

Complete genome of devastating soybean pathogen assembled

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Asian soybean rust. Credit: Peter van Esse

An international research collaboration has successfully assembled the complete genome sequence of the pathogen that causes the devastating disease Asian soybean rust.

The research development marks a critical step in addressing the threat of the genetically-complex and highly-adaptive fungus *Phakopsora pachyrhizi* which has one of the largest genomes of all plant [pathogens](#). Asian [soybean](#) rust has a devastating impact on soybean, an internationally important crop with 346 million tonnes produced globally.

In conditions favourable to its spread, the rust can destroy up to 90% of the soybean harvest. At present soybean growers in major areas of cultivation such as Latin America must use chemicals to protect crops.

The largest producer of the soybean is Brazil, where the combined cost of losses and disease control measures is US \$2 billion per season.

The new dataset comprises the [genome sequence](#) of three isolates (K8108, MG2006 & PPUFV02) of which one has been assembled at chromosome level detail (PPUFV02). These three genomes will be hosted by the Joint Genome Institute and will be made available over the coming weeks.

The three genomes will be repeat masked and annotated in the same way, to facilitate direct comparisons and inferences for the [research community](#). This will enable researchers to study the molecular mechanisms of the pathogen, paving the way for breeding and engineering of disease-resistant crops.

The [international consortium](#) behind the project comprised 11 research and industry partners: The 2Blades Foundation, KeyGene, the Joint Genome Institute (JGI), Bayer, Syngenta, the Brazilian Company of Agricultural Research (Embrapa), l'Institut National de la Recherche Agronomique (INRA—France), the German Universities of Hohenheim and RWTH Aachen, The Sainsbury Laboratory, and the Federal University of Viçosa (Brazil).

The soybean rust pathogen is highly adaptive and disease resistance genes present in soybean have been overcome rapidly, and the pathogen is building resilience against the current generation of fungicides. These two factors leave few solutions for controlling the disease in the field.

Two of the three isolates that the consortium have sequenced are from Brazil, where the impact of soybean rust is a huge problem for farmers.

Phakopsora pachyrhizi has a highly complex [genome](#), it is 60 times bigger than the yeast genome, composed of 93% repetitive elements and possesses two nuclei.

This complexity has delayed progress on the sequencing of this pathogen, and meant that high-end, next-generation sequencing technologies were required to complete the task.

Given the importance of this disease, KeyGene made their PromethION machine (an industry first) and their sequencing and bioinformatics experts available pro bono. This way ultra-long DNA-sequencing reads of the pathogen and a high quality nanopore assembly were produced. This allowed Dr. Yogesh Kumar Gupta from the 2Blades group to generate a chromosome level assembly of the isolate PPUFV02, of which the DNA was provided by their long-term collaborator Prof. Sérgio Brommonschenkel at the Federal University of Viçosa (Brazil).

The consortium has also generated a transcriptome atlas of all the fungal structures and infection stages of the pathogen.

"Asian soybean rust is a critical challenge for soybean growers," said Dr. Peter van Esse, leader of the 2Blades Group at The Sainsbury Laboratory, Norwich, one of the collaborators.

"A chromosome level genome assembly allows the scientific community

to study, in unprecedented resolution, components of the pathogen that are critical for causing disease. This is a critical first step towards the design of transformative control strategies to combat this highly damaging pathogen."

The three soybean rust genomes will be hosted by the Joint Genome Institute and are available here - mycocosm.jgi.doe.gov/Phapa1

Provided by John Innes Centre

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