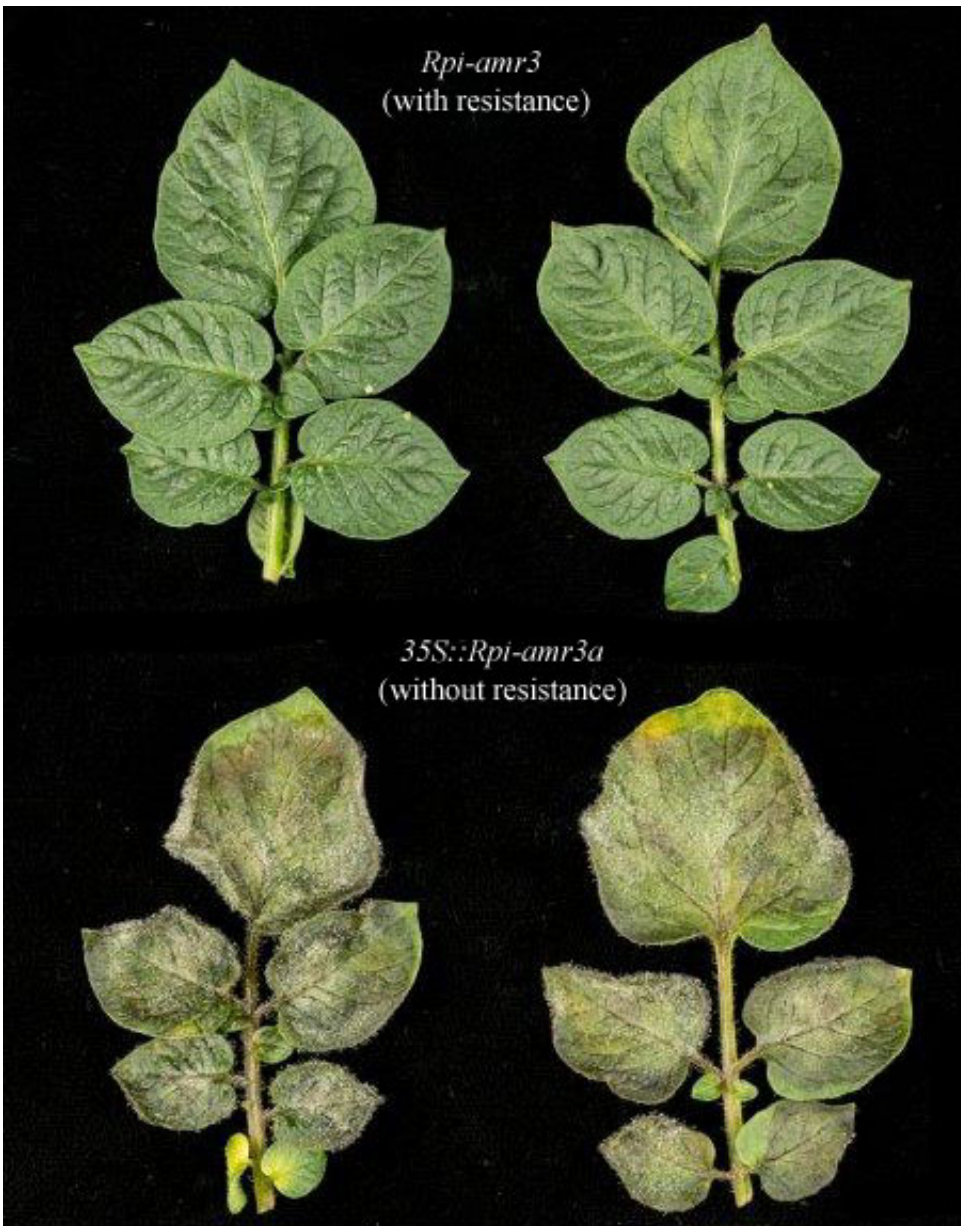


New technique accelerates isolation of potato late blight resistance genes

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Several candidates were introduced into a model species, of which one (*Rpi-*

amr3) successfully provided broad-spectrum blight resistance. Credit: The Sainsbury Laboratory

A team of scientists from The Sainsbury Laboratory (TSL) and The Genome Analysis Centre (TGAC) have developed a new method to accelerate isolation of plant disease resistance genes. The team have also identified a brand new source of blight resistance genes in *Solanum americanum*, a wild relative of the potato.

Plant pathogens such as late blight can evolve rapidly to overcome resistance genes, so scientists are constantly on the hunt for new resistance genes. Professor Jonathan Jones and colleagues from his lab at TSL pioneered the new technique, called "SMRT RenSeq", and believe it will significantly reduce the time it takes to define new resistance genes.

The team plan to stack several resistance genes together in one plant, to make it much harder for pathogens to evolve to overcome the plant's defences. It is hoped the deployment of this new technique will improve commercial crops and will lead to higher yields, significantly reduced environmental impact and lower costs for the producer and eventually the consumer.

Potato late blight remains a major threat to potato and tomato production, with world-wide crop losses estimated to be in excess of £3.5 billion. Prevention measures and crop losses cost UK potato farmers around £55 million a year, and on farm blight management can account for as much as half of the total cost of potato production.

Managing the disease requires frequent application of fungicides, which incurs not only a significant economic cost but also environmental costs.

Genetic resistance can be introduced into crop species, which reduces the need for chemical spraying. However, using conventional breeding techniques, deploying [genetic resistance](#) is long and laborious.

Sources of new plant resistance genes are difficult to find. The TSL team investigated the wild potato relative, *Solanum americanum*, which carries several resistance genes, and by using the new technique, rapidly isolated a new resistance gene, Rpi-amr3.

SMRT RenSeq makes the process of finding, defining and introducing genetic resistance far quicker and easier by combining two sequencing techniques: 'RenSeq' (Resistance gene ENrichment SEQuencing) and 'SMRT' (Single-Molecule Real Time sequencing).

The technique consists of two main steps:

1. A sub-set of DNA sequences are "captured" using a method that selects for long DNA molecules that carry a sequence that is commonly associated with resistance genes.
2. These DNA molecules are sequenced multiple times to make sure the code is determined as accurately as possible using the novel long-read SMRT technology.

This results in a very reliable DNA sequence for each candidate resistance gene. Genetic analysis of the results enabled the team to define which of these candidate genes were linked to blight resistance. Following this, the SMRT RenSeq method also enabled the team to identify and define the parts of the genome which regulate the resistance genes. Several candidates were introduced into a model species, of which one (Rpi-amr3) successfully provided broad-spectrum blight resistance. The Platforms & Pipelines Group at TGAC performed the sequencing, led by David Baker.



Professor Jonathan Jones and colleagues from his lab at TSL pioneered the new technique, called 'SMRT RenSeq', and believe it will significantly reduce the time it takes to define new resistance genes. Credit: The Sainsbury Laboratory

Professor Jonathan Jones said: "Engineering disease resistance genes into crops is a continuous battle to stay one step ahead of new strains of disease, and scientists are constantly investigating how to speed up this process. This [new technique](#) significantly reduces the time and cost of isolating candidate resistance genes, and has great potential for application to other desirable traits in potato and in other crops."

TGAC Project lead and Plant & Microbial Genomics Group Leader at TGAC, Dr Matt Clark, said: "Our cultivated potatoes and tomatoes are

highly susceptible to potato blight, as thousands of years of selective breeding has brought with it a huge loss in genetic variation. However, within closely-related wild species, it is possible to find natural resistance to such pathogens. Finding and using disease resistance genes from closely related plants is critical in the arms race against crop pathogens. This technique accelerates the process and we hope will help reduce crop losses to disease."

This paper is one of three papers which will be published together in *Nature Biotechnology* on Monday 25 April 2016. The other two papers focus on finding new [resistance genes](#) for soybean rust (by Dr Peter Van Esse, The Sainsbury Laboratory) and wheat stem rust (by Dr Brande Wulff, the John Innes Centre).

More information: Accelerated cloning of a potato late blight–resistance gene using RenSeq and SMRTRT sequencing, *Nature Biotechnology*, [DOI: 10.1038/nbt.3540](https://doi.org/10.1038/nbt.3540)

Provided by John Innes Centre

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