

## **Tracking a crop disease could save millions of lives**

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Scientists have discovered why one of the world's most important agricultural diseases emerged, according to research published in the September issue of the *Journal of General Virology*. Maize streak virus (MSV) causes the main virus disease of Africa's most important food crop. By comparing the genome of the virus to those of its less harmful relatives, scientists have discovered how and why MSV became a serious pest and spread so rapidly across Africa.

"Given the fragility of African agriculture and perpetual famine risks with millions of lives at stake, MSV is actually one of the most important plant pathogens worldwide," said Dr Darren Martin from the University of Cape Town in South Africa. "We wanted to learn more about how the virus emerged and spread so we can develop new ways to fight the diseases it causes."

There are many different strains of MSV but only one of these causes a severe disease in maize. The others cause relatively mild infections in other grassy food crops such as wheat, oats and sugarcane. Scientists have known for some time now that the "maize adapted" MSV strain is peculiar; all versions of the virus that have been sampled throughout the entire African continent are genetically almost identical. The researchers looked at strains of the virus that infect natural grasses and compared these to the maize adapted strain. The results show that the maize adapted strain is even more unique than was previously thought.

"We found that the maize adapted virus infects a greater variety of



grasses than any of the other MSV strains," said Dr Martin. "The virus appears to be spreading around Africa faster than the other strains too. When we compared the genomes of 11 different strains of MSV, we discovered that lots of genes had been exchanged between the strains in a process called recombination. We also found that every MSV that causes severe disease in maize has descended from an ancestral virus that was the recombinant offspring of two relatively harmless wild grass infecting viruses. This chance recombination event could be the reason MSV has become such a serious problem."

All available information suggests that over 100 years ago, two grass adapted MSVs recombined to produce a new "wide-host range" strain that could infect a greater variety of other plants than its parents. This meant the virus could survive the winters in wild grasses more effectively than its relatives – something that potentially increased the speed at which it spread across Africa. The ability of this recombinant strain to infect many different host species may have also enabled it to rapidly adapt to maize – a process that today has led to its emergence as an economically important crop disease.

"Understanding the chain of events that trigger the emergence of novel pathogens is a major goal of epidemiologists worldwide," said Dr Martin. "There is a lot of circumstantial evidence suggesting how evolutionary processes like recombination might trigger the emergence of a pathogen but there are actually very few well documented examples of this having occurred."

The next step is to carry out rigorous tests to provide more evidence for the specific biological causes of the emergence of MSV. The researchers also hope to develop different genetic strategies to help the crops resist disease. "Comparing important pathogens with their "agriculturally irrelevant" relatives can tell us useful stuff about the pathogens," said Dr Martin. "Knowing that maize adapted MSVs are unusually mobile I hope



will prompt scientists to test MSV resistance genes against the large bank of virus strains that we have catalogued from across Africa."

"We are currently testing various resistance strategies, some in an advanced stage of development, using many of the viruses we've sampled. Complex genetic strategies like stacking resistance genes and targeting different virus components that cannot be simultaneously exchanged by recombination might ultimately be the only way to control the disease."

Source: Society for General Microbiology

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