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Review paper

Emerging plant virus disease: the case of maize yellow mosaic virus

Bayissa Regassa

Ethiopian Institute of Agricultural Research, Ambo Agricultural Research Centre, Ambo, Ethiopia.

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***Correspondence**
Bayissa Regassa
bregassa2019@gmail.com

A group of plant viruses and individual viruses have emerged as major threats to crop production worldwide. Emergent plant viruses are often mediated *via* an insect vector and with increasing global trade. Also, the emergence of a virus in a new geographical area may be initiated by the introduction of infected plant materials (propagative materials or seeds). The novel virus, named *Maize yellow mosaic virus* (MaYMV) consists potentially in a new constraint to maize production worldwide. MaYMV epidemics are multi-component systems resulting from interactions among the viruses, vectors and host plants. MaYMV was transmitted by corn leaf aphid, *Rhopalosiphum maidis*, but not mechanically. In addition to maize, MaYMV was harbored by alternative hosts such as sugarcane, itch grass sugarcane, *Panicum miliaceum*, and *Sorghum bicolor.* Knowledge of the ways in which a virus maintains itself in the absence of a living host and spreads in the field is essential for the development of effective management measures. More research is needed to assess MaYMV in weeds and wild hosts, whether transmitted through seeds and the relative abilities of different aphid species to transmit MaYMV within and between different grass species to know the virus ecology and infection pathway to maize, to aid the development of an effective integrated disease management tactic.

Key words: *alternative host, distribution, emerging virus, symptoms, transmission*

INTRODUCTION

Epidemics of existing plant virus diseases and the emergence of novel virus diseases have become a major threat to subsistence and commercial agriculture. Rapid climatic changes create favorable conditions for development and an increase in the spread of plant viruses due to direct or indirect influences on population dynamics of virus-transmitting insect vectors (Prasannath et al., 2015). Obtaining the epidemiological information needed for each virus patho system involves gathering information about the main source of infection, how the virus spreads in and out of plants, how it spreads to invade new sites, and how it survives without growing time. After that, a clear picture is needed of the factors that cause the virus to be infected, which are the most important ones that often spread and delay their epidemic (Roger, 2004).

Emerging plant disease

Emerging diseases are defined as those that occur in a population for the first time, or that may have existed previously but are rapidly increasing in incidence or spatial areas in the past 20 years causing considerable damage (Damstegt, 1999; Castillo et al., 2015). Globally, the number of newly emerged plant diseases has increased dramatically in the last few years. A comprehensive study of international infectious plant disease by Aronson et al. (2004) showed that among plant viruses, viruses account for about half (47%) of new plant diseases followed by fungi (30%), bacteria (16%), phytoplasma, nematode, and others take up the remaining 7%. A virus that already exists when conditions allow or when it is introduced to a new environment or new viruses or a new type of vector or biotype can cause a recurrent plant virus infection.

Factors Influencing Virus Disease Emergence

There can be various different factors that enable the emergence of a plant virus disease. These include genetic variables such as random mutations, recombination, long-distance spread to new agroecosystems and changes in vector population dynamics (Rojas and Gilbertson, 2008). An authoritative study on the factors deriving the global emergence of plant virus shown that introduction from other countries makes up 71%, followed by a change in vector numbers (16%), climate (5%), recombination (5%) and farming practices (3%) (Aronson et al., 2004). The main factors contributing to the emergence of plant viruses are agricultural production systems based on mono-cropping with low genetic diversity and high crop density; trade-in plant germplasm and live vegetation that move viruses, hosts, and vectors to new locations; climate change affecting the distribution area of hosts and vectors; and the potential of viruses for rapid evolution and adaptability (Jones, 2009; Elena et al., 2014). Humans are well-known for their direct or indirect transmission of the virus. Specifically, people donate 1) a new virus or type of virus that is often linked to the movement of seeds or plant-based substances as a result of germplasm or seed trade, 2) a new vector or biotype (e.g., aphids, whiteflies, thrips and whiteflies) and, 3) a new crop or new species at risk during crop diversification. A weak isolation/quarantine system where viral testing can be performed using reliable and sensitive techniques such as ELISA and PCR may contribute to this situation. Humans can also indirectly induce changes in agronomic activities due to modern agricultural practices by planting monocultures or exotic plants, by introducing agricultural practices such as irrigation to improve the spread of the virus, or by relying too much on chemical controls that vector-resistant. In addition to humans, viruses can be introduced into the world by using air vectors at borders as many can fly long distances. Finally, annual or long-term climate change can increase the spread of viruses (Abraham, 2019). Increased temperature changes affect host plant physiology, metabolic pathways, nutritional status, phenology and morphology (Canto et al*.,* 2009; Jones and Barbetti, 2012). Heat stress and rising temperatures increase the susceptibility of hosted plants to viral infection and decrease rather give the virus firmness that causes infection (Mitchell et al*.,* 2005). Increased temperatures in addition change the repetitive levels of plant virus, the systematic movement of individual virus found in mixed infections (Jones, 2016).

The emergence of Maize yellow mosaic virus

The novel virus, called *Maize yellow mosaic virus* (MaYMV, classified in genus *Polerovirus* of the family *Luteoviridae*), was first reported to infect maize (*Zea mays* L.) in China in 2016 (Chen et al*.,* 2016). All members of the *Luteoviridae* are of great economic importance (Ellis et al*.,* 2013). The *Luteoviridae* family currently comprises 26 virus species in three genera and a novel *polerovirus*, the MaYMV of the *Luteoviridae* family was first identified as the most threat to a crop plant (maize) of paramount economic value. The virus was identified from the symptomatic field-grown maize plants showing yellowing, whitish to yellow stripes, and mosaic on maize and sugarcane (Chen et al., 2016; Palanga et al., 2017; Guide et al., 2018; Sun et al., 2019).

History and Global distribution of MaYMV

MaYMV is likely to be a new menace to maize production worldwide (Gonçalves et al., 2020). It has been estimated that MaYMV causes yield losses of 10-30% (Bernreiter et al., 2017). MaYMV was first reported in the world in maize from Asia, China in 2016 (Chen et al., 2016) and thereafter MaYMV in maize plants was reported and identified in other countries of Asia, Latin America and Africa.

Table 1. ***Maize yellow mosaic virus*** **global distribution.**

Continent/Country	Year (first report)	Reference
LATIN AMERICA		
Brazil		Gonçalves et al., 2017
Ecuador	2017	Bernreiter et al., 2017
ASIA		
China	2016	Chen et al., 2016
South Korea	2018	Lim et al., 2018a
AFRICA		
Nigeria	2017	Yahaya et al., 2017
Tanzania	2018	Read et al., 2018
Burkinefaso	2017	Palanga et al., 2017
Kenya	2018	Massawe et al., 2018
Rwanda	2018	Massawe et al., 2018
Uganda	2018	Massawe et al., 2018
Ethiopia	2018	Guide et al., 2018
South Africa	2020	Welgemoed et al., 2020

MaYMV Alternative hosts

In-plant virus disease management, it is important to understand the role of alternate hosts in the emergence and development of disease epidemics (Regassa et al., 2021). Since the emergence of MaYMV, this virus was found to infect diverse plants in the family *Poaceae,* including maize (Gonçalves et al., 2017), itch grass (*Rottboellia cochinchinensis*) and sugarcane (*Saccharum* spp.) in Nigeria (Yahaya et al., 2017), *Panicum miliaceum*, and *Sorghum bicolor*in South Korea (Lim et al., 2017). MaYMV infecting sugarcane also reported in China (Sun et al., 2019). In addition to maize, the detection and identification of MaYMV in perennial sugarcane, itch grass, *Panicum miliaceum*, and *Sorghum bicolor*, indicate their potential roles as reservoir hosts of the virus. The identified alternative hosts (Weed and cultivated plants) of plant viruses including MaYMV are epidemiologically important and maintain the virus inoculum in the absence of the host plants in the field, and support the survival of the virus for continuous infection (Regassa et al., 2021).

MaYMV Transmission mechanism

Insect transmission is the most widely distributed method of transmission of a plant virus in the field. Because of the strong boundary of the cell wall and plant stability, many plant viruses need vectors to be transmitted to new host plants or to a new habitat (Blanc and Drucker, 2011). About 80% of plant viruses depend on insect vectors for transmission, and plant viruses show a high degree of specificity of a group of insects that can transmit them. Vectors of plant viruses are very different taxonomically and can be found in arthropods, nematodes and fungi (Froissart et al., 2002; Hull, 2002). The *Polerovirus* genus is one of three genera established in the family *Luteoviridae*; the other two have been *Luteovirus* and *Enamovirus* (King et al., 2018). *Poleroviruses* are transmitted in a circular, non-propagating way by several species of aphids (*Aphididae*, Insecta), but not by mechanical or seed means (Krueger et al., 2013). MaYMV is a member of *Poleroviruses*, a transmission study conducted by (Gonçalves et al., 2020) shows that the maize leaf aphid, *Rhopalosiphum maidis* is a MaYMV vector based on transmission tests using any infected plants collected. "daughter" infected plants as sources of MaYMV. The MaYMV classification obtained by aphid transmission created symptoms of mosaic. The study also revealed that MaYMV was not transmitted by infected plants (corn) to healthy plants by mechanical means.

Identification methods of MaYMV

Plant viruses are generally can be diagnosed and identified by using a various technique including symptom observation, particle morphology observation under an electron microscope, mechanical or vector transmission to indicator host plants, detection using virus-specific antibodies (serological assay) (Davis and Ruabete, 2010, Regassa et al., 2020) and nucleic acid based (polymerase chain reaction) (Bhardwaj and Kulshrestha, 2020).

Reverse transcription polymerase chain reaction

The universal PCR technique is applicable directly to DNA plant viruses (Hema and Konakalla, 2021); it is not directly applicable to most plant viruses that have RNA genomes. Including MaYMV, about 70 % of identified plant viruses have RNA genome (Bhat and Rao, 2020). For the identification and detection of RNA viruses, Reverse transcription polymerase chain reaction (RT-PCR) is a standard method, which involves the first step of reverse transcription that converts single strand RNA to a complementary DNA (cDNA) copy with the aid of the enzyme reverse transcriptase before the starting of PCR (Bhat and Rao, 2020). RT-PCR has been used to detect MaYMV in maize (Planga et al., 2017; Guadie et al., 2018; Read et al., 2018), sugarcane and itch grass (Yahaya et al., 2017; Sun et al., 2019).

Sequencing

Sequencing is a very reliable technique for virus identification. Next-generation sequencing (NGS) is one of modern identification techniques that have been used in the diagnosis of new unidentified plant viral diseases. NGS-based identification methods share a few familiar processes, for example the extraction of total nucleic acid (DNA or RNA) from the infected host plants, followed by fragmentation of the DNA for library preparation. By implementing a set of synthetic DNA adapters and primers to the fragmented DNA, one can use different sequencing chemistries and platforms for analysis (Mehetre et al., 2021). MaYMV has been identified using NGS after extraction of RNA from maize leaves (Chen et al., 2016; Palanga et al., 2017; Gonçalves et al., 2017; Welgemoed et al., 2020).

Management of MaYMV

Generally, plant virus disease management measures are aimed either at decreasing the virus source, or at preventing virus spread within the crop. However, management for newly emerged plant virus needs an understanding of the economic importance of a particular virus to a crop, the selection of which control measures to use requires detailed ecological and epidemiological knowledge (Makkouk and Kumari, 2009). MaYMV is newly emerged in the world; and hence, much is not known about its epidemiology except vector (aphids) (Goncalves et al., 2020) and few alternative hosts identified (Lim et al., 2017; Yahaya et al., 2017; Sun et al., 2019). Plant virus diseases including MaYMV are intrinsically difficult to manage directly by use of chemical pesticides; however, integrated management methods which include cultural practices such as removal of infection sources, field sanitation, removal of alternative hosts, use of healthy seed (virus free seeds); chemical pesticides to control insect vectors indirectly through seed treatment and foliar spray are the most possible management measures of plant viral diseases (Regassa et al., 2020; 2021). The removal of symptomatic plants, known as roguing, is a phtyosanitary control measure that is widely used to remove sources of virus infection from within crops (Makkouk and Kumari, 2009).

CONCLUSION

Since MaYMV is a newly emerged disease, despite its potential impact, much is not known about its epidemiology and control measures. Adequate field and laboratory research-based information will be required including more assessments of alternative hosts that the virus overwintering, insect vectors that transmitting the virus from plant to plant and associated factors that contribute to MaYMV disease epidemics including cropping system, cultural practices and environmental condition. Plant virus diseases including MaYMV are intrinsically difficult to manage directly by use of chemical pesticides; however, integrated management methods which include cultural practices such as removal of infection sources, field sanitation, removal of alternative hosts, use of healthy seed (virus-free seeds); chemical pesticides to control insect vectors indirectly through seed treatment and foliar spray are the most possible management measures of plant viral diseases. For such an approach to succeed, the epidemiology and associated factors influencing the geographical spread of the disease should have to be studied.

COMPETING INTERESTS

Not applicable.

ETHICS APPROVAL

Not applicable.

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