



## The Identity and Role of Maize Cuarto Virus in Mal de Rio Cuarto Disease

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**Disease caused by Mal de Rio Cuarto virus (MRCV) causes devastating crop losses for many producers in Argentina.** In the late 1990s, MRCV affected about 1.2 million acres of maize which resulted in \$120 million in losses. The disease continues to be an annual threat to maize production in Argentina. This MRCV is of particular economic concern to U.S. hybrid seed companies as Argentina produces many of the hybrid seeds for the U.S. market. Future hybrids intended for the U.S. market are also tested on Argentine research plots.

The ever-threatening MRCV is a species of virus in the Reoviridae family, genus *Fijivirus*. There are two other very closely related fijiviruses, Maize rough dwarf virus (MRDV) and Rice black-streaked dwarf virus (RBSDV). The characteristic symptoms of MRCV infections are swellings, referred to as enations, occurring on the underside of leaves. These enations actually look like tiny tumors that run along the leaf veins. The economically significant effect of the virus infection is the dwarfing of the maize which produces smaller plants that are far less productive. Although the three viruses are related and the effects of the diseases are similar, little is known about MRCV compared to MRDV and RBSDV.

## OBJECTIVES

The objectives of this study were to first identify any possible differences in mild and severe MRCV; characterize the relationships; and then develop a reliable assay for identification. The complete genome sequence of RBSDV was determined by a Japanese group and was available from GenBank. Partial genome sequence information was obtained by an Italian group for MRDV. Argentine scientists had sequenced five segments for MRCV.

Using available information on RBSDV and MRDV, OARDC scientists determined that there are 10 genome segments for MRCV isolates that produced both mild and severe symptoms. Once the genome segments for MRCV isolates were determined, scientists were then able to partially sequence the remaining segments.

## CHALLENGES

The major problem with developing control methods for MRCV is that up until this project, there were no reliable techniques to determine if a plant is infected by MRCV, MRDV, or RBSDV. Assays that are based on antibodies rose against the viruses and were not sensitive enough to distinguish between them. In particular, there was no sequence data available to scientists for MRCV. Thus, in order to work toward the goal of controlling MRCV in maize, the first step was to identify the genome sequence and then, using that information, develop an assay or test to accurately and reliably identify the viruses.

## ACHIEVEMENTS

The information obtained on MRCV sequence during this project provided enough information to allow OARDC scientists to develop species-specific primers using RT-PCR or reverse transcription-polymerase chain reaction. RT-PCR is a highly specific and extremely sensitive method for detecting the viral genome. The primers were tested to ensure that they reacted with all of the samples of MRCV and that they did not react with the other fivirus (MRDV or RBSDV) samples. These tests were successful in accurately identifying between the three different species of virus.

## FUTURE

Completion of the sequences of incomplete genome segments is planned and will be published for use by other scientists throughout the world. Development of control techniques has already started with industry funding in the amount of \$41,250 to look at the possibilities of using a technique called vascular puncture inoculation. This inoculation technique has the potential to allow scientists to develop a maize hybrid either resistant or partially resistant to Mal de Rio Cuarto disease.



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