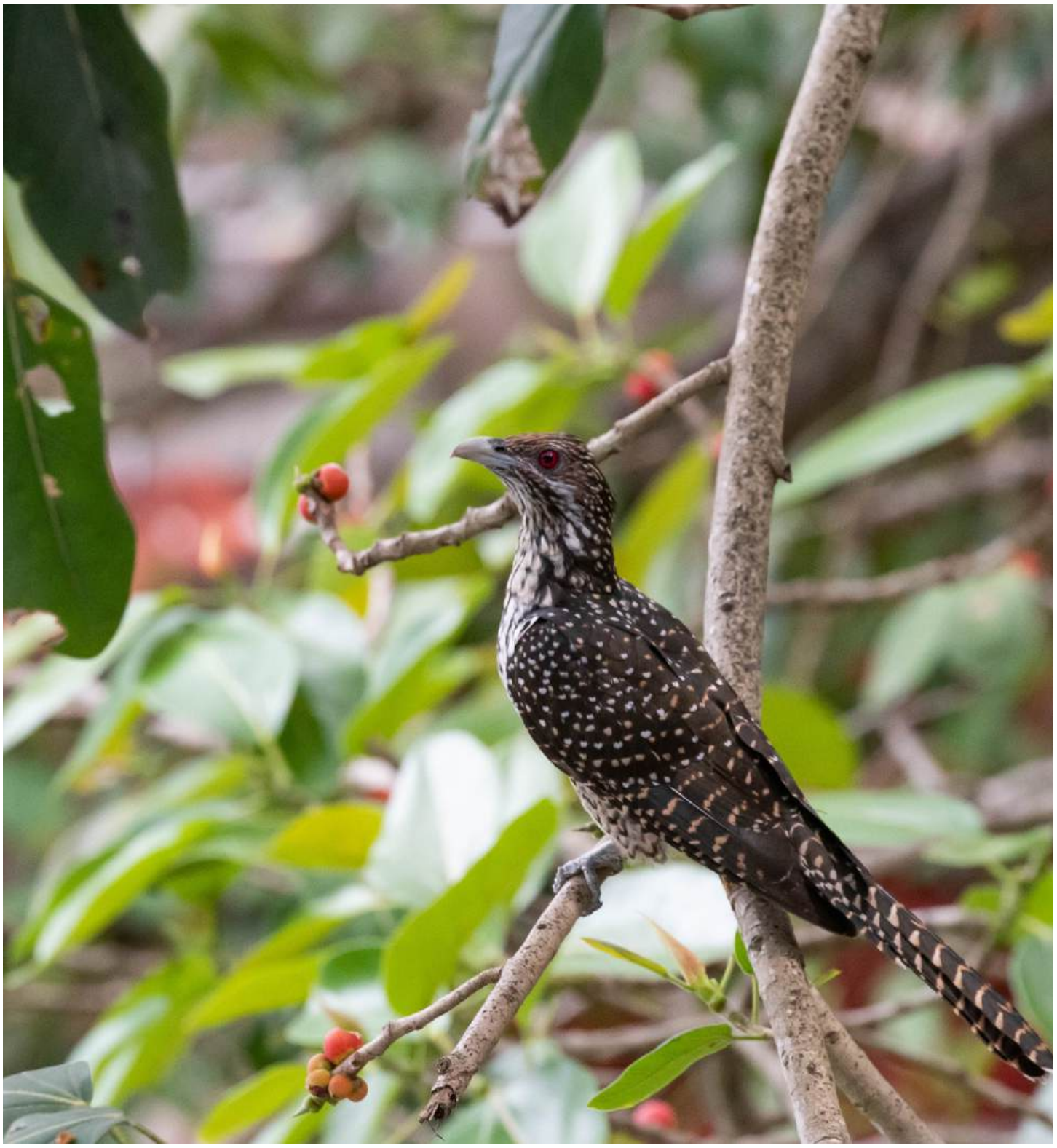
Do not miss out on this exciting opportunity to be a part of the Inter-University Biology Quiz Competition 2024! The registration deadline is April 30, 2024.

Scan the QR code to access the registration form and secure your spot in this academic challenge

JOIN OUR
Membership

The IOBSL extends a warm invitation to all passionate individuals interested in the diverse realms of biology to join its esteemed community today

To join the IOBSL and become part of this dynamic community, visit our website
https://www.iobsl.org/how-to-join-the-institute



Photograph by

Dr. Praneeth Ratnayake, M. I. Biol. (Sri Lanka)

Submit your research to

Sri Lankan Journal of Biology (SLJB)

SLJB provides high quality, comprehensive and broad coverage in all areas of Biology. The journal publishes original scientific research articles that describe significant research findings. SLJB encourages the submission of original contributions in all fields of basic and applied research involved in Biological Sciences.

Read the submission guidelines

FEATURE ARTICLES

Lighting Up Microbes: Identifying with Carbon Quantum Dots

Fluorescence microscopy, particularly with quantum dots (QDs), has garnered attention for molecular structure identification. Carbon quantum dots (CDs), a biocompatible alternative to traditional QDs, have become prominent in bacterial cell imaging due to their size tunability and stable fluorescent activity. CDs have proven effective in labeling bacteria, facilitating the visualization of infection processes, viability assessment, bacterial type identification, and quantification. Current trends in CDs focus on environmentally friendly synthesis, improved quantum yield, functionalization for enhanced applicability, and the development of multifunctional CDs with antibacterial properties. This article provides insights into the evolving landscape of microbial imaging and highlights the strides made in utilizing CDs for advanced applications.

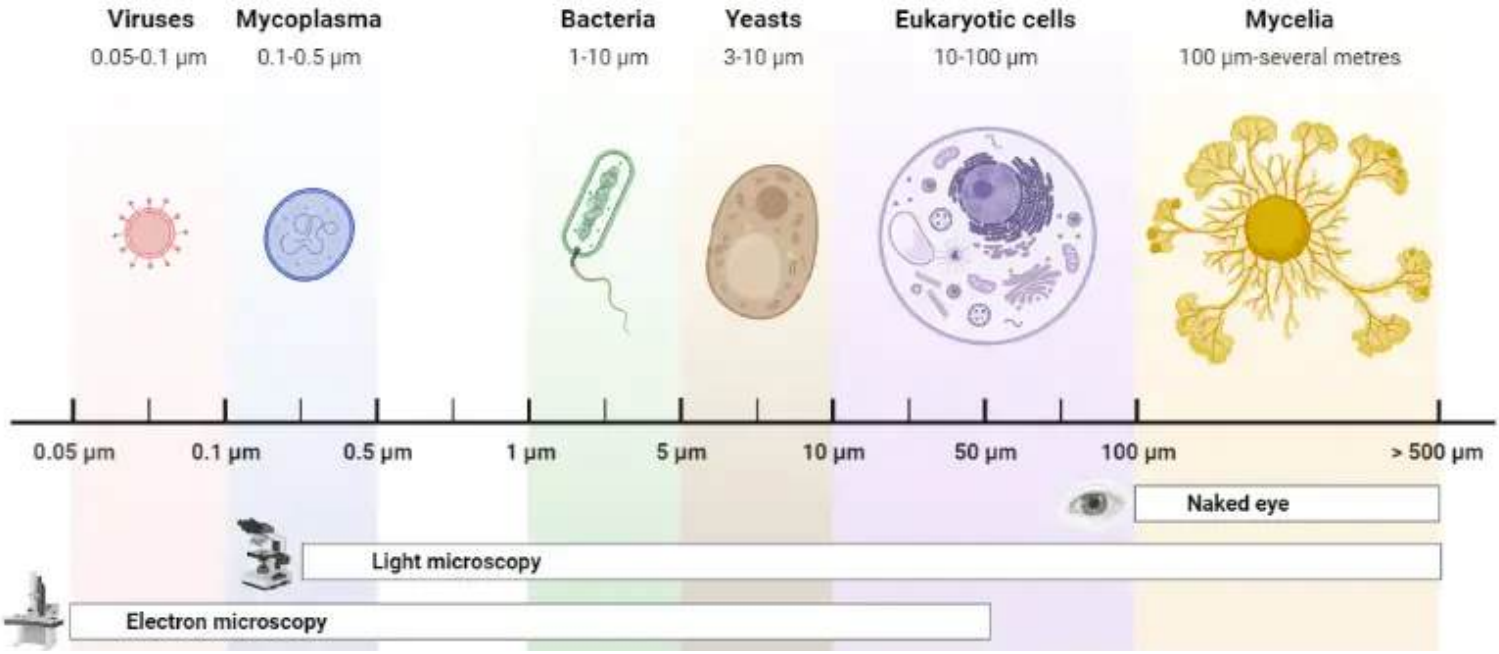


Figure 1 Different types of microbes with their size range
Source: Tankeshwar, A. (2024) *Sizes of representative bacteria, viruses, yeasts, and human cells* [online]. Available at: https://microbeonline.com/size-of-bacteria/ (Accessed: 21 April 2024)

What are microbes?

Microbes are an essential part of the existence of life on Earth. They are believed to be generating half of the oxygen that the residents of the plant breathe.

Even if life without higher organisms is a possibility, life without microbes will be just a dream! They are believed to be found in large quantities everywhere, and some could even think of the microbial life present beyond the earth. For example, the gastrointestinal (GI) tract has become home to more than 100 trillion microorganisms. They can be beneficial to man, animals, and plants in many ways, but fear is also associated with the possible harmful effects. The most common example that we are familiar with is the deadly infections that lead to several deaths. These microorganisms could be mainly bacteria, archaea, yeast, single-cell eukaryotes, viruses, and parasites.

Microbes are characterized by brief generation times, compact genome sizes, and diminutive structural configurations. Bacterial cells typically fall within the size range of 1 µm, while viruses may exhibit even smaller dimensions, often reaching 0.1 µm. Given their microscopic nature, these cells elude identification by the unaided eye and necessitate scrutiny through advanced microscopic and electron microscopy techniques. Figure 1 illustrates various microbial types along with their respective size ranges.

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How can we see microbes?

Microbial cell imaging is a broad topic that is generally used to study specific cellular structures or constituents such as flagella, microbial cell walls, fimbriae, and inner cellular structures such as the nucleus, mitochondria, endoplasmic reticulum, and Golgi apparatus of microbes. When it comes to viruses, the identification of cellular structures is a difficult task via light microscopy, hence requiring the use of electron microscopy techniques like transmission electron microscopy (TEM). This is primarily due to the ultrasmall size of viruses.

The identification of many of these structures is important for understanding the mechanisms of cellular interactions and developmental stages, such as biofilm formation and disease occurrence involving multiple microbial species. In such cases, cell-to-cell communication that is built up via the microbial cellular structures and the outer environment is a critical factor. Therefore, the identification of such mechanistic approaches via imaging will be useful to deduce the morphological variations within different microbes as well as to address the fundamental phenomena related to microbial growth and survival. High-resolution imaging of microbial structures is commonly performed using scanning electron microscopy (SEM), TEM, and atomic force microscopy (AFM) as indicated in Figure 2.

Fluorescence imaging of microbes

Among various imaging techniques, fluorescence microscopy holds a special place in the identification of the molecular structures of microbes. Over the past decade, there has been significant focus on developing new fluorescent probes for microbial identification. Fluorescence imaging allows for conventional imaging of molecular structures, cell tracking,

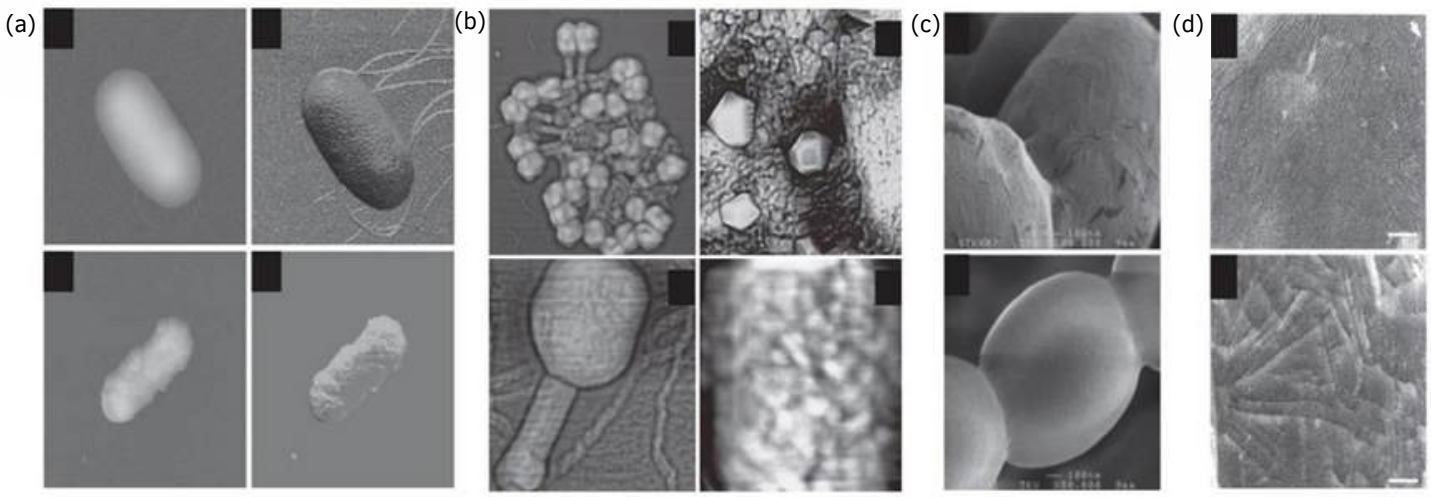

Figure 2 Different microscopic images of bacteria, fungi and other microorganisms under the advanced microscopic techniques. (a) Atomic force micrographs of *Pseudomonas syringae* pv. *Tabaci*, (b) Atomic force micrographs of T4 phages, (c) Cryo-field emission scanning electron micrographs of *Streptomyces coelicolor*, (d) Transmission electron micrographs of freeze-fractured replicas of fungal conidia.
Source: Kim (2016)

and biosensing. Recent advancements have widened the applicability of fluorescence imaging, making it versatile and specific for single and multicolor imaging purposes. In this regard, genetically engineered fluorescent proteins that emit color and chemically designed organic fluorophores are the two key pathways that have been followed by many scientists in recent years. Nevertheless, these approaches are far behind the desired outcome due to temporary fluorescence activity and the inability to perform multimodal imaging with vibrant colors, largely due to their broad emission spectra. Therefore, the development of multicolor emissive, stable, and biocompatible fluorescent dyes has always been challenging.

Quantum dots as fluorescence imaging agents

Among many different types of fluorescent probes, QDs have gained special attention in recent years due to their size-tunable stable fluorescent activity. QDs are generally semiconductor nanomaterials composed of a core and a shell. Examples include cadmium selenide (CdSe), lead selenide (PbSe), or indium arsenide (InAs). However, due to the toxicity effects associated with the heavy metals present in QDs, the development of biocompatible, photoluminescent, and cost-effective alternative QDs has gained research interest thereafter. Among different QDs, 2-10 nm-sized CDs have gained special attention in bacterial cell imaging (Figure 3).

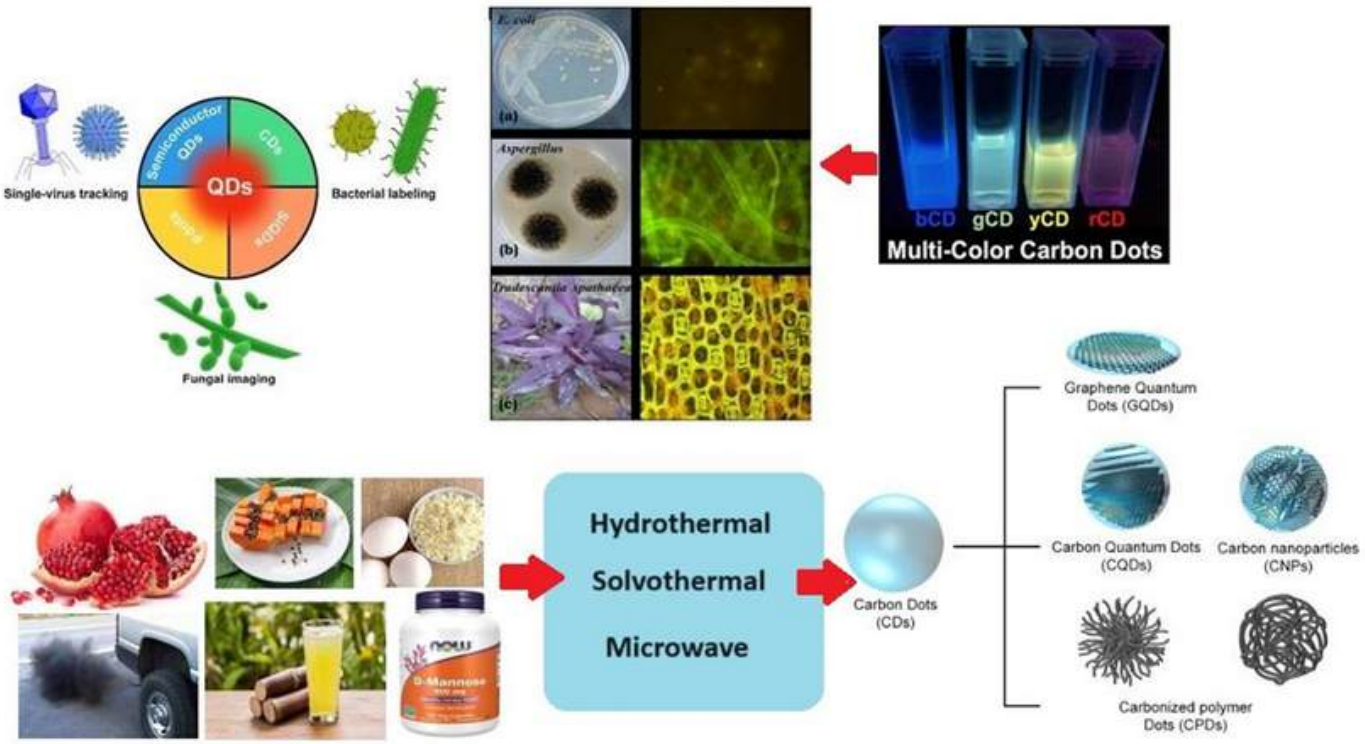

Figure 3 Different types of carbon dots synthesized via various synthetic approaches used on fungal and bacterial imaging

Source: Sharma, Sharma and Bera (2022); Gao et al (2018)

Carbon quantum dots as fluorescence imaging agents

Compared with other QDs, CDs are known for their excellent ability to absorb energy in the near UV-visible region, resulting in emissions mainly in the visible and near-infrared (NIR) regions. Additionally, among the many other QDs used for optical imaging, CDs are biocompatible, yielding brighter emissive colors that are excitation-dependent, typically emitting in the green and blue regions. Depending on the chemical structure of the CDs, four major types of CDs have been utilized in microbial imaging. These include CDs with a definite crystal structure, CDs with a few graphene layers with functional groups, carbon nanodots, and carbonized polymer-based CDs.

Various source materials, as indicated in Figure 3, have been utilized for the generation of different CDs. Many of these sources are plant-based or plant-derived materials or extracted from natural waste. These materials have then been subjected to treatment approaches such as hydrothermal synthesis (solubilized in water and treated at an elevated temperature of 170℃, pressure of 1 bar for 12 hours) or solvothermal synthesis (solubilized in a solvent other than water and treated at elevated temperature and pressure, typically 1 bar). In addition, some research has also focused on the use of microwave irradiation for the generation of CDs.

The said CDs have primarily been utilized to label the bacteria (Figure 4) such as *Escherichia coli*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*, to visualize the

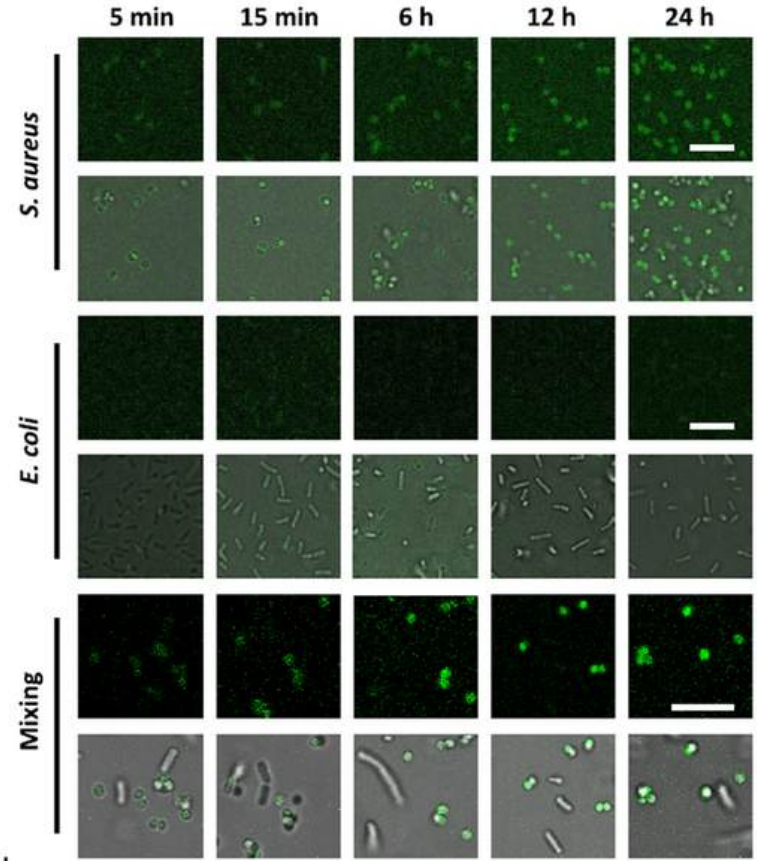

Figure 4 Confocal images of *Staphylococcus aureus* and *Escherichia coli* treated with CDs (100 μgmL $^{-1}$) for 5 min, 15 min, 6 h, 12 h, and 24 h
Source: Yan et al (2021)

steps during an infection that involve the attachment to the host cell, entry into cells, replication inside cells, and possible antibacterial activity included by CDs, as indicated in Figure 5. Furthermore, fluorescence tagging with CDs has been employed for viability assessment (Figure 6), identification of the bacterial type, and quantification of the bacteria. More importantly, rapid diagnosis of bacteria is crucial for effective clinical treatment, reducing mortality during deadly diseases, and identifying hazardous bacterial species in various ecosystems.

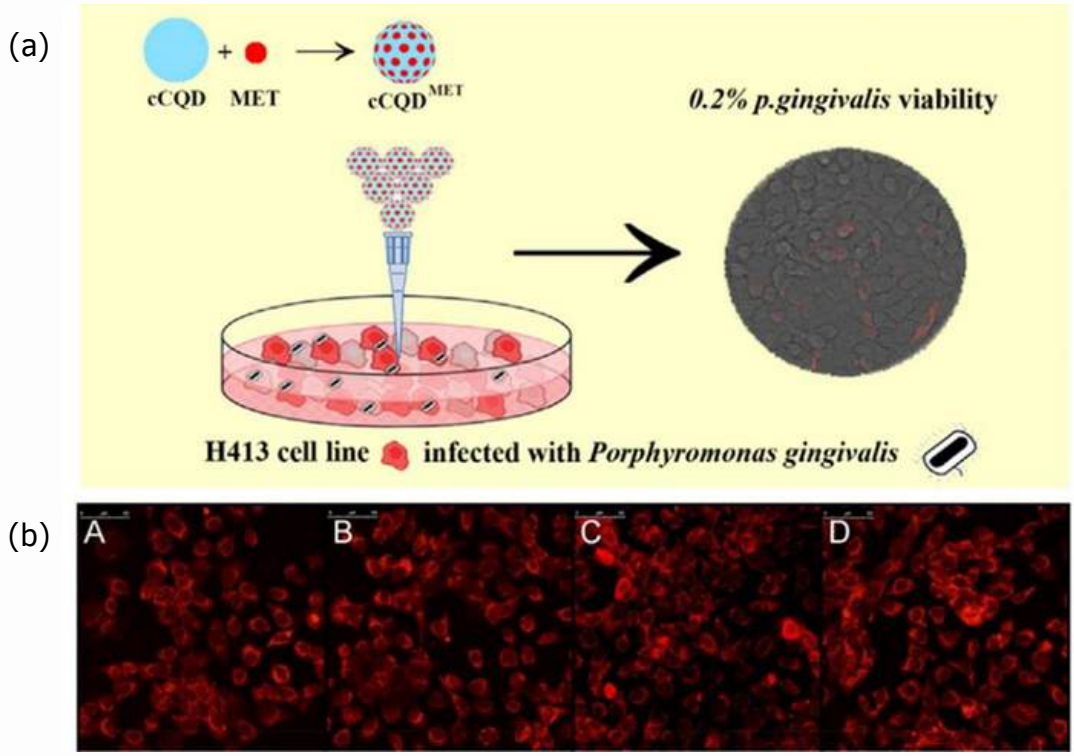

Figure 5 (a) Carbon quantum dots (CDs) killing intracellular *Porphyromonas gingivalis*, (b) Cellular uptake of CDs with increasing fluorescence intensity of internalized CDs over a 4 h period
Source: Jiang et al (2023)

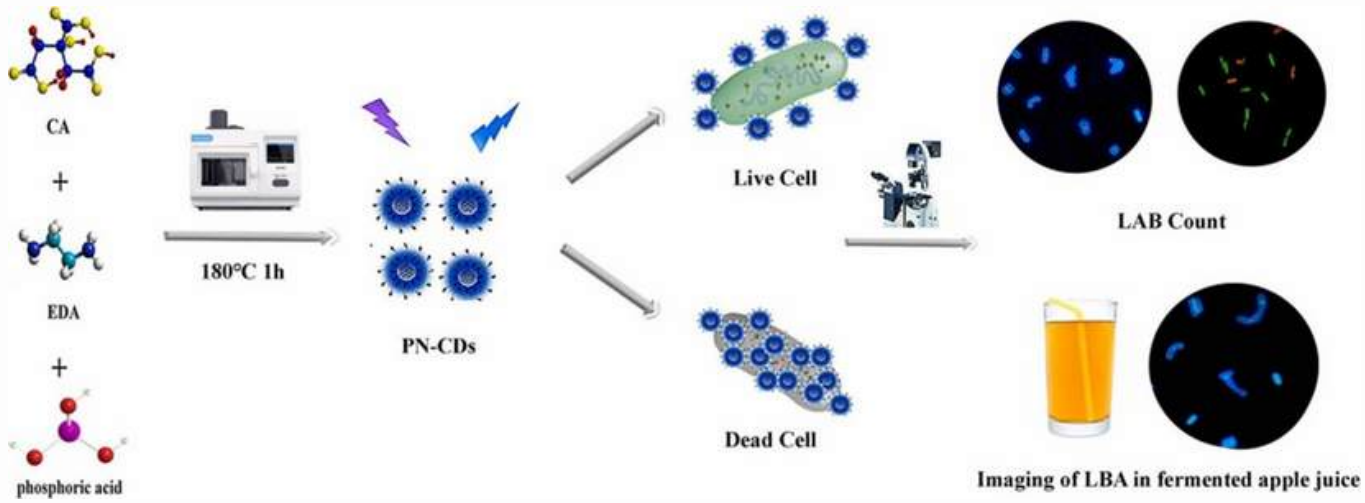

Figure 6 Carbon quantum dots tracking the viability of lactic acid bacteria in apple juice
Source: Fu et al (2023)

Current news and updates about CDs

The novel trends in CDs include the shift towards greener synthetic approaches, improving the quantum yield, further functionalization of CDs to improve applicability and increase specific interactions with microbes, doping of CDs with nitrogen and sulfur to improve photostability, as well as the formation of CDs nanocomposites and the development of multifunctional CDs for simultaneous imaging and providing antibacterial effects.

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The Battle Against the Hidden Killers: An Overview of Human Fungal Infections, Diagnosis, and Treatment

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Human fungal pathogens, the “hidden killers”, can pose a range of infections and create an unprecedented burden on human health. These infections could vary from superficial skin conditions to life-threatening systemic diseases (Figure 1). The increasing number of fungal infections and related deaths each year poses a rising threat to human health. This growing trend is often attributed to climate change, heightened pathogen virulence, and the increasing prevalence of immunocompromised individuals worldwide. Despite an estimated 3.5–5.1 million fungal species, only a few hundred, nearly 300 species, are linked to human fungal diseases. Notably, *Aspergillus*, *Candida*, *Cryptococcus*, *Exophiala*, *Pneumocystis*, and *Trichophyton* contribute to most fatalities.

Nature of fungal pathogenesis in humans

In the battle against human fungal diseases, antifungal agents play a crucial role, incorporating chemical compounds and natural products in the management and prevention of these diseases. Apart from these antifungal agents, various methods, approaches, and strategies are employed globally in managing human fungal diseases. Classification of human pathogen infections takes various approaches, primarily based on the site of infection, pathogen acquisition route, and the type of virulence exhibited by the pathogen. These classification methods help us to understand the diverse nature of fungal infections in humans and contribute to diagnostic and treatment strategies. However, despite advances in antifungal and other recommended advanced therapies, poor outcomes and high mortality rates persist due to the inadequate availability of treatments in some countries and poor diagnostic practices.

Fungal infections originate from two main sources: exogenous and endogenous mycoses. Exogenous mycoses occur when disease is transmitted to individuals through external

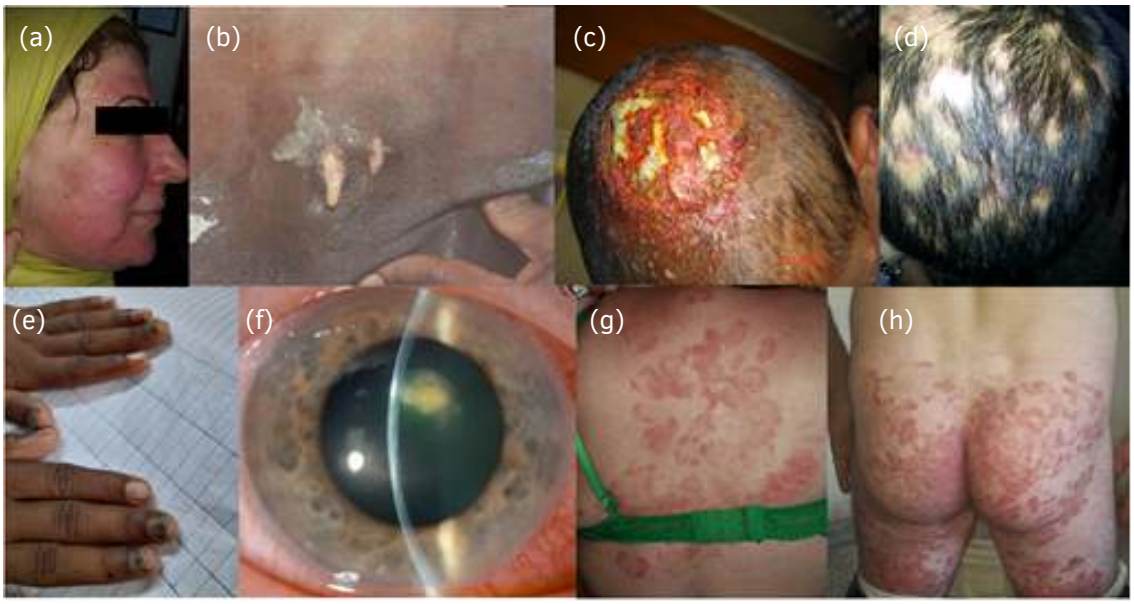

Figure 1 Clinical images showing fungal infections in different sites of the human body
Photo credit: a, c, d, g, h: Khalifa E. Sharquie (Department of Dermatology, College of Medicine, University of Baghdad); b: Tsidiso Gugu Maphanga (Centre for Healthcare-Associated Infections, Antimicrobial Resistance and Mycoses (CHARM), National Institute for Communicable Diseases, Division of National Health Laboratory Service, Sandringham, South Africa); e: Sarah A. Ahmed (Radboud university medical center, Netherlands) and Mawahib A.I. Ismail (Mycology Reference Laboratory, University of Khartoum, Khartoum, Sudan); f: Darren Ting (Academic Unit of Ophthalmology, Institute of Inflammation and Ageing, University of Birmingham, Birmingham, UK), and Khadim Diongue (Cheikh Anta Diop University, Dakar, Senegal).

routes, such as airborne, cutaneous, or percutaneous contacts. For instance, Coccidioidomycosis (valley fever) caused by *Coccidioides immitis* and *C. posadasii* can be inhaled by humans when the spores rise in dust storms. Subsequently, the pathogen can infect the lungs and surrounding tissues, leading to diverse symptoms including cough, fatigue, fever, headache, muscle aches or joint pains, and rashes. On the other hand, endogenous mycoses occur when the pathogen is acquired through colonization or reactivation of a fungus from latent infections. For instance, *Cryptococcus neoformans* can infect the lungs or the central nervous system, causing pneumonia-like symptoms including fever, cough, shortness of breath, and chest pains.

Fungi exhibit different types of virulence, which can be classified into two categories: primary infections and opportunistic infections.

Primary fungal infections typically occur in individuals with a normal immune system and are usually the result of inhaling fungal spores. These infections tend to develop at a slower rate. Examples of primary fungal infections include Blastomycosis (caused by *Blastomyces dermatitidis*), coccidioidomycosis (caused by *Coccidioides immitis*), histoplasmosis (caused by *Histoplasma capsulatum*), and paracoccidioidomycosis (caused by *Paracoccidioides brasiliensis*). In contrast, opportunistic infections occur almost exclusively in immunocompromised hosts with weakened immune defence mechanisms. Factors leading to immunocompromise include conditions such as HIV infection, diabetes mellitus, lymphoma, organ transplantations, acute lymphocytic leukaemia, and other hematologic cancers. Early diagnosis of fungal diseases is critical for effective treatment in both primary and opportunistic infections.

Diagnosis of human fungal infections

Diagnosis of fungal infection has traditionally relied on preliminary methods such as direct microscopic examination of clinical samples, histopathology, and tissue and body fluid biopsies. However, with advancements in medical technology, novel approaches including serological methods, imaging techniques, and molecular-based assays are now widely used in fungal disease diagnosis.

A biopsy is a procedure for removing cells, tissues, or fluid from the body for examination. Biopsy samples obtained from infected areas are used for diagnosis. Tissue biopsies or biological fluid samples from the site of infection can be cultured on a suitable medium to isolate the fungi responsible for the infection. Moreover, culturing facilitates the selection of the most suitable treatment options. Cultured fungi can then be examined further by microscopy, either as dried smears or wet mounts, with or without specific staining. Direct microscopy enables the identification of fungal morphological features such as fungal hyphae, fruiting structures, or spores.

Serological tests are employed to determine the antibody response in the body against fungal infections, offering a non-culture-based diagnosis approach. Several technologies are now available including galactomannan (GM), latex agglutination test (LAT), complement fixation (CF) tests, and enzyme immunoassay (EIA). Galactomannan, an immunodominant polysaccharide component found in the cell walls of *Aspergillus* species, serves as an emblematic biomarker in medical mycology.

The GM test detects fungal cell wall antigen galactomannan from patient specimens such as serum, cerebrospinal fluid (CSF) samples, and bronchoalveolar lavage (BAL) fluid. LAT is a rapid test that detects fungal antigens in patients with systemic fungal infections, and the test kits are commercially available with a surface of latex particles coated with antibodies specific to certain types of fungi. Saliva, urine, serum, or CFS obtained from the patients can be used for the LAT. In the CF test, the fungal antigens and positive controls are used to detect antibodies in the patient's serum. This test aids in the diagnosis of specific fungal diseases such as histoplasmosis, blastomycosis, coccidioidomycosis, and aspergillosis.

It is not always recommended to perform routine biopsies in immunosuppressed patients. Hence, imaging methods are pivotal as they are informative and non-invasive. Diagnostic imaging in fungal infections typically targets structural changes that may occur later in the host-fungal interaction process, often seen in established infections. Common imaging techniques include chest X-ray (plain radiography), computerized tomography (CT) scanning, magnetic resonance imaging (MRI), and ultrasound (US) scans. Additionally, molecular imaging has emerged as a novel approach, allowing physicians to visualize molecular and cellular changes inside the body. This provides unique information to assist in diagnosing, evaluating, treating, and managing various diseases, including cancer and invasive fungal infections.

In the last decade, the development of nucleic acid amplification technologies including various quantitative PCR technologies and molecular sequencing technologies, revolutionized the research in the medical mycology field. These technologies enable rapid detection and identification of fungi present in clinical samples. Currently, sequence-based methods are widely applied for the identification of unknown fungi grown in cultures. The choice of locus depends on the type of fungi being studied, with ITS-rDNA sequence data commonly used for preliminary identification of fungal pathogens. The integration of sequence data and the construction of multi-locus phylogenetic trees in recent studies have significantly enhanced the accuracy and reliability of identifying human fungal pathogens. In addition, other main molecular-based techniques include pulse-field gel electrophoresis, restriction enzyme analysis, random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), microsatellite length polymorphism (MLP) typing, and DNA microarrays.

Despite the availability of advanced diagnostic methods, there are many challenges associated with their use. These challenges include laborious processes, difficulties in the sample collection and isolation, high cost, relatively low growth rates or sensitivity, and the invasive nature of the specimens required for certain tests. In addition, signs and symptoms of fungal infections are nonspecific, making it challenging to differentiate colonization from invasive disease. Blood cultures, commonly used for diagnosis, often yield negative results. Furthermore, many patients, particularly those immunocompromised, may be unable to undergo invasive diagnostic procedures due to their condition, further complicating the diagnosis process.

Therapeutics for fungal diseases

Fungal infections are commonly treated with antifungal drugs, which selectively target and eliminate fungal pathogens from the host with minimal toxicity to the host. These treatments are available globally in the form of oral or intravenous medications, lotions, creams or powder, mouthwash or lozenges, eye drops, or shampoo.

Currently, three classes of antifungal agents are used for treating invasive fungal diseases (IFDs) based on their inhibition targets: ergosterol inhibitors, 1,3-β-D-glucan synthase (GS) component FKS1 inhibitors, and flucytosine interfering with RNA and DNA metabolism. Ergosterol, a sterol present in fungal cell membranes, plays a crucial role in maintaining cell membrane integrity. Azoles and polyenes, which belong to the ergosterol inhibitor class, target this compound. GS is involved in synthesizing 1,3-β-D-glucan, which is the major component of the fungal cell wall. Echinocandins such as caspofungin, micafungin, and anidulafungin are considered the most widely used GS inhibitors worldwide. Flucytosine, a pyrimidine, inhibits DNA and RNA synthesis in fungi by incorporating itself into the growing nucleic acid chain, thereby preventing further extension. Combinations of flucytosine with other antifungals are recommended for treating refractory cases, including infections caused by resistant fungi, and invasive fungal infections (IFIs) associated with biofilms and vegetation formation.

Nanotechnology-based formulations are reported to be a promising therapy against fungal infections. Nanoparticles effectively deliver drugs to the target site, promoting reduced toxicity and increased bioavailability of the antifungal agent. Therefore, they offer an advantage in the treatment of IFIs. The two major drawbacks limiting the applications of nanoparticles in drug delivery systems are environmental toxicity issues associated with nanoparticle synthesis and the biocompatibility of nanoparticles. However, the emerging trend of green synthesis of nanoparticles, which involves synthesizing nanoparticles using biomacromolecules from natural resources, overcomes these drawbacks.

In addition to the above-mentioned therapies, RNA-based therapies are also currently being studied for their potential use in the treatment of fungal infections. RNAi-based therapies have been researched for various intracellular infections mediated by fungi. Furthermore, nanocarrier-mediated delivery of siRNA (small interfering RNA) and shRNA (short hairpin RNA) molecules have also been found to overcome the various delivery challenges associated with these biotherapeutics.

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Chaperones to the Rescue: Tackling Neurodegenerative Diseases and Potential Therapeutic Applications

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Protein misfolding has been identified as a contributing factor in several neurodegenerative conditions, such as Alzheimer's disease (AD), Huntington's disease (HD), Amyotrophic Lateral Sclerosis (ALS), and Parkinson's disease (PD). One common characteristic observed among individuals affected by these illnesses is the aggregation of deposits consisting of misfolded proteins. The occurrence of abnormal protein folding can lead to toxicity by either impairing or enhancing protein function, or both. One promising treatment strategy for these diseases is to use protein-remodeling factors to correct misfolded proteins and restore protein structure and function back to its native state. Hence, the interaction between chaperones and protein folding/degradation pathways plays a vital role in developing novel therapeutic drugs for these neurodegenerative diseases.

Chaperone-mediated protein homeostasis

Molecular chaperones are indispensable proteins that interact with unfolded and partially folded polypeptide chains, thereby impeding their aggregation and precipitation. Several molecular chaperones were initially characterized as heat shock proteins (Hsp) due to their upregulation in response to higher temperatures.

The folding and re-folding of substrate proteins, also known as clients, are essential for maintaining their functional state and structure. This process is facilitated by a network of molecules called chaperones and co-chaperones, which are highly conserved across various organisms. Molecular chaperones function by interacting with other proteins, thereby stabilizing them and assisting in achieving their native conformation. With a widespread presence in cells, they play a crucial role in facilitating the folding of recently produced proteins, as well as the re-establishment of partially folded proteins into their respective three-dimensional configurations.

Chaperones play a crucial role in maintaining intracellular protein homeostasis by engaging protein degradation pathways responsible for regulating the continuous turnover of proteins and eliminating misfolded proteins. Molecular chaperones in bacteria are called Caseinolytic peptidase B (ClpB), while in yeast and plants, they are called heat-shock protein (Hsp)104 and Hsp101, respectively. Conversely, metazoans lack ClpB. In recent times, ClpB and Hsp104 have become the main focal points of protein research and the development of novel therapeutic drugs.

Caseinolytic peptidase B (ClpB)/heat-shock protein (Hsp)104 regulation

In an ATP-dependent manner, Hsp100 disaggregases (known as Hsp104 in *Saccharomyces cerevisiae* and ClpB in *Escherichia coli*) drive aggregated substrates as single polypeptides through their central pores, forming hexameric rings.

It is believed that Hsp70 first detects the substate and binds to the surface of aggregates, facilitating the transfer of the aggregated substrate to Hsp100. Subsequently, Hsp100 disaggregases break down the aggregates by pulling peptide loops through their central channel in an ATP dependent manner.

The reactivation and breakdown of protein aggregation controlled by ClpB are closely linked to two additional molecular chaperones, namely DnaK/Hsp70 and DnaJ, as well as a nucleotide exchange factor known as GrpE that operates in a cyclic manner. Nevertheless, the precise mechanism by which ClpB facilitates the reactivation and disintegration of protein aggregates remains unknown. The hexameric form of bacterial ClpB, which possesses biological activity, has a molecular weight of 575 kDa. When nucleotides such as ATP or ADP are present, six monomers of ClpB, each weighing 95 kDa, assemble to form a functional hexameric ClpB complex (Figure 1).

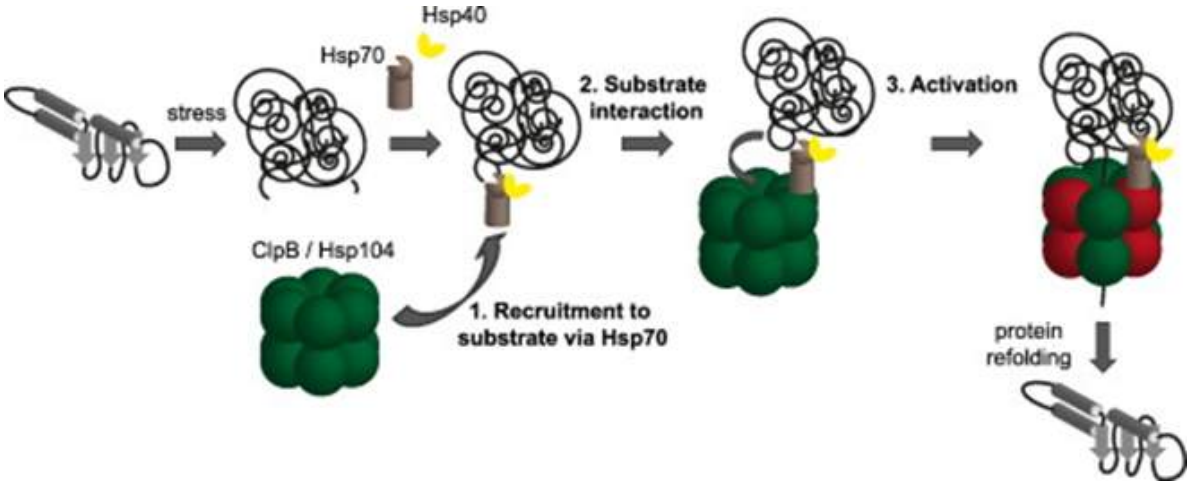


Figure 1 Substrate interaction of hexameric ClpB and Hsp104. Co-chaperone Hsp40 and Hsp70 are important in substrate recognition and interaction. Folded proteins become misfolded proteins due to cellular stress. These misfolded proteins are recognized by Hsp70 (brown) and Hsp40 (yellow) and guided towards ClpB/Hsp104 (green). Misfolded proteins are exraected trhough its central channel of ClpB/Hsp104 by ATP hydrolysis (red). These exreacted linear polypeptides are folded/recycled back to active proteins again.
Source: Kummer et al (2016)

Each ClpB monomer (also Hsp104) has a structure made up of many unique domains, including an N-terminal domain (NTD), two AAA+ nucleotide-binding domains (NBD1 and NBD2) that bind to ATP and hydrolyze ATP, a middle domain (MD) inserted into NBD1 that has a coiled-coil structure, and a short region at the C-terminal. When these monomers undergo self-association, they create a constricted channel located in the middle of the hexamer. ClpB breaks the aggregated proteins and releases them as single polypeptides by using ATP as the energy source (Figure 2).

The structure of each Hsp104 monomer (each weighing 104 kDa) shares a similar domain arrangement with ClpB. The Hsp104 hexamer has a central channel that spans its entire length. Polypeptides extracted from aggregates are propelled through the central channel of both ClpB and Hsp104 using ATP. *In vitro* experiments have demonstrated that Hsp104 chaperones can reconstruct amyloid conformers and denatured proteins. Sequence variations in the middle domain (M-domain) of ClpB and Hsp104 are responsible for chaperone activation. The M-domain also regulates the ATPase activities of ClpB and Hsp104 and is responsible for the interaction with DnaK/Hsp70 chaperones (Figure 2).

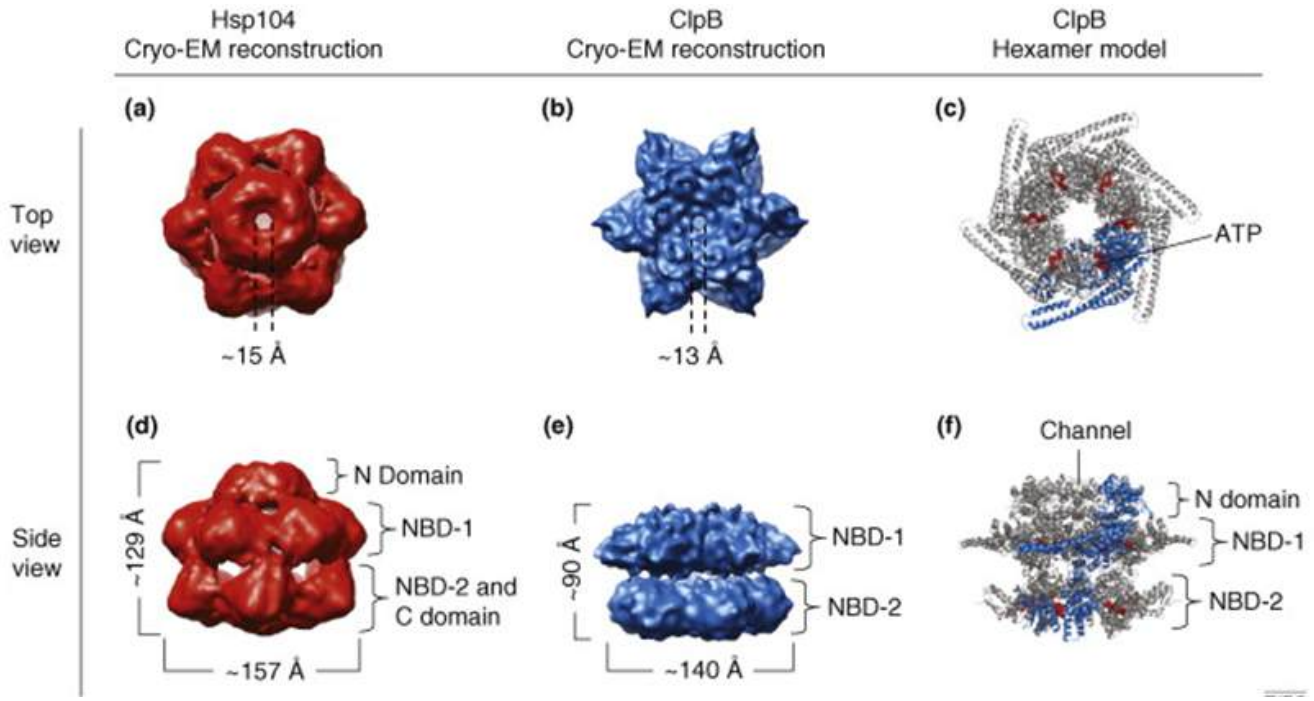


Figure 2 Three-dimensional cryo-EM reconstruction of hexameric ClpB and Hsp104 models. The length, width and the size of the central channel is shown in Angstroms (Å). NBD: Nucleotide Binding Domain. (a) and (d) are Hsp104 protein viewed from top and side. (b) and (e) are ClpB protein, viewed from top and side. Hsp104 and ClpB has a central channel of 15 Å and 13 Å, respectively. Hsp104 has following dimensions: length 129 Å, width 157 Å. ClpB has following dimensions: length 90 Å, width 140 Å. ClpB hexamer bound to ATP is shown in (c) and (f). A single protomer is shown in blue and the position of ATP in red as a CPK model in (c) and (f).
Source: Doyle et al (2009)

Human protein disaggregase system

For a long time, it has been thought that humans might possess protein disaggregase related to the Hsp100 family found in bacteria, fungi, and plants. However, identifying such a protein disaggregase has proven challenging until the revelation that the collaboration between Hsp110, Hsp70, and Hsp40 can effectively disaggregate and reactivate proteins. Hsp110, is an essential component of the mammalian cytosolic disaggregase machinery, exhibits the ability to collaborate with Hsp70 and Hsp40 in the process of disaggregating preformed aggregates and amyloids. Hsp110 engages in collaborative and synergistic interactions with Hsp70 and two distinct types of Hsp40 cochaperones to effectively resolve substantial protein aggregates. Given the extensive array of potential complexes that may form between various Hsp70s and Hsp 40s, it is hypothesized that distinct and specific complexes could be utilized to dissolve various protein aggregates. While it is possible that a particular combination may be utilized in specific neuronal subtypes, it is also possible that a specific combination could target α-synuclein disaggregation, while another combination could target tau disaggregation.

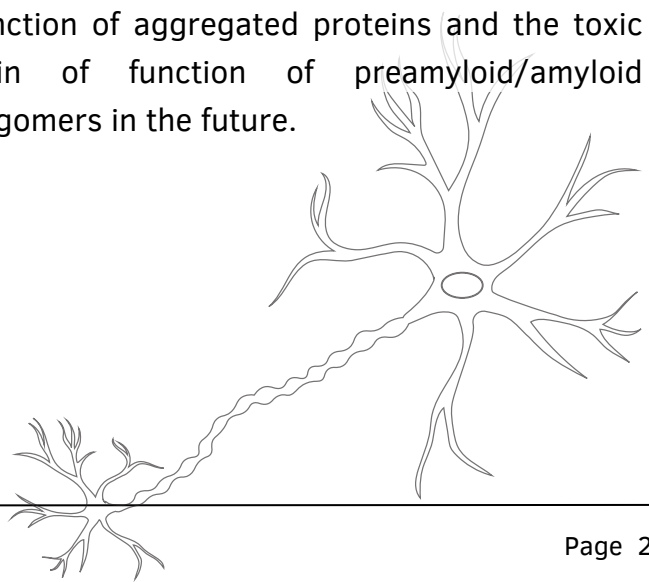
Powerful amyloid-remodeling system

The term "intracellular inclusions" refers to the signature lesion of PD, which consists of Lewy bodies made of alpha synuclein protein (alpha-syn), amyloid versions of the tiny pre-synaptic protein. Inhibition of fibrillization by Hsp104 was potent for both alpha-syn and PD-linked variants.

The hallmarks of AD include neurodegeneration in certain subcortical regions and the cerebral cortex, as well as widespread shrinkage of the brain. Internal neurofibrillary tangles containing amyloid protein tau and external neuritic plaques containing primarily beta amyloid 42 and beta amyloid 40 (Ab42 and Ab40) are the defining pathogenic lesions of AD. It has been reported that Hsp104 inhibits the *de novo* fibrillization of Ab42.

Potential future directions

The amyloid-remodeling activity of Hsp104 is exceptionally potent, and it combines the hydrolysis of ATP with the rapid dismantling of amyloid fibers. It has not been possible to definitively identify a metazoan homologue or analogue of Hsp104. Furthermore, no activity has been discovered in metazoa that combines protein disaggregation with renaturation processes. The unique ability of Hsp104 to deconstruct cross beta sheets and preamyloid oligomers opens a potential new avenue of application in metazoan systems. Reversing amyloid formation and breaking down formed amyloids could serve as an initial solution for addressing amyloid associated disorders. By employing these chaperones in a metazoan system, we may address both the loss of function of aggregated proteins and the toxic gain of function of preamyloid/amyloid oligomers in the future.



Surprisingly, despite being a yeast protein, Hsp104 is extremely well tolerated in metazoan systems and does not exhibit any overt toxicity. However, to apply these systems in a mammalian setup, initial studies on ClpB for its specific substrate recognition mechanisms are vital, as ClpB and Hsp104 share certain structural and functional features.

The concept of modifying the proteostasis network has limitations despite its great potential. For example, while increased expression of protein-remodeling proteins may help improve protein folding and combat neurodegenerative diseases, it may also stimulate cell division, potentially leading to cancer. To address neurodegenerative disease effectively, the development of novel strategies for small-molecule modulators of protein-remodeling systems and the creation of customized protein-remodeling systems will be crucial for rewiring and restoring the proteostasis network.

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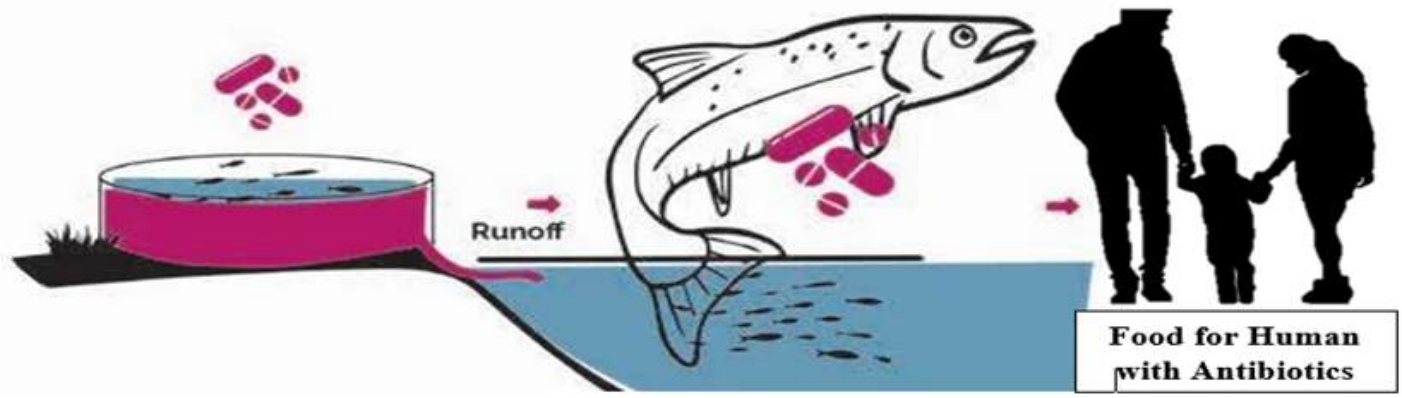
The Escalating Emergence of Antibacterial Resistance in Aquaculture Poses a Crisis for Human Health



Aquaculture has rapidly grown worldwide as a major industry, providing not only economic income and high-quality food products but also employment opportunities to hundreds of thousands of skilled and unskilled workers. Furthermore, aquaculture will play an important role in meeting the increased demand for protein-rich food. However, diseases in aquaculture systems are now considered as one of the critical limiting factors in the industry, with particular attention focused on shrimp aquaculture.

Recent studies have shown that antimicrobial drugs, including antibiotics, have been approved and used in many countries to treat bacterial diseases in aquaculture. The widespread use of antibiotics in aquaculture systems has exerted a very strong selection pressure, leading to the emergence of antibiotic-resistant bacteria.

Antibiotics usage in aquaculture

The Food and Agriculture Organization (FAO) estimates that 10,259 tons of antibiotics were used globally in aquaculture in 2021, with usage projected to increase by 33% to 13,600 tons annually by 2030. The Asia-Pacific region accounts for the most significant portion of worldwide antibiotic use in aquaculture, with China alone accounting for 57.9% of usage in 2021.

When disease outbreaks occur on commercial fish farms, farmers tend to add antibiotics into the feed, regardless of whether the causative agent is a virus or bacteria. This practice is especially prevalent in low- and middle-income countries in Asia and Africa, such as Bangladesh, Sri Lanka and Nigeria, where there is lack of diagnostic tools for identifying fish diseases. Consequently, the overuse of antibiotics poses a significant challenge in these regions.

Moreover, these countries often have fewer restrictions on the sale of antimicrobials compared to countries in Europe and elsewhere. Additionally, even when antibiotic use is regulated, the rules are often not strictly enforced.

Development of antibiotic resistance

The most significant concern regarding antibiotic release into the environment is the development of antibiotic resistance, leading to reduced therapeutic potential against human and animal pathogens. Inappropriate and irrational use of antimicrobial agents provides favorable conditions for the emergence, spread, and persistence of resistant microorganisms. The longer the duration of exposure to antibiotics, the higher the risk of resistance development, regardless of the severity of the need for the antibiotic. Consequently, antibiotic resistance to specific antibiotics becomes more prevalent, necessitating a greater need for alternative treatments.

Spread of antibiotic resistance to human

Aquatic environments can serve as a source of drug-resistant bacteria, which can be directly transmitted and cause infections in humans. Aquaculture is increasingly recognized as a contributing factor to the rise of resistance in microorganisms affecting humans. This often begins with the introduction of antibiotics into the water, either through fish excretions or from antibiotics present in fish products themselves.

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Transmission to humans can occur through direct contact with water or aquatic organisms, ingestion of contaminated drinking water, or through the handling or consumption of aquaculture products. Direct transmission from aquatic environments to humans can involve human pathogens, such as *Vibrio cholera*, *Vibrio vulnificus*, *Shigella* species, and *Salmonella* species, or opportunistic pathogens, such as *Aeromonas hydrophila*, *Pseudomonas shigelloides*, and *Escherichia coli*. The presence of antimicrobial-resistant *Salmonella* species in aquatic environments is most likely attributable to contamination from human, animal, or agricultural sources.

Present status of antibiotic contaminations and antibiotic resistance in aquaculture effluent water in Sri Lanka

The effluent from aquaculture sites showed higher concentrations of antibiotics, particularly those belonging to the tetracycline group, compared to other selected antibiotics tested. Levels of oxytetracycline (OTC) in shrimp hatcheries ranged from 0.056 ± 0.001 µg/ml to 0.234 ± 0.014 µg/ml, which were comparably higher than OTC levels observed in food fish farms (0.008 ± 0.012 µg/ml - 0.221 ± 0.012 µg/ml) and ornamental fish farms (0.009 ± 0.011 µg/ml - 0.031 ± 0.005 µg/ml). Similarly, increased levels of tetracycline (TET) were detected in shrimp hatcheries (0.012 ± 0.019 µg/ml - 0.112 ± 0.017 µg/ml) compared to ornamental fish (0.001± 0.002 µg/ml - 0.002 ± 0.031 µg/ml) and food fish farms (0.001 ± 0.031 µg/ml - 0.076 ± 0.022 µg/ml), respectively.

In aquaculture farms in Sri Lanka, *Bacillus* sp., *Acinetobacter* sp., *Achromabacter* sp., *Staphylococcus* sp., *Micrococcus* sp. were identified as the most abundant genera exhibiting resistance to TET and OTC.

Risk to animal and human health

Previous studies have shown that aquaculture farms serve as sources of TET and antibiotic resistance bacteria (ARB). The presence of TET resistance (TETr) bacteria, particularly potential opportunistic pathogens isolated from the aquaculture environment, and the detection of TETr genes highlight the urgent need for establishing a monitoring system to regulate antibiotic usage in aquaculture. The presence of ARB in farm water may lead to fish diseases and eventually, production losses at fish farms.

Antibacterial agents may disturb the microflora of the human intestinal tract, increasing the risk of certain infections. When individuals take antibiotics for any reason, it increases the risk of infections caused by particular pathogens that have developed resistance to those antibiotics. This not only increases the frequency of treatment failure but also increases the severity of infection due to antibiotic resistance, leading to a prolonged duration of illness, an increased frequency of bloodstream infections, and increased hospitalization.

Mitigating antibiotic usage in aquaculture

Antibiotic use in aquaculture is driven by production intensification and the rise of aquatic animal diseases in various farmed aquatic species. Due to crowded farming conditions, a large portion of the antibiotics used in aquaculture are administered to prevent illness rather than treat infection. The World Health Organization (WHO) estimates that by 2050, antimicrobial resistance will be responsible for 4.7 million deaths in the Asia region. In Sri Lanka, the National Strategic Plan (NSP) 2017-2022 was developed in collaboration with WHO in 2016. The NSP is developed under five key strategies aligned with the strategic objectives of the Global Action Plan: improving awareness and understanding of antimicrobial resistance through effective communication, strengthening the knowledge and evidence base through surveillance and research, reducing the incidence of infection through effective sanitation, hygiene, and infection prevention measures, optimizing the use of antimicrobial medicines in human and animal health, and preparing the economic case for sustainable investment and increasing investment in new medicines, diagnostic tools, vaccines, and other interventions. Further studies providing clear evidence of the link between inappropriate antibiotic use in aquaculture and antibiotic residues, as well as antibiotic resistance in bacterial pathogens, are needed to develop the appropriate control strategies.

The use of antibiotics in aquaculture exerts selective pressure, leading to the emergence of reservoirs containing ARB and transferable resistance genes in fish pathogens and other bacteria in the aquatic environment. Furthermore, resistance genes from aquatic bacteria can disseminate through horizontal gene transfer, potentially reaching human pathogens. Genes conferring resistance against clinically relevant antibiotics which are carried on mobile genetic elements that replicate in pathogens are considered an immediate threat to the successful treatment of human clinical infections. Hence, it is crucial to implement efforts aimed at preventing the development and spread of antimicrobial resistance in aquaculture. These efforts focus on improving management practices, regulating the use of antimicrobial agents, implementing prudent use guidelines, and monitoring both the use of antimicrobial agents and antimicrobial resistance levels.

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Greenhouse Gas Emissions in Wastewater Treatment Plants: Righting the Wrong Towards Livability

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Climate and emissions

Climate change is a critical global issue that has garnered widespread attention in recent years (Figure 1). Despite its long-standing history, the present state of global climate change is alarming, as evidenced by the continuous increase in net anthropogenic greenhouse gas (GHG) emissions and cumulative CO_2 emissions since 1850. The issue of climate change is anticipated to present significant challenges to governments, industrialists, and individuals in the future. The resulting changes in resource usage, production, and economic activities are expected to have far-reaching consequences.

To address this challenge, GHG inventories have emerged as an essential tool for understanding the sources and trends of GHG emissions and removals. A GHG inventory is a list of emission sources and their associated emissions, calculated using standardized techniques. These inventories are developed by organizations for several reasons, including managing GHG risks and addressing opportunities for reduction, participating in GHG programs, engaging in the GHG market, and receiving credit for taking early voluntary action.

GHG emissions in wastewater treatment

To combat global warming and climate change, the Kyoto Protocol was established, aiming to maintain atmospheric GHG concentrations at non-significant levels.

The first step in achieving this goal involves preparing inventories to monitor and reduce GHG emissions. As a result, companies, institutions, and organizations require reliable methods for calculating and tracking their GHG emissions. In contrast to industrial applications, wastewater treatment can be a significant source of GHG emissions. Therefore, addressing emissions from wastewater treatment plants (WWTPs) holds the potential to reduce overall GHG emissions (Figure 2) while also improving the sustainability and efficiency of wastewater treatment processes. This is crucial for mitigating climate change and ensuring the environmental sustainability of water management systems.

The benefits of WWTPs extend beyond protecting public health and the environment.

Figure 1 Greenhouse gas emissions
Source: Shutterstock (2016) *Coal fired power station silhouette at sunset, Pocerady, Czech republic* [online]. Available at: https://www.shutterstock.com/image-photo/pocerady-november-14-2016-coal-fired-1619145415 (Accessed: 24 March 2024)

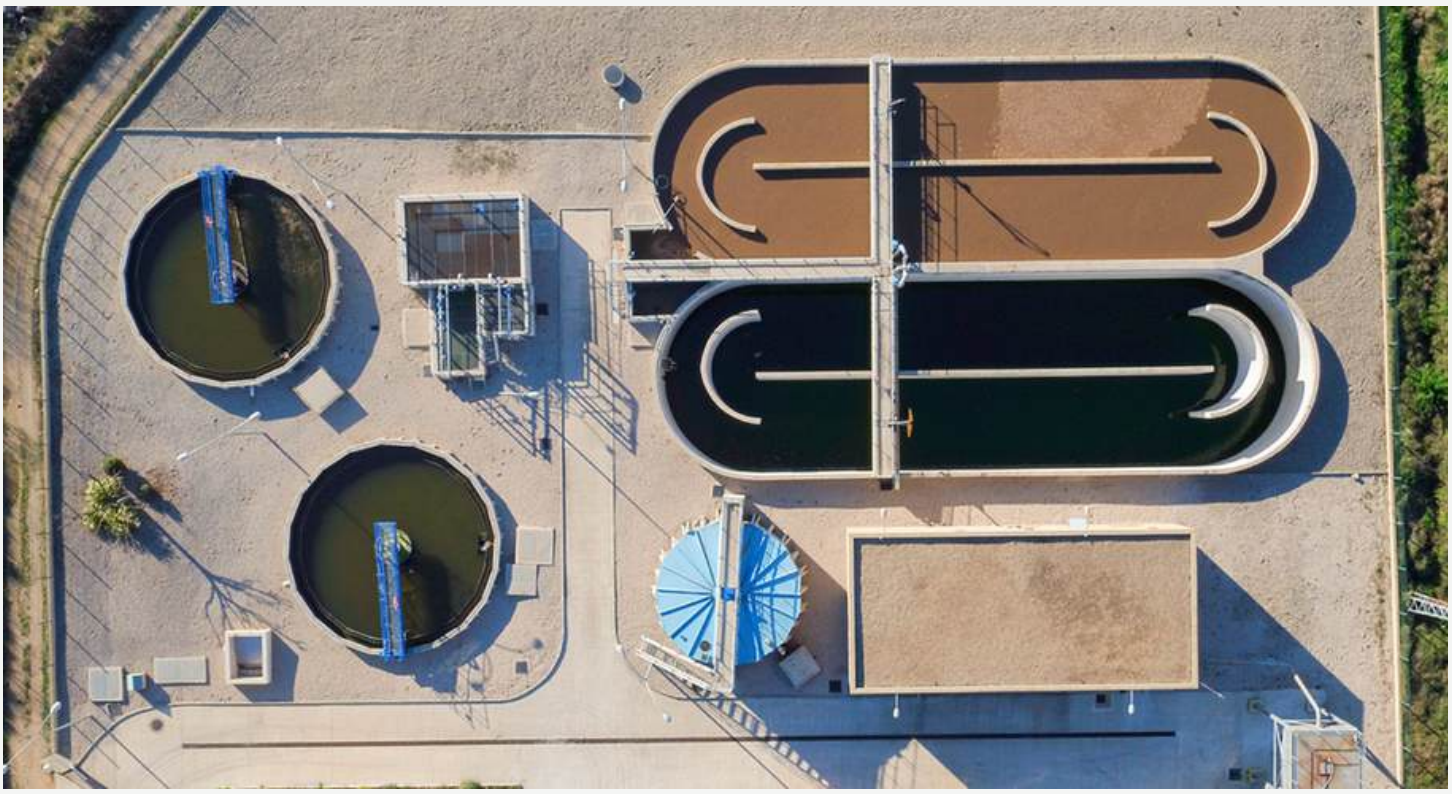

Figure 2 Wastewater treatment plant (WWTP)
Source: https://www.acciona.com/updates/articles/acciona-participate-initiative-to-capture-carbon-dioxide-produced-wastewater-treatment-plants/?_adin=02021864894 (Accessed: 24 March 2024)

These plants can also contribute to economic growth by providing a reliable source of water for industries and agriculture. For example, treated wastewater can be used for irrigation, reducing the need for freshwater and increasing crop yields. In addition, some industries, such as power plants, rely on a steady supply of water, which can be provided by WWTPs. Moreover, WWTPs can generate renewable energy from wastewater by using anaerobic digesters to break down organic matter and produce biogas, which can be used as a source of energy. This not only reduces the environmental impact of wastewater treatment but also provides an additional source of energy.

Assessing footprints: GHG and carbon inventories

Current research carried out to develop a GHG inventory of acommon WWTP in Sri Lanka. This inventory spans one year and includes emissions from direct and indirect sources, such as energy consumption, employee commuting, and wastewater treatment processes. Notably, the plant has no GHG removal processes. To carry out this assessment, the study relied on the Intergovernmental Panel on Climate Change (IPCC) guidelines published in 2006 and the GHG protocol. The IPCC guidelines provide a standardized methodology for estimating GHG emissions and removals. On the other hand, the GHG protocol provides a set of guidelines and tools for businesses and organizations to measure and manage their GHG emissions.

The top-down approach and the bottom-up are two types of approaches used in collecting activity data. Top-down inventories involve gathering information on a large scale, where data is collected and analyzed by national or international agencies or offices.

This method involves compiling data from multiple sources, such as governmental statistics, reports, and surveys. For example, utilizing default values from IPCC guidelines for GHG inventories and emission factors from reports and other sources belong to this category. On the other hand, bottom-up inventories typically gather and consolidate data from localized sources, such as utility bills or other locally provided information. In contrast to the top-down inventory approach, which relies on aggregated data from national and international sources, the bottom-up approach focuses on collecting and analyzing detailed data from a specific region or population. For example, collecting data for energy consumption from electricity bills belongs to this approach. The IPCC also recommends using a hybrid approach that combines elements of both top-down and bottom-up approaches to estimate GHG emissions and removals.

In this study, energy and waste were the two sectors considered for preparing the GHG inventory, among the five sectors mentioned in the IPCC guidelines for national GHG inventories. Based on the GHG compiled inventory, it is clear that a total of 1065.20 tCO_2e (carbon dioxide equivalent) has been emitted for the year. It is evident that Scope 2 emissions (The World Resources Institute has developed scopes of emissions: Scope 1, Scope 2, and Scope 3 to help organizations understand and categorize their emissions sources) had a significant impact on the overall GHG emissions and in terms of the total GHG emissions, Scope 1 emissions have contributed the most, followed by Scope 2 emissions, while Scope 3 emissions have made a minimal contribution.

Research findings

The results indicate that the WWTP has a significant GHG emission, with an average annual CO_2e emission of 1065.21 tons. The major contributors to these emissions were purchased electricity and biological treatment processes. The study suggests various strategies for reducing GHG emissions, including implementing energy efficiency measures, reusing treated wastewater, utilizing sludge for fertilizer manufacturing, and enhancing wastewater treatment processes. These findings hold the potential for informing the development of mitigation strategies aimed at reducing GHG emissions from WWTPs in similar contexts.

A SWOT analysis was carried out for the study, revealing significant practical implications for the future design and operation of centralized WWTPs. The GHG inventory provided a comprehensive understanding of emissions from the plant, offering several key benefits. Firstly, the establishment of a baseline for emissions and progress tracking towards emission reduction goals provided a roadmap for effective emissions management. This facilitated the implementation of strategies to reduce GHG emissions from the plant. Moreover, the identification of significant sources of emissions through the GHG inventory informed future design and operation decisions, highlighting areas where targeted improvements could positively impact emission reduction efforts. This approach can lead to a more efficient and environmentally friendly plant operation, critical for meeting sustainability targets.

Additionally, the GHG inventory provided the opportunity for cost savings by identifying inefficiencies and areas for improvement. This can help reduce operational costs and improve the financial stability of the plant, providing significant benefits in the long run. Accurately quantifying GHG emissions from a WWTP may require extensive data collection and analysis, which can be time-consuming and expensive, especially if specialized expertise or equipment is needed. The process of quantifying GHG emissions is crucial, and it requires an expert to avoid inaccurate quantification, which could lead to incorrect conclusions and recommendations. However, despite the best efforts, the GHG inventory may not capture all emission sources due to a lack of data or clear methodologies for quantification, resulting in an incomplete understanding of the plant's GHG emissions. Conducting a GHG inventory can lead to the implementation of GHG reduction strategies that have the potential to improve plant efficiency and reduce operating costs. Implementing these strategies can help the plant reduce its carbon footprint, generating positive publicity and increasing stakeholder engagement in sustainability initiatives.

Additionally, the results of the GHG inventory can contribute to the development of policies and regulations concerning GHG emissions from WWTPs. However, implementing GHG reduction strategies may require significant capital investments or operational changes, such as installing energy-efficient equipment or altering treatment processes, posing a risk to the plant's financial stability or operational capacity. Moreover, if the GHG inventory reveals high emissions, the plant's sustainability efforts may be viewed negatively by stakeholders and the public, potentially leading to reputational harm.

In summary, the study emphasizes the importance of not only reusing treated water to reduce the demand for freshwater resources but also quantifying GHG emissions through treated wastewater discharge, thereby, reducing GHG emissions through such pathways. The selection of the best options will depend on factors such as environmental, social, and economic feasibility. As the global community strives to mitigate climate change and achieve sustainable development goals, understanding and mitigating GHG emissions from WWTPs emerge as critical imperatives. By clarifying the intricate nexus between WWTPs and GHG emissions, this research aims to direct policy formulation, and technological innovations towards a more sustainable and resilient future.

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Trait-Based Approaches to Understanding Plant Community Assembly in Response to Climate Change

Organisms do not live in isolation; rather, they are interconnected with each other and their surrounding environment. In a broad sense, the environment, inclusive of the organisms themselves, constitutes an ecosystem. An ecosystem is a geographic area where plants, animals, other organisms, weather, and landscapes collaborate to create a web of life. The subdiscipline of ecology known as "plant ecology" is devoted to studying plant interactions, abundance, and distribution within ecosystems. It explores how environmental conditions affect plant survival, abundance, community dynamics, and the interactions plants have with other creatures. Plant community assembly is a critical component of ecology, as it controls the composition and operation of ecosystems. Environmental filtering (EF), biological interactions, and stochastic processes such as dispersal filtering (DF) are some of the elements that influence the community assembly process.

Random occurrences and chance play a significant role in forming communities, whereas niche-based processes such as DF emphasize the influence of environmental conditions on species distribution and abundance.

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Knowing the functional traits of species and their interactions with their environment is facilitated by trait-based techniques, which have become essential tools in the field of plant ecology. These methods enable the identification of important characteristics influencing community assembly and the prediction of species responses to environmental changes. Ecophysiological trait trade-offs play a crucial role in establishing niche differences and determining species fitness. These traits have been studied by applying trait-based techniques to analyze the functional responses of tree species to ongoing climate change.

Climate change dramatically impacts plant communities, leading to modifications in biomass dynamics and trait spectrum in old-growth forests. By demonstrating how variations in several traits are arranged along resource acquisition trade-offs and emphasizing the significance of wood density in determining species survival, tolerance, and defense mechanisms under various environmental conditions, trait-based approaches can aid in explaining these changes.

In summary, trait-based techniques offer essential insights into the functional traits of species and their reactions to environmental changes. Niche-based and stochastic elements together drive the complicated process of plant community formation. Understanding community assembly and the effects of climate change on plant communities is essential for forecasting and controlling ecological responses to climatic changes.

Theoretical framework of trait-based ecology

Plant functional characteristics include any morphological, physiological, or phenological variables that indirectly impact plant fitness by influencing the three main aspects of plant performance: growth, reproduction, and survival. These functional characteristics were first categorized into "soft" and "hard" traits by Hodgson and coworkers. "Soft" traits, such as particular leaf area, leaf water content, dry mass, plant height, relative length of root, seed quantity, or mass, were identified as less expensive and more accessible measures for the function of interest. Conversely, "hard" traits, such as photosynthesis, respiration, transpiration, growth rates, plant water potential, water usage efficiency, and stomata conductance, were considered to reflect the function of interest but were either expensive or difficult to measure.

In plant ecological studies, trait-based approaches are widely used to understand how individual species interact with their environment and with each other. The primary focus lies on elucidating the interplay between natural processes, niche-based environmental filtering, and niche-based species sorting in an interactive context. The importance of floral features in community assembly processes at high altitudes has been investigated using trait-based methodologies, revealing that floral traits play a significant role in plant community assembly (Figure 1). These methods can also aid in enhancing the assessment of community assembly reactions to environmental changes and identifying non-random patterns.

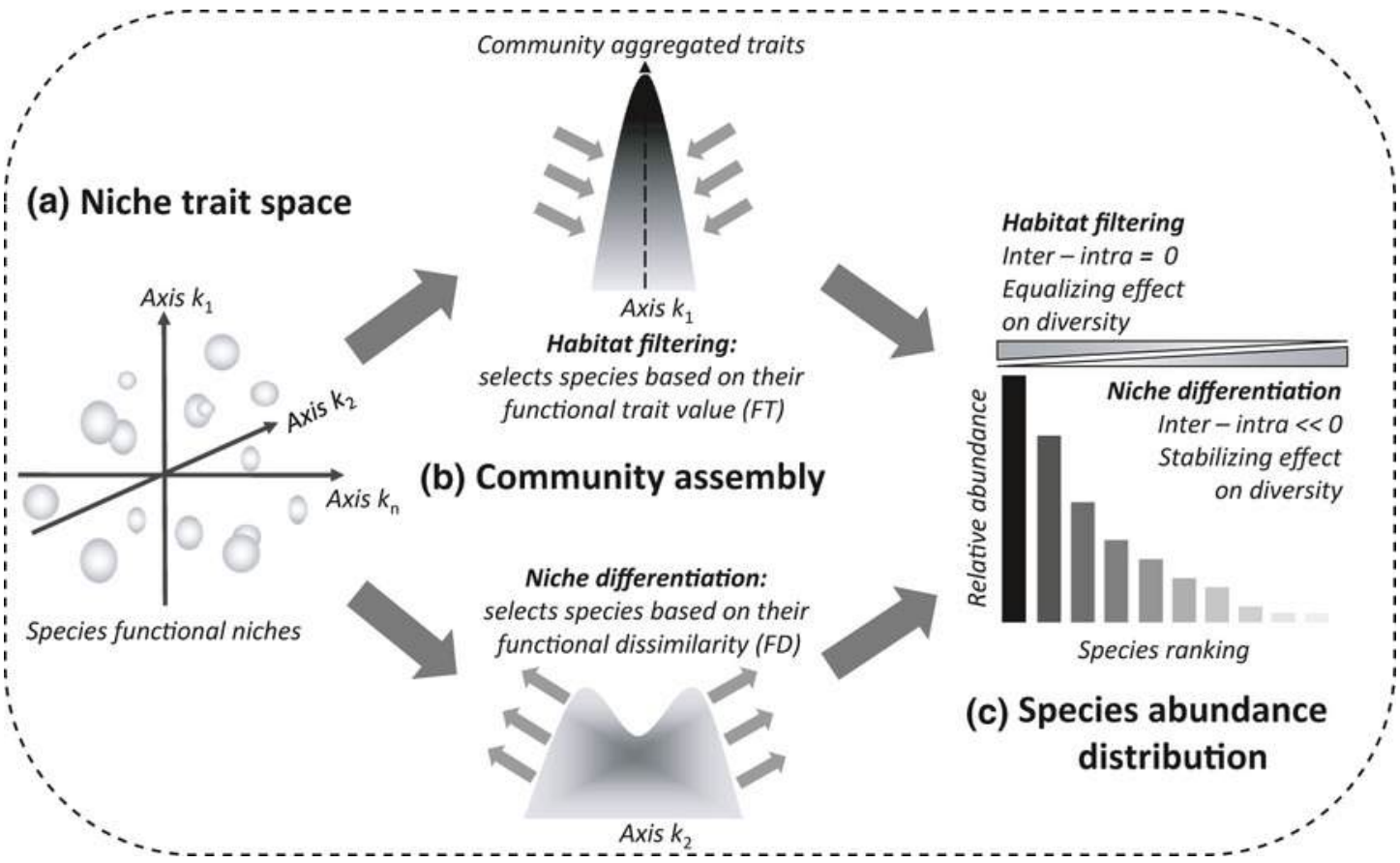

Figure 1 Predicting species abundance from plant functional traits: a conceptual model highlighting the importance of niche differentiation (ND) and habitat filtering (HF) in competitive communities. Source: Maire et al (2012)

Recent advancements in the modeling of trait-based plant community assembly have led to the development of new models predicting the relative abundance of species from a regional species pool. Using these models can enhance our knowledge of community assembly processes and their influence on how plants respond to their environment.

Methods in trait-based ecology

Functional characteristics are essential to reflect plant strategies for resource acquisition, competition, and stress tolerance. These characteristics inform us how plants interact with other species and their environment, forming their ecological strategy and responses to different environmental conditions.

Resource acquisition: Specific leaf area (SLA), leaf nitrogen content (LNC), and leaf dry matter content (LDMC) are functional parameters that indicate how plants maximize the efficiency of their utilization of resources. In resource-rich environments, plants can optimize photosynthesis and growth by adopting a rapid resource acquisition strategy, leading to increased SLA and LNC. These characteristics enable plants to effectively compete for resources in their surroundings and adapt to changes in the availability of resources (Figure 2).

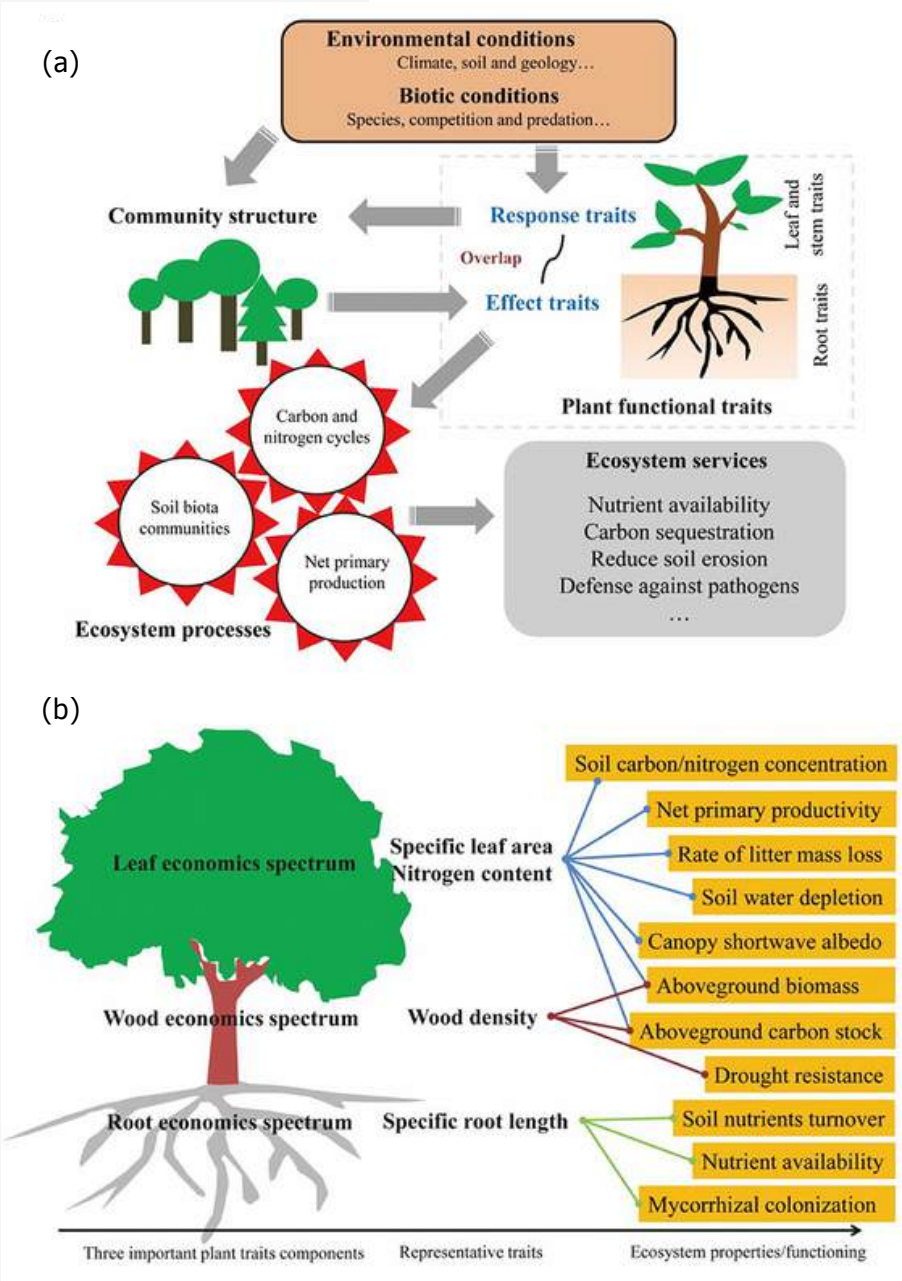

Figure 2 How plant functional traits determine ecosystem functioning (a) and some specific examples (b) Source: Liu et al (2021)

Competition: A plant's capacity to compete within a community is influenced by characteristics related to competition, such as plant height and root length. A plant's capacity to obtain resources below ground and outcompete other species can be influenced by specific root characteristics. In contrast, taller plants may have a competitive edge when securing light. A plant's strategy for prevailing in resource competition scenarios is reflected in its functional features that enhance competitiveness.

Stress tolerance: A plant's capacity to endure environmental stresses such as drought, high temperatures, or nutrient shortages is indicated by functional features associated with stress tolerance, such as LDMC and leaf area (LA). Plants with higher LDMC and lower SLA are often better suited to withstand stressful situations because they conserve resources and reduce water loss through transpiration. These characteristics demonstrate how a plant survives and thrives in harsh conditions.

Functional traits provide insights into plant strategies for resource acquisition, competition, and stress tolerance. Researchers can gain valuable insights into how plants compete for resources, adapt to their environment, and cope with stress by examining these characteristics. This information contributes to shaping the ecological strategies and community dynamics of plants.

Climate change and plant community dynamics

Plant communities are significantly impacted by climate change, which can result in changed species interactions, phenological changes, and range shifts of certain species. Rising global temperatures, changing precipitation patterns, and a notable rise in extreme weather events such as storms, cyclones, floods, fires, and drought all contribute to these changes. Trait-based evaluations of plant community responses to climate change have been established through case studies. For instance, a survey of the feedback between plants and soil revealed that the effects of climate change on these interactions would affect the carbon cycle and may even cause the plant-soil feedback to decouple during range shifts. Additionally, research on plant communities in the New World suggests that species distributions are changing due to climate change, leading to changes in the composition of plant communities.

Functional characteristics play a crucial role in mediating plant responses to the stresses induced by climate change. We may connect processes seen in individual plants to the dynamics of plant populations, species distribution patterns, and ecosystem functioning through functional traits. Insights into how plants adapt to their environment, compete for resources, and cope with environmental challenges can be gained from traits such as leaf, root, and reproductive traits, which represent methods for resource acquisition, competition, and stress tolerance. However, the measurement of functional traits requires considerable time and resources, and there is often a limited amount of trait data available for specific species or ecosystems. These drawbacks make trait-based approaches less effective in assessing community assembly responses to environmental changes and detecting non-random patterns.

Challenges and future directions

A significant obstacle in the study of trait-based ecology is trait plasticity, which can cause variations within species and influence the relationship between functional traits and environmental factors. This makes it more challenging to identify the underlying mechanisms guiding community assembly and ecosystem functioning. Another issue is the scaling problem, where functional traits may vary between spatial and temporal scales, making it challenging to generalize patterns and correlations with external influences.

Additionally, the availability of data presents a substantial constraint because the absence of comprehensive and standardized trait databases can impede the creation of trait-based models and the capacity to compare functional features across species and ecosystems. Future directions for trait-based research in understanding plant community responses to climate change involve incorporating genetic data to understand the underlying mechanisms driving functional trait variation and evolution. Genetic data provide insights into the genetic basis of functional traits and their responses to environmental changes. Additionally, integrating multi-trait analyses can enhance our understanding of the complex relationships between functional traits and environmental factors. Such analyses can offer insights into the trade-offs and synergies between functional traits and their role in community assembly and ecosystem functioning.

With a changing climate, trait-based approaches hold great promise for guiding conservation and ecosystem management initiatives. These techniques offer insights into the mechanisms behind community assembly and ecosystem functioning by comprehending the intricate interactions between species and their environment. Such insights are vital for the effective management of ecosystems and conservation planning. Trait-based methods also enable the prediction of how ecosystems will respond to changes in their environment, which can aid in the development of management plans aimed at mitigating the effects of climate change on plant communities and ecosystems.

Trait-based techniques are essential for understanding how plant communities respond to climate change and gaining insight into how different species react to environmental changes. By integrating genetic data, multi-trait studies, and extensive trait databases, we can enhance our understanding of the dynamics of plant communities and guide efficient ecosystem management tactics. In order to understand plant ecology in a changing world and ensure sustainable conservation and management methods for our ecosystems, interdisciplinary collaboration and comprehensive approaches are essential.

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The
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Epiphany,
What DNA
Can be;
=
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===== You are the bearer
Of viral DNA, as from
Cap to the nadir,
Are rippling cascades.
You lift Mendel's pea,
You craft Mullis's tea,
You draw Curie's tree.
Opuses of evolution,
RNA viruses to whales,
Barcoded only by thee.
Polymerase to bases, a
Polymath to chemistry,
Filled like Dolly's ovum.
To entrust a daydream,
As a genius and genie
Make a virus palpable
To unambiguity. Balmy
& wonky ballroom you
Are, a beret on, mixed
With salts and buffers,
And dancing the feet
To a lively, snappy jive.
DNA multiply in you.
A viral heirloom within
A chamber, catalyzing
Company into crowds.
Inside you, remains the
Journey to serendipity,
To amplify a locus,
For a fortnight,
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lony.

Dr. Dilantha Gunawardana
M. I. Biol. (Sri Lanka)
Smart Media

NATURE CAPTURES

Poecilotheria ornate (Fringed ornamental/Ornate tiger spider)
IUCN Red List status: Endangered

Poecilotheria ornata, commonly known as the fringed ornamental or ornate tiger spider, is a notable arboreal tarantula endemic to Sri Lanka. This species exhibits remarkable characteristics in morphology, behaviour, and venom composition. With a legspan potentially reaching up to 25 cm in females, *P. ornata* ranks among the largest members of its genus, second only to *P. rufilata*. Detailed descriptions of both female and male individuals highlight distinct colourations and markings. Females exhibit greenish-yellow or purplish tinges dorsally, while males are generally greenish-brown with less prominent markings. Behavioural observations indicate that *P. ornata* constructs asymmetric funnel webs in tree holes to capture flying insects, its primary prey. Remarkably, it may engage in a mutualistic relationship with frogs especially with *Uperodon nagaoi*, sharing tree holes and potentially offering protection from predators.

While *P. ornata* bites are not typically fatal, they are considered medically significant, causing intense pain and muscle cramping. Understanding the intricate biology and ecological interactions of *P. ornata* contributes to both scientific knowledge and conservation efforts aimed at preserving this fascinating species and its habitat.

Photographs by

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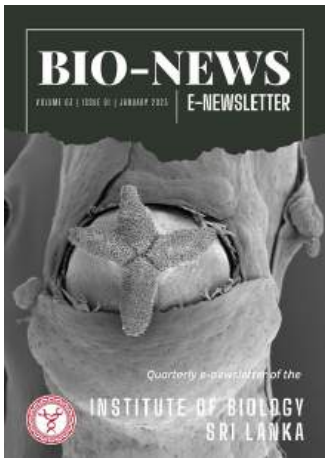

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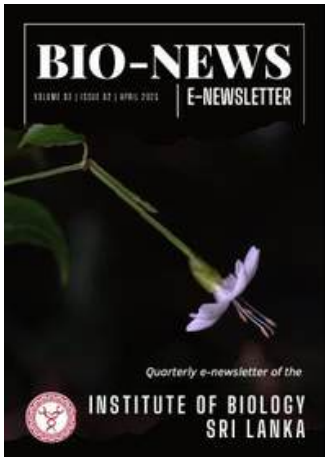

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