

Science

FINDINGS

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"Science affects the way we think together."
Lewis Thomas

Disease Detectives: Mapping the Risk of Invasive Forest Pathogens Under a Changing Climate



J.B. Friday

Widespread tree mortality caused by the myrtle rust pathogen (*Austropuccinia psidii*) in an ohia forest on the Hawaiian island of Molokai in 2019. Researchers identified genetic subgroups of the pathogen and projected where it can be expected to thrive across the globe as climates change.

"Diseased nature oftentimes breaks forth in strange eruptions."

— William Shakespeare

Most plants within the Myrtaceae (myrtle) family may be unfamiliar to many of us in the Pacific Northwest, but products from these plants, such as cloves, allspice, eucalyptus oil, or guava, are likely more familiar. The myrtle family includes more than 7,000 species of evergreen trees and shrubs found in the tropics or subtropics. Many of the trees have eye-catching flowers or foliage that are used in floral arrangements or planted in gardens. They are also sources of fruits, essential oils, or timber products that are traded around the world.

Many plants in the myrtle family are particularly vulnerable to myrtle rust, a disease of

the foliage or other green tissue that is caused by the fungal pathogen *Austropuccinia psidii*. After the spores of the myrtle rust pathogen land on a plant's vibrant green leaves, the symptoms and signs of myrtle rust disease soon appear. First, small purple spots emerge. Within these spots, yellow pustules form; these pustules contain spores that can cause new infections. As the infection matures, the yellow becomes grey, and soon, if there are many spots, the leaves wither and fall away. Any newly formed foliage that is infected also may die shortly thereafter. If the tree continues to lose its energy-producing leaves, it dies.

As the spores are carried by the wind or rain farther through the forest, orchard, or plantation, more trees are infected by this fungal pathogen. Eventually, large areas of a forest can succumb to the disease.

IN SUMMARY

Brown root rot (caused by *Phellinus noxius*) and myrtle rust (caused by *Austropuccinia psidii*) are natural disturbances in their native tropical and subtropical forest ecosystems. A tree infected with either fungal pathogen becomes unhealthy and likely dies, sometimes within 3 months. These pathogens are threatening forest ecosystems around the world as they spread through international trade or other means, such as by wind or through the soil. Climate change also is creating environmental conditions that will allow these pathogens to survive in novel forest ecosystems where they haven't been found historically.

An international team headed by researchers with the USDA Forest Service and Colorado State University analyzed the genetics of the two pathogens and mapped their likely spread based on the current locations of the various subgroups of each pathogen and contemporary and projected future climates. They found that distinct genetic subgroups of each pathogen occupied different ecological niches and caused varying damage to host trees.

The genetic diversity of these pathogens creates a potent threat, and this information is critical for agencies that regulate trade. The Hawaii Department of Agriculture, for example, is working with the USDA Animal Plant Health Inspection Service to prohibit the importation of plants in the myrtle family from locations where myrtle rust pathogens of a specific genetic subgroup are known to occur.



Rose apple (*Syzygium jambos*), a plant in the Myrtaceae family, showing signs and symptoms of myrtle rust: bright yellow, powdery spores on both sides of the leaf; red, deformed leaves and stems; and dead leaves.

“Forest diseases cause more long-term damage to forest ecosystems than all other natural disturbances combined, including beetles and wildfires,” explains Mee-Sook Kim, a research plant pathologist with the USDA Forest Service, Pacific Northwest Research Station. “And, forest disease impacts will continue to increase due to invasive pathogens, climate change, and other disturbances.”

Such a situation is playing out in Australia. Nearly a decade ago, myrtle rust emerged in eastern Australia, where diverse Myrtaceae species reside. The source of the myrtle rust pathogen is unknown, but it possibly arrived on infected plant material, or perhaps spores survived a trip across the ocean. In this new forest ecosystem, the myrtle rust pathogen spread widely, and many Myrtaceae species had little defenses to resist infection by this novel pathogen. The native guava (*Rhodomyrtus psidioides*) proved especially vulnerable. The once-widespread plant is now at risk for imminent extinction. An estimated 15 more woody species within the Myrtaceae family are also at risk for extinction on the Australian continent.

The Forest Service and other forestry agencies around the world employ plant and forest pathologists, such as Kim, to study forest pathogens and find methods to prevent their spread or mitigate their effects once they are detected.

A research team led by Kim; Ned Klopfenstein, a research plant pathologist at the Forest Service’s Rocky Mountain Research Station; and Jane Stewart, an associate professor who heads a tree pathology lab at Colorado State University, has developed one such tool that shows promise—a bioclimatic model that accurately predicted the appearance of myrtle

rust pathogen in eastern Australia and other areas around the world.

An Outbreak in Hawaii

The myrtle rust bioclimatic model originated during an earlier myrtle rust outbreak, this one on the other side of the Pacific Ocean. As the regional forest pathologist for the Forest Service’s Pacific Southwest Region, which includes California, Hawaii, and the U.S.-Affiliated Pacific Islands, Phil Cannon is accustomed to fielding questions about diseased trees.

In 2005, he fielded a call from Janice Uchida, a plant pathologist with the University of Hawaii, and Eloise Kilgore, with the Hawaii Department of Agriculture. They had observed what appeared to be myrtle rust on the exotic and invasive rose apple tree (*Syzygium jambos*). “Furthermore, 6 months after they found this pathogen in Honolulu, it could be found across every island in the Hawaiian chain,” says Cannon. “The myrtle rust pathogen can spread very fast.”

Myrtle rust is a forest disease with a well-documented history. The myrtle rust pathogen was first found in 1884 on guava (*Psidium guajava*) growing in Brazil; fast-forward 136 years, and the pathogen is now found in Florida, South and Central America, the Caribbean, and more recently in Southeast Asia, South Africa, Australia, and other regions.

Although the current subgroup of the myrtle rust pathogen didn’t appear to be causing much harm to the ohia tree, the pathologists fear that more aggressive subgroups of this pathogen could prove lethal to ohia. This would have devastating ecological consequences as the ohia tree is the most widespread native tree

species in Hawaii; it comprises 80 percent of trees in Hawaii.

“If the Hawaiian Islands lose the ohia tree, they face major ecological problems because considerable biodiversity is associated with ohia, and it’s the predominant tree in their watersheds,” Cannon explains.

To dive into myrtle rust’s genetics, Cannon reached out to Kim and Klopfenstein, both of whom he had worked with for more than two decades on forest pathogen research. “Mee-Sook is a leader of molecular genetics for forest pathogens in the Western United States,” he says. He also reached out to Acelino Alfenas, professor of plant pathology in Universidade Federal de Viçosa, Brazil. Alfenas tasked Rodrigo Graça, one of his Ph.D. students at the time, to collect numerous samples of myrtle rust from different host trees and different geographic locations in Brazil and bring these samples to the United States under an Animal Plant Health Inspection Service importation permit. The myrtle rust pathogen was genetically characterized at Washington State University and the Forest Pathology Lab at the Rocky Mountain Research Station in Moscow, Idaho.

Kim and Klopfenstein welcomed the new research project. With Graça, they developed a plan to investigate the pathogen. “Because the myrtle rust pathogen is associated with diverse hosts across a wide geographic area, our collaborative research began with characterizing the genetic diversity within this species,” Kim explains.

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Researchers have only recently begun to understand the genetic diversity of fungal pathogens. “Historically, fungi were identified morphologically,” says Stewart. “I’m finding that a lot of fungi with similar morphology can represent either different species or different biotypes, which can have different ecological behaviors.”

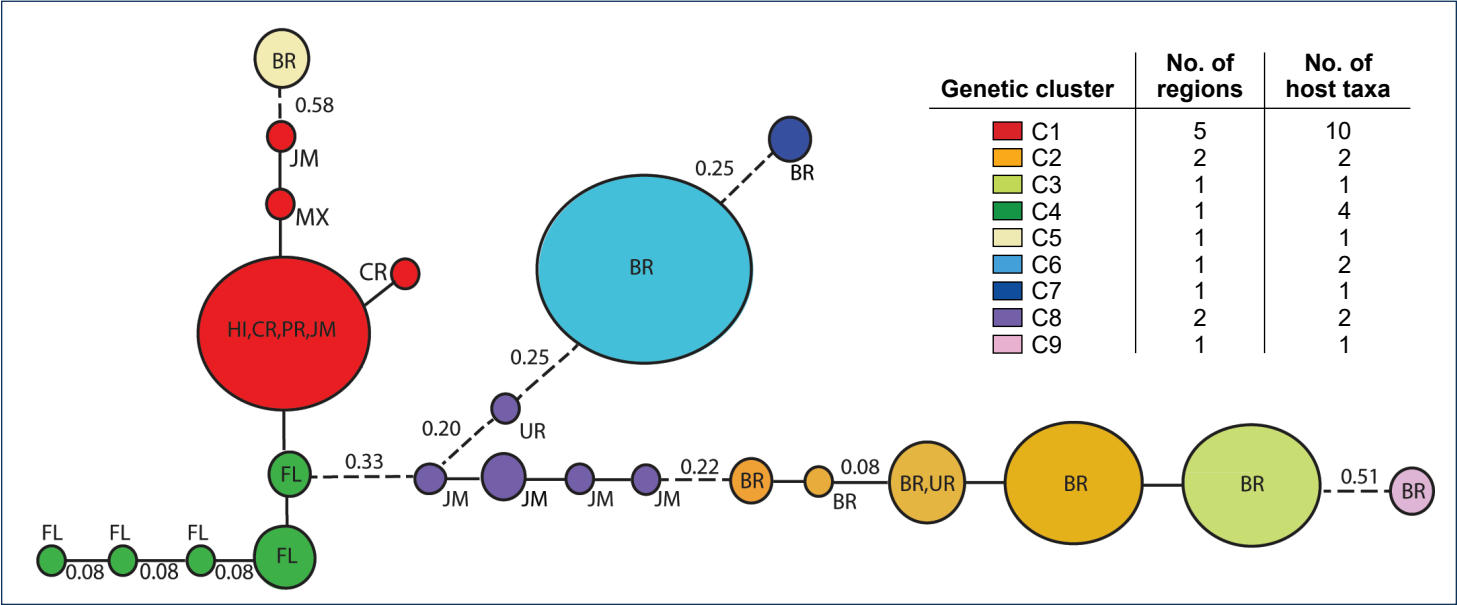
Researchers from six countries (Brazil, Costa Rica, Jamaica, Mexico, Uruguay, and the United States) collected 226 samples of myrtle rust and sent them to Stewart’s lab where her team analyzed their genetics. As Uchida and Kilgore suspected, there were indeed at least three different strains or subgroups of myrtle rust pathogen, which Stewart calls “biotypes.” These biotypes were named Pandemic, Guava-Brazil, and Eucalypt/Rose apple-Brazil. The Pandemic biotype was found in Hawaii.



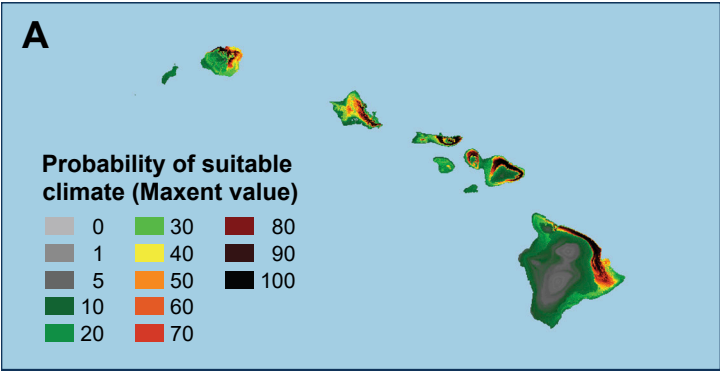
KEY FINDINGS



- *Phellinus noxius* and *Austropuccinia psidii* are invasive fungal pathogens that cause, respectively, brown root rot and myrtle rust, a foliar disease. Trees infected with these pathogens grow more slowly and can die from the disease. If these diseases are widespread, they can negatively affect an entire forest ecosystem.
- Genetic analyses determined that these two fungal species comprise several subgroups that occupy distinct niches and pose a threat to more plant species than originally known. More than 7,000 tree species in the Myrtaceae family are potential hosts of the myrtle rust pathogen.
- Bioclimatic models are used to predict current and future distribution of the brown root rot and myrtle rust pathogen subgroups. This technique can also be applied to other invasive forest pathogens.



The genetic analysis of myrtle rust samples revealed several unique pathogen genotypes that could be grouped in nine distinct genetic clusters (C1 through C9); each with characteristic host trees and geographic distribution. Circle size is proportional to genotype frequency, and distances between circles reflects genetic distance.



Geographic areas predicted to have suitable climate for the Pandemic subgroup (C1 and C4 genetic clusters) of the myrtle rust pathogen, which is currently found in Hawaii. Although only the Pandemic subgroup of the myrtle rust have been found in Hawaii, bioclimatic modeling indicates the potential distribution of other genotypes, should they be introduced. Color shades ranging from green to red represent the increasing probability of suitable habitat for the pathogen.



Potential distribution of the Eucalypt/Rose apple-Brazil subgroup (C2 and C3 genetic clusters) of the myrtle rust pathogen if it were introduced to Hawaii. The state has banned imports of the plants in the myrtle family that can host these subgroups of the myrtle rust pathogen and pose a threat to the native ohia tree.

To better understand the different ecological niches where these genetic subgroups are found, John Hanna, a biological science technician also with the Rocky Mountain Research Station, worked with the team to develop a model that combined the climate data of 19 climate variables, such as annual mean temperature, annual precipitation, and precipitation of the driest quarter, with the GPS locations of the pathogen samples. From this model, they created a map to predict where myrtle rust pathogen and its pathogen subgroups could occur under the contemporary climate and where it could potentially occur in the future as a result of climate change.

“Before we published, John Hanna’s models had predicted that myrtle rust pathogen could occur in eastern Australia, New Zealand, New Caledonia,” Klopfenstein says. “It turned out exactly as the models had predicted, and that started giving us faith in the models.”

The model also predicted that the Eucalypt/Rose apple-Brazil subgroup could survive in Hawaii, while the Pandemic subgroup would find a suitable climate in Brazil. Both invasive scenarios pose great threats to the Myrtaceae plants in each of the respective geographic regions.

An Outbreak in Oceania

This modeling approach, which was developed by John Hanna, proved successful for another emerging forest pathogen that Cannon brought to the team for analysis. In 2009, he contacted the foresters of the 10 most populated U.S.-Affiliated Pacific Islands and asked if they had any forest pathogen issues. A couple responded, describing the same issue. A “black sock” would appear around the bottom of the tree, and the tree was often dead within the next few months.

Cannon visited several islands to observe the disease firsthand, and he determined its likely cause was *Phellinus noxius*, which causes a disease known as brown root rot (also known as black sock disease). “When a tree becomes infected, it starts losing its leaves, and about 3 months later, it often falls over because this fungal pathogen has destroyed the wood,” he explains. “It’s just a sensational fungal pathogen to work on. I’ve never seen anything consume wood like this fungus.”

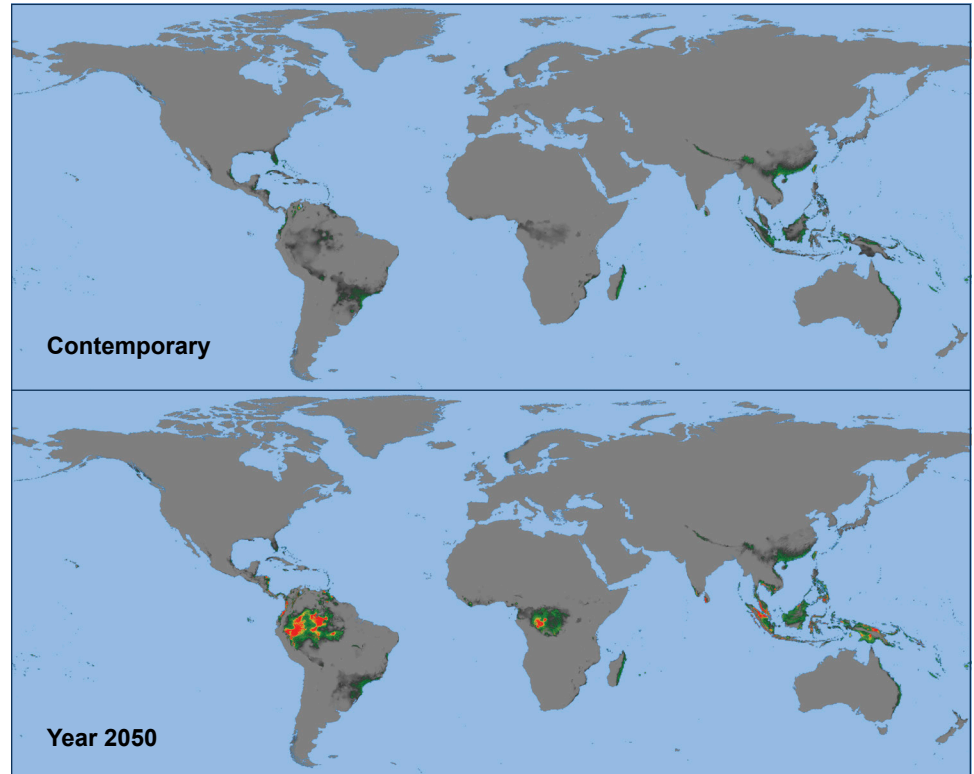
In some situations, the disease was used as a forest management tool. “In some Oceania islands, brown root rot disease has been there for a long time,” explains Klopfenstein. “They learned to use the disease for clearing small forest patches so they could grow other crops, like sweet potatoes.”

Yet, on other islands, the disease was killing a food source. “One of the most seriously affected trees are breadfruit (*Artocarpus altilis*),” Cannon says. “Breadfruit is the staple that, after fish, provides the most valuable food on most of these US-Affiliated Pacific islands.”

Like myrtle rust, the origin of brown root rot disease is also unknown. Cannon reached out to Kim, Stewart, and Klopfenstein to see if they were interested in studying this pathogen’s genetics as well. They accepted the challenge and used a similar approach to that developed for myrtle rust. Cannon and collaborators from Japan, Hong Kong, Taiwan, Malaysia, and Oceania sent 95 samples to Kim and Stewart for analysis.

Foresters and land managers in eastern Asia had a vested interest in learning more about this forest pathogen due to the cultural importance of their trees that were vulnerable to brown root rot disease.

“In Hong Kong, older trees were so culturally important that the government would spend tens of thousands of dollars for metal scaffolding to prevent these trees from falling on people,” Klopfenstein says. “People had a spiritual



Bioclimatic models produced by John W. Hanna

Brown root rot is currently found in regions of Oceania and eastern Asia. Bioclimatic models suggest that the pathogen can likely survive in many other regions, including Hawaii and Florida, if introduced. Color shades ranging from green to red represent the increasing probability of suitable habitat for the pathogen.



Ned Klopfenstein

A college student in Saipan, the largest of the Northern Mariana Islands, helps survey for trees infected with brown root rot.



LAND MANAGEMENT IMPLICATIONS



- Identifying genetic subgroups of forest pathogens and their geographic distribution is essential for addressing threats of invasive pathogens and developing forest management approaches to mitigate the ecological damage from the diseases caused by these pathogens.
- Forest managers can use information about current and predicted future distributions of invasive forest pathogens to plan and implement strategies designed to minimize the impacts of pathogens on diverse forest ecosystems.
- Bioclimatic modeling can inform development of regulatory policies and guidelines to prevent the importation of invasive forest pathogens or pathogen subgroups into countries with vulnerable forest crops or ecosystems.

relationship with these trees. In Taiwan, they had street trees that were of high value, so they were doing fungicide injections. We typically only think about these tree diseases in the abstract because they aren't in our backyards, but when you see how people have immediate concerns to their livelihoods and culture, this sheds a new light on how we consider the impacts of these tree diseases."

The genetic analyses revealed the brown root rot pathogen had substantial genetic diversity and at least three distinct subgroups: eastern Asia, western Oceania/Japan/Taiwan, and American Samoa. More worrisome, more than 400 tree species are vulnerable to brown root rot. Results from a bioclimate model revealed that although brown root rot is currently found in eastern Asia and Oceania, this fungal pathogen could potentially survive in South America, Africa, Europe, the Caribbean, and the Southeastern United States.

Preventing Future Outbreaks

The bioclimate modeling and genetic research that Kim, Stewart, Klopfenstein, and their colleagues have undertaken has greatly aided the state agencies tasked with managing for invasive tree pathogens and federal agencies that oversee the import and export trade. Because of the team's findings that Hawaii's ohia trees are vulnerable to the Eucalypt/Rose apple-Brazil subgroup of the myrtle rust pathogen, the Hawaii Department of Agriculture is working with the USDA Animal Plant Health Inspection Service to prohibit the importation of Myrtaceae species that could carry the Eucalypt/Rose apple-Brazil pathogen subgroup.

Stewart's lab is developing a tool that regulatory agencies can use to test plant material for

the presence of different biotypes or subgroups of the myrtle rust pathogen. "If a new subgroup is present, they can prevent that material from entering into the country or state," Stewart says. And, because the results will be available within a couple hours, "this tool will certainly be helpful from a management and regulatory perspective."

Taking these proactive measures to prevent the establishment of an invasive forest pathogen is key, says Klopfenstein. "Usually, people don't worry about an invasive pathogen until after it has invaded," he says. "And, once a pathogen has invaded, there's very little we can do to stop it from spreading. If we can prevent the entry of an invasive pathogen, we've accomplished a big service."

Managers of the forested landscapes will also benefit from this research, says Kim. "The genetic characterization of forest pathogen coupled with bioclimate modeling helps inform management about forest disease. This kind of information can be used to establish quarantine, regulatory policies, and other strategies for disease management."

Genetics work also is underway to help foresters in states and territories grappling with other forest pathogens and diseases. As for what makes this work possible, Kim emphasizes that this research relies on collaboration. "Without international collaboration, we couldn't have accomplished our genetic characterization and bioclimate modeling," she explains. "With invasive forest pathogens, international collaboration is probably the most important key to accomplishing this work."

"The general formula of [ecological] management for the future might be, think globally and act locally."

—Rene Jules Dubos,
microbiologist

For Further Reading

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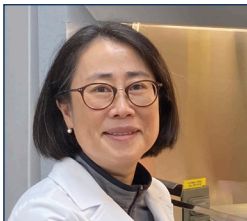
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