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# Advances in Science

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Ecology and biodiversity**

## **FEATURES**

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**Wing pattern diversity in butterflies**

**The link between biodiversity and happiness**

**Fungi: The good, the bad and the mysterious**

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## Advances in Science

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**On the cover:** Animals play important roles as seed dispersers in the tropical forests of Asia (Khao Yai National Park, Thailand) [Photos: Jun Ying LIM]

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# Wing pattern diversity in butterflies

Butterfly wing patterns are adaptations to survive in particular environments and in other cases, the consequence of sexual selection by choosy mates

## Introduction

Given the ongoing loss of biodiversity, biologists like myself, who have always pursued fundamental questions in biology, must reckon with the right path forward. Should we spend the little time we all have preventing further species from going extinct, so that our children and grandchildren can still see and appreciate those increasingly rare species? Or spend our time trying to understand the general principles that generated the diversity we have come to cherish in the first place? I have picked this second path, not because I do not fully support research in species conservation, but simply because I am endlessly curious about diversity, and cannot help but follow where this curiosity takes me.

In the final year project of my undergraduate studies, I set out to answer how and why butterflies have evolved their astonishingly diverse and beautiful wing patterns. Little did I realise that I would continue trying to answer these questions thirty years later. It has always seemed mysterious to me how such patterns arise on the wings and how they evolve. Some of these patterns should be better than others at offering protection from predators, or at attracting mates, so why are they not all the same? Why do butterflies display such astonishing wing pattern diversity? And what is the underlying genetic mechanisms?

## Eyespot wing pattern diversity

Due to the magnitude of the diversity involved, my efforts are focused on primarily trying to understand the forces and mechanisms that generate wing pattern diversity in a genus of satyrid butterflies with eyespots, called *Bicyclus*. These are small brown butterflies that live in Africa. They are sister to a genus that lives



Figure 1: Butterflies from the family *Nymphalidae*, showing a diversity of eyespot patterns that have evolved over a long period of millions of years.

in Singapore and other parts of Asia, called *Mycalesis*. *Bicyclus* is selected because I was trained to rear one species as an undergraduate student, and this species has now adapted to laboratory rearing conditions. It has a row of eyespots on its wings, and our team has primarily been focusing on examining eyespot diversity across the genus.

Over the years, we made progress at answering some questions surrounding eyespot wing pattern diversity in this genus and more broadly across the nymphalid species (see Figure 1 and 2). By inferring the ancestral wing patterns across the evolutionary tree of *Bicyclus*, we discovered that most of the eyespots that are exposed to predators (i.e. those that are always visible when the butterfly is at rest with the wings closed over its body) are extremely conserved, and the number of eyespots hardly ever change over the course of evolution. We think that these eyespots are important in deflecting the attacks of predators towards the wing margin [1]. In experiments involving the praying mantids, it has been shown that instead of the butterfly body, these raptorial predators attack the eyespots on the wings. As a result, the butterfly can still fly away with its ripped wings

to see another day, and to lay more eggs.

These exposed eyespots are also mostly found in higher numbers on the hindwings relative to the forewings. If the butterfly displays too many eyespots on the forewings, the attacks shifts more anteriorly, towards the forewing, and this is detrimental to the butterfly. The forewing is important for lift-offs, and rips on this wing will prevent a swift escape from subsequent attacks. Although, eyespots are mostly a good defence for butterflies, they need to be placed judiciously on the wings and kept in low numbers on the forewings.

## Eyespots playing a role in sexual selection

Our ancestral reconstruction of wing patterns also showed that those eyespots that were hidden mostly on the dorsal sides of the wing evolve at very rapid rates. These hidden eyespots are exposed to prospective mates during courtship, but are hidden from predators when it is at rest. However, there was no clear directionality regarding how these hidden dorsal eyespots changed in numbers over the course of evolution: over millions of years, some lineages gained eyespots,

while others lost them, and males and females did not necessarily gain or lose eyespots at the same time. This pattern of evolution hints that these eyespots are likely playing a role in sexual selection, rather than in natural selection. In sexual selection, preferences are often arbitrary, fickle, and anything goes – much like how thin ties were preferred in men’s fashions in the 1960s, then fat ties were preferred in the 1970s, and then back to thin ties in the 1980s.

In laboratory experiments, we discovered that males and females of at least one *Bicyclus* species notice these eyespots on the wings of the opposite sex and they prefer a specific number of them! They notice when additional eyespots are present, or when some eyespots are missing. In both cases, they dislike these new patterns when given a choice of whom to mate with. The species we rear in the laboratory displays a clear preference for patterns of its own species (the so-called “wildtype” pattern), and this might explain how species can tell each other apart in the field. However, these preferences are not necessarily fixed: females can “learn” to prefer novel patterns in the wings of males. Learning happens when females are exposed to an unusual wing pattern during the first few hours of their adult lives, before they become sexually receptive. Whether this learning ability accelerates the evolution of one pattern to another is still unclear, but it is something we are interested in pursuing further.

### Recent research findings

The most recent advance from our team was the discovery of how eyespots

might have first appeared on the wings of butterflies. As an undergraduate I read a book by the astrophysicist Fred HOYLE, called “*The Intelligent Universe*”, where he suggested that the large eyespots of the saturniid moths could not have evolved gradually, as is usually described in evolution, because there would be no advantage for moths caught in intermediate steps of the eyespot evolution, such as those carrying “eyespot with faded colour rings”. Hoyle’s scepticism of gradual evolution led him to advocate for a kind of creationism, concluding that some traits just had to spring into being, fully formed, and in their current complex states. All these years after reading his book, I am finally able to answer his conundrum: we have discovered that eyespots are likely to have evolved from mutations that produce a discrete rather than a gradual change in phenotype [2]. We have shown that eyespots reuse many of the genetic mechanisms that are used to make antennae and legs. When these programmes are re-activated in the cells of the wing, they lead to eyespot patterns instead of limb-like outgrowths. We are still exploring why this happens but have discovered that the same set of genes are switched on in the development of antennae, legs and eyespots using exactly the same set of activation switches.

Another cool discovery is that we had previously estimated that eyespots evolved initially on the hindwings alone. This is estimated to have happened around 70 million years ago when dinosaurs still roamed the Earth, and humans had not yet evolved. Millions of years later, however, several lineages of butterfly independently gained the ability to



Figure 2: *Taenaris catops* is a butterfly which can be found in West Papua, Indonesia. [Photo credits: Yulia BERESHPOLOVA and Kristof ZYSKOWSKI]

develop eyespots on the forewings as well. More recently, we discovered that an important regulatory gene, called a Hox gene, was likely involved in eyespot origins. This gene is only expressed in hindwings but not in forewings. When it is disrupted using genetic engineering, several hindwing eyespots disappeared. This outcome shows that the Hox gene is essential for eyespot development and might have been instrumental in allowing eyespots to first evolve on hindwings [3].

The evolution of all the myriad of bizarre and novel butterfly wing patterns must each have its own interesting ecological and adaptive back-story. Perhaps my laboratory’s contribution to help preserve the habitats that sustain these fabulous insects may be simply to create awareness and awe of how millions of years of evolution can create such inventive and alternative solutions to the same old problems facing all organisms, such as escaping from predators and attracting mates. Butterflies are constantly evolving new ways to do this, mostly by varying their colours and their patterns.

For more details, please visit: <https://lepdata.org/monteiro/>

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Antónia MONTEIRO is a Professor with the Department of Biological Sciences, NUS. Her laboratory rears butterflies all year around, but now moths, praying mantises, and damselflies, are also frequent visitors.

### References

[1] Chan IZW\*; Ngan ZC; Naing L; Lee Y; Gowri V; Monteiro A\*, “Predation favours *Bicyclus anynana* butterflies with fewer forewing eyespots” PROCEEDINGS OF THE ROYAL SOCIETY B - BIOLOGICAL SCIENCES Volume: 288 Issue: 1951 Article Number: 20202840 DOI: 10.1098/rspb.2020.2840 Published: 2021.

[2] Murugesan SN\*; et. al., “Butterfly eyespots evolved via cooption of an ancestral gene-regulatory network that also patterns antennae, legs, and wings” PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA Volume: 119 Issue: 8 Article Number: e2108661119 DOI: 10.1073/pnas.2108661119 Published: 2022.

[3] Matsuoka Y\*; Monteiro A\*, “Hox genes are essential for the development of eyespots in *Bicyclus anynana* butterflies” GENETICS Volume: 217 Issue: 1 Article Number: iyaa005 DOI: 10.1093/genetics/iyaa005 Published: 2021.

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# The link between biodiversity and happiness

Spending time in biodiverse green and blue spaces can improve our health and contribute to the well-being of the planet

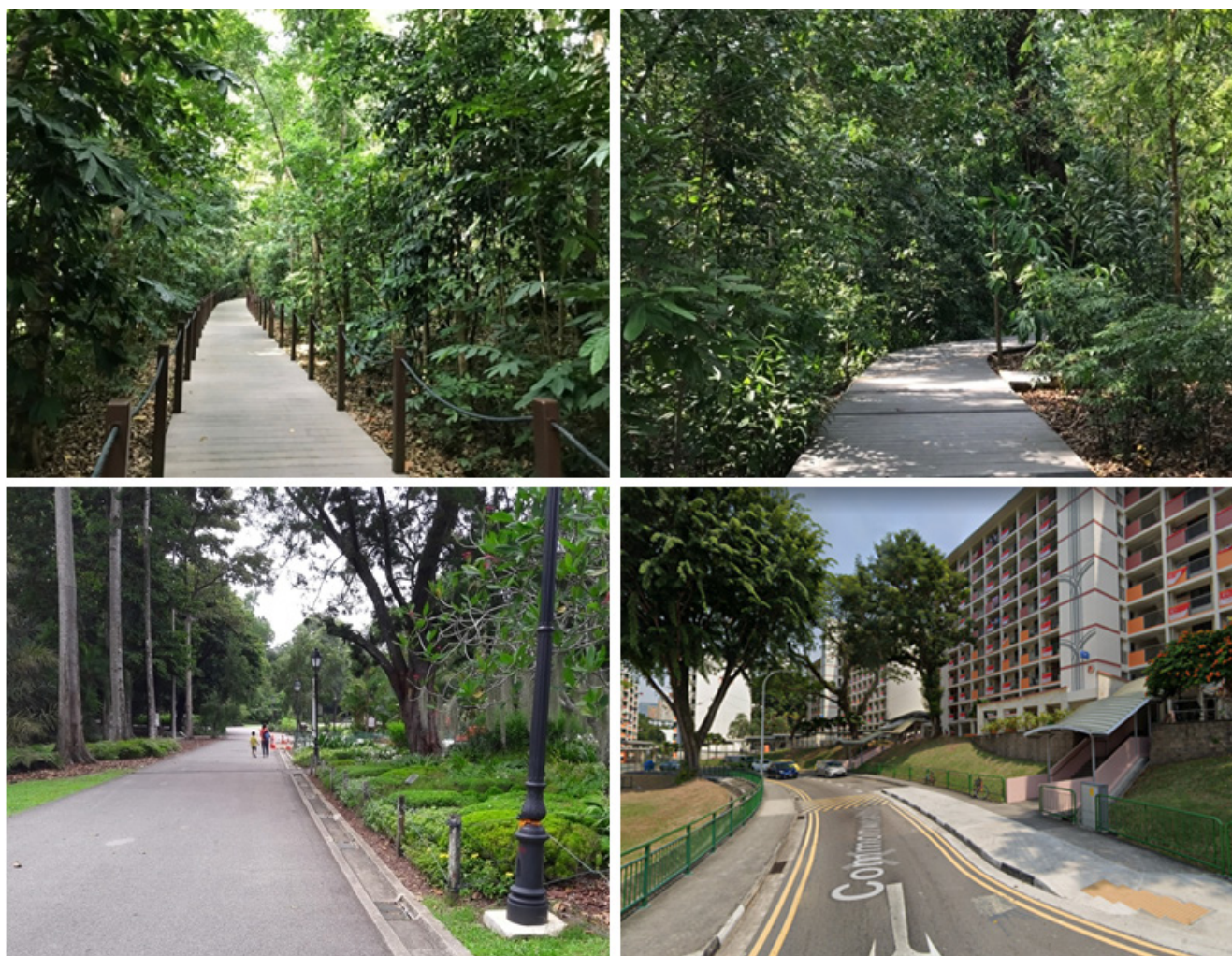


Figure 1: Examples of trails used in research studies to understand the link between biodiversity and happiness. The visuals show (top panels) the Windsor Nature Park, (bottom left) a manicured trail in a park and (bottom right) an urban trail.

## Introduction

Living in densely populated cities can pose a toll to our well-being. Our fast-paced lifestyle -juggling work with family duties while being bombarded by information on social media - can be overwhelming. These stressful conditions were further exacerbated by the COVID-19 pandemic. Faced with this extreme pressure, Singaporeans, like most other citizens in this world, used green and blue spaces to seek respite.

Although there is consensus that spending time in nature is beneficial for

human health, it is not clear whether any form of “nature dose” can provide the same type of benefits. At the BioEcon laboratory, our research team tries to dig deeper to understand more about the specific aspects of the nature dose that are more likely to bring joy to our lives.

## Diversity is the spice of life

As part of one of our research studies, participants were allocated to nature walks consisting of itineraries that ranged from a completely urban setting, to manicured urban parks to

pristine forests teeming with diverse wildlife (see Figure 1) [1]. It was found that the level of the perceived biodiversity by the participants played a mediating role in their capacity to feel relaxed and, as a result, to enjoy positive moods (“feel happier”) (see Figure 2). With positive moods being a precursor of mental health, our results point to the importance of conserving intact habitats, which harbour greater biodiversity, to fully receive the restorative benefits of being in nature.

In a different study, a survey was performed on a total of 1,500

Singaporean participants. This study provided another instance showing the importance of diversity in natural spaces and it being an important element that makes life more interesting and enjoyable. Using analytical methods, a significant link was found between the extent of the diversity of the different types of green and blue spaces which the participants had visited weekly and the satisfaction level with their current lifestyle [2]. In other words, it is not simply a matter of frequently visiting a nearby park. It is equally important that the visits to these manicured parks are also combined with visits to other nature reserves and blue spaces. Indeed, diversity is the spice of life.

### Why do some people love spending time in nature while others hate it?

In 1984, Biologist E.O. WILSON posed the biophilia hypothesis which suggests that humans have an innate tendency to seek connections with nature and other forms of life. In reality, human affinity to nature is quite varied. While some people love hiking in the great outdoors regardless of the hot weather and presence of mosquitoes, others would rather spend the afternoon lazing at home watching television or serials.

Why is there this difference? Is it the way we were brought up that makes us love nature or are we born this way naturally? To answer these questions, our team used a twin study, which allows for exploring the overall role of genes in the development of a particular trait. In a nutshell, the study compared the similarities in the time spent in nature between identical and non-identical twins. The similarities were found to be stronger among identical twins, which

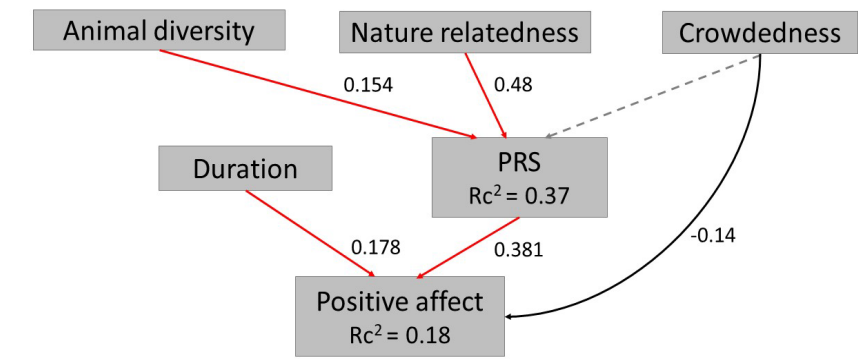


Figure 2: Structural equation models depicting the relationship between the characteristics of the walk and subsequent change in positive affect (positive mood) from a study performed by the researchers. PRS: Perceived Restorativeness Scale.

suggested a genetic component to our love for nature. Indeed, the orientation towards nature derived from our study was estimated to be 46% heritable. This means that “nurture” is still the main determinant of our love for nature. These results would reconcile both the biophilia hypothesis and the large variability in nature orientation that is observed.

### Would climate change threaten the biodiversity-happiness link?

Given the importance of spending time outdoors for our well-being, it is worrying whether climate change could sever our connections with nature. With the climate becoming increasingly warmer, exacerbated by the urban heat island effect, spending time in nature may become thermally uncomfortable. Moreover, extreme weather events like droughts could affect the composition and diversity of the ecosystems around us, reducing their appeal. Climate change, which reduces the liveability of Singapore and our capacity to enjoy its diverse nature, could potentially have severe economic and health

consequences.

In future research efforts, we plan to work towards identifying solutions which help our ecosystems become more resilient to climate change so that they can continue to provide the biodiversity-happiness link for our enjoyment. This could include research studies on the pattern of people’s daily activities under different climatic conditions by using GPS traces from their mobile phone signals. Other related studies could include different ways on the use of greenery to cool down the ambient temperature of our urban environment. Interestingly, the inverse relationship could also be true: would exposing people to nature get them to act more sustainably, contributing to mitigate the effects of climate change? Our initial results seem to validate this point, further reinforcing the idea that spending time in nature has a wide variety of benefits for people and the planet.

For more details, please visit: <https://blog.nus.edu.sg/bioeconlab/>

Roman CARRASCO is an Associate Professor with the Department of Biological Sciences, NUS. He completed his PhD in spatial bioeconomic modelling at Imperial College London. His research focuses on developing spatial models that combine ecology and economics to answer sustainability questions. Prof Carrasco is currently the Assistant Head of the Department of Biological Sciences and helps coordinate the MSc in Biodiversity Conservation and Nature-based Climate Solutions.

#### References

[1] T. Nghiem, et. al., “Biodiverse urban forests, happy people: Experimental evidence linking perceived biodiversity, restoration, and emotional wellbeing” URBAN FORESTRY & URBAN GREENING Volume: 59 Article Number: 127030 DOI: 10.1016/j.ufug.2021.127030 Published: 2021.

[2] C.-c. Chang, et. al., “Life satisfaction linked to the diversity of nature experiences and nature views from the window” LANDSCAPE AND URBAN PLANNING Volume: 202 Article Number: 103874 DOI: 10.1016/j.landurbplan.2020.103874 Published: 2020.



# Fungi: The good, the bad and the mysterious

Origin and evolution of plant-fungus associations and their functional roles in the ecosystems

## Introduction

For most of us, fungi appear either as the delicious (or not) components on our dinner table, or as the obnoxious moulds causing food spoilage and various diseases. However, fungi are far more than these. Their presence is ubiquitous, from soil to oceans and the air that we breathe in. They also live within other organisms, ranging from plant leaves and roots to the human gut and skin. Fungi have long established intimate interactions with other organisms. Some fungi can promote the health of other organisms, while others are pathogens. However, for the vast majority, their ecological roles remain elusive. In fact, even their presence is elusive as many fungi are only known to us as DNA fragments obtained from environmental samples. With increasing interest in the study of environmental microbes, more and more new fungal species are being discovered. It has been estimated that the total fungal species ranges from one to 10 million, while those known number only around 150,000.

As one of the few mycological laboratories in Southeast Asia, our team focuses on two fundamental questions -- what fungi are there in the local ecosystems and what do they do? As mycologists, our work involves documenting the fungal diversity in the region and characterising their ecological functions. This advances our understanding of fungi and also helps with efforts in adjacent fields such as bio-conservation and bio-remediation.

## Mangrove endophytic fungi – the diversity and their ecological functions

Since our establishment last year, our team has been exploring fungal diversity in mangrove forests. We are particularly interested in fungi that live within mangrove trees – the

endophytic fungi. These fungi, by definition, are living within the hosts but generally do not cause any disease symptoms. In fact, many of them are known to promote host resistance to biotic and abiotic stresses and play roles in maintaining the health of plants. The endophytic fungi, even though mostly invisible to us, are an integral part of the ecosystem which includes the mangroves. However, little is known about the mangrove endophytic fungi, especially in this region.

Since December 2021, our team has sampled 80 trees from 11 mangrove species in Pulau Ubin and isolated over 700 different strains of endophytic fungi from 80 genera (see Figure 1 and 2). Most of these endophytic fungi were not selective with their host tree and could be found in various tree species. However, many of them showed preference for certain types of plant tissue. For instance, the most common fungi from our collection, *Colletotrichum*, was mostly found in the leaves. *Trichoderma*, the fungi often known as the plant helper, was mainly associated with the branches and roots but rarely with the leaves.

Interestingly, there was a significant proportion of plant pathogens in our endophyte cultures. Among the top 10 most abundant fungal genera, five of them are known to be plant pathogens, making up 33% of the total number of endophyte strains. This is quite intriguing as all the samples were obtained from healthy plant tissues. With so many pathogens present, it is puzzling why the mangrove trees are not displaying any notable disease symptoms. A possible explanation could be the “beneficial” interactions among the different endophytes. As different endophytes compete for resources, it is likely that their actions inhibit each other’s growth and as a result none of them are able to proliferate.

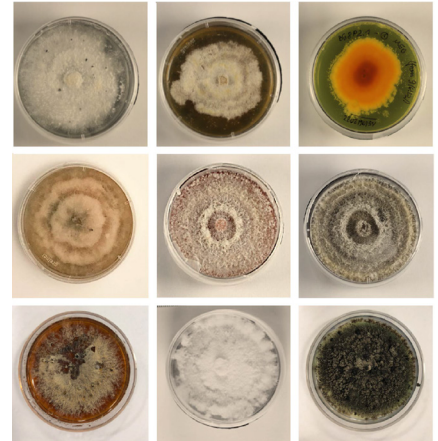


Figure 1: Examples of endophyte fungi growing in culture.

Experiments are being conducted in culture conditions to investigate the interactions between these endophytic fungi. Our team has also identified many latent pathogens in our culture collection. Latent pathogens reside quiescently in healthy hosts. When the host plants are stressed and their immune systems are weakened, these fungi switch on their pathogen mode and start to attack the hosts. Given the prevalence of latent pathogens in our mangrove forests, environmental stresses could potentially trigger disease outbreaks in them.

## Reverse ecology – are the ecological functions of fungi linked to their genomes content?

While experiments using fungal cultures can help us assess certain parameters associated with fungi, the ecological functions performed by them in nature are much harder to quantify. For many fungi species, their ecological functions are described based on limited observations and/or extrapolations from related ones. With the rapid accumulation of fungal genome data, there exists an opportunity to infer the functions of these fungi using a reverse ecology approach. This could be achieved by establishing a suitable

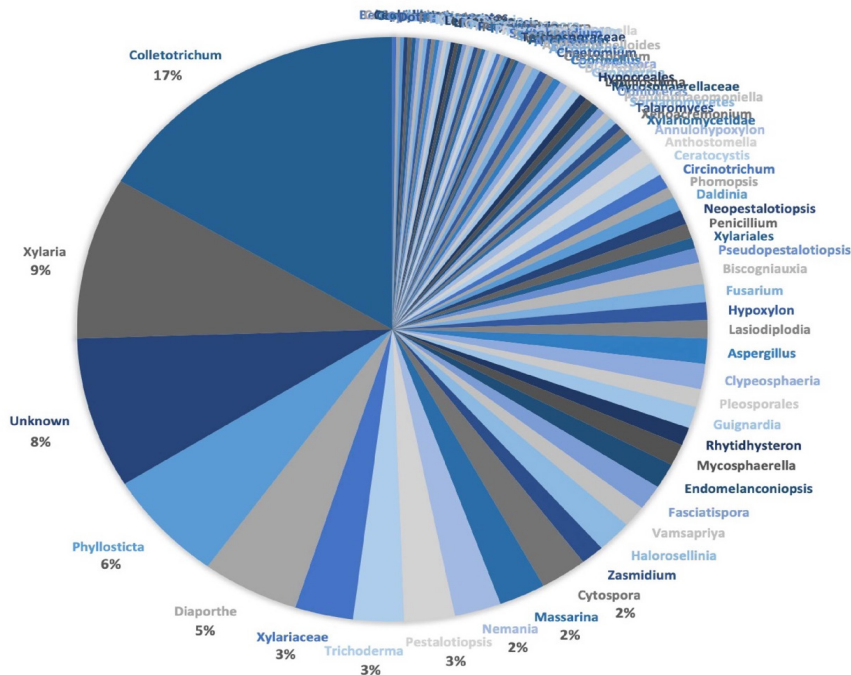


Figure 2: The relative abundance of fungal genera among our endophyte collections.

relationship between the genome content and the related ecological functions provided by the fungi.

To tackle this question, our team focused on the genes involved in encoding the secreted proteins in the fungi. Fungi utilise these secreted proteins to digest food, to defend themselves against predators and competitors, and to deal with various abiotic stresses. Therefore, the composition of these secreted proteins is believed to be tightly linked to the ecological functions provided by the fungi.

Our team performed a kingdom-wide study to study the above hypothesis. A comparative analysis on 132 fungal genomes revealed that the saprotrophic fungi (i.e. fungi that obtain their nutrients from non-living organic materials and degrade them in the process) generally

possess a large number of digestive enzyme genes [1]. In contrast, fungi living within their hosts, such as parasites or mutualistic symbionts, had much fewer digestive enzyme genes. These findings fit well with our expectations. As decomposers, the saprotrophic fungi secrete digestive enzymes into the environment to break down the complex bio-polymers (e.g. cellulose) into small simple molecules (e.g. glucose) which can be readily absorbed by the fungi. For symbiotic fungi, their food is generally available as smaller molecules within the hosts so the need for digestive enzymes is low. In addition, when the fungi secrete more enzymes, they are more likely to be detected by the host defence systems. Therefore, symbiotic fungi tend to possess fewer number of digestive enzymes compared with their saprotrophic relatives. Also, the symbiotic fungi have an inherent

need to avert or damp down the hosts' immune system. This is often achieved by using "small secreted proteins (SSP)". In our study, a higher proportion of SSPs has been observed in symbiotic fungi compared with saprotrophic fungi. Further analysis proved a statistically significant correlation between secreted protein composition and fungal ecological guilds.

In addition to the "expected" findings described, there were surprises as well. The most interesting and alarming example is the distribution of CotH protein. This protein has been found in the Mucormycosis-causing black fungi. These opportunistic pathogens are commonly found in the environment and pose no threat to healthy humans. However, they can cause the deadly Mucormycosis in immune-compromised patients. As an example, there has been a report from India on black fungus infections in COVID 19 patients. Studies have shown that CotH protein plays a key role in the invasion of the host cells by the fungi.

In our study, CotH was found with a surprisingly wide distribution among the sampled genomes. Given the opportunistic nature of the black fungi, this wide distribution of CotH suggests that there might be many more potential human pathogens than those currently known. In addition to CotH, a number of other pathogenicity-related proteins were found in saprotrophic fungi. Do these saprotrophic fungi have other ecological roles? Do the pathogenicity-related proteins have other functions? Either way it invites further investigation.

For more details, please visit: <https://www.dbs.nus.edu.sg/staffs/ying-chang/>

Ying CHANG is an Assistant Professor with a joint appointment at the Department of Biological Sciences, NUS and Yale-NUS college. Her research focuses on the characterisation of species and functional diversities of fungi using multiple approaches ranging from culturing-based experiments, to comparative genomics and metagenomics.

Reference

[1] Chang Y\*; Wang Y; Mondo S; Ahrendt S; Andreopoulos W; Barry K; Beard J; Benny GL; Blankenship S; Bonito G; Cuomo C; Desiro A; Gervers KA; Hundley H; Kuo A; LaButti K; Lang BF; Lipzen A; O'Donnell K; Pangilinan J; Reynolds N; Sandor L; Smith ME; Tsang A; Grigotiev IV; Stajich JE; Spatafora JW, "Evolution of zygomycete secretomes and the origins of terrestrial fungal ecologies" ISCIENCE Volume: 25 Issue: 8 Article Number: 104840 DOI: 10.1016/j.isci.2022.104840 Published: 2022.





# Wildlife and ecosystem functioning

Understanding the downstream effects of the biodiversity crisis is crucial for self-sustaining Southeast Asian forests

## Introduction

The tropical forests of Southeast Asia (SEA) are among the most biodiverse and productive ecosystems in the world. However, defaunation from decades of overhunting and habitat degradation have reduced many areas into “empty forests”, impoverished ecosystems where only a few small-sized or resilient animal species remain. The scale of the problem is staggering. In an analysis of monitored wildlife populations, the 2022 WWF Living Planet Report shows that monitored wildlife populations in the Asia-Pacific have declined in abundance by over 50% on average since 1970 [1], though it is worth noting that these estimates are possibly underestimates: population-level data for many animal species is lacking and these numbers do not account for the wholesale loss of habitat for wildlife.

Moreover, while these numbers reflect a crisis for wildlife, they do not fully capture the impact of defaunation on natural ecosystems. As animals play many important functional roles in tropical forest ecosystems such as seed dispersal, pollination and the regulation of plant populations, there is growing concern that the pervasive decline or loss of animal populations, also known as defaunation, may lead to downstream effects on ecosystem structure and diversity. Some studies have even shown that the loss of large animal seed dispersers may lead to the gradual erosion of the carbon capacity of forests, as typically carbon-dense animal dispersed trees are gradually replaced by those of less carbon-dense wind dispersed species. The “emptying” of forests in SEA may thus undermine global efforts to reduce greenhouse gas emissions, avert biodiversity loss and restore degraded habitats.

But despite the potential long-term

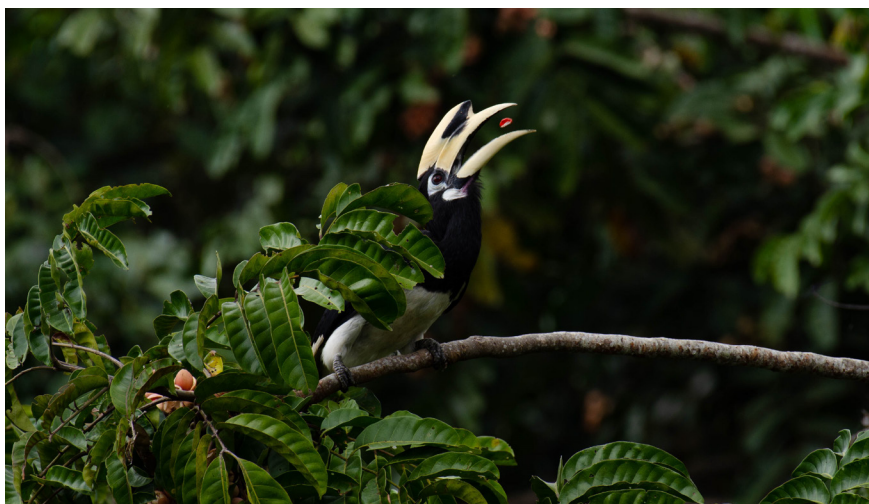


Figure 1: Hornbills play important roles as seed dispersers in the tropical forests of Asia (Khao Yai National Park, Thailand) [Photos: Jun Ying LIM]

consequences of defaunation on natural ecosystems, its impacts – particularly in SEA – remain poorly understood. At the Plant Ecology, Evolution and Biogeography laboratory, we study how plants and animals interact to shape ecosystems as well as how human impacts may be affecting this crucial dynamic.

## Building seed-dispersal network models

Seed dispersal is a crucial part of the life cycle of plants. Seeds that find a foothold far from their parent plants may enjoy reduced competition for resources or threat from “natural enemies” such as herbivores which may be found in higher densities near adults. As a testament to the importance of this crucial ecological process, up to 90% of the woody species in tropical forests rely on animals for seed dispersal (see Figure 1). Thus in many ways, seed dispersal underpins the rich plant diversity of our tropical forests.

Unsurprisingly, plants have evolved an incredible diversity of ways to attract and entice fruit-eating animals, from fleshy seeds to juicy pulps and far-reaching scents. Considering that different plants

employ different strategies to attract seed dispersers, predicting how the loss of seed dispersers will impact SEA forest ecosystems is not straightforward. Seed dispersal interaction data in the region is not readily available, missing for many species, and the collection of such data is labour intensive while only providing snapshots of an animal’s preferences in a particular area.

To leverage the existing but sparse observational data, my laboratory employs a big-data analytical approach. Together with wildlife and seed dispersal ecologists from across the region, we are compiling the largest seed dispersal database for the region. Using this database, we will develop new statistical methods (including machine learning approaches) that can make probabilistic predictions of interaction probabilities between seed dispersers and various plants in the region. The novelty of our models is that it constructs these statistical relationships by using information on both the animal species and the plants themselves. As a simple example, the size of a seed that a given fruit-eating bird can disperse is fundamentally limited by how large it can open its mouth. With trait information

on both animal and plant, one can make predictions on the likelihood of an interaction between any given plant-animal pair. Such models will allow us to project the true impact of defaunation on plant diversity in SEA forests, identify important frugivores for conservation prioritisation, and also species with high restoration potential.

### Estimating the impact of defaunation on forest carbon

The loss of large seed dispersers will lead to a gradual change in the species composition of tree communities, with potentially detrimental effects on forest carbon. However, it is unclear if such an effect may be expected in SEA, where the forests contain a higher proportion of wind-dispersed species such as the emblematic dipterocarps. Furthermore, while large animals often serve as seed dispersers, they also influence vegetation composition and structure in other ways. Large herbivores such as elephants disturb the vegetation as they move and forage in forest understoreys. Such activities can have significant effects on the functioning of the ecosystem. For example, the mortality of small trees caused by African forest elephants has a paradoxical effect of promoting the abundance of larger and more carbon-dense trees, thus increasing the above-ground carbon storage of African rainforests [2] (see Figure 2).

To explore the influence of SEA animals on above-ground carbon stocks of forests in the region, my laboratory has put together data from over 5,000 forest plots, the culmination of work from hundreds of forest ecologists in the region and beyond. Using structural equation models, we will examine the

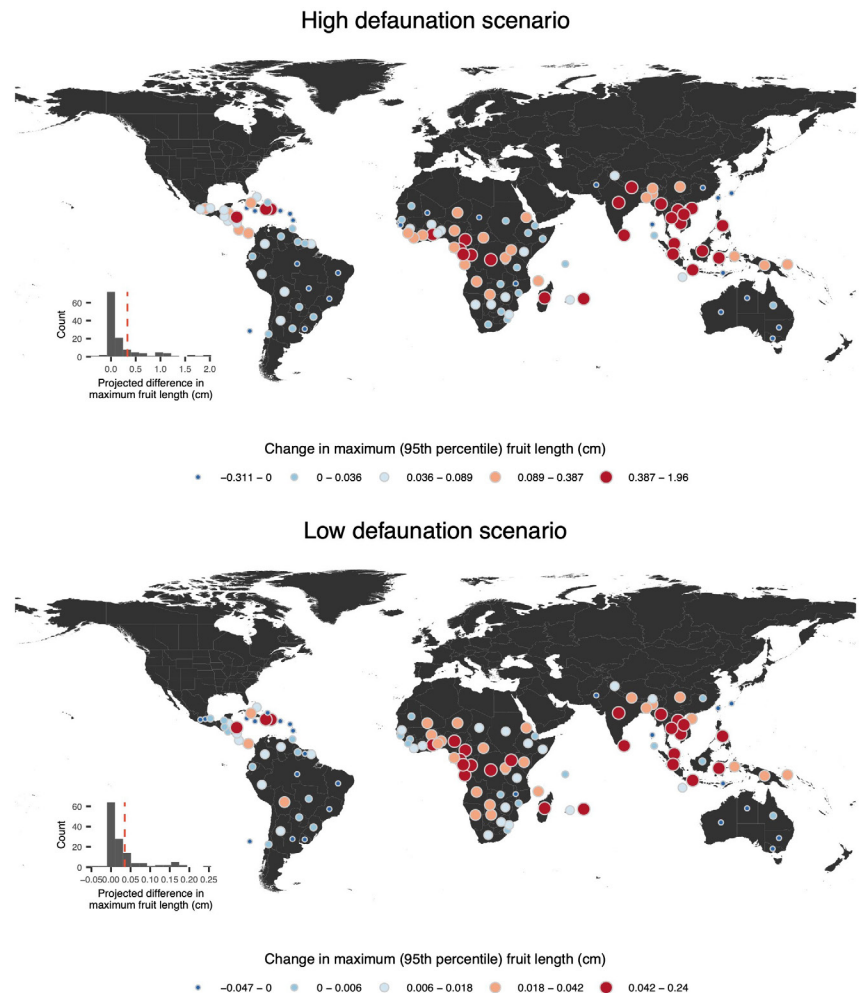


Figure 2: Estimates of the magnitude of ecological and evolutionary change in fruit size (proxy for defaunation impact) for tropical palms to keep up with the potential loss of large mammalian seed dispersers. Tropical ecosystems in Southeast Asia are projected to be particularly vulnerable to defaunation, especially due to the extinction risk of large fruit-eating mammals such as rhinos and elephants. Modified from [2].

complex, causal relationships between climatic factors, and local fauna and forest structure at these sites. Subsequently, we will investigate how these changes in animal assemblages may then shape the capacity of SEA forests to store carbon.

laboratory will shed light on the myriad ways that wildlife enrich the biodiversity and ecosystems of SEA, and hopefully pave the way for holistic and sustainable strategies towards their greater protection.

Ultimately, the research from my

For more details, please visit: <https://peeb-lab-nus.com/>

Jun Ying LIM is an Assistant Professor with the Department of Biological Sciences, NUS and a principal investigator at the Centre for Nature-based Climate Solutions. He studied and trained at Imperial College London (2009–2013), later receiving a Ph.D. in Integrative Biology from University of California, Berkeley (2013–2018). After post-doctoral stints at the University of Amsterdam and Nanyang Technological University, he joined NUS as a faculty member in 2021. His research focuses on the ecology, evolution and biogeography of tropical ecosystems, with a focus on plant-animal interactions.

#### References

- [1] WWF (2022) Living Planet Report 2022 – Building a nature-positive society. Almond R.E.A., Grooten M., Juffe Bignoli D. & Petersen T. (Eds). WWF, Gland, Switzerland.
- [2] Berzaghi F, et al. “Carbon stocks in central African forests enhanced by elephant disturbance” NATURE GEOSCIENCE, 12,725–729. DOI: 10.1038/s41561-019-0395-6 Published: 2019.
- [3] Lim JY, et al. “Frugivore-fruit size relationships between palms and mammals reveal past and future defaunation impacts” NATURE COMMUNICATIONS, 11:4904. DOI: 10.1038/s41467-020-18530-5 Published: 2020.



## Lee Kong Chian Natural History Museum (LKCNHM)



The skeleton of the first record of a sperm whale in Singapore which was found dead off Jurong Island on 10 July 2015.

The Lee Kong Chian Natural History Museum (LKCNHM) is Singapore's only natural history museum, and a leading institution in Southeast Asian biodiversity research, education, and outreach. It is home to over a million biological specimens from Southeast Asia.

At the Museum, specimen-based research and curation are at the heart of scientists' main activities. Examples of research carried out over the past two years include an intensive survey of the Mandai forest, led by entomologist Dr HWANG Wei Song. Using a range of collection methods, the study generated more than 16,000 DNA barcodes and estimated more than 2,800 putative species to be present. Additionally, the discovery of a new freshwater fish species in Singapore, the saddle barb (*Barbodes sellifer*),

by vertebrates curator Mr Kelvin LIM, and Museum Honorary Research Affiliate Dr Maurice KOTTELAT, has emphasised the scientific significance of the Nee Soon Swamp Forest which is the last substantial pocket of freshwater swamp forest in Singapore. Such discoveries help to raise the conservation significance of our local forests and inform both restoration and development plans.

The Museum also organises a variety of educational and outreach programmes suitable for all ages with regular collaborations in place that host enticing workshops and competitions. In 2021, LKCNHM collaborated with St John's Island National Marine Laboratory to host the STEP Environment Camp, aimed at nurturing environmental stewardship among 100 youth participants from

across Asia. Additionally, a partnership with the NUS Centre for Nature-based Climate Solutions to equip educators with knowledge on climate change, biodiversity and nature-based solutions also took place.

As a safe-keeper of Singapore's natural heritage, the Museum not only seeks to share knowledge with the public, but also recognises the value of our collections among the scientific community, which supports biodiversity research and conservation in Singapore and the region.

Overall, we hope that all who visit the Museum can be empowered to become environmental stewards in their own way, and act as guardians of Singapore's natural biodiversity.

For more details, please visit: <https://lkcnhm.nus.edu.sg/>



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