

# Researchers sequence myrtle rust genome

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Dr Peri Tobias wearing a T-shirt printed with some of the billion letter genetic code of the myrtle rust fungus.  
Credit: University of Sydney

The invasive fungus myrtle rust has been attacking native plants, driving some to the brink of extinction. Dr Peri Tobias and her team hope that sequencing the entire genome can help the plants fight back.

Scientists in Australia and New Zealand have built the entire genetic map of the fungus responsible for myrtle rust, an invasive disease that has brought at least three [native plant species](#) to the brink of extinction since its introduction to Australia a decade ago.

The result is the world's largest assembled [fungal genome](#), taking up a billion letters of DNA genetic code. If you printed the genome it would take up more than 400,000 A4 pages.

This discovery marks an important step towards unlocking genetic features of *Austropuccinia psidii*, which drives the disease threatening myrtle [plants](#) in Australia and New Zealand. Commonly affected plants in Australia include horticultural staples such as bottlebrush, paperbark trees, lilly pillies, tea-trees and many eucalyptus species.

The research has been published in the journal

*G3: Genes, Genomes, Genetics*.

The genome project was initiated by Professor Robert Park led by Dr Peri Tobias from the School of Life and Environmental Sciences and the Sydney Institute of Agriculture at the University of Sydney. Dr Tobias said: "Assembling this genome was a huge collaborative effort. We were dealing with the output of new DNA sequence chemistry, new technology and newly developed software.

"This invasive fungus is very problematic for Australian plants of the Myrtaceae family such as eucalypts, paperbark and tea-tree. Some lesser-known species, like the native guava, scrub stringybark and silver malletwood, are now on the verge of extinction."

Dr Tobias said that the genome of this fungus, which originates in South America, is so large because it is bloated with transposable elements, genetically unstable regions that can allow the introduction of new mutations.

"We think the [transposable elements](#) have been beneficial to the fungus by enabling it to adapt to infect new hosts. We are working to test these ideas experimentally," she said.

The University of Sydney is a global leader in rust fungus research and is this year celebrating a centenary of research into the rust fungus that affects global wheat crops.

The rust is widespread on Australia's east coast from southern New South Wales to far north Queensland. It is also found in nursery production sites around Melbourne.

The NSW Department of Primary Industries says that movement of myrtle plants in Australia is regulated and Tasmania, Western Australia, Northern Territory and South Australia have quarantine restrictions for the importation of myrtle plant products.

Worldwide there are 5500 plant species potentially affected by myrtle rust disease.

plants resistant to the fungus for better management of the disease."

Collaborator on the project and co-author Dr Grant Smith is a principal scientist at Plant & Food Research in New Zealand. He said: "If you're going to go after a pathogen, it is important to get some understanding of its genome."

**More information:** Peri A Tobias et al. *Austropuccinia psidii*, causing myrtle rust, has a gigabase-sized genome shaped by transposable elements, *G3 Genes/Genomes/Genetics* (2021). DOI: [10.1093/g3journal/jkaa015](https://doi.org/10.1093/g3journal/jkaa015)

At the time myrtle rust arrived in New Zealand in 2017, there was limited understanding of the *A. psidii* genome. Dr Smith came to Australia to present New Zealand's research intentions, which included sequencing the genome. While there, he was approached by Dr Tobias from the University of Sydney to work collaboratively on sequencing.

Provided by University of Sydney

"Instead of us trying to re-sequence what had already been started, we decided to pool our resources and effort to build on what Peri and her colleagues had begun," Dr Smith said.

He said that genome sequencing is like working on a three-dimensional jigsaw puzzle. The output from a sequencing instrument is millions of small segments. These are then assembled and aligned back to the chromosomes – the building blocks of a genome – from which they originated.

The genome took three months to assemble using the University of Sydney's high-performance computing facility.

"Other rust fungi have 80 million base pairs. *Austropuccinia psidii* is more than 10 times as big," said Dr Benjamin Schwessinger, a senior lecturer at the Australian National University and one of the collaborators on the project. By comparison, the virus causing COVID-19 has about 30,000 bases, about 27,000 times smaller.

Now that the genome has been sequenced, it can be used as a tool to investigate how *A. psidii* infects plants in the myrtle family and to look for ways to facilitate disease resistance. The team has started using the [genome](#) to get an idea of which pathogen genes and which host genes are interacting at the earliest points in the infection process.

Dr Tobias said: "We are looking at what makes

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