Journal of Environment and Earth Science
ISSN 2224-3216 (Paper) ISSN 2225-0948 (Online)
Vol.16, No.1, 2026 www.iiste.org

Emerging plant virus disease: the case of Maize Yellow mosaic virus: Review

Bayissa Regassa
Ethiopian Institute of Agricultural Research, Ambo Agricultural Research Centre, Ambo, Ethiopia

Abstract
Groups of plant viruses and individual viruses have emerged as major threats on crop production worldwide. Emergent plant viruses are usually mediated via an insect vector in increasing global trade, the emergence of a virus in a new geographical area may be initiated by the introduction of infected plant materials (propagative materials or seeds). Once introduced, the successful emergent virus expands into a new place via activity of an existing insect vector or, less frequently, through spread by physical contact. 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 between 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*. More studies are vital to evaluate MaYMV in weeds and wild hosts, whether transmitted through seed and the relative abilities of different aphid species to acquire and transmit MaYMV within and between different grass plants to understand the virus ecology and infection pathway to maize, to aid the development of an integrated disease management strategy.
Key words: Alternative host, Distribution, Emerging virus, Symptoms, Transmission
DOI: 10.7176/JEES/16-1-01
Publication date: February 28th 2026

1. Introduction

Epidemics of existing plant virus diseases and emergence of novel virus diseases have become a serious threat to subsistence and commercial agriculture. Maize yellow mosaic virus, a member of the genus Polerovirus, was first reported in the world in China in 2016 (Chen et al., 2016) and the recent reports of new cases in various parts of the world indicate that the virus is potentially emerging globally. Rapid climatic change creates favorable conditions for development and an increase in the spread of plant virus due to direct or indirect influences on population dynamics of virus-transmitting insect vectors (Pautasso *et al*., 2012).

Obtaining the critical epidemiological information required for each virus pathosystem includes collecting information on the nature of the primary virus infection source, how the virus spreads into and within crops, how far it spreads to invade new sites and how it survives outside the main growing period. After that, a clear picture is required of the factors that cause the epidemic of the virus concerned, which are the most important ones that tend to spread and delay their epidemic (Jones, 2001).

2. 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 (Castillo *et al*., 2015, Damstegt, 1999). Globally, the number of newly emerged plant disease has increased dramatically in the last few years. A comprehensive study of an 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 / viruses or a new type of vector or biotype can cause a recurrent plant virus infection.

2.1. Factors Influencing Virus Disease Emergence

There can be many factors that facilitate the emergence of a plant virus. These include genetic variables such as random mutations, recombination, long-distance migration 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 change in vector numbers (16%), climate (5%), recombination (5%) and farming practices (3%) (Aronson *et al*., 2004). The main factors contributing to 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 the like, 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 the 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).

2.2. The emergence of Maize yellow mosaic virus

The novel virus, named *Maize yellow mosaic virus* (MaYMV, classified in genus *Polerovirus* of 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 significant economic importance (Ellis *et al*., 2013). The family *Luteoviridae* currently includes 26 virus species in three genera and a novel *polerovirus*, MaYMV belonging to the family *Luteoviridae* was first identified in a crop plant (maize) of paramount economic value. The virus was identified from the field-grown maize plants showing yellow mosaic symptoms on the leaves.

The 5642 genomes of complete MaYMV long nucleotides shared the highest sequence of nucleotide sequences (73%) in the *Maize yellow dwarf virus*. Since MaYMV belongs to the *Polerovirus* genus, plant strains of the genus *Polerovirus* have genes of monopartite RNA about 5-6 kb long (Andrew *et al*., 2012) containing six open reading frames (ORF) called ORF0 I -ORF5, with three non-translated (UTRs), including 51 UTR, 31 UTR, and intergenic UTR between ORF2 and ORF3 (Mo *et al*., 2010; Krueger *et al*., 2013). ORF0-derived proteins have been shown to act as RNA-silencing suppressor (RSS) Mangwende *et al*., 2009; Kozlowska-Makulska *et al*., 2010) differs from members of the Luteovirus genus that lack ORF0 (Miller *et al*., 1995).

2.2.1. History and Global distribution of MaYMV

MaYMV consists potentially in a new constraint to maize production worldwide (GonÃ§alves *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, Chania in 2016 (Chen *et al*., 2016) and thereafter MaYMV in maize was reported and detected in other countries of Asia, Latin America and Africa.

Table 1. *Maize yellow mosaic virus* global distribution. This table provides the year in which first it has been reported in.

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
Ethiopia	2018	Guide *et al*., 2018

2.2.2. MaYMV symptoms

In most areas, MaYMV was identified from samples taken from symptomatic maize leaf 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**).

Figure 1. Maize yellow mosaic virus symptoms on maize: A= Yellowing, B= whitish to yellow strips, C and D= mosaic. **Source:** Chen *et al.,* 2016 and Palanga *et al*., 2017

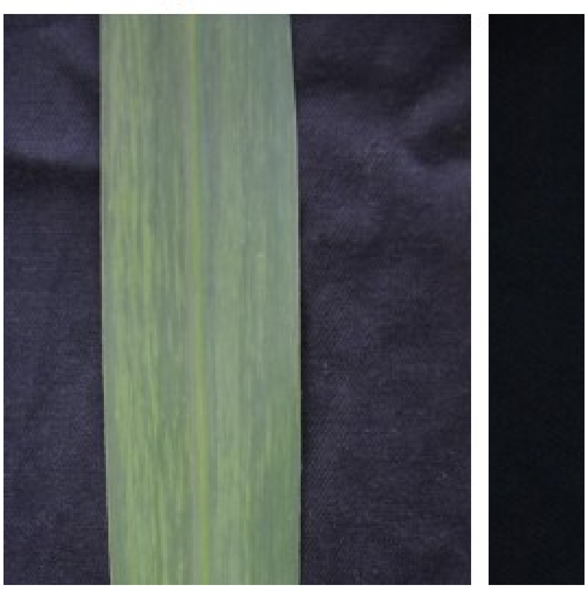

Figure 2. MaYMV symptom (yellowish stripes and mosaic) in sugarcane**.** *source:* **Sun *et al*., 2019**

2.2.3. 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. 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. Weed and cultivated plants identified as alternate hosts of MaYMV are epidemiologically important and maintain the virus inoculum in the absence of the host crop in the field, and support the survival of the virus for continuous infection.

2.2.4. MaYMV Transmission mechanism

Insect transmission is the most widely distributed method of transmission of 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 virus 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).

Plant viruses can be transmitted from plant to plant in different ways. They can be transmitted mechanically without the need for vectors (Luria *et al*., 2017; Wilstermann and Ziebell, 2019). Viruses can also be transmitted by seeds, pollen, or vectors such as fungi, mites, or nematodes (Hull, 2014). Phloem-feeding insects, such as whiteflies (Hemiptera: *Aleyrodidae*) and aphids (Hemiptera: *Aphididae*) are the most common carriers of plant viruses (Hogenhout *et al*., 2008). Aphids can be found all over the worldwide, and many species of aphids can act as virus vectors for one or more virus species (Stevens and Lacomme, 2017). It is estimated that about 50% of insect-vectored plant viruses are dependent on aphids for their transmission (Nault, 1997).

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.

2.3. Conclusions and recommendations for future research

Since MaYMV is newly emerged disease, despite its potential impact, much is not known about its epidemiology and control measures. Adequate field and laboratory research-based information including on its, 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. The knowledge of virus transmission and its survival are to understand how the disease transmits from infected to health plants, the virus spreads between and among maize fields and understanding the association of disease intensity with different cropping systems and cultural practices will help to identify the most important variables and focus efforts to develop sustainable management strategies.

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. More studies are vital to evaluate MaYMV in weeds and wild hosts, whether transmitted through seed and the relative abilities of different aphid species to acquire and transmit MaYMV within and between different grass plants to understand the virus ecology and infection pathway to maize, to aid the development of an integrated disease management strategy. Regular field monitoring, assessment of virus symptoms and rouging-out diseased maize plants are help to prevent further spread by insect vectors.

3. References

Abraham, A. 2019. Emerged Plant Virus Disease in Ethiopian Agriculture: Causes and Control Options. *Ethiopian Journal of Agricultural Science*, 29 (1), 39- 55.

Anderson, P. K, Cunningham, A. A., Patel, N G., Morales, F. J., Epstein, P. R., Daszak. P. 2004. Emerging infectious diseases of plants: pathogen pollution, climate change and agrotechnology drivers. *Trends in Ecol. & Evol*. 19: 535-544.

Andrew, M. Q. K., Michael, J. A., Eric, B. C., Elliot, J. L. 2012. Virus taxonomy. In Virus Taxonomy: Ninth Report of the International Committee on the Taxonomy of Viruses; Elsevier Academic Press Inc.: San Diego, CA, USA, pp. 1045–1053.

Bernreiter, A., Garcia Teijeiro, R., Jarrin, D., Garrido, P., Ramos, L. 2017. First report of maize yellow mosaic virus infecting maize in Ecuador. *New Disease Reports* 36:11

Canto, T., Aranda, M. A., Fereres, A. 2009. Climate change effects on physiology and population processes of hosts and vectors that influence the spread of hemipteran-borne plant viruses. *Glob. Chang. Biol*. 15, 1884–1894.

Chen, S., Jiang, G. Z., Wu, J. X., Liu, Y., Qian, Y. J., Zhou, X. P. 2016. Characterization of a novel polerovirus infecting maize in China. *Viruses* 8:120.

Damsteegt V. 1999. New and Emerging Plant Viruses. APSnet Features. Online. doi: 10.1094/APSnetFeature-1999-0999

Elena, S. F., Fraile, A. and Garcıá –Arenal, F. 2014. Evolution and emergence of plant viruses. *Adv. Virus Res*. 88, 161–191. doi: 10.1016/B978-0-12-800098- 4.00003-9

Gonçalves, M. C., Godinho, M., Alves-Freitas, D. M. T., Varsani, A., Ribeiro, S. G. 2017. First report of maize yellow mosaic virus infecting maize in Brazil. *Plant Disease* 101:2156–2157.

Gonçalves, M. C., Ramos, A., Nascimento, T., Harakava, R., Duarte, P. A., Lopes, R.S. 2020. Aphid transmission of maize yellow mosaic virus: an emerging polerovirus. *Tropical Plant Pathology* https://doi.org/10.1007/s40858-020-00374-5

Guadie, D., Tesfaye, K., Knierim, D., Winter, S., Abraham, A. 2018. Survey and geographical distribution of maize viruses in Ethiopia. *Eur. J. Plant Pathol*. 153, 271–281.

Hogenhout, S. A., Ammar, E.-D., Whitfield, A. E., Redinbaugh, M. G. 2008. Insect vector interactions with persistently transmitted viruses. *Annual Review of Phytopathology*, 46, 327–359. https://doi.org/10.1146/annurev.phyto.022508. 092135

Jones, R. A. C. 2009. Plant virus emergence and evolution: origins, new encounter scenarios, factors driving emergence, effects of changing world conditions, and prospects for control. *Virus Res*. 141, 113–130. doi: 10.1016/ j. virusres.2008.07.028

Jones, R. A. C. 2016. *Future Scenarios for Plant Virus Pathogens as Climate Change Progresses. Advances in Virus Research, 87–147.*

Jones, R. A. C., Barbetti, M. J. 2012. Influence of climate change on plant disease infections and epidemics caused by viruses and bacteria. CAB Rev. 7 (22), 1–32. http://www.cabi. org/cabreviews.

King, A. M. Q., Lefkowitz, E. J, Mushegian, A. R., Adams, M. J., Dutilh, B. E., Gorbalenya, A. E., Harrach, B., Harrison, R. L., Junglen, S., Knole, N. J., Kropinski, A. M., Krupovic, M., Kuhn, J. H., Nibert, M. L., Rubino, L., Sabanadzovic, S., Sanfacon, H., Siddell, S. G., Simmonds, P., Varsani, A., Zerbini, F. M., Davison, A. J. 2018. Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses. *Arch Virol*. 163:2601–31.

Kozlowska-Makulska, A., Guilley, H., Szyndel, M. S., Beuve, M., Lemaire, O., Herrbach, E., Bouzoubaa, S. 2010. P0 proteins of European beet-infecting poleroviruses display variable RNA silencing suppression activity. *J. Gen. Virol*. 91, 1082–1091. [CrossRef] [PubMed]

Krueger, E. N., Beckett, R. J., Gray, S. M., Miller. W. A. 2013. The complete nucleotide sequence of the genome of Barley yellow dwarf virusRMV reveals it to be a new Polerovirus distantly related to other yellow dwarf viruses. *Front Microbiol*. 4:205.

Krueger, E. N., Beckett, R.J., Gray, S. M., Miller, W. A. 2013.The complete nucleotide sequence of the genome of Barley yellow dwarf virus-RMV reveals it to be a new Polerovirus distantly related to other yellow dwarf viruses. *Front. Microbiol*. 4.

Lim, S., Yoon, Y., Jang, Y. M., Bae, S., Lee, Y. H., Lee, B.C. 2018a. First report of maize yellow mosaic virus on *Zea mays* in South Korea. Plant disease. 102 (9), 1864.

Lim, S., Yoon, Y., Jang, Y. W., Bae, D. H, Kim, B. S., Maharjan, R., Yi, H, Bae, S., Lee, B. C., Lee, Y. H., Park, C. Y., Lee, S. H., Moon, J. S. 2018b. First report of Maize yellow mosaic virus infecting Panicum miliaceum and Sorghum bicolor in South Korea. Plant Dis. 102:689.

Luria, N., Smith, E., Reingold, V., Bekelman, I., Lapidot, M., Levin, I., Dombrovsky, A. 2017. A new Israeli tobamovirus isolate infects tomato plants harboring Tm-2^2 resistance genes. PLoS One, 12(1): e0170429. https://doi.org/10.1371/ journal. pone.0170429

Mangwende, T., Wang, M. L., Borth, W., Hu, J., Moore, P. H., Mirkov, T. E., Albert, H. H. 2009. The P0 gene of Sugarcane yellow leaf virus encodes an RNA silencing suppressor with unique activities. *Virology*. 384(1):38-50

Miller, W.A.; Dinesh-Kumar, S.P.; Paul, C.P. Luteovirus gene expression. Crit. Rev. Plant Sci. 1995, 14, 179–211.

Mo, X.H., Chen, Z. B., Chen, J. P. 2010. Complete nucleotide sequence and genome organization of a Chinese isolate of Tobacco vein distorting virus. *Virus Genes*, 41, 425–431.

Nault, L. R. 1997. Arthropod transmission of plant viruses: A new synthesis. Annals of the Entomological Society of America, 90(5), 521–541. https://doi.org/10.1093/aesa/90.5.521

Palanga, E., Longué, R. D. S., Koala, M., Néya, J. B., Traoré, O., Martin, D. P., Peterschmitt, M., Filloux, D., Roumagnac, P. 2017. First report of maize yellow mosaic virus infecting maize in Burkina Faso. *New Disease Reports* 35:26

Read, D. A., Featherstone, J., Rees, D. J. G., Thompson, G. D., Roberts, R., Flett, B. C., Mashingaidze, K., Berger, D. K., Welgemoed, T., Pietersen, G., Schulze, S. E., Kiula, B., Kullaya, A., Mbega, E. 2018. First report of maize yellow mosaic virus (MaYMV) on maize (Zea mays) in Tanzania. *Journal of Plant Pathology* 101:203

Stevens, M., & Lacomme, C. 2017. Transmission of plant viruses. In H. F. van Emden & R. Harrington (Eds.), *Aphids as crop pests* (pp. 323–361). Wallingford, UK: CABI.

Wilstermann, A., Ziebell, H. 2019. Tomato brown rugose fruit virus (ToBRFV). JKI Data Sheets—Plant Diseases and Diagnosis, 1, 1–4. https://doi.org/10.5073/20190607-160917

Yahaya, A.A., Rwahnih, M., Dangora, D. B., Gregg, L., Alegbejo, M. D., Lava Kumar, P., Alabi, O. J. 2017. First report of maize yellow mosaic virus infecting sugarcane (Saccharum spp.) and itch grass (Rottboellia cochinchinensis) in Nigeria. *Plant Disease* 101:1335.

Ellis, M. H., Silva, T. F. Stiller, W. N., Wilson, L. J., Vaslin, M. F. S. Sharman, M., Llewellyn, D. J. 2013. Identification of a new Polerovirus (family Luteoviridae) associated with cotton bunchy top disease in Australia. *Australas. Plant Pathol*. 42, 261–269

Froissart, R., Michalakis Y, Blanc S. 2002. Helper component-transcomplementation in the vector transmission of plant viruses. *Phytopathology*, 92: 576-579.

Hull, R. 2002. *Matthew's Plant Virology*. Academic Press, New York, NY, USA.

Sun, S.R., Chen, J.S., Yang, J., Huang, X.C., Huang, M. T., Gao, S. G. 2019. *The American Phytopathological Society*, 103 (9). https://doi.org/10.1094/PDIS-04-19-0762-PDN

Jones, R. A. C. 2001. Developing integrated disease management strategies against non-persistently aphid-borne viruses: A model program. *Int. Pest Man. Rev*. 6:15–46.

Pautasso, M., Doring, T.F., Garbelotto, M., Pellis, L. and Jeger, M. J. 2012. Impacts of climate change on plant diseases-opinions and trends. European Journal of Plant Pathology. doi: 10.1007/s10658-012-9936.

Rojas M. R., Gilbertson, R. L. 2008. Emerging plant viruses: a diversity of mechanisms and opportunities. *Plant virus evolution*, pp.27-51.