

## New sequencing technique will make cloning genes for disease resistance in plants easier

[The] constant evolutionary arms race between plants and pathogens, whereby the organisms causing disease in plants are mutating to avoid plant defences, causes the plants to evolve through changes in their own genetic makeup. This is where a huge variety of R [Resistance] genes come into play that are highly similar in structure and DNA sequence.

Researchers at the Earlham Institute (EI), The Sainsbury Laboratory (TSL) and the James Hutton Institute, have found a new way to decipher these large stretches of DNA to discover and annotate pathogen resistance in plants.

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Dr Matt Clark, ... lead author of the study, said: "Wild relatives of crops contain a huge repertoire of novel genes that could be used to breed more resistant varieties that need less pesticide treatments. When it comes to identifying key genes it can be very difficult for researchers to find the exact resistance gene due to the sheer similarity of their DNA sequences.

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Professor Jonathan Jones, Senior Scientist at TSL and co-author, said: "This improvement to the RenSeq method will greatly facilitate building reliable inventories of R genes in multiple plant species, helping us clone additional genes that could protect our crops."

**The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis. Read full, original post:** Forming a second line of plant defence – capturing disease-resistant DNA