

Searching big data for disease resistance in crops

May 4 2016, by , Sciencenetwork Wa



Credit: AI-generated image ([disclaimer](#))

Researchers at the Centre for Crop and Disease Management are using big data approaches to study fungal genome evolution, which will one day lead to a better understanding of crop protection.

The CCDM, which is co-funded by Curtin University and the Grains

Research and Development Corporation (GRDC), has carried out research led by Dr James Hane.

Dr Hane is searching for atypical evolutionary relationships between [genes](#) in different species to help find genes that cause crop disease.

"The vast majority of genes are inherited vertically, that is, they are passed down from parent to child in the normal way," Dr Hane says.

"However very occasionally and especially in microbes, genes can "jump" across vast evolutionary distances—which is referred to as lateral gene transfer.

"We are comparing thousands of genomes in a large-scale evolutionary analysis to narrow down where genes have laterally transferred or "jumped" between species."

Genes that have been laterally transferred may hold clues to genes that help the pathogen survive, evolve and cause disease, Dr Hane says.

"For instance, we know at some point in history a very potent fungal disease gene—called ToxA—jumped from the pathogen causing yellow spot disease to the pathogen causing septoria nodorum blotch disease in wheat.

"Both pathogens are evolutionarily distant, yet they have the same gene that causes infection.

"We are looking for more genes like ToxA by comparing thousands of genomes and looking for unusual evolutionary patterns where genes are shared exclusively between two distantly related species, using the supercomputing resources at the Pawsey Supercomputing Centre."

By using the supercomputer Magnus, Dr Hane is currently searching a database of more than 3500 species, including fungi, bacteria, archaeobacteria, oomycetes, insects, plants and algae.

The process is computationally intense, Dr Hane says, as all of the genes from each species need to be compared to all of the genes in all other species resulting in more than 12 million comparisons, each with about 10,000 to 20,000 genes each.

"Genome sequencing and comparative genomics have come a long way, only 10 years ago we were working with just a handful of fungal species with whole genomes, now there are hundreds," Dr Hane says.

"We've moved our studies from working on a single reference genome for a single species, to comparing hundreds of genomes of the same [species](#)—with the increase in scale yielding new insights and improved accuracy."

Dr Hane says the results of his work in combination with others at the CCDM will be passed onto breeding companies to help breeders and growers to select disease-resistant crop cultivars.

This article first appeared on [ScienceNetwork Western Australia](#) a science news website based at Scitech.

Provided by Science Network WA

Citation: Searching big data for disease resistance in crops (2016, May 4) retrieved 17 July 2024 from <https://phys.org/news/2016-05-big-disease-resistance-crops.html>

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