

# Emerging Plant Viral Diseases and Their Impact on Global Agriculture

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## Introduction

Emerging viruses pose a significant threat to plant, animal, and human health, with many causing devastating losses in crop production. An emerging virus is generally defined as one that has recently evolved or appeared in a new environment, enabling it to spread and establish within new ecological niches. These viruses may be entirely novel or previously known pathogens that have become more prevalent due to environmental or ecological changes, or through the development of new variants. In the case of plant viruses, key drivers of emergence include changes in agricultural practices and the long-distance movement of plant materials. While some emerging plant viruses cause severe epidemics and attract significant public and scientific attention due to their economic impact, others may emerge without immediately leading to major outbreaks or losses. Despite the diversity of viruses and hosts, several common mechanisms underlie virus emergence. For plant viruses, insect vectors often mediate their spread. However, the globalization of trade has increasingly led to the introduction of infected plant materials such as seeds, cuttings, or other propagative materials into new geographic regions. Once introduced, an emerging virus may successfully establish itself through interaction with local vectors or, less commonly, through mechanical means such as physical contact. Genetic variability plays a crucial role in virus emergence across all biological systems. Mechanisms such as mutation, reassortment, and recombination allow viruses to adapt, evade host defences, and potentially expand their host range. These genetic changes can lead to the evolution of new viral strains capable of surviving and thriving in novel environments, thereby increasing the likelihood of disease outbreaks across plant, animal, and human populations.

## Recently Emerging Plant Viruses on Different Plant Hosts

We are currently facing numerous emerging viruses affecting a wide range of host plants. Most of these are transmitted by whiteflies and belong to the following genera and families: *Torradovirus* (family

*Secoviridae*), *Crinivirus* (family *Closteroviridae*), *Begomovirus* (family *Geminiviridae*). In addition to these, other significant genera include *Ipomovirus* (family *Potyvoviridae*) and *Carlavirus* (family *Betaflexoviridae*).

## Maize Lethal Necrosis (MLN)

A major example of an emerging plant virus disease is Maize Lethal Necrosis (MLN). In 2011, a severe outbreak of MLN was reported in the Southern Rift Valley of Kenya. MLN is caused by a synergistic infection of Maize chlorotic mottle virus (MCMV; genus *Machlomovirus*, family *Tombusviridae*) and one of several potyviruses from the family *Potyvoviridae*. In Kenya, MLN was initially associated with Sugarcane mosaic virus (SCMV), a potyvirus with a global distribution. Although, SCMV has long been present worldwide, the emergence of MLN is mainly attributed to the more recent spread of MCMV. First identified in the early 1970s, MCMV spread slowly and was largely confined to the Western Hemisphere until the 1990s. However, starting around 2010, MLN rapidly expanded across South-eastern Asia, sub-Saharan East Africa, and more recently, South America (notably Ecuador). The disease has since affected a vast region of nearly 1.2 million km<sup>2</sup> stretching from Ethiopia in the north to Tanzania in the south and from Kenya in the east to the Democratic Republic of the Congo (DRC) in the west.

In Kenya, 2013 saw the highest MLN-related losses, particularly in western Kenya, with significant damage also reported in the highlands of central Kenya and the Rift Valley. Over 50% of farmers in western Kenya were affected, experiencing yield losses of up to 50%. Nationwide, maize losses were modelled at 500,000 metric tons (MT), representing approximately 22% of total maize production. In Uganda, yield losses were similarly estimated at up to 50%. Across Ethiopia, Kenya, Rwanda, Tanzania, and Uganda, the economic toll on smallholder farmers was projected between USD 291 to 339 million, with even greater annual losses forecasted over the following five years. In Ecuador, MLN outbreaks in Guayas Province during the 2015-2016-season resulted in 25-40% yield losses, prompting the government to

declare a state of emergency. Projected economic losses for the 2016–2017 season were between USD 64–100 million. Although quantitative data are lacking, Taiwan reported substantial losses during the 2014–2015 season. In China, direct economic damage from MLN exceeded USD 2 billion, equating to more than 10 million metric tons of maize lost.

### Tomato leaf curl New Delhi virus

*Tomato leaf curl New Delhi virus* (ToLCNDV) is a bipartite begomovirus (genus *Begomovirus*, family *Geminiviridae*) transmitted in a circulative and persistent manner by the whitefly *Bemisia tabaci*. First reported in India in 1995, ToLCNDV has become a serious pathogen of tomato (*Solanum lycopersicum*), especially in northern India, causing substantial yield losses. Over the past decade, it has expanded its host range beyond solanaceous crops to include several vegetables and fiber crops. Originally confined to South and Southeast Asia with occurrences in India, Pakistan, Bangladesh, Thailand, Indonesia, and Taiwan. The virus has more recently spread westward to Iran and across the western Mediterranean Basin, including Spain and Italy, where it has caused severe outbreaks in cucurbit crops grown in both greenhouse and open fields.

ToLCNDV now poses a significant global threat due to its rapid geographical expansion and broad host range. It has been documented to infect at least 43 plant species across Asia, the Middle East, North Africa, and Southern Europe. While initially associated with tomato leaf curl disease, the virus is now widely recognized for causing major losses in cucurbit crops as well. Its continued spread is facilitated by international trade, climate adaptability, and efficient transmission by whiteflies, underscoring the urgent need for effective disease management strategies, including resistant cultivars, vector control, and coordinated surveillance efforts.

### Wheat Streak Mosaic Disease

Wheat streak mosaic disease (WSMD) is the second most significant viral disease affecting wheat globally, first reported in 1922 in the United States. It is now prevalent across many major wheat-growing regions, including Australasia, Europe, the Middle East, Central Asia (Iran, Kazakhstan), East Asia (China), sub-Saharan Africa (Nigeria, Zambia, South Africa), South America (Brazil, Argentina), and North America (USA, Mexico, Canada). Although outbreaks

are often sporadic, they can be devastating. In particular, WSMD is considered the most destructive wheat virus disease in the Great Plains of North America, an area spanning over 1.3 million km<sup>2</sup>.

WSMD is caused by Wheat streak mosaic virus (WSMV), which is transmitted by the wheat curl mite, a tiny eriophyid mite. Unlike yellow dwarf disease (YDD), which is more severe under cool conditions, WSMD tends to cause the most damage when wheat is grown under warm conditions. Similar to YDD, WSMD also results in shrivelled grains and poor seed quality, often rendering the harvest unmarketable. Beyond wheat, WSMV has a broad host range, also infecting barley, maize, oats, rye, sorghum, and various annual grasses, further complicating its management and control.

### Faba bean necrotic yellows disease

Faba bean necrotic yellows disease (FBNYD) is a highly destructive viral disease of faba bean, first reported in Syria in 1986, and now widespread across 17 countries from Spain to Pakistan, including regions in North Africa, the Middle East, Yemen, and the Horn of Africa. It is considered the most economically important virus disease of faba bean in many of these areas, with epidemics capable of causing up to 90% yield loss. Notably, in the early 1990s, severe outbreaks in Middle Egypt forced a geographical shift in faba bean cultivation to the Nile Delta. FBNYD is caused by the *Faba bean necrotic yellows virus* (FBNYV), classified under the genus *Nanovirus*, family *Nanoviridae*, and is transmitted in a persistent manner by three aphid species: *Aphis craccivora*, *A. fabae* (black bean aphid), and *Acyrtosiphon pisum* (pea aphid). While faba bean is the primary host, FBNYV also infects other legume crops such as common bean (*Phaseolus vulgaris*), cowpea (*Vigna unguiculata*), chickpea (*Cicer arietinum*), lentil (*Lens culinaris*), various wild and pasture legumes, and non-leguminous species in the genus *Amaranthus*, making its management particularly challenging.

### Tomato brown rugose fruit disease

Tomato brown rugose fruit virus (ToBRFV) is a rapidly emerging RNA virus that poses a significant threat to global tomato production. First identified in greenhouse-grown tomatoes in Jordan in 2015, with the initial outbreak traced back to Israel in 2014, ToBRFV causes severe crop losses, often with disease incidences approaching 100%. The virus primarily

infects tomato, though pepper can also serve as a host. Since its emergence, ToBRFV has been reported in at least 35 countries across four continents, highlighting its aggressive spread. Transmission occurs mainly through contaminated seeds and mechanical contact during routine horticultural activities, making its containment and management particularly challenging for growers worldwide.

### **Southern rice black-streaked dwarf disease**

Southern rice black-streaked dwarf virus (SRBSDV) was first discovered in 2001 and caused devastating outbreaks in Vietnam and China during 2009–2010, posing a major threat to rice production in Asia. The virus is currently restricted to East and Southeast Asia and is transmitted in a persistent, circulative manner by the white-backed planthopper (*Sogatella furcifera*). In addition to rice, SRBSDV also infects maize and Chinese sorghum, affecting multiple staple crops. Infected seedlings exhibit severe dwarfing, excessive tillering, and produce small spikes and barren grains, with affected plants often developing brown roots, leading to substantial yield losses (Zhou et al., 2013). SRBSDV belongs to the genus *Fijivirus*, family *Reoviridae*, and is characterized by virus particles containing a 10-segmented double-stranded RNA genome.

### **Cotton blue disease (CBD)**

Cotton blue disease (CBD) is a viral disease caused by *Cotton leaf roll dwarf virus* (CLRDV), a positive-sense single-stranded RNA virus transmitted by the aphid *Aphis gossypii* in a circulative-persistent manner. First recorded in Maharashtra, India (Mukherjee et al., 2016), CBD is now known to occur in Africa, Asia, and the Americas, although CLRDV has only been definitively identified as the causal agent in Brazil. Infected cotton plants exhibit small, thick, brittle, and leathery leaves with a deep green to bluish hue and yellow veins. Other symptoms include reddening of petioles and veins, downward leaf rolling, stunted growth, and a bunchy, zig-zag branching pattern due to shortened internodes. These morphological changes result in significant growth suppression and yield loss, making CBD an emerging concern in cotton-growing regions.

### **Grapevine Red Blotch disease**

Grapevine red blotch-associated virus (GRBaV) is a newly identified virus of grapevines and a proposed member of a novel genus within the family

*Geminiviridae*. First reported in California in 2008, GRBaV is linked to red blotch disease, which significantly affects vineyard profitability by reducing fruit quality and delaying ripening. In red-berried grapevine cultivars, symptoms appear as red blotches that expand across the leaf blade, while in white-berried cultivars, symptoms are subtler, manifesting as irregular chlorotic areas that may turn necrotic late in the season. GRBaV has been reported across major grape-growing regions in North America, with two distinct phylogenetic clades identified. The virus has been found in wine and table grape cultivars, interspecific hybrids, and rootstocks in several U.S. states, including California, Oregon, Washington, New York, and Texas, as well as in British Columbia and Ontario, Canada, posing a growing threat to grape production across the continent.

### **Conclusion**

Over the past two decades, plant viruses both as individual species and in groups have increasingly emerged as major threats to global crop production. This emergence is driven by multiple mechanisms, including long-distance dispersal through human activities, which allows viruses to establish in new agroecosystems. Regardless of whether they possess DNA or RNA genomes, plant viruses exhibit genetic variability through mutation, reassortment, and recombination, giving rise to novel or more virulent variants. The emergence and spread of these viruses are often closely tied to the proliferation of insect vectors, as seen with begomoviruses, criniviruses, and tospoviruses, whose outbreaks are linked to the global spread of their insect hosts. Factors such as international trade of plant materials, agricultural expansion into new regions, and the intensification of commercial farming further heighten the risk of new virus emergence. Although advances in molecular technologies like PCR, genome sequencing, and microarrays have improved the early detection of emerging viruses, identifying novel agents remains a complex task that demands both cutting-edge tools and innovative research strategies.

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