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COVER STORY

The Sri Lanka Frogmouth (B*atrachostomus moniliger*), found in the dense forests of Sri Lanka and the Western Ghats, is a master of camouflage, often returning to the same roost for months. Its nest, a mossy pad lined with down and disguised with lichens and bark, cradles a single chick whose wide-mouthed, eager expression captures a moment of pure, animated curiosity. This rare sighting from Sinharaja highlights both the bird’s extraordinary adaptation and the hidden wonders of our forests.

Photograph by Vimukthi R. Gunasekara
Department of Zoology and Environment Sciences
Faculty of Science, University of Colombo

BIO-NEWS

CONTENTS

IOBSL COUNCIL - 2024/2025

Standing (Left to Right): Dr. V. K. Fernando (Treasurer), Dr. S. Ediriweera (Council Member), Dr. P. K. C. B. Wijerathna (Council Member), Dr. A. M. Wickramasuriya (Editor), Prof. Hiran Amarasekera (Secretary for International Relations), Dr. K. G. S. U. Ariyawansa (Council Member), Dr. P. Dharmasena (Council Member), Dr. I. U. Kariyawasam (Council Member), Dr. D. Dayananda (Assistant Editor), Mr. K. M. S. Ruvinda (Assistant Treasurer)

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Absent: Dr. W. M. T. P. Ariyarathne (Council Member)

IOBSL NEWS AND EVENTS

Sri Lankan Biology Olympiad 2024

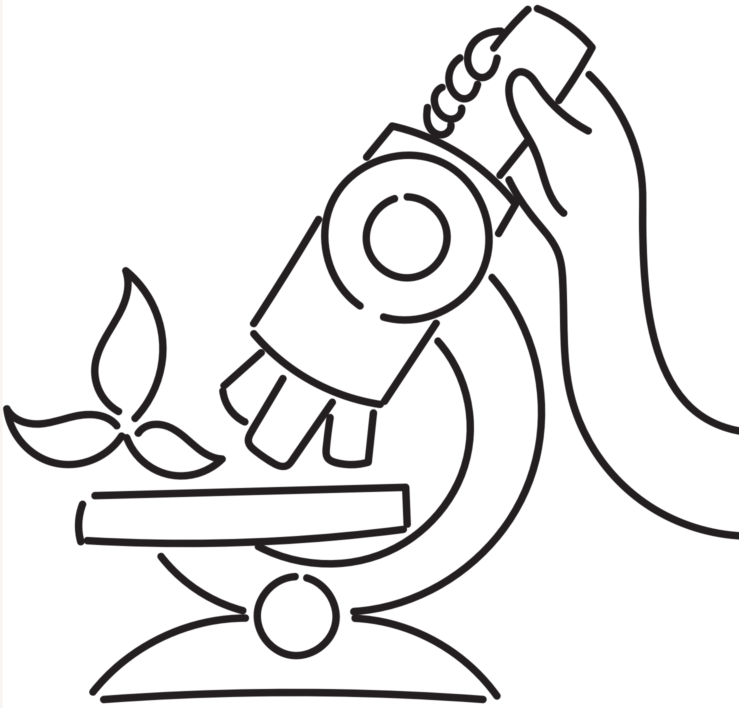
The Sri Lankan Biology Olympiad 2024 was successfully held on November 3, 2024, recognizing the brightest young minds in biology. Jathukeshan Saieswaran (S. Thomas' College, Mount Lavinia) and K.A.D.I. Pulasthi Gajaba Wijerathna (Ananda College, Colombo) emerged as the top achievers in the Gold Medal category.

This year, a total of 13 Gold Medals, 16 Silver Medals, 21 Bronze Medals, and 31 Merit Awards were awarded to outstanding performers.

The top 15 eligible candidates from the Gold and Silver Medal categories will participate in the second round of training for the International Biology Olympiad (IBO) 2025 selection. The prestigious IBO 2025 will be held from July 20–27, 2025, at Ateneo de Manila University, Philippines.

Congratulations to all the winners! Your dedication and hard work are truly commendable.

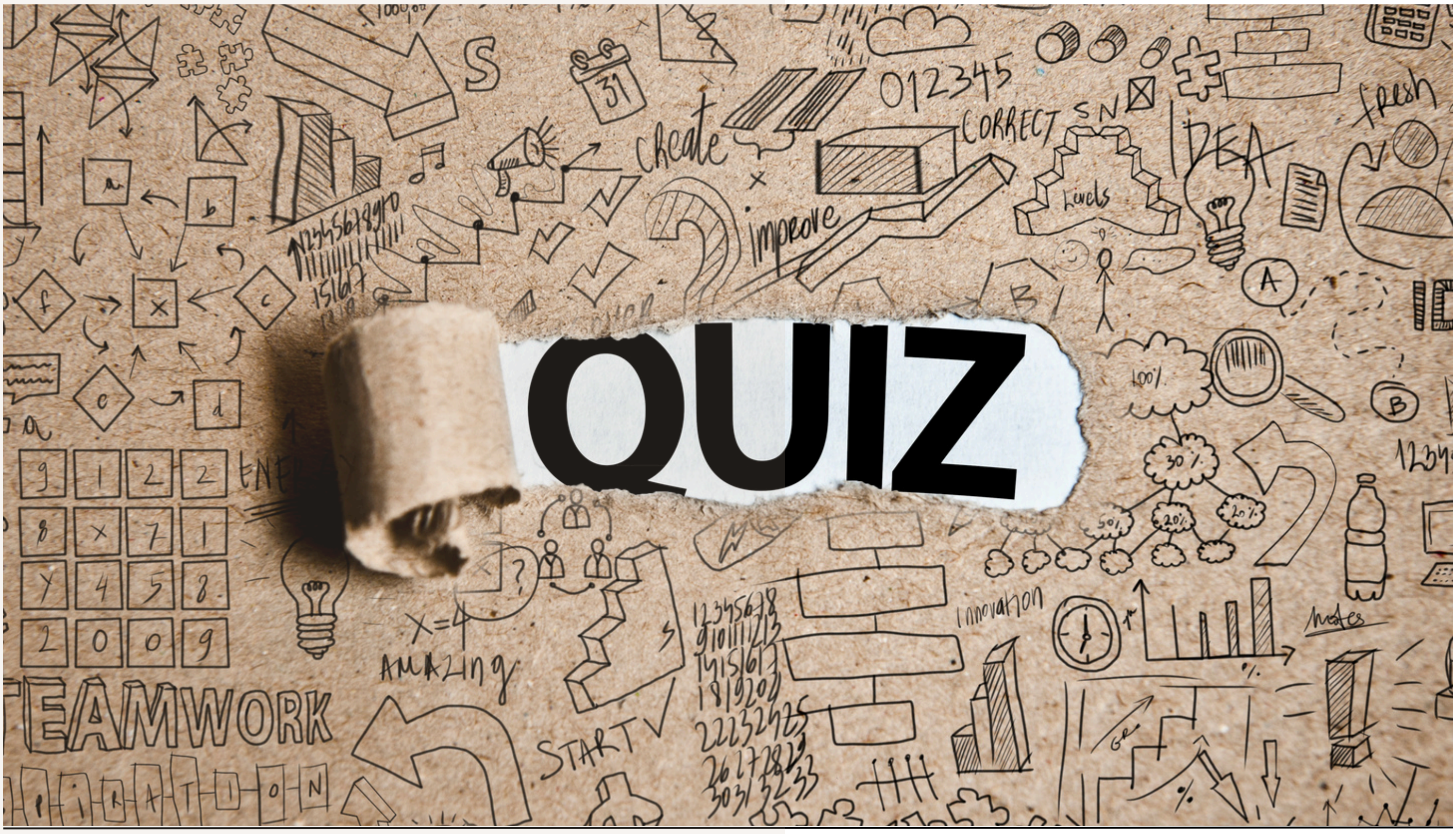
Inter-University Biology Quiz Competition 2025: A Platform for Future Biologists



The Inter-University Biology Quiz Competition, organized by the IOBSL, was held for the 8th consecutive year, continuing its tradition of fostering academic excellence among undergraduate students. This year's competition, open to students from state and UGC-approved universities, was conducted in two stages.

Stage I of the quiz took place online via the LMS platform on 3rd May 2025, with 38 enthusiastic undergraduates participating. Based on their performance, the top 10 scorers have been selected to advance to Stage II.

Stay tuned for further updates!



INSTITUTE OF BIOLOGY
SRI LANKA
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INTER-UNIVERSITY BIOLOGY CHALLENGE 2025

IOBSL is organizing a Biology Challenge Competition for interdisciplinary teams of undergraduates selected from state and non-state universities in Sri Lanka to develop an attractive and challenging proposal to nourish the IOBSL theme "Biological innovation for food security and sustainable green economy".

Eligibility
Undergraduates of State and Non-State Universities of Sri Lanka

Team composition
Four-member team consisting of students from different disciplines including one student from the discipline of biology

Structure of the Challenge
Submission of novel, feasible and cost-effective proposals and a presentation that nourishes the theme of IOBSL. Each team is expected to collaborate with an industrial partner or the Industry Liaison Centres of the University.

Awards
1st, 2nd and 3rd places will be awarded with certificates and Cash Prizes at the Annual Sesssions of IOBSL.

- **Deadline for Registration**
  1st of June 2025
- **Deadline for Submission**
  1st of July 2025
- **Notification of the winners**
  1st of August 2025

Click here for guidelines.
Register online - click here

Registration fee - Rs.1000/- per team
Please refer the guidelines for the account details.

For more information contact, E-mail: iobchallenge2025@gmail.com

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Dr. Chamika Wijerathna
University of Sri Jayewardenepura
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Applications Open for the Young Scientist Award 2025

The IOBSL is pleased to announce that applications are now open for the prestigious **Young Scientist Award 2025**. This award aims to recognize outstanding young biologists who have demonstrated excellence in research and made significant contributions to the advancement of the field of Biology in Sri Lanka.

Eligible candidates are encouraged to apply and showcase their scientific achievements and dedication to biological sciences. The award serves not only as a recognition of individual merit but also as a celebration of the potential and promise of the next generation of Sri Lankan biologists.

Apply now and be recognized for your contribution to the future of Biology!

For more information and application guidelines, please visit the official website of the IOBSL.

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Sri Lanka

YOUNG SCIENTIST AWARD 2025

APPLY BEFORE
31st July 2025

Aim:

- To recognize young biologists who excel in research and have contributed to the development of the field of Biology in Sri Lanka

Eligibility Criteria

- Applicants must be below 40 years of age by the closing date of the applications.
- The applicants will be evaluated on their contribution to 5 areas: research, innovation, grants, leadership and other contributions to the field of Biology.
- This is a lifetime award and will not be awarded to previous winners.

For Further Details:

Visit Our Website

Application Form

The winner will be awarded a medal at the inauguration ceremony of the 45th annual sessions of the Institute of Biology Sri Lanaka.

Call for Abstracts – 45th Annual Sessions of the Institute of Biology, Sri Lanka

The IOBSL is pleased to announce that its 45th Annual Sessions will be held on **26th September 2025.** IOBSL members are now invited to submit abstracts under the timely and impactful theme: **“Biological Innovation for Food Security and Sustainable Green Economy.”**

Abstracts are welcomed under the following four thematic tracks:

- Zoology and Environmental Sciences
- Plant Sciences and Agriculture
- Molecular Biology and Biotechnology
- Microbiology and Chemical Biology

INSTITUTE OF BIOLOGY, SRI LANKA (IOBSL)
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45TH ANNUAL SESSIONS
2025

CALL FOR ABSTRACTS

SUBMISSION DEADLINE
22ND JUNE 2025

BIOLOGICAL INNOVATION
FOR FOOD SECURITY AND
SUSTAINABLE GREEN ECONOMY

SUB THEMES

- ✓ Zoology and Environment Sciences
- ✓ Plant Sciences and Agriculture
- ✓ Molecular Biology and Biotechnology
- ✓ Microbiology and Chemical Biology

Submission Link
https://forms.gle/Q67E3hsuUiHRJgbCA

More Information : https://www.iobsl.org/

Don’t miss this opportunity to showcase your research and contribute to shaping the future of biology in Sri Lanka.

For abstract guidelines and submission details, please visit the IOBSL website.

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

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

Y Chromosome Is Disappearing: Can Men Live Without The Y Chromosome?

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Introduction: a shrinking Y chromosome with a big role

According to popular self-help books, men and women exhibit distinct differences as if they hail from different planets, but what separates them are radically different chromosomes.

Sex determination systems exhibit extraordinary diversity and versatility throughout the tree of life. While the sex of most animals is determined by sex chromosomes at the time of fertilization, the sex of most turtles and all species of crocodilians is determined by environmental cues such as temperature. However, in humans and other mammals, primary sex determination is by chromosomal configuration; females have two X chromosomes (XX), while males possess one X and Y chromosome (XY).

The X chromosome is a genetic powerhouse containing about 900 genes, while the Y chromosome is diminutive, carrying only about 55 genes. Despite its small size, this tiny chromosome plays a vital role in determining male sex by triggering the development of the testis in an embryo.

Even if this vital chromosome is evolutionarily robust, however paradoxically, it is in steady decline. Nearly 97% of its ancestral genes have been lost during the last 180 million years. If this deterioration keeps up at its current rate, the human Y chromosome may disappear in around 4.6 million years, potentially leading to extinction, which will have profound impacts on reproduction and the survival of the male sex in mammals.

Origin of sex chromosomes: a tale of divergence

The origin and evolution of sex chromosomes have been interesting to many scientists. Sex chromosomes evolved from a pair of ordinary autosomes approximately 180 million years ago. Increasing investment in one sex role while decreasing in the other might cause gonochorism to evolve from hermaphroditism gradually. Alternatively, sex-role sterility mutations can cause gonochorism to evolve quickly, ultimately leading to the creation of sex chromosomes. Since the mutations are not anticipated to occur simultaneously, it is anticipated that the transition will involve a brief condition of androdioecy or gynodioecy. Without recombination to repair mutations, genes on the Y began to degrade through a process known as Muller’s ratchet. Over millennia, the Y shrank, retaining only a few essential genes related to testis development and sperm production. An XY sex chromosomal system develops if the initial mutation is a dominant female-sterility mutation followed by a recessive male-sterility mutation; a ZW system is produced by the opposite combination of mutations. Thus, interestingly, this degeneration is not uniform across species. Some animals, like birds and snakes, use this ZW sex-determination system where females are the heterogametic sex, and their W chromosomes are also degenerative, but many have stabilized.

Establishment of sexual phenotypes in humans

In 1959 scientists identified the region of the Y chromosome that determines sex. It was found that a gene on the Y chromosome known as the sex-determining region of the Y, or Sex-determining Region of the Y chromosome (SRY), was the key regulator of sex determination. The mere presence of this region is sufficient for sex determination. The *SRY*, which serves as a master switch for testis development, was discovered, marking a significant advancement.

This *SRY* gene encodes a unique transcription factor that activates a testis-forming pathway at about week seven of embryonic development. The early undifferentiated embryo has two systems of ducts, Wolffian and Müllerian ducts, which can be developed into the male and female reproductive tracts, respectively. In the presence of the SRY gene, the indifferent gonad develops into a testis. The testis begins producing two hormones, testosterone and anti-Müllerian hormone, or AMH. Testosterone and one of its derivatives, dihydrotestosterone, induce the formation of other organs in the male reproductive system, while AMH causes the degeneration of the Müllerian duct. In females, who do not contain the SRY protein, the ovary-forming pathway is activated by a different set of proteins. The fully developed ovary then produces estrogen, which triggers the development of the uterus, oviducts, and cervix from the Müllerian duct.

Shrinking of Y chromosome

For many years, scientists have been captivated and perplexed by the long-term evolutionary decline of the human Y chromosome. The Y chromosome stays mostly isolated throughout meiosis, in contrast to other chromosomes that recombine during this process, enabling them to repair and rearrange genetic information. Except for two little pseudoautosomal areas, it does not recombine with the X chromosome for the majority of its length. This absence of recombination shields the Y from potentially hazardous interactions with the X chromosome, but it also makes the Y more susceptible to the buildup of mutations and the eventual erasure of genes.

Just roughly 55 of the 1,438 genes that were once thought to be shared with the X chromosome are still present in the current human Y. These genes that have been kept are by no means redundant, even with this drastic reduction. The majority are necessary for the development of the testis, spermatogenesis, and transcriptional regulation processes that are vital for sex differentiation and male fertility. It is interesting to note that although the Y chromosome's story has frequently been presented as one of decline and imminent extinction, new research suggests that this genetic deterioration may have reached a plateau. The existence of extensive palindromic sequences in the male-specific region of the Y chromosome (MSY) is one of the main characteristics that has contributed to this stability.

One arm of a palindrome can be used as a template to fix mutations in its mirror copy, a rare but significant process known as intrachromosomal gene conversion. The integrity of the Y chromosome's remaining genes may be preserved by this intrinsic self-healing mechanism, which is specific to the chromosome. Therefore, the Y chromosome seems to have evolved an evolutionary strategy to preserve the core genes necessary for male life and reproduction, even though it has lost the majority of its ancestral genes.

The Y chromosome differs significantly from other human chromosomes in terms of structure. Heterochromatin, satellite DNA, retrotransposons, and repetitive elements are all closely spaced throughout it. The Y is particularly difficult to examine using conventional sequencing techniques because of these repeated and tightly coiled sections. This intricacy made the Y chromosome one of the human genome's least well-characterized for many years. The last significant step in the thorough mapping of all human chromosomes was not reached until 2022, when scientists from the Telomere-to-Telomere (T2T) Consortium successfully published the first complete and gapless sequence of the Y chromosome. The mechanisms underlying Y chromosome degradation, population genetics, and Y-linked disorders can now be better understood thanks to this discovery.

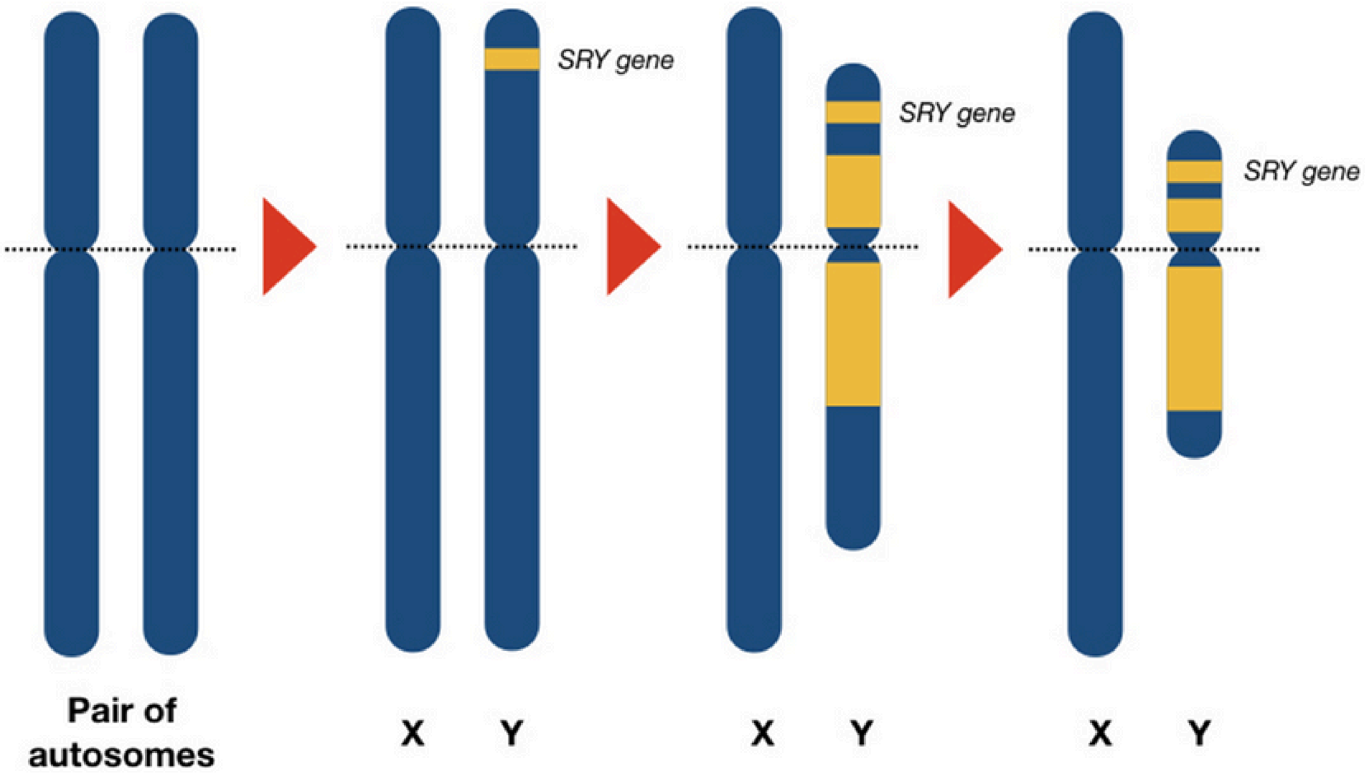

Figure 1 Evolution of the Y chromosome from the autosomes
Source: https://karyotypinghub.com/is-the-y-chromosome-really-disappearing-lets-findout-a-scientific-answer/

Sex determination in the future

While the human Y chromosome is unique in its trajectory, it is not alone in its evolutionary challenges. Interestingly, other mammals have already navigated this genetic crisis. Two rodent species, the Japanese spiny rat (*Tokudaia* sp.) and the mole vole (*Ellobius* sp.) have entirely lost their Y chromosomes and continue. These examples suggest that the disappearance of the Y chromosome may not spell extinction, but rather survival. However, the development of novel sex-determining genes found on other chromosomes has allowed these species to persist and procreate.

Researchers have already identified a duplicated region near the SRY-box transcription factor 9 (*SOX9*) gene, a key player in sex development, that seems to act as a new sex-determining gene. Thus, it will replace the need for SRY.

When combined, these results cast doubt on the notion that the Y chromosome is doomed. It has had significant gene loss in the past, yet stability and some evolutionary innovation are characteristics of its present. In this sense, the Y chromosome's tale is one of resilience and change rather than just degradation. Instead of being a chromosome in crisis, it might really be a chromosome in evolutionary transition, losing old genes to make room for a future characterized by creativity and flexibility rather than frailty.

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The Ocean's Hidden Treasure: Pigmented Bacteria Isolated from Marine Algae as a New Source of Antioxidants and UV Protection

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Marine ecosystems cover approximately 71% of the planet and support nearly 80% of global biodiversity. Marine microbes represent over 95% of the total marine biomass, with bacterial densities reaching up to one billion cells per litre of seawater. However, regardless of their ecological significance, the diversity and taxonomic characterisation of marine bacteria remain largely underexplored. Among these microbial communities, planktonic bacteria, including cyanobacteria and eubacteria, reveal diverse ecological interactions, with some species forming close associations with eukaryotic hosts, such as marine macroalgae commonly known as seaweed. In recent years, there has been an emerging interest in studying these symbiotic relationships, particularly within the substructure of the seaweed-bacteria holobiont concept. This concept unfolds the functional integration between seaweed and its associated phycoplane bacteria, collectively fostering a dynamic biological unit that contributes to macroalgal health, physiology, and resilience. Sri Lanka, an island nation situated in the Indian Ocean, hosts a rich diversity of marine macroalgae (Figures 1a and 1b). However, despite this extensive biodiversity, much of its marine microbial diversity remains unexplored.

Marine algae-bacterial interaction

The phycoplane, consisting of all exposed seaweed surfaces, serves as a dynamic interface for marine algal-bacterial interactions, where algae secrete exudates to captivate beneficial microbiota, including pigmented bacteria (Figure 1c), which reciprocate by inducing algal growth, development, and survival. These interactions are open-specific, as seen in the morphogenesis stimulation of *Monostroma oxyspermum* by *Cytophaga*, *Flavobacterium*, and Bacteroides and the association between diatoms and proteobacteria (*Roseobacter* sp., *Sulfitobacter* sp.) and Bacteroidetes (*Cytophaga* sp., *Flavobacterium* sp.).

These interactions can be categorized into three main types: nutrient exchange, signal transduction, and gene transfer. In nutrient exchange, algae liberate dissolved organic carbon (DOC), which phycoplane-associated bacteria (PAB) assimilate while producing essential compounds like vitamin B12, phytohormones, and siderophores. In signal transduction, algae have the potential to produce chemicals that regulate bacterial quorum sensing and biofilm formation, while some bacteria, such as those from *Shewanella*, *Streptomyces*, and *Bacillus*, secrete algicidal metabolites affecting algal growth. Horizontal gene transfer has also been detected, as evidenced by bacterial-origin genes in *Seminavis robusta* chloroplasts and Dinoflagellate minicircle genomes.

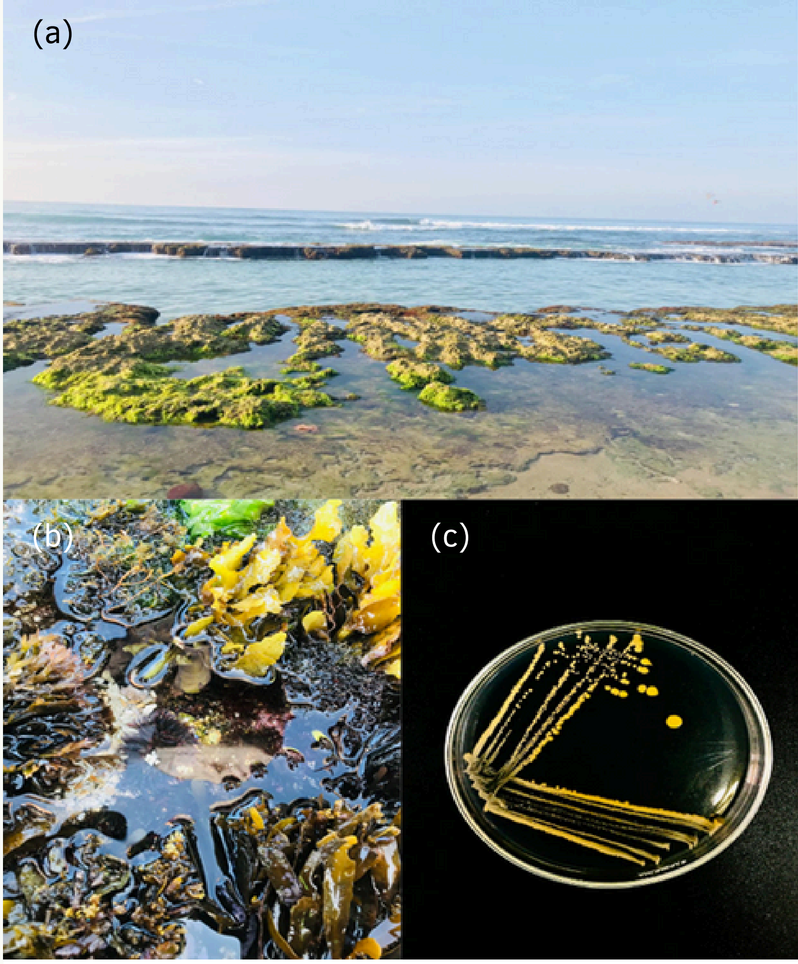

Figure 1 (a) Coastal ecosystem at Thalpe Beach, Sri Lanka; (b) Close-up view of weeds and seaweeds at Thalpe; (c) Yellow pigment-producing bacteria isolated from *Padina minor yamada*.

These interactions, classified into mutualism, commensalism, or parasitism, emphasize that PAB and algae often function as holobionts to tolerate harsh conditions and pathogen attacks. Quorum sensing (QS) further mediates interspecies communication through autoinducers like N-acyl-homoserine lactone (AHL) and 2-alkyl-4-quinolone (AQ), triggering gene expression based on signal thresholds. The diversity and composition of the phycoplane community are determined by internal factors such as oxygen levels, exudates, oxidative stress, antifouling agents, and attachment mechanisms like MSHA-pili and curli-protein fibres (*Pseudomonas tunicata* attachment to *Ulva lactuca*), as well as external factors like light, temperature, salinity, and interactions with fungi and viruses. Ultimately, bioactive compounds, signaling molecules, and other metabolites within the phycoplane and ambient microenvironment serve as significant mediators of these complex algal-bacterial interactions.

Antioxidant properties of marine bacterial pigments

Reactive oxygen species (ROS), such as hydrogen peroxide (HOOH), superoxide (O_2^-), and hydroxyl radicals (HO·), are highly activated molecules produced by cellular metabolism and external environmental factors like UV radiation, temperature, and pollutants, leading to oxidative stress in marine organisms. In cellular signaling, biofilm formation, and defensive mechanisms; the excessive production of ROS can be resulted in oxidative stress, and the destruction of DNA, proteins, lipids, and other biomolecules, ultimately affecting marine organism's growth, reproduction, immunity, and overall survival. To counteract with the oxidative stress, marine organisms employ enzymatic (e.g., catalases, superoxide dismutase, glutathione peroxidase) and non-enzymatic (e.g., vitamins, minerals, phenolic metabolites, and bacterial pigments like carotenoids and melanin) antioxidant mechanisms. Interestingly, bacterial pigments neutralize free radicals by donating electrons, breaking oxidative chain reactions, and chelating metal ions such as lead, iron, and copper to prevent free radical formation. Additionally, carotenoids scavenge singlet oxygen, further enhancing antioxidative protection.

UV-protective potential of marine bacterial pigments

Bacterial pigments, as secondary metabolites, play a significant role in UV protection through various mechanisms. The UV protection mechanisms of these pigments primarily rely on their ability to absorb UV radiation and dissipate the absorbed energy as heat, preventing ROS formation and cellular damage. The major UV-blocking pigments include melanins, mycosporines, scytonemin, and carotenoids, along with prodigiosin and violacein, which also exhibit photo-protective properties. Melanins, heteropolymeric pigments formed via tyrosine metabolism, not only protect against UV radiation but also aid in stress tolerance and biofilm formation. Mycosporines, with their unique chromophore structures, function as UV-absorbing molecules while also serving as antioxidants and thermal protectants. Scytonemin, a yellow-brown pigment found in cyanobacteria, absorbs UV radiation and exhibits anti-inflammatory and anti-proliferative properties.

Carotenoids, derived from isoprenoid pathways, contribute to photoprotection while also possessing antioxidant, anti-inflammatory, and anti-cancer properties.

The biosynthesis of these pigments involves various metabolic pathways, including tyrosine metabolism for melanins, the shikimate pathway for mycosporines, aromatic amino acid biosynthesis for scytonemin, the melvonate and methylerythritol 4-phosphate pathways for carotenoids, and specific gene clusters for prodigiosin and violacein.

Biotechnological and industrial applications of bacterial pigments

Bacterial pigments have significant biotechnological applications, particularly in skin care and sunscreen formulations due to their UV-blocking properties. Pigments such as violacein and prodigiosin have shown promising UV-blocking potential when used as additives in commercial sunscreens, while melanin is a strong candidate as a direct active sunscreen ingredient. Given the harmful effects of synthetic UV filters such as endocrine disruption, allergenic reactions, cytotoxicity, and negative impacts on marine ecosystems, naturally derived, biodegradable, and non-toxic bacterial pigments present sustainable alternatives as UV filters. Beyond sun protection, bacterial pigments hold significant therapeutic potential due to their antioxidant, antimicrobial, anticancer, cytotoxicity, anti-obesity, anti-inflammatory, and wound-healing properties, and they have further applications in drug delivery, photothermal therapy (PTT), photodynamic therapy (PDT), and photoacoustic imaging (PAI).

Additionally, bacterial pigments can be used as natural, eco-friendly alternatives to synthetic dyes in the textile industry, offering benefits such as UV-blocking, antimicrobial, and anti-odour properties. Their applications extend to other industries, including candle making, paper production, soap manufacturing, and ink formulations for pens and highlighters. Unlike synthetic dyes derived from fossil fuels, bacterial pigments are renewable, non-toxic, and chemically modifiable, making them a viable alternative for industrial use while addressing stability and extraction challenges associated with other natural pigments.

Bacterial pigments offer a promising and eco-friendly alternative to synthetic dyes which are associated with significant environmental and health hazards. Historical reliance on natural pigments emphasizes their value, yet modern technological advancements in biotechnology and synthetic biology have developed their potential for large-scale production. Extensive research on marine bacterial pigments has highlighted their capacity to produce a wide range of pigments with applications in food, textiles, cosmetics, and pharmaceuticals. The continuous exploration of untapped habitats and the development of advanced production techniques are set to drive future innovations, positioning bacterial pigments as a sustainable and versatile resource for various industries.

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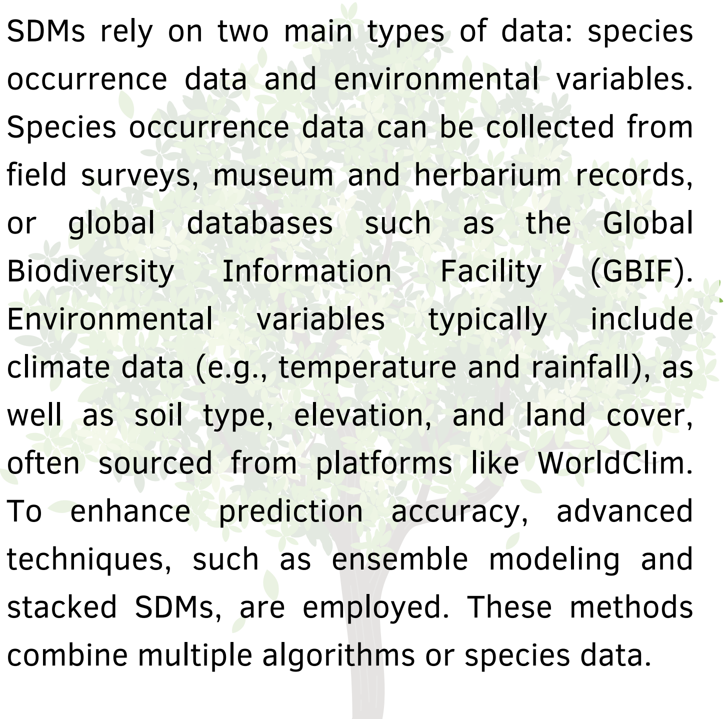
UPDATES ON THE LATEST RESEARCH

Species Distribution Modeling: A Powerful Tool for Biodiversity Conservation

Species distribution modeling (SDM) is a computational approach used to predict where species are likely to occur based on their relationship with environmental factors such as climate, soil, and topography. Recent advances in species distribution models serve as a vital approach in biodiversity conservation, biogeography, macroecology, and facilitating the generation of geographic maps by correlating species' occurrence records with environmental variables.



SDMs rely on two main types of data: species occurrence data and environmental variables. Species occurrence data can be collected from field surveys, museum and herbarium records, or global databases such as the Global Biodiversity Information Facility (GBIF). Environmental variables typically include climate data (e.g., temperature and rainfall), as well as soil type, elevation, and land cover, often sourced from platforms like WorldClim. To enhance prediction accuracy, advanced techniques, such as ensemble modeling and stacked SDMs, are employed. These methods combine multiple algorithms or species data.

In here, we explore key SDM approaches and their applications in Sri Lankan biodiversity conservation. An overview of the analysis workflow is provided in Figure 1.

Ensemble modeling: strengthening predictions

Ensemble modeling combines multiple SDM algorithms, such as generalized linear models (GLM), random forest, and maximum entropy (MaxEnt), to produce more robust predictions. Instead of relying on a single model, ensemble approaches average or weight results from different methods, thereby reducing uncertainty and improving reliability.

For example, in Sri Lanka, ensemble models have been used to predict the habitat suitability of endemic plant species like *Memecylon*, helping researchers in identifying areas most at risk from climate change. By integrating multiple algorithms, scientists can better assess how environmental shifts may impact species distributions and prioritize conservation efforts accordingly.

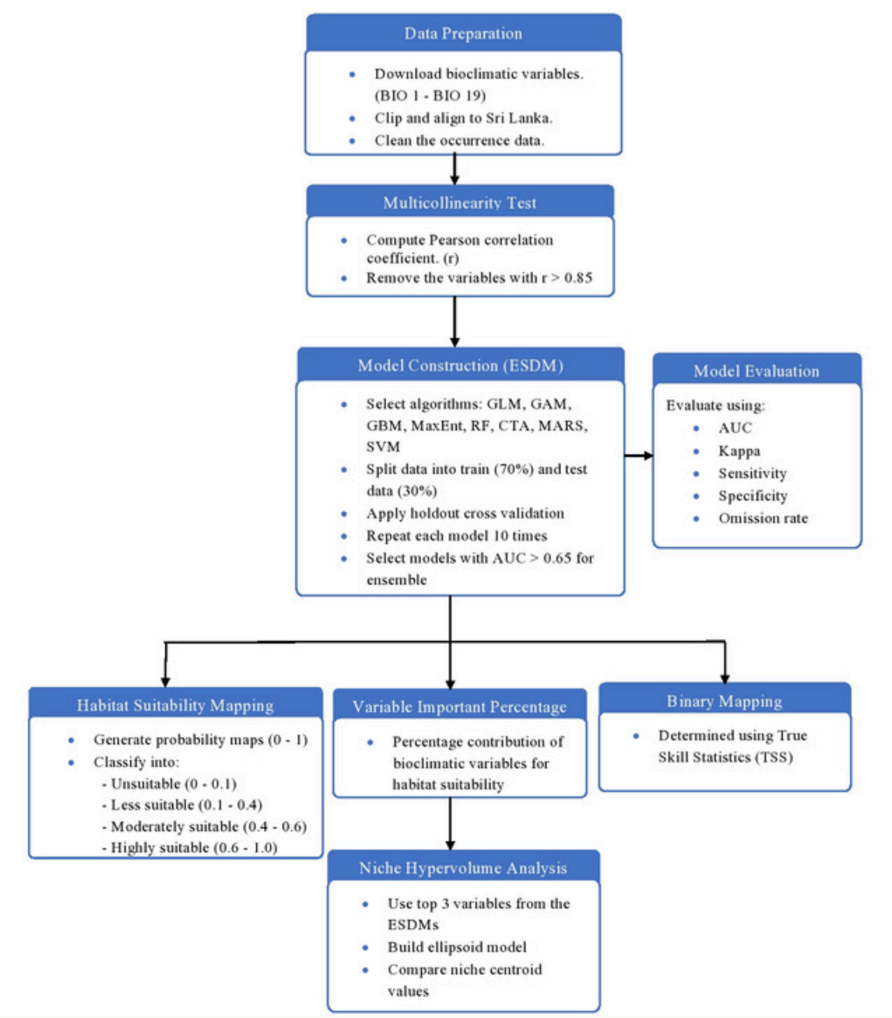


Figure 1 Analysis workflow of ensemble distribution modelling

Stacked and joint species distribution models

Stacked SDMs (SSDMs) combine individual species models to predict broader biodiversity patterns, such as species richness or endemism. This approach is particularly useful for conservation planning in diverse ecosystems like Sri Lanka's rainforests, where multiple species coexist.

Joint SDMs (JSDMs) take this a step further by incorporating species interactions, such as competition or mutualism, into the modeling process. These models are valuable in complex ecosystems, where plant communities vary significantly with altitude and microclimates.

Incorporating disturbance factors

To generate accurate predictions, SDMs must consider both natural and human-induced disturbances. Key factors include land-use changes such as deforestation and urbanization, which reduce available habitat. Climate change also plays a major role by altering temperature and rainfall patterns, forcing species to shift their ranges. Additionally, the spread of invasive species can outcompete native flora, further threatening biodiversity.

Current research in Sri Lanka

Several ongoing studies in Sri Lanka highlight the importance of SDMs in conservation efforts. One project focuses on *Stemonoporus*, a genus of endemic dipterocarp trees found in the wet zone. Using SDMs, researchers are mapping their distribution to identify priority areas for conservation.

Another study investigates two *Syzygium* species with distinct ecological niches, aiming to predict how climate change may affect their future ranges. Preliminary findings suggest that montane species could experience significant habitat loss.

Similarly, research on *Memecylon* uses SDMs to project habitat shifts under different climate scenarios, highlighting the vulnerability of narrow endemics in high-altitude regions (Figure 2). Studies on *Impatiens* distribution also show alarming declines in certain species, largely due to habitat destruction (Figure 3).

Conservation implications and future directions

The insights generated from SDMs are crucial for planning effective conservation strategies. In Sri Lanka, these models support habitat prioritization, ecological restoration, and the design of protected areas, particularly under dynamic climate regimes. By identifying future suitable habitats, SDMs can also guide translocation and assisted migration efforts for climate-sensitive species.

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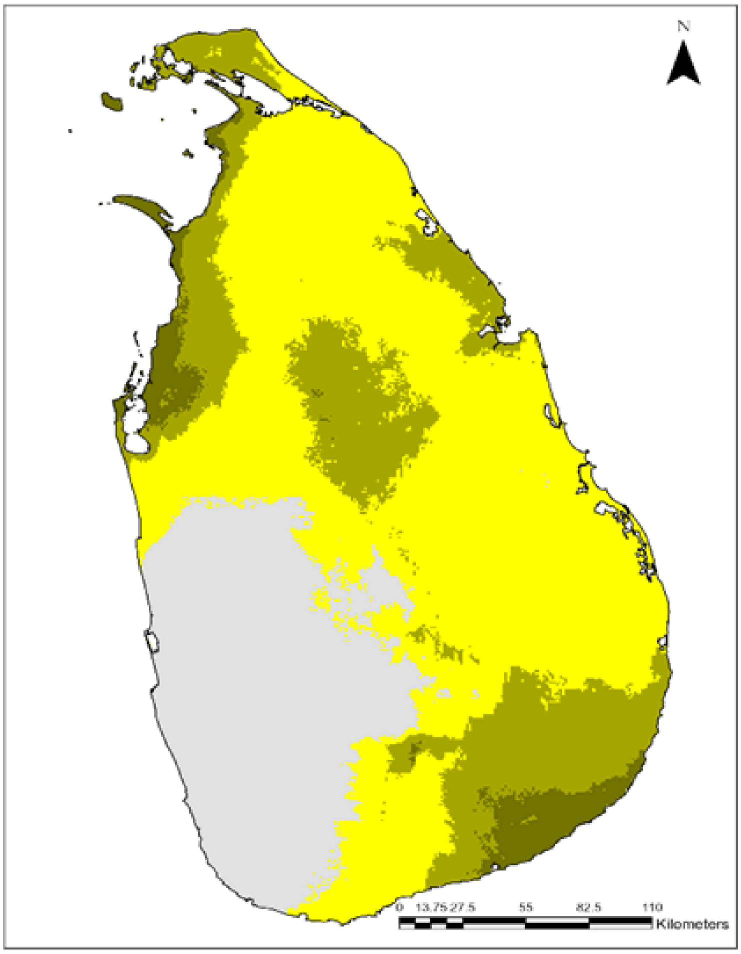

Figure 2 *Syzygium cumini* habitat suitability for year 2050

Moreover, incorporating socio-environmental data such as proximity to human settlements, roads, and deforestation rates enhances the real-world applicability of SDMs. As new technologies emerge, including remote sensing and machine learning, the resolution and accuracy of SDMs are expected to improve, offering even greater utility for policy-making and conservation planning. Recent research has shown that combining SDMs with genomic vulnerability assessments could help in identifying populations most at risk from climate change. This integrated approach demonstrates that incorporating genetic information can substantially alter conservation priorities compared to using SDMs alone.

Looking forward, integrative approaches that combine SDMs with phylogenetics, population genetics, and ecological monitoring will further enhance our understanding of biodiversity dynamics. As computational power increases and methodological approaches continue to evolve, SDMs are becoming more sophisticated and biologically realistic. The integration of genomic data is especially promising, allowing models to account for adaptive potential and population-level variation in environmental tolerances.

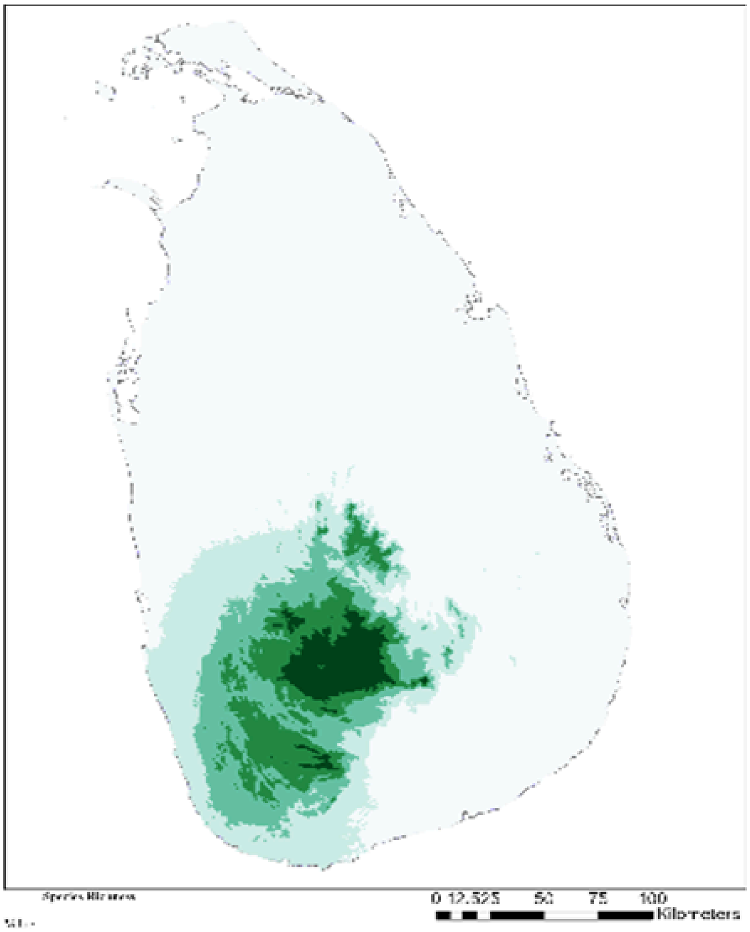

Figure 3 Predicted spatial extent of *Impatiens* genus areas for 2090

Ongoing research in Sri Lanka not only contributes to local conservation efforts but also serves as a valuable model for similar efforts in other tropical biodiversity hotspots. With the development of artificial intelligence, these technologies can be utilized in research and development processes for both flora and fauna. Additionally, integrating these technologies with biogeography and emerging fields like spatial phylogenetics opens new frontiers in biodiversity conservation.

SDMs are essential tools for conserving biodiversity in Sri Lanka and worldwide. From ensemble models to niche dynamics studies, these techniques help scientists to predict how species may respond to environmental changes and to guide conservation efforts.

Ongoing research on endemic species like *Stemonoporus*, *Syzygium*, *Memecylon*, and *Impatiens* highlights the urgent need to protect Sri Lanka's unique flora, a hotspot of endemism under growing threats. By refining SDM techniques and addressing their limitations, researchers and conservationists can more effectively safeguard ecosystems for future generations.

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Breast Cancer in Women: A Brief Guide to Types, Symptoms, Risk Factors, Detection, and Management

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Breast cancer is caused by the uncontrolled growth of cells in the breast tissue, leading to the formation of tumours. Breast cancer is the second most prevalent form of cancer worldwide. Although it can affect both men and women, the risk is significantly higher among women (Global Cancer Statistics, 2022). Data from GLOBOCAN indicate that breast cancer accounts for approximately 1 in 8 cancers diagnosed globally, with a total of 2.3 million cases. Despite its high incidence, the mortality rate associated with breast cancer is comparatively lower than that of lung, liver, and stomach cancers, with 666,103 deaths reported in 2022.

Breast cancer is a carcinoma type of cancer which starts in the skin or tissue that covers the internal organ or gland. It is considered a heterogeneous disease since it consists of different subtypes with distinct characteristics, including variations in histology, biology, clinical presentation, behavior, and response to treatments. Considering histopathology, breast cancer is classified into invasive and non-invasive (in situ) types, each with distinct subtypes. Non-invasive breast cancer includes Ductal Carcinoma In Situ (DCIS), which is confined to the milk ducts and has not spread to the surrounding tissue, representing an early form of breast cancer. Another type, Lobular Carcinoma In Situ (LCIS), occurs in the lobules (milk-producing glands) and it has a high risk of developing invasive breast cancer.

Invasive breast cancer contains Invasive Ductal Carcinoma (IDC), the most common type, accounting for 70-80% of cases. IDC begins in the milk ducts and invades nearby breast tissue. Another subtype, Invasive Lobular Carcinoma (ILC), originates in the lobules and can spread to adjacent tissues, often posing detection challenges in mammograms. The second most common invasive breast cancer is lobular carcinoma (10%).

Subtypes of molecular genetic classification are luminal A, luminal B, human epidermal growth factor (HER2) overexpression, and triple negative breast cancer (TNBC). The subtypes are defined by the expression of estrogen receptor (ER), progesterone receptor (PR), and HER2.

- Luminal A: ER+/HER2−
- Luminal B: ER+/HER2+
- HER2-overexpression: ER−/HER2+
- Triple-negative (TN): ER−/PR−/HER2−

Breast cancer can be categorized into 5 stages: stage 0, I, II, III, and IV. The designated type explains the level of differentiation and likelihood of spreading. Level 1 is usually considered a low risk of spread, while levels higher than 3 denote highly differentiated and a higher likelihood of spreading. Stage of the breast cancer is also described by the "TNM" system which is a system used to describe the amount of cancer that has spread.

- **T:** Size of the tumor (in centimeters)
- **N:** Number of nearby lymph nodes with cancer
- **M:** Metastasize of the cancer to the other parts of the body (0 = no spread, 1 = it has spread)

The heterogeneity of breast cancer with respect to molecular markers, location, and grade necessitates personalized approaches for diagnosis and therapy to optimize the outcomes of each subtype.

Symptoms

A lump in the breast or armpit, thickening or swelling in a part of the breast, and irritated or dimpled breast skin are significant warning signs of breast cancer. Additionally, redness or flaky skin, pain in the nipple area and an inverted nipple are notable symptoms. Nipple discharge other than breast milk, including blood, along with any changes in the size or shape of the breast, should prompt immediate medical attention. Pain in any area or an inflamed appearance of the breasts are also symptoms. These symptoms highlight the importance of regular self-examinations of the breasts and prompt reporting of any abnormalities to ensure early detection and treatment. There are some non-cancerous (benign) breast conditions which are not life-threatening, but some could be linked with a high risk of getting breast cancer later.

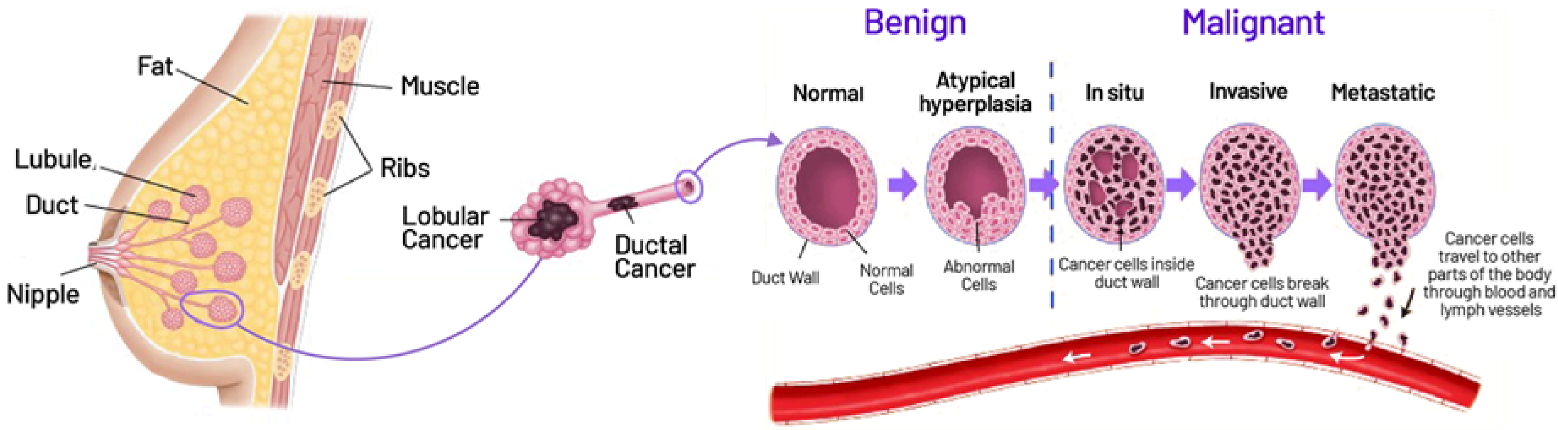

Figure 1 Progression of breast cancer
Source: https://www.saintjohnscancer.org/breast/breast-cancer/types-of-breast-cancer/

Risk factors

Breast cancer is a multifactorial disease. Among them, the risk factors are genetic mutations, family history of breast cancer, reproductive history, having dense breasts, lifestyle, environmental factors, old age, and even a combination of factors. Breast cancer typically affects women over the age of 50.

Genetic mutation: Having mutations in certain genes, such as *BRCA1* and *BRCA2*, increases a woman's chance of developing breast or ovarian cancer. BRCA proteins play a major role in repairing damaged cells in the breast and ovaries and keep other cells growing normally. Germline mutations in the *BRCA1* and *2* genes are responsible for only 16% of all hereditary breast cancers. Patients who carry mutations in one or both *BRCA* genes have a high risk of having breast cancer. However, *BRCA1* or *BRCA2* mutations do not guarantee that a person will be diagnosed with breast cancer in the future.

Women with a *BRCA1* mutation, as well as women who do not inherit a breast cancer gene mutation, may be at increased risk for developing breast cancer due to single nucleotide polymorphisms (SNPs) in chromosomal segments. Moreover, mutations in the *P53* gene which is a tumor suppressor gene, can cause breast cancer too.

Family history of breast cancer: Women who have a *BRCA1* or *BRCA2* mutation and are diagnosed with breast cancer frequently have a family history of breast, ovarian, or other cancers. Some are more likely to have a genetic predisposition linked to breast cancer if they have blood relatives on either maternal or paternal side of the family who had breast cancer diagnosed before age 50 or if there is both breast and ovarian cancer on the same side of the family or if they have a relative with triple-negative breast cancer (TNBC) or if there are other cancers in the family in addition to breast such as prostate, thyroid, melanoma, stomach, pancreatic, uterine or if there is a known abnormal breast cancer gene in their family.

Reproductive history: Usually, women experience menarche around the age of 12 and menopause by around 55 years. However, there are exceptions. Women who begin menstruation before the age of 12 or undergo menopause after the age of 55 have an increased risk of developing breast cancer. This elevated risk is attributed to prolonged exposure to estrogen and progesterone, resulting from an extended reproductive hormonal cycle.

Having dense breasts: Having dense breasts means there are more connective tissues than fatty tissues. Because of that, lumps cannot be detected using mammograms. So, those women should undergo other screening tests to determine whether they are cancer-free. Women with high-dense breasts have a 2-fold risk compared to women with low density.

Lifestyle and environmental factors: Increased alcohol consumption and lack of exercise are linked with the occurrence of breast cancer. The risk may be higher in individuals with a diet of rich saturated fats and low fruits and vegetables.

Some environmental factors that affect breast cancer are radiation and chemical exposure. Radiation therapy to the chest area in the past can increase the chances. Carcinogenic chemicals include substances such as xenoestrogens, asbestos, formaldehyde, and heavy metals like mercury and arsenic.

Detection and diagnosis

Early detection and diagnosis can be done by tests such as mammograms, ultrasounds, other imaging tests, and biopsies. If the scan or examination reveals an abnormality, a biopsy is done to take out a small piece of breast tissue, which will be sent to the laboratory for testing. Early detection through screening allows for early treatment, while insights into tumor biology and molecular subtypes have enabled the development of targeted therapies, improving treatment effectiveness and patient prognosis. Therefore, advances in molecular understanding of breast cancer have significantly reduced the mortality rates.

The 5-year survival rate for breast cancer varies greatly across the globe, from 80% or more in wealthy nations to 60% in middle-income nations and fewer than 40% in low-income nations. The results of many investigations indicated that the relative survival rate is highest at age 50 and thereafter declines with advancing age.

Management

Up to stage two, breast cancer is curable. Women with a family history of breast cancer are advised to begin screening ten years younger than their relative was diagnosed. Ignoring breast cancer symptoms when they appear is one of the major reasons for delaying the diagnosis.

Major treatment options of breast cancer are radiotherapy, chemotherapy, endocrine therapies or combinations of these treatments. Hormonal therapy can be used to treat ER+ and PR+ types. TNBC causes approximately 15–20% of breast cancers. There are no targeted therapies for this type of breast cancer. Adjuvant therapy is an additional treatment given alongside the main treatment to improve its effectiveness. It reduces the risk of cancer recurrence.

One of the most common cancers in the world is breast cancer. Even though it is a heterogeneous disease, genetic mutations play a crucial role. It is very important to identify the cancer at its early stages. Monthly breast self-examinations and more regular screenings by a physician at least once a year are recommended for women with a family history of breast cancer. Another important fact about breast cancer is adjuvant therapy. It lowers the chance of the patient getting the cancer again. Combination of molecular genetics and modern technologies in personalized medicine improves treatment, reduces side effects, and improves prognoses for patients with breast cancer.

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Advancements in the Diagnosis and Treatment of Leptospirosis: Challenges and Innovations

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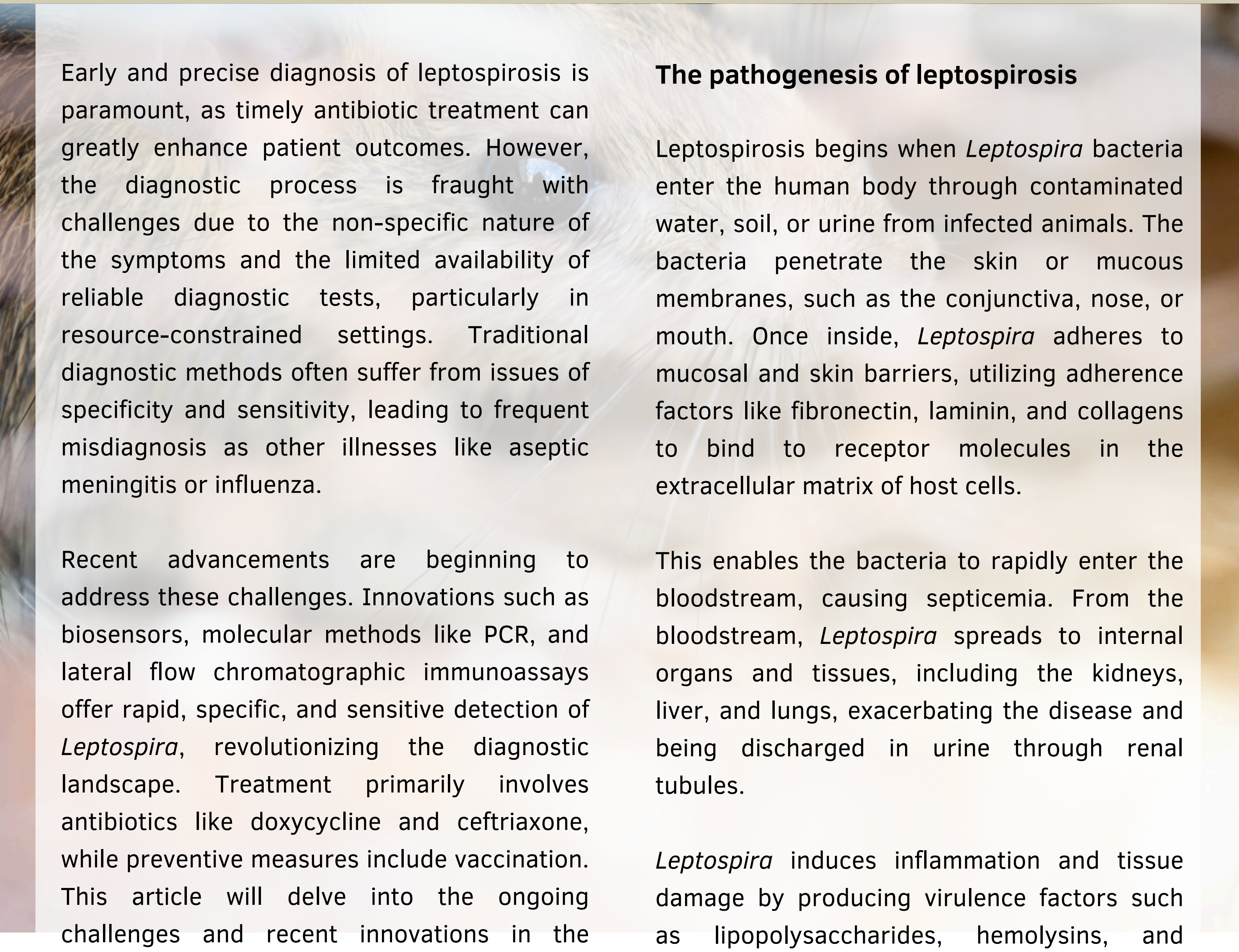
Leptospirosis, a pervasive zoonotic disease caused by *Leptospira* bacteria, poses a significant public health threat across Sri Lanka and the globe. Its prevalence is especially pronounced in tropical and subtropical regions, where environmental and socioeconomic factors facilitate its spread. While rodents are the primary reservoirs, recent studies have highlighted the presence of *Leptospira* in the urine and feces of other animals, including cattle, dogs, and pigs. The clinical manifestations of leptospirosis are notably diverse, ranging from mild, flu-like symptoms to severe, life-threatening complications affecting multiple organ systems.

Leptospirosis in Sri Lanka is endemic and exhibits seasonal outbreaks, particularly during the monsoon periods. The Department of Epidemiology has reported a significant outbreak of Leptospirosis, with 5,000 cases recorded in Sri Lanka during the first six months of 2024, predominantly from the central, southern, and north-central provinces. This notable increase in cases warrants considerable public health attention and discussion within the community. The spike in incidence highlights the need for enhanced surveillance, preventive measures, advanced diagnostic methods, treatments, and public awareness to mitigate the spread of this zoonotic disease.

High-risk groups include farmers, agricultural workers, and individuals involved in animal husbandry, exposed through occupational activities and recreational pursuits such as swimming or wading in contaminated water bodies.



Early and precise diagnosis of leptospirosis is paramount, as timely antibiotic treatment can greatly enhance patient outcomes. However, the diagnostic process is fraught with challenges due to the non-specific nature of the symptoms and the limited availability of reliable diagnostic tests, particularly in resource-constrained settings. Traditional diagnostic methods often suffer from issues of specificity and sensitivity, leading to frequent misdiagnosis as other illnesses like aseptic meningitis or influenza.

Recent advancements are beginning to address these challenges. Innovations such as biosensors, molecular methods like PCR, and lateral flow chromatographic immunoassays offer rapid, specific, and sensitive detection of *Leptospira*, revolutionizing the diagnostic landscape. Treatment primarily involves antibiotics like doxycycline and ceftriaxone, while preventive measures include vaccination. This article will delve into the ongoing challenges and recent innovations in the diagnosis and treatment of leptospirosis, emphasizing the critical need for continued research, enhanced surveillance, collaborative efforts, and integration of new technologies to mitigate the impact of this global health concern.

The pathogenesis of leptospirosis

Leptospirosis begins when *Leptospira* bacteria enter the human body through contaminated water, soil, or urine from infected animals. The bacteria penetrate the skin or mucous membranes, such as the conjunctiva, nose, or mouth. Once inside, *Leptospira* adheres to mucosal and skin barriers, utilizing adherence factors like fibronectin, laminin, and collagens to bind to receptor molecules in the extracellular matrix of host cells.

This enables the bacteria to rapidly enter the bloodstream, causing septicemia. From the bloodstream, *Leptospira* spreads to internal organs and tissues, including the kidneys, liver, and lungs, exacerbating the disease and being discharged in urine through renal tubules.

Leptospira induces inflammation and tissue damage by producing virulence factors such as lipopolysaccharides, hemolysins, and metallopeptidases, which trigger pro-inflammatory cytokines and hepatocyte apoptosis.

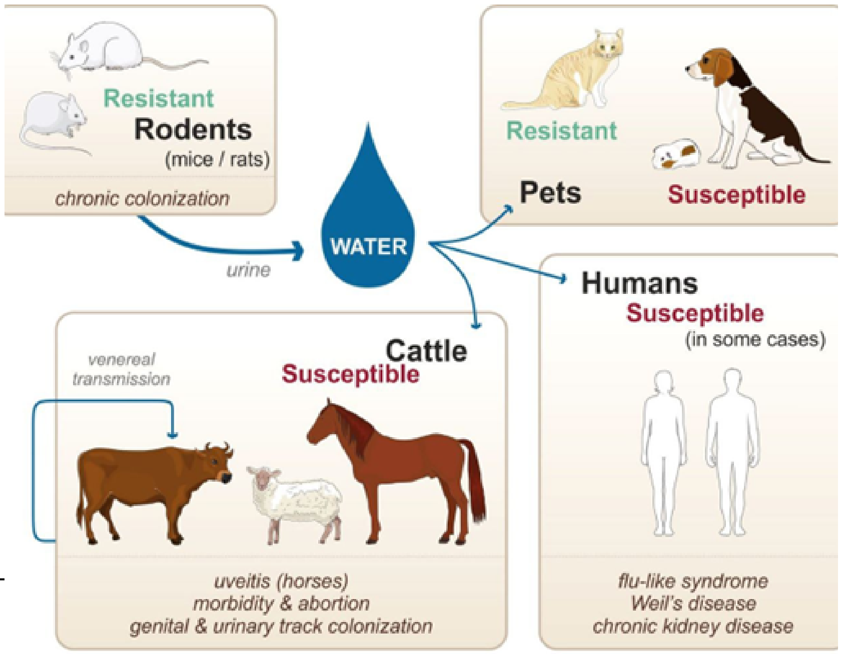


Figure 1 Zoonotic cycle of leptospirosis, susceptibility of various accidental hosts, and transmission modes.
Source: Bonhomme and Werts, (2022); Zheng et al (2023)

The bacteria's ability to cause systemic infection results in symptoms like high fever, myalgia, lymphadenectasis, hemorrhage, and jaundice. The pathogenesis of leptospirosis involves complex interactions between *Leptospira* and the host immune system, where the bacteria evade the immune response and cause significant tissue damage. These mechanisms underscore the invasive nature of *Leptospira* and its capability to cause widespread systemic infection, leading to the development of leptospirosis (Figure 1).

Specific and nonspecific symptoms

Leptospirosis exhibits a wide spectrum of symptoms and non-specific symptoms such as fever, headache, chills, muscle aches, vomiting, nausea, diarrhea, abdominal pain, cough, and occasionally a rash, often leading to misdiagnosis. These symptoms can closely mimic those of other viral illnesses like influenza, dengue, or malaria. However, leptospirosis can also manifest with specific symptoms that aid in its differentiation from other febrile illnesses. These include conjunctival suffusion (reddening of the eyes without discharge), jaundice or frank icterus (yellowing of the skin and eyes), renal failure with oliguria (decreased urine output), hemorrhagic features, and systemic inflammatory response or shock. The severe form of leptospirosis, known as Weil's disease, is particularly notable for the combination of jaundice and renal failure and can involve other organ systems such as the lungs, heart, and central nervous system. In summary, while the non-specific symptoms of leptospirosis can easily be confused with other diseases, the presence of specific symptoms like conjunctival suffusion, jaundice, and renal failure can help distinguish it from other causes of acute febrile illness.

Evolution of leptospirosis diagnostic methods

The traditional diagnostic methods for identifying leptospirosis include serological tests, microscopy, and culture. The Microscopic Agglutination Test (MAT) is the gold standard among serological tests, requiring a comprehensive panel of *Leptospira* serovars as antigens. Other serological tests like Enzyme Linked Immunosorbent Assay (ELISA) and Indirect Hemagglutination Assay (IHA) detect antibodies but often suffer from limitations in specificity and sensitivity. Microscopy, including dark-field microscopy and histochemical stains like Warthin-Starry, can directly visualize *Leptospira* in body fluids or tissues, but requires a high bacterial load and is prone to inaccuracies (Figure 2). Culture methods, although definitive, are impractical for immediate diagnosis due to the slow-growing nature of *Leptospira*, which can take up to three months to culture.

These traditional methods have significant limitations, especially in the early stages of infection when antibodies are not yet present, and sensitivity is low. However, modern diagnostic approaches offer promising alternatives. Molecular methods, such as PCR and isothermal amplification techniques, detect *Leptospira* DNA, providing rapid and sensitive diagnosis, particularly in the early stages of infection.

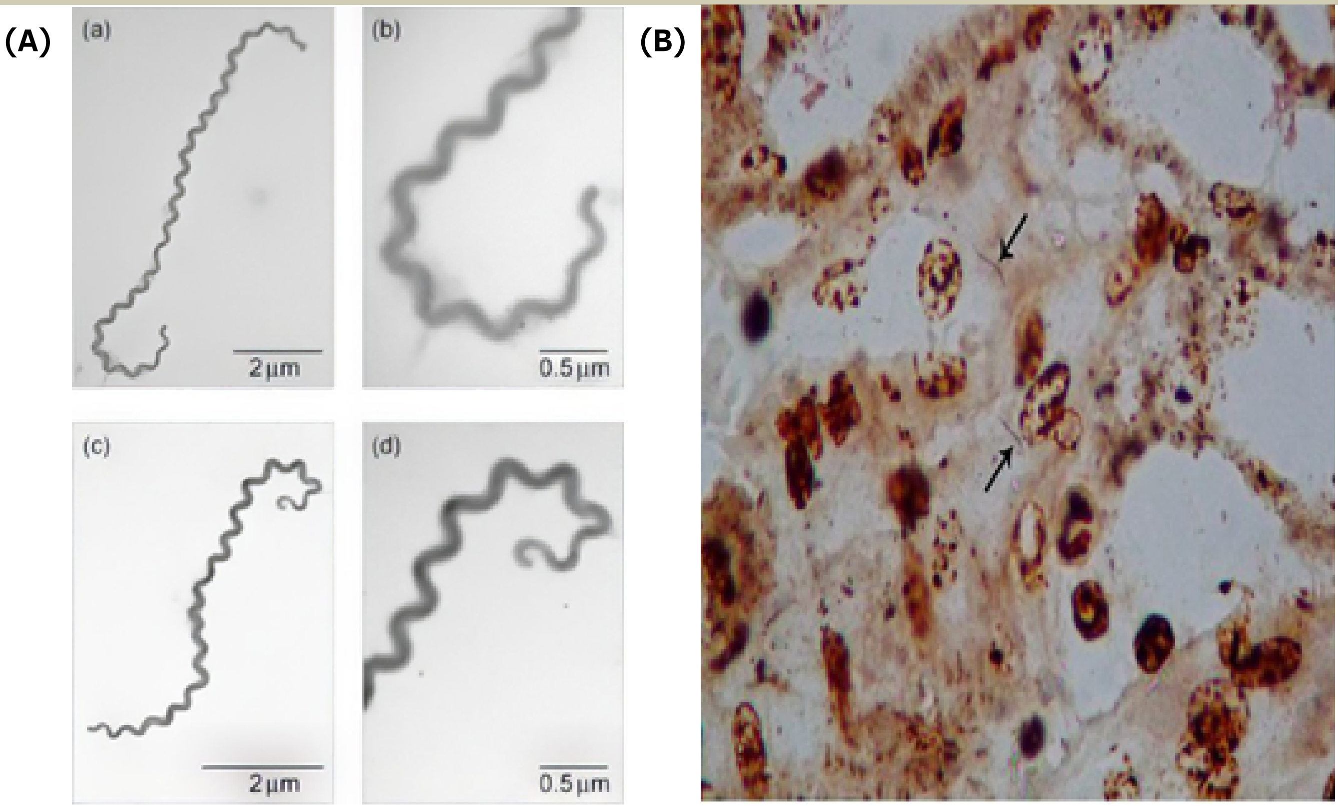


Figure 2 Electron micrographs of leptospires. The images illustrate (Aa, Ac) the elongated, helically coiled structure and (Ab, Ad) the distinctive hook-like feature observed at the extremities of some bacterial cells (A), Warthin-Starry staining of the kidney tissues. Presence of filiform, dark brown *Leptospira* (arrows) on the apical surface of epithelial cells in the cortex (B)
Source: Fraga et al (2015); Azizi, Kheirandish, & Rahimi (2014)

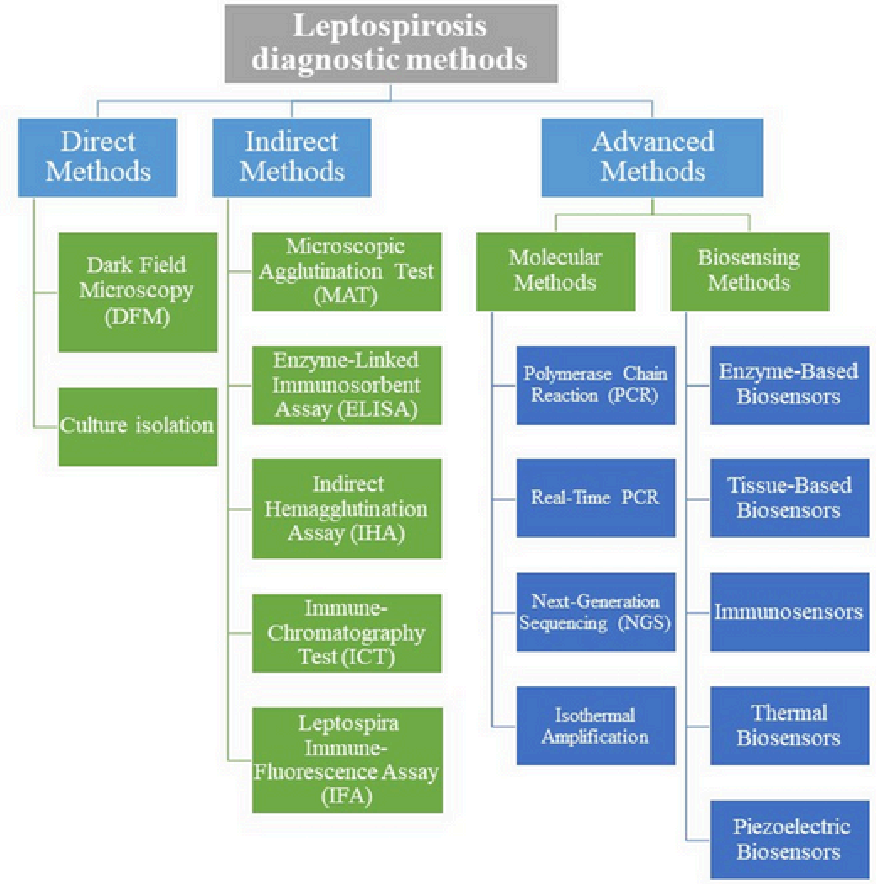


Figure 3 Diagnostic methods of leptospirosis

Novel biosensors, lateral flow assays, and genomic analysis provide insights into *Leptospira* that aid in developing more effective diagnostic tests and treatments. The advancement of these modern techniques is crucial for enabling early and accurate identification of leptospirosis, particularly in resource-limited settings (Figure 3).

Impact on public health

Leptospirosis exerts a substantial burden on public health, and it is prevalent in tropical and subtropical regions like Sri Lanka, where environmental factors and socio-economic conditions facilitate its transmission. The clinical manifestations of leptospirosis can lead to severe complications such as organ failure, hemorrhage, and death, placing significant strain on healthcare systems. The challenge is compounded by its non-specific symptoms, which often result in misdiagnosis, delaying effective treatment, and complicating public health efforts to control its spread.

Preventive methods

Several preventive strategies are crucial in combating leptospirosis. Improved sanitation and hygiene practices are essential, especially in high-risk environments such as agriculture, construction, and outdoor recreational areas. Vaccination, while currently limited, remains an effective preventative measure, particularly for individuals at high risk of exposure.

Enhancing public health surveillance and reporting mechanisms is vital for better understanding the epidemiology of leptospirosis and guiding targeted prevention strategies. Education and awareness campaigns play a pivotal role in informing at-risk populations about the modes of transmission and preventive measures. Additionally, environmental management initiatives, including effective rodent control measures, are essential to minimize contamination of water and soil.

Innovations

Innovative approaches are revolutionizing the diagnosis, treatment, and prevention of leptospirosis. Molecular diagnostic methods such as PCR offer rapid and accurate detection of *Leptospira*, enabling the timely initiation of treatment. Biosensors and lateral flow assays provide rapid, specific, and sensitive diagnostics, particularly beneficial in resource-limited settings where traditional methods may be inaccessible. Genomic analysis of *Leptospira* enhances understanding of its genetic diversity, facilitating the development of more effective diagnostic tools and treatment strategies. Novel treatment modalities, including providers and public health officials, are pivotal in advancing the understanding and management of leptospirosis on a global scale. These efforts are crucial in mitigating the impact of this pervasive zoonotic disease, both locally in Sri Lanka and globally.

Advancements in the diagnosis and treatment of leptospirosis are crucial in addressing the significant public health challenges posed by this zoonotic disease. Leptospirosis presents with a wide range of symptoms, often leading to misdiagnosis, and its pathogenesis involves complex interactions between the bacteria and the host's immune system. Traditional diagnostic methods have limitations in sensitivity and specificity. However, recent innovations such as molecular diagnostics, biosensors, and lateral flow assays offer rapid, specific, and sensitive testing, facilitating early and accurate diagnosis.

Effective management of leptospirosis also requires enhanced preventive strategies, including improved sanitation, vaccination, and public awareness campaigns. Educating at-risk populations and implementing environmental management measures are essential to reduce the disease's prevalence. Continued research and global collaboration are vital to develop more effective diagnostic tools, treatment strategies, and preventive measures. By integrating new technologies and fostering international cooperation, the impact of leptospirosis on global public health could be mitigated.

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NATURE CAPTURES

Impatiens repens

A stunning endemic treasure of Sri Lanka, this bright yellow-flowered perennial gracefully trails across the landscape. Known locally as **"ගල් දෙමට" (Gal Demata)**, *Impatiens repens* features thick, fleshy, reddish stems that support delicate leaves with subtle crimson hues. Its solitary blossoms bring bursts of sunshine-yellow to shaded areas, while its traditional use in Ayurvedic medicine highlights the union of nature's beauty and healing power in one remarkable plant.

Photograph by
Mr. A. M. Kosala L. Abeykoon, S. Biol. (Sri Lanka)
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A vibrant Northern Cardinal (*Cardinalis cardinalis*) perched gracefully with its crimson feathers strikingly contrasted against the serene winter landscape.
Captured location – North America (Pennsylvania, USA)

The Northern Cardinal (*Cardinalis cardinalis*), also known as the common cardinal or red cardinal, is a passerine songbird widely distributed across North America. Male birds are renowned for their brilliant red plumage, while female birds display a more subtle brownish hue with warm red accents. The species gets its name from the red-robed cardinals of the Roman Catholic Church. Male cardinals owe their vivid coloration to dietary carotenoids, which they metabolize to produce uniquely pigmented feathers. Cardinals exhibit strong monogamous behavior, often forming long-term pair bonds. Their breeding and molting cycles are influenced by their unique photoperiod-dependent hormonal regulation. Additionally, cardinals lack a well-defined migration pattern, they mostly favor dense thickets for nesting and foraging. These vibrant red cardinals add a splash of color even to the coldest winter landscapes. Revered for their beauty, Northern Cardinals hold the distinction of being the state bird of seven U.S. states: Illinois, Indiana, Kentucky, North Carolina, Ohio, Virginia, and West Virginia.

Photograph by
Ms. Udeshi Wickramarachchi, A. I. Biol. (Sri Lanka)
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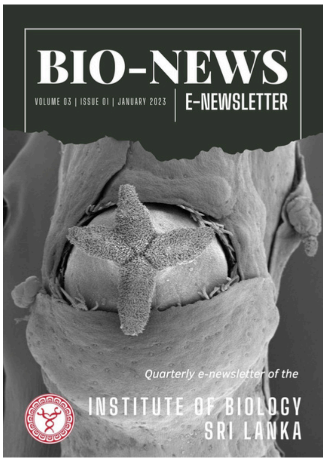

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