Tomato RNA Viruses in Burkina Faso

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ABSTRACT

Tomato (*Solanum lycopersicum* L.) is one of most widely consumed vegetables in the world and second most important vegetable crop in Burkina Faso. It is recognized today as contributing to the achievement of food security and the generating of incomes, both in urban and rural areas. Despite this importance, tomato crops were confronted with numerous constraints including RNA viruses are economically important biotic factors hindering profitable tomato production. The increased numbers of new RNA viruses and emergence of host resistance-breaking strains of known viruses are causing significant tomato yield losses. Knowledge and understanding of RNA virus biology and ecology are important for development of disease management strategies to combat these viruses in tomato production. This review highlights current knowledge on the main tomato RNA viruses in Burkina Faso, with particular focus on their characteristics, disease symptoms, yield losses, and modes of virus transmission and elimination. This information is presented to provide a basis for diagnostic and disease management strategies for these pathogens in tomatoes. A list is also included of tomato-affecting RNA viruses present in other countries that are threats to the tomato crop health.

Keywords: Tomato, viruses, yield losses, disease management strategies.

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most important vegetable crops in the world. With more than 36 tons per hectare in 2021 (FAOSTAT, 2023), tomato is one of the most important vegetable crops. In 2021 in Africa, the total tomato production was 21 million tons (approx. 13 tons ha^{-1}), in Burkina Faso, total production was approx. 291,000 tons and average yield was 17 tons ha^{-1} (FAOSTAT, 2023). Tomato cropping is a major source of income in Burkina Faso, particularly for rural and periurban communities and foreign income earner.

In view of the significance of tomato as a cash crop in Burkin Faso, the constraints to its production should be regularly reviewed with the ultimate goal of addressing them. Among these constraints include; low soil fertility high cost of seeds, shortage of improved varieties, lack of proper and adequate inputs, lack of technical knowhow at the farm level and severe attack by diseases and insect pests. Fungal, bacterial and viral diseases are reported as the most serious threats in tomato production (Blancard *et al.*, 2012).

Viral plant diseases cause significant production losses each year worth several billion dollars globally (Rivarez *et al.*, 2021). Tomatoes can be infected by many different viruses, with 312 viral pathogens being reported, of which 84 are RNA viruses (Rivarez *et al.*, 2021). RNA viruses are highly variable, and are one of the largest groups of causing significant diseases in eukaryotes, particularly tomatoes. Each growing season RNA viruses cause epidemics of emerging or re-emerging diseases (Green, 1991; Pringle, 1999 and Scholthof *et al.*, 2011). The main RNA viruses infecting tomato belong to nine families (*Secoviridae, Tospoviridae, Virgaviridae, Bromoviridae, Bunyaviridae, Closteroviridae, Flexiviridae, Luteoviridae* and *Potyviridae*), from which 13 genera are of economic importance, namely *Crinivirus, Potyvirus, Alfalfamovirus, Cucumovirus, Tospovirus, Ilarvirus, Tombusvirus, Luteovirus, Nepovirus, Potexvirus, Tobamovirus, Topocuvirus,* and *Tymovirus* (Green, 1991; Pringle, 1999 and Scholthof *et al.*, 2011).

Despite recurrence of reports of RNA viruses, very few studies on tomato RNA viruses have been carried out in Burkina Faso. Generally, the studies on tomato viruses in this country have concentrated on DNA viruses (Ouattara, 2017). Six species of RNA viruses have been reported in Burkina Faso on marketable crops (tomato, potato, pepper), including *Cucumber mosaic virus* (CMV), *Tomato spotted wilt virus* (TSWV), *Pepper veinal mottle virus* (PVMV), *Potato virus X* (PVX), *Tomato mosaic virus* (ToMV) and *Potato virus Y* (PVY), (Barro *et al.*, 2007; Ouédraogo, 2012; Ivo, 2024 and Zampaligré, 2024). Only PVMV, CMV and TSWV have been identified on tomatoes in this country (Ouédraogo, 2012; Ivo, 2024 and Zampaligré, 2024). This low representation of RNA viruses responsible for tomato diseases could be because only limited surveys have been carried out in this country. The detection methods previously used in have involved serological tests (ELISA), which have limitations (Barro, 1994 and Ivo, 2024). The actual diversity of RNA viruses could therefore be greater than the three RNA viruses

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identified so far. However, implementation of effective disease control strategies require adequate knowledge of RNA virus diversity in Burkina Faso.

The present paper reviews the important tomato RNA viruses in Burkina Faso, including their impacts, host range, and management strategies that can be implemented according to the specific circumstances of each viral pathosystem. Additionally, a list is included of RNA viruses that threaten tomato crop health.

Tomato Production in Burkina Faso

Originally from South America, the tomato was domesticated in Mexico. Its introduction in Spain and Italy, and from there, into other European countries, was in the first half of the sixteenth century (Figure 1). Tomato cultivation spread from Europe to South and East Asia, Africa particularly in Burkina Faso and the Middle East through a combination of historical, cultural and economic factors (Blancard *et al.*, 2012).

Burkina Faso is a coastal continental country whose economy is based on agriculture and livestock. More than 84% of the working population derive their incomes from agriculture. The country has three climatical areas with varied agricultural production systems. Tomato has been cultivated for many decades. Introduced in the 1930s, tomato production was concentrated in the western part of the country during the 1960s and 1970s (Bidon, 1995). Production then increased from the 1980s, with the construction of many hydraulic infrastructures and land irrigation. The area of harvested tomatoes increased from 150 ha to 17 000 ha over the five decades from 1970 to 2021 (FAOSTAT, 2023). Tomato production increased from 14,000 tons in 1970 to 305,000 tons in 2015 (FAOSTAT, 2023). Since then, however, production has declined and then remained at approx. 200,000 tons per year (FAOSTAT, 2023), probably due to biotic and abiotic stresses. The main agro-ecological market gardening areas of the country are the Boucle du Mouhoun, Centre-Est, Cascades, Est, Nord, Sud-Ouest, Centre-Sud and Centre-Ouest (Figure 2) (MASA, 2013).

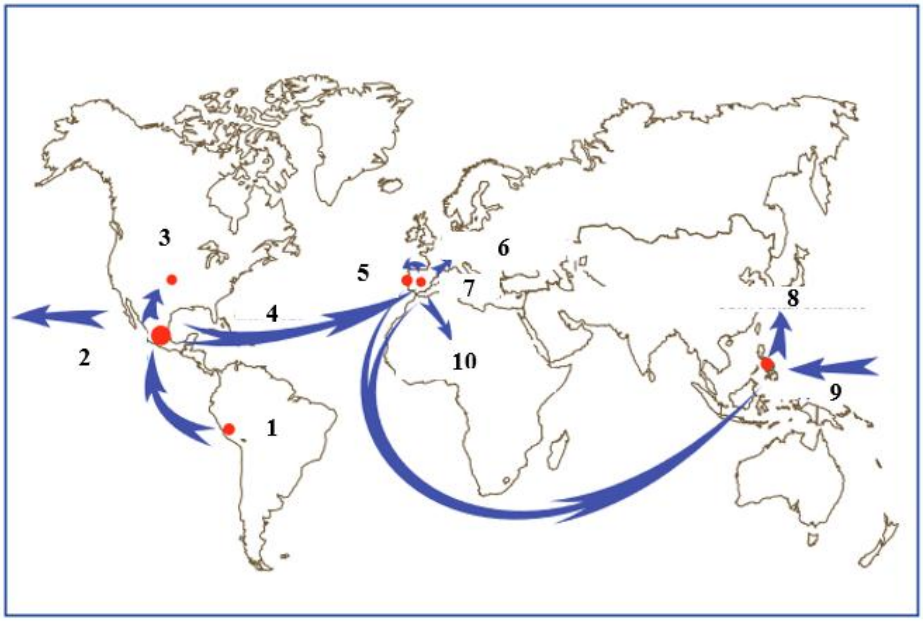

Figure 1. Map to show the possible expansion of the tomato crop worldwide (Blancard *et al.*, 2012)

(1) Peru, (2) Mexico (domestication), (3) US, (4) After 1523, (5) Portugal, (6) Other European countries, (7) Espain, (8) Other Asian countries, (9) Philippines, (10) Africa and the middle East.

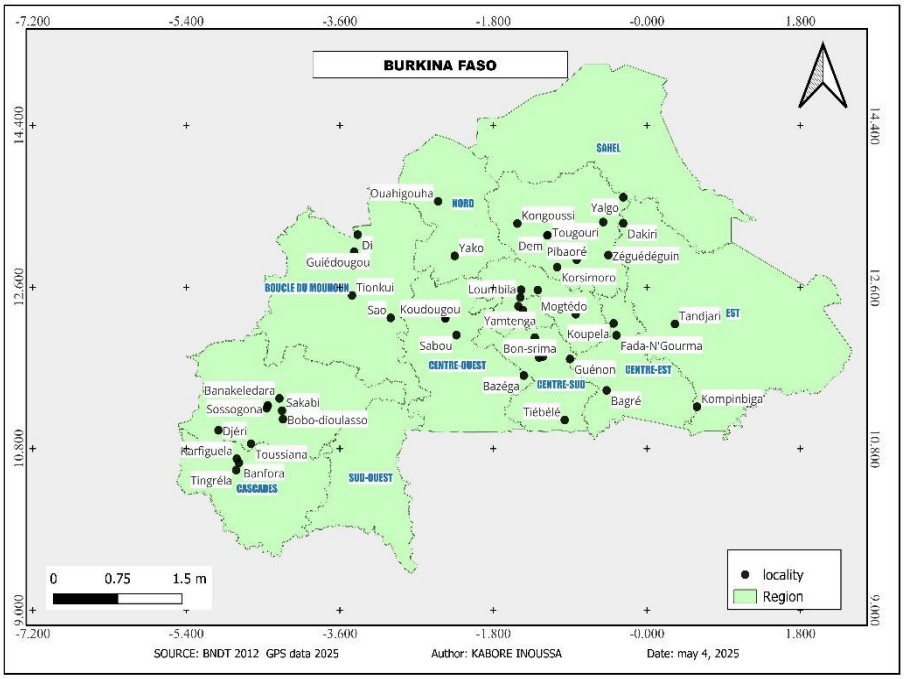

Figure 2. Map of Burkina Faso, with the main regions and localities for tomato production indicated

Main Tomato Accessions Grown in Burkina Faso

A large number of tomato accessions are grown in Burkina Faso, including Diva F1, Roma VF, Rossol VFN, Mongal F1, Petomech, Cobra 26 F1, Emerald F1, Admiral F1, UC 82 B, Arbra F1, Sibra F1, Martyna F1, Tomy F1, TSX-F1 Cerise, Sahara F1, Tropimech F1 and TSX-F1 (MASA, 2013 and Kaboré, 2022). The fruit may have a quite different morphology and size depending on the variety: more or less large, oval, flattened, slightly flattened, pear-shaped, ribbed, rounded, elliptical, heart-shaped, rectangular, cylindrical, obovate, or smooth (Figure 3). These varieties are mainly produced by foreign companies, and are marketed by the seed import and sales companies TIGRE AGRO, BOUTAPA, NANKOSEM, SAPHYTO, KING AGRO, SOPAGRI, SEMAGRI, EXOTIMEX and NANKOSEM. In recent years, research has evaluated adaptation of imported tomato varieties to the Burkina Faso agro-ecological conditions, as well as creation of new varieties. The new varieties that have been introduced include FBT1, FBT2, FBT3, FBT4 and FBT5, created by the Institut de l'Environnement et de Recherches Agricoles (INERA), In order to increase the availability of tomatoes in all seasons (Rouamba *et al.*, 2013). The advantages of these FBT varieties are their adaptability to hot-humid seasons, making fresh tomatoes available during this period of each year. Also, varieties FBT3 and FBT4 are recognized as resistant to aphids and *Thrips tabaci* (Kere, 2016). Consequently, these varieties deserve particular attention regarding their levels of resistance to RNA viruses.

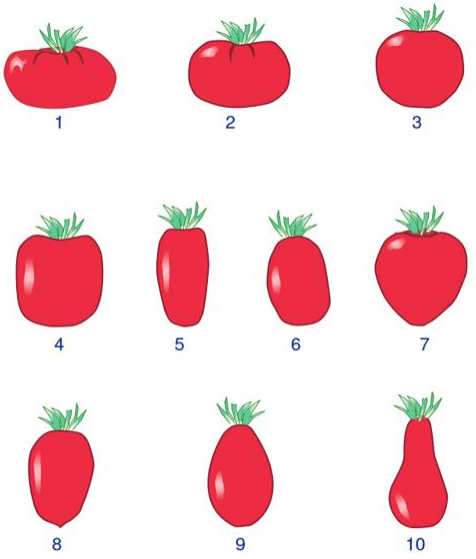

Figure 3. Morphology of tomato fruit (longitudinal section)

(1) Flattened, (2) slightly flattened, (3) round, (4) rectangular, (5) cylindrical, (6) elliptical, (7) heart shaped, (8) obovate (9) oval and (10) pear shaped.

Rna Viruses Affecting Tomato in Burkina Faso

***Pepper veinal mottle virus* (PVMV; genus *Potyvirus*, family *Potyviridae*)**

PVMV is a single-stranded RNA virus with flexuous particles, measuring 770 x 12 nm (ICTVdB, 2006) (Figure 4). The virus particles are 6% nucleic acid and 94% protein, and are typically located in the cytoplasm of all parts of infected host plants. The virus has a thermal inactivation point (TIP) of 55-60°C, longevity *in vitro* (LIV) of 7-8 d, and a dilution end point of 10^{-3}-10^{-4} (ICTVdB, 2006). This virus was first reported in Africa in Senegal (Bouhot, 1968), and is now distributed in many countries, particularly in West Africa, including Niger, Burkina Faso, and Ivory Coast (Konaté and Traoré, 1999). The virus strains infect at least 35 species of *Solanaceae* and nine species in five other plant families (*Aizoaceae, Amaranthaceae, Apocynaceae, Chenopodiaceae*, *Rutaceae*) (Brunt *et al.*, 1990). Crops such as *Capsicum frutescens, C. annuum*, *Solanum lycopersicum*, and *Solanum melongena* have been reported as the principal hosts of PVMV (Konaté & Traoré, 1999 and Nitiema & Sombié, 2019). This virus is transmitted by six species of aphids, including *Aphid craccivora, A. spiraecola, A. fabae, A. gossypii*, *Myzus persicae*, and *Rhopalosiphum maidis*, with *Myzus persicae* and *A. gossypii* being the most important aphid vectors (Alegbejo and Abo, 2002).

PVMV can be mechanically inoculated and transmitted to several *Fabaceae, Amaranthaceae*, and *Asteraceae* hosts, in addition to *Solanaceae* (Green and Kim, 1991), but is probably not seed-transmitted (Green and Kim, 1991). This virus can cause tomato yield losses of up to 43% in Burkina Faso (Ivo, 2024). Leaf symptoms expressed on plants infected with PVMV include chlorotic vein banding, mottling and mosaic (Nitiema & Sombié, 2019 and Ivo, 2024).

***Cucumber mosaic virus* (CMV; genus *Cucumovirus*, family *Bromoviridae*)**

CMV has a wide host range, affecting more than 1200 plant species in 100 families, and can be transmitted by mechanical inoculation of plant sap and over 80 species of aphids in a non-persistent manner (Pratap *et al.*, 2012). Morphologically, CMV particles are isometric with diameter of 29 nm (Figure 5). This virus is stable, but with thermal inactivation at 65 to 70°C. It can survive *in vitro* for 7 d at 24°C, 10 d at 4°C, and several weeks at -25°C (Palukaitis and García-Arenal, 2003). CMV has been reported on tomato in Burkina Faso, as well as pepper and cucumber, and these three are the primary hosts in this country (Ouédraogo, 2012). CMV symptoms include leaf mosaics, chlorotic spots, necrosis, and deformation in some cases (Ouédraogo, 2012). Young tomato plants are more susceptible to CMV than plants that have reached the flowering stage. Early infections affect host growth, development, and yields., and early affected plants may be stunted and bushy. Incidence of severe forms of the virus, causing filiform and necrotic host symptoms, may vary from year to year or season to season (Green and Kim, 1991). CMV causes crop yield losses of up to 30% (Ouédraogo, 2012).

CMV is transmitted by more than 80 insects, including 33 aphid genera, in a non-persistent mode, *Myzus persicae*, *Aphis craccivora*, *Aphis gossypii, and Aphis craccivora*, are the most important vector species (Ouédraogo, 2012). CMV is also transmitted in tomato seeds (Bragard *et al.*, 2013).

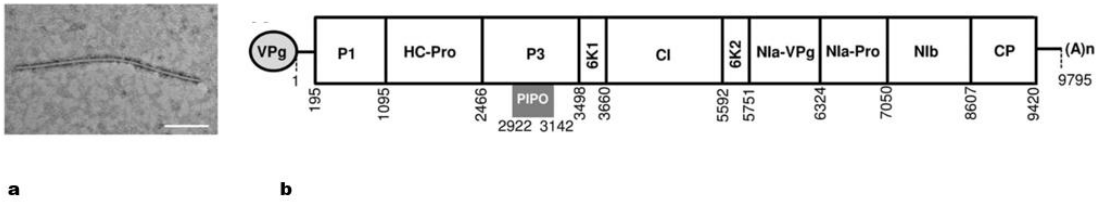

Figure 4. (a) A single *Pepper veinal mottle virus* (PVMV) particle. (b) Genome organization of *Pepper veinal mottle virus* (Xiang *et al.*, 1999)

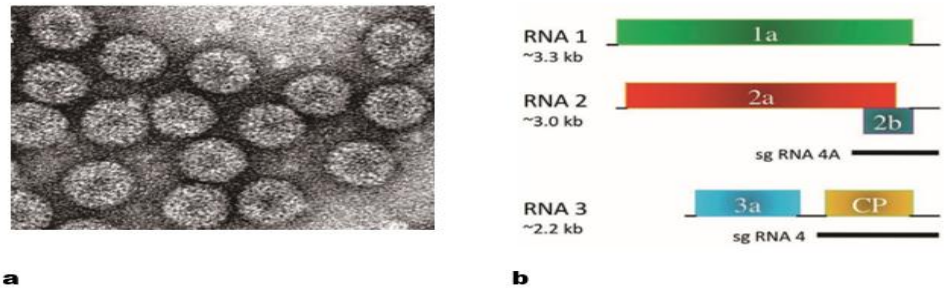

Figure 5. (a) *Cucumber mosaic virus* (CMV) particles which are 29 nm in diameter. (b) Genome organization of CMV (Scholthof *et al.*, 2011)

***Potato virus X* (PVX; genus *Potexvirus*, family *Flexiviridae*,)**

PVX; is the type member of potexvirus, and this genus was described in 1931 as "*Potato virus X*". This virus has been reported in potato and other plants in several regions of Burkina Faso (Barro, 1994). Vein-clearing and mottling are characteristic symptoms of PVX infections. Vein clearing typically develops 7 d after infection, followed by the characteristic green-banding (Barro and Konaté, 1998). PVX is typically transmitted via host pollen or seeds, by contaminated farming equipment, or from plant-to-plant contact between healthy and infected foliage or roots (Blancard *et al.*, 2012 and Barro & Konaté, 1998). PVX does not have known invertebrate vectors (Barro and Konaté, 1998). PVX particles are flexuous filaments of length 450 to 580 nm and diam. 13 nm, with helical symmetry and a pitch of 3.3-3.7 nm. The PVX genome is a positive single-stranded RNA (6.4 kb) protected by a protein shell (Barro and Konaté, 1998) (Figure 6). The virus causes significant losses in many important crops, especially in solanaceous plants such as *Solanum lycopersicum* L., *Nicotiana tabacum* L., and *Capsicum annuum* L.) (ICTVdB, 2006).

The PVX genome contains five ORFs which express the following products: ORF1, the viral polymerase; ORFs 2 to 4 express the triple gene block (TGB) movement proteins, and the TGB1 protein encoded by ORF2 is also a suppressor of RNA silencing; and ORF5 is the coat protein. There are two subgenomic RNAs, expressing, respectively, the TGB proteins and the coat protein (Scholthof *et al.*, 2011).

***Tomato spotted wilt virus* (TSWV; genus *Orthotospovirus*, family *Tospoviridae*)**

TSWV an orthotospovirus that was initially isolated from tomato crops. It contains a membrane-bound quasi spherical particle of diam. 80 to 120 nm, 5 to 10 nm surface projections (Figure 7), which occur in all parts of infected host plants (Francki *et al*., 1991 and Hull, 2014). The TSWV genome has three segments of ssRNA (the L segment is negative sense of 8.90 kb, the M and S segments are ambisense of lengths, respectively, 4.82 and 2.92 kb) (Figure 7). The virus is transmitted by thrips, and replicates in the thrips vectors and in plant hosts (Bragard *et al.*, 2013). Although TSWV has been reported in many other countries, recent dispersal of Western flower thrips (*Frankliniella occidentalis*), the major vector of TSWV, led to re-emergence of TSWV as a major agricultural pest in the 1980s with the international value of losses estimated to be more than US$1 billion annually (Goldbach and Peters, 1994). TSWV occurs in Burkina Faso (Subrahmanyam *et al.*, 1992). The virus has the largest host range of any plant virus, infecting over a thousand plant species, in 279 genera from 84 families of dicotyledons and monocotyledons, including tomato, amaranth, pepper, peanut, watermelon, tobacco, and cowpea (Alegbejo, 2015). Symptom expression due to TSWV infections include conspicuous chlorotic or necrotic rings on leaf stems resulting to stunted plant growth and on fruit during early infection causing reduced size, Fruit can become malformed and unmarketable with chlorotic or necrotic ring spots due to virus replication, symptoms that may only develop when the fruit become fully ripe and red (Subrahmanyam *et al.*, 1992). TSWV reduced tomato yield by 36% in Burkina Faso (Zampaligré, 2024). TSWV infections often reduce fruit quantity, quality, and market value, causing significant value reductions for thus low-income farmers (Van de Wetering *et al.*, 1992).

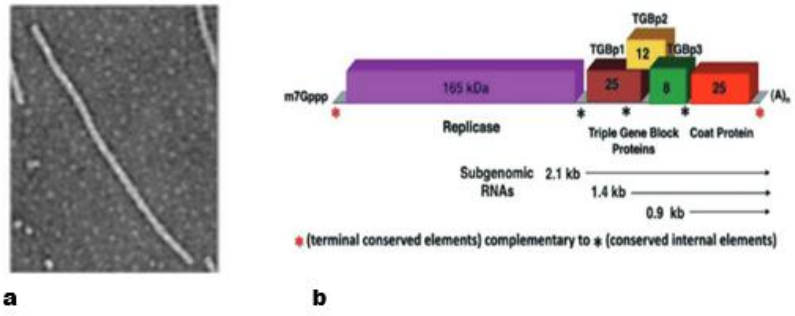

Figure 6. (a) *Potato virus X* (PVX) particles. (b) Genome organization of *Potato virus X* (Scholthof *et al.*, 2011)

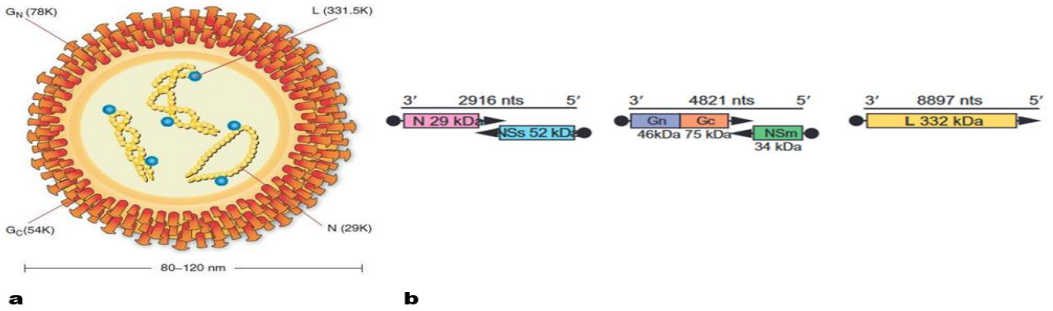

Figure 7. (a) Diagram of a *Tomato spotted wilt virus* (TSWV) particle. (b) Genome organization of TSWV (King *et al.*, 2012). The S, M, and L RNA genomic segments are encapsidated by the nucleoprotein, are in association with L protein molecules, and from plan-handle structures due to the complementary of their 5′ and 3′ ends. The glycoproteins GN and GC are embedded within the virus envelope

The L RNA segment of TSWV has a single ORF encoding the RNA polymerase. Each of the other two RNA segments has two ORFs expressed by the antisense strategy. The M segment 3′ ORF expresses the glycoproteins which form the spikes on the particle, and the 5′ ORF expresses P34, the movement protein. The S segment 3′ ORF expresses P29, the nucleocapsid protein, and the 5′ ORF expresses a suppressor of RNA silencing.

***Potato virus Y* (PVY; genus *Potyvirus*, *family* Potyviridae)**

PVY particles are flexous, and of length approx. 750 nm and width 11 nm (Brunt *et al*., 1990). This virus is the type member of potyvirus, and the genus shows significant variability expressed in several of its hosts. The PVY genome is a unipartite single-stranded molecule of positive-sense ssRNA, of approx. 9.7 kb, where the 5′ end has a VPg and the 3′ end is polyadenylated (Figure 8). Particles sediment as one component (145 S_{20w}) in purified preparations. PVY has a thermal inactivation point (TIP) of 50 to 62°C, longevity *in vitro* (LIV) of 7 to 50 d, and a usual dilution end point of approx. 10^{-2}-10^{-6} (Brunt *et al*., 1990 and Alegbejo, 2015). The virus in many countries, but has a narrow host range in the tropical regions, and infects tomato and pepper in some African countries (Barro, 1994). In Burkina Faso, PVY has only been reported on pepper and potato (Konaté and Traoré, 1999). The virus is found mainly in field crops, and frequently in protected crops. It is very damaging in warm regions on potato and pepper. Plants infected with PVY express typical symptoms of mottling which later develops as a green mosaic. Age or developmental stage of host plants at which infection occurs determines the severity of foliage symptoms and yield reductions caused by PVY (Barro *et al.*, 2007). The virus has a wide host range, including crops such as pepper, tomato, potato, eggplant, tobacco, and weeds (*Portulaca oleracea*, *Senecio vulgaris*, *Solanum nigrum*, *Physalis* spp.). PVY is transmitted by *Myzus persicae* and more than 40 aphid species, in a nonpersistent manner (Bragard *et al.*, 2013). The virus is also mechanically transmitted hosts in the *Amaranthaceae*, *Asteraceae*, *Chenopodiaceae*, and *Fabaceae*, in addition to *Solanaceae*, but probably does not spread by contact or in seed. PVY is responsible for important diseases

capable of causing up to 16% yield losses of pepper fruit (Barro *et al.*, 2007).

***Tomato mosaic virus* (ToMV; genus *Tobamovirus*, family *Virgaviridae*)**

Tomato mosaic virus was first reported on tomato in 1909, in Connecticut, United States of America (ICTVdB, 2006). This virus was long considered to be a strain of *Tobacco mosaic* v*irus* (TMV), but further characterization showed that it has different serological, genomic and host range properties, permitting separate nomenclature. ToMV particles are morphologically identical to those of TMV, and are rigid rods, measuring approx. 300 × 15 nm (Figure 9). This virus has an *in vitro* (LIV) longevity of 500 d, dilution end point (DEP) of 10^{-5}-10^{-7}, and thermal activation point (TAP) of 85-90°C (Alegbejo, 2015). ToMV has wide in international distribution. Several strains have been reported, and two pathotypes (0 and 1) were reported on tomato in Africa (Nono-Womdim *et al.*,1996). *Tomato mosaic virus* has been reported as an important viral disease in Burkina Faso (Barro *et al.*, 2007). Although its incidence has decreased significantly with the use of resistant tomato varieties, recent use of new susceptible types has shown that the virus is still a threat. Various symptoms have been associated with ToMV infections, including crinkling, mosaic mottling, and curling of leaves, and stunted growth of infected tomato plants (Alegbejo, 2015).

ToMV can infect many different hosts, although probably fewer than *Tomato mosaic virus*. Its main hosts are in the *Solanaceae*, including *Capsicum frutescens* and *C. annuum* (Barro *et al.*, 2007). ToMV is less common on other Solanaceous hosts, *Nicotiana tabacum*, *Petunia hybrida*, *Physalis alkekengi*, *P. peruviana*, *P. subglabrata*, *P. heterophylla*, *P. longifolia*, *P. virginiana*, *Solanum tuberosum*, and recently, *S. muricatum*. There is no report of natural vectors for the virus, but it can be transmitted by mechanical inoculations, contact between plants, grafting, and is up to 94% transmitted in tomato seeds. Hoon and Jin (2002) reported that contaminated seeds carrying the virus on seed coat and in infested plant debris are the primary ToMV inoculum sources in the field. Yield losses of more than 25% have been reported from severe ToMV infections of pepper in Burkina Faso (Barro *et al.*, 2007).

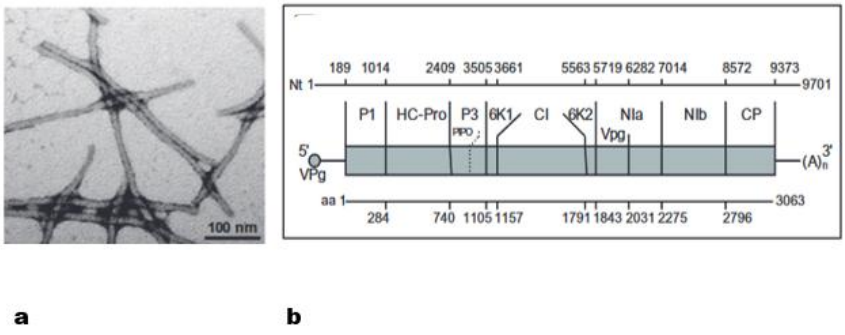

Figure 8. (a) Particles of *Potato virus Y* (PVY). (b) Genome organization of *Potato virus Y* (PVY) (Jakab *et al.*, 1997)

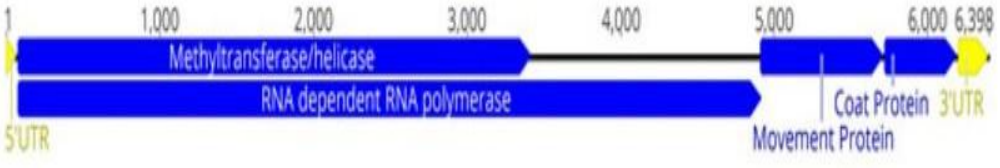

Figure 9. Genetic map of the ToMV genome. The numbers represent nucleotide bases, while the blue and yellow regions indicate the putative coding genes and 5′UTR, and the yellow region indicates the 3′UTR flanking region (Arinaitwe *et al.*, 2018)

Impacts of Rna Viruses on Tomatoes in Burkina Faso

As early as the 1990s, RNA virus diseases in vegetable crops, particularly tomatoes, attracted attention of the scientific community (Barro, 1994). In Burkina Faso, other studies addressed some epidemiological aspects of these diseases, and highlighted their increasingly wide distribution (Barro *et al.*, 2007). Recent research showed that tomato crops were affected by *Cucumber mosaic virus* (CMV), *Pepper veinal mottle virus* (PVMV) and *Tomato spotted wilt virus* (TSWV), with mainly four phenotypes in the affected fields (Figure 10), and with prevalences of 30% for CMV, 43% for PVMV, and 40% for TSWV (Ouédraogo, 2012 and Ivo, 2024). These viruses can reduce tomato crop yields and alter product quality and affecting the economy of the country. As a result, RNA viruses cause problems to tomato growers, forcing these farmers in some gardening sites cease tomato production.

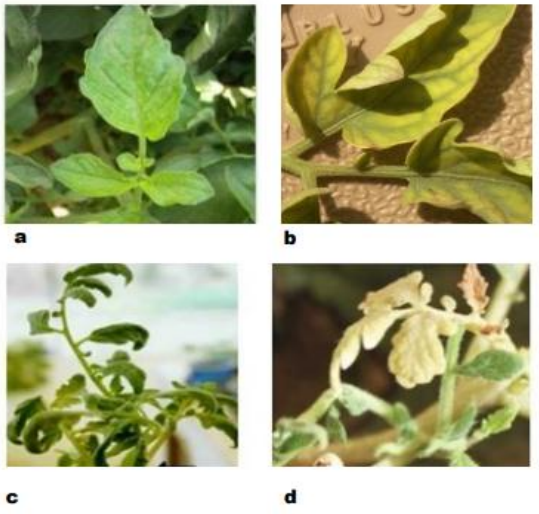

Figure 10. Four main phenotypes of RNA virus diseases on tomato plants in Burkina Faso. (a) Phenotype a, caused by *Cucumber mosaic virus*, resulting in yellow mosaic on a tomato leaf. (b) Phenotype b, causing leaf discolouration caused by *Pepper veinal mottle virus*. (c) Phenotype c, and (d) Phenotype d, causing thread-like leaves in tomatoes without necroses, caused by *Cucumber mosaic virus* (Ouédraogo, 2012 and Ivo, 2024)

Strategies to Combat Spread of Tomato Rna Viruses in Burkina Faso

Tomato cropping is important in Burkina Faso, for economic and social reasons. However, tomato production faces difficulties which include infections by RNA viruses that reduce crop yields and quality, and consequently market gardener incomes. Given the common presence and impacts of these viruses, farmers and phytosanitary professionals must adopt practices to limit the spread of these viruses. Among these are prophylactic (preventive) control, chemical management, and host genetic control. Current Relevant knowledge on each of these approaches is for Burkina Faso is summarized in the following sections.

Prophylactic control of RNA viruses

Prophylactic methods are defined as sets of agricultural management techniques aimed at satisfying specific needs of the cultivated plants and preventing pathogen development. When host plants are in optimal development conditions, they present maximum resistance to RNA viruses. The viruses can survive on or in debris of diseased plants, on weeds and other related host plants, and sometimes in host seeds. As part of the preventive measures for RNA virus diseases, Barro (1994) and Ouédraogo (2012) suggested the following specific appropriate measures:

- choose appropriate crop cultivation sites (gardens in open fields, or under cover). The land for tomato plants must be well drained, and improved with by amendments (e.g. organic manure, liming), and additions of balanced manure;
- respect cultural transplanting and planting practices, taking account of plant spacings, within and between crop rows. Risks of developing virus diseases causing yield losses vary depending on the production system. For example, monoculture tomato fields can be more susceptible to viral infections than mixed crop types, as monocultures have common genetic makeups and common vulnerability to disease-causing RNA viruses.

Control of insect-transmitted RNA viruses

Chemical control is most commonly used by farmers to control vectors of RNA viruses (*Aphis gossypii*, *Bemisia tabaci*, *Aphis craccivora* and *Thrips tabaci*). These insects can become threatening regardless of using virus preventive measures. In Burkina Faso, over the period 2009 to 2018, insecticides were increasingly used and the dominant phytosanitary products to protect agricultural production. In this country, and elsewhere in tropical Africa, most phytosanitary measures carried out by farmers were not effective against RNA viruses. Reasons included: inadequate farmer knowledge for

identification of pathogens and pest insects; most pesticide products are not approved or kept in good condition; and recommended doses are not respected. For example, 90% of pesticides used in Burkina Faso during the 2015/16 agricultural season were purchased from local markets, without guarantees of product conformity and quality, and 71% of pesticides formulated for use on cotton crops were used on tomatoes during the same period (Kolié, 2009). This misuse probably creates residues problems in food products, with associated health risks to farmers and consumers, and create biological imbalances in crop production. This situation requires alternative means of pest and pathogen management, which will reduce hazardous use of insecticides.

Host plant genetic control

Host genetic control involves adoption of resistant or tolerant crop varieties by farmers, when these are available. These methods are simple to apply and effective, if the varieties selected meet required market expectations, which include plant shape, fruit type, and high yield. Tomato variety improvement companies developed hybrid tomatoes (F1) under different commercial names (e.g. Cobra, Mongal, Rossol). These types are qualified as resistant or tolerant to virus diseases and/or pests by their marketing companies. Notwithstanding these research efforts, breeding for tomato resistance to some virus diseases has not been successful to date. Most of these marketed varieties are not adapted to local hot and humid growing conditions, and are also inaccessible most farmers due high costs for purchase of new seeds each season. In Burkina Faso, INERA has, therefore, developed five new varieties of wintering tomato called Farako-Bâ Tomato (FBT), and these include FBT1, FBT2, FBT3, FBT4 and FBT5. Among these, FBT3 and FBT4 are recognized as resistant to insect vectors of RNA viruses (*Aphis gossypii, Bemisia tabaci, Aphis craccivora* and *Thrips tabaci*) (Kere, 2016). Consequently, all of the FBT varieties require particular attention to assess their levels of resistance to RNA viruses.

International Status of Other Rna Viruses Infecting Tomato

Many RNA viruses are reported on tomatoes. The most widespread of these viruses are outlined below, and these RNA pathogens are important factors reducing tomato production.

***Tomato chlorosis virus* (ToCV) and *Tomato infectious chlorosis virus* (TICV) (ToCV and TICV; genus *Crinivirus*, family *Closteroviridae*)**

Viruses in crinivirus (closteroviridae) are transmitted by whiteflies. These viruses have bipartite genomes each composed of two ssRNA genomic segments which are separately coated in filamentous virions (Kiss *et al.*, 2013). RNA-1 encodes proteins involved in virus replication, and RNA-2 (and RNA-3) encodes proteins involved in viral encapsidation, movement, and vector transmission (Martelli *et al.*, 2002). Their infections in plants can be confused with nutritional disorders and phytotoxicity, due to the obvious interveinal yellowing of leaves and leaf fragility, leading to reductions in crop yields (Alfaro-Fernández *et al.*, 2009). *Tomato infectious chlorosis virus* (TICV) and *Tomato chlorosis virus* (ToCV) can infect tomato. ToCV was first described by Wisler *et al.* (1998), and is now present in many countries, causing yield losses due to reductions in fruit size. ToCV has been shown to infect 25 crop and weed species (Alfaro-Fernández *et al.*, 2007), while TICV can infect 22 weed species that may be TICV reservoirs (Alfaro-Fernández *et al.*, 2009). Both of these viruses are spread by the greenhouse whitefly (*Trialeurodes vaporariorum*), and ToCV can also be transmitted by other whitefly species, including several biotypes of *Bemisia tabaci*. Although both viruses probably have only tomato as their primary host, they can infect a range of plant species including common weeds. Criniviruses are limited to host phloem, and are transmitted semipersistently by whiteflies (*Bemisia tabaci*) and *Trialeurodes vaporariorum* and *T. abutiloneus*) (Wisler *et al.*, 1998). Of these viruses is restricted to host phloem tissues, so neither *Tomato chlorosis virus* nor *Tomato infectious chlorosis virus* can be mechanically transmitted. These viruses are also not known to be seed transmitted. These viruses are spread semi-persistently via whitefly transmission. Once carrying the virus, insects can transmit it during 3 to 5 d. Two to three weeks after being infected with either TICV or ToCV, tomato plants begin to produce leaf symptoms, including irregular chlorotic mottling and interveinal yellowing (chlorosis) which intensify with time while the leaf veins remain green (Wintermantel, 2004).

***Tomato brown rugose fruit virus* (ToBRFV; genus *Tobamovirus*, family *Virgaviridae*)**

Tobamovirus includes several economically important viruses, such as *Tobacco mosaic virus* and *Tomato mosaic virus*. ToBRFV was first detected in field-grown tomatoes, which showed typical mosaic symptoms, leaf narrowing and yellow or brown rugose spots on the fruit (Salem *et al.*, 2016 and Luria *et al.*, 2017). These infections caused severe yield losses in Israel in 2014 (Luria *et al.*, 2017), and in Jordan in 2015 (Salem *et al.*, 2016). After these discoveries of ToBRFV, the virus was found to be widespread, and to date has been detected 35 countries across North America, Asia, Europe, and Africa (EPPO, 2022).

The ToBRFV genome is a single-stranded, positive-sense RNA of approx. 6.4 kb, encoding four open reading frames. The genomic RNA is encapsidated into virions that are rod-shaped and approx. 300 nm long and 18 nm in diameter. Tobamovirus virions are stable and can survive in plant debris or on seed surfaces for long periods. In protected facilities such as greenhouses, ToBRFV is transmitted primarily by mechanical contact, including propagation materials, plant debris, contaminated soil, growth media, circulating water, workers' farming practices, and culture tools (Dombrovsky & Smith, 2017 and Oladokun *et al.,* 2019).

ToBRFV incidence in affected crops has been estimated to be from 50 to 100% (Salem *et al.,* 2016 and Alkowni *et al.,* 2019), with observed yield reductions of 10 to 55% (Avni *et al.,* 2021).

Tomato infected plants exhibit mild to severe mosaic and deformation of leaves, and fruit may develop brown rugose (rough) patches, marbling, and deformations. The peduncles and calices often become necrotic and fail to produce fruit. Yellow blotches, brown or black spots, and rugose wrinkles appear on tomato fruit. ToBRFV can infect more than 40 host species of *Apocynaceae*, *Asteraceae*, *Amaranthaceae,* and *Solanaceae*, but tomato and pepper are the only species that are the natural hosts of ToBRFV (Salem *et al.,* 2016 and Luria *et al.,* 2017).

***Tobacco mosaic virus* (TMV; genus *Tobamovirus*, family *Virgaviridae*)**

Tobacco mosaic virus, the first virus to be described, was first recorded on tobacco in the Netherlands in 1886 and in Russia in 1892. TMV was selected as a type virus for tobamovirus and virgaviridae. This virus has been the subject of many fundamental studies, particularly at the molecular level. Infected pepper plants are usually stunted, and deformed, with raised bumps and mottled leaves, in addition to dark and light green areas (Kumar *et al.,* 2011). Other symptoms include leaf mosaic and curling, and stunted fruit growth, and infected fruit shrink and ripens unevenly (Kumar *et al.,* 2011).

TMV is a seed-borne pathogen, and can spread by mechanical means such as hand, cutting and other tools, but not by insect vectors. TMV infects at least 125 different crop hosts, including tobacco, tomato, chilli, and cucumber (Kumar *et al.,* 2011). TMV has long been associated with tomato mosaic disease, but a specialized form of the virus (*Tomato mosaic virus*, ToMV) has been recognized to be much more competitive on tomato (Kumar *et al.,* 2011).

***Tomato bushy stunt virus* (TBSV; genus *Tombusvirus*, family *Tombusviridae*)**

Tomato bushy stunt virus was first isolated in 1935 in Ireland from tomato, and was later observed on tomato England (Tomlinson *et al.,* 1982). TBSV is a unipartite, isometric, single-stranded, positive-sense virus, with particle diameter of 33 nm (Martelli *et al.,* 1988; 2001). TBSV virions are non-enveloped icosahedral T = 3 particles assembled from 180 coat protein subunits (42 kDa) whose arrangement causes a granular appearance on the virion surface. The particles are ∼33 nm in diameter, and are composed of 17% RNA and 83% protein. The TBSV genome consists of a positive-sense single-stranded RNA of approx. 4.8 kb, which lacks the 5′-cap or 3′-poly(A) tail typical for eukaryotic mRNAs (Hull, 2014). TBSV is widespread and causes economically important diseases in several crops (Martelli *et al.,* 2001), in Central and Western Europe, Africa (Nigeria), and North America (Alegbejo, 2015). The virus is thought to be passively transmitted in water or by soil-borne organisms. This has been reviewed in detail by Rochon *et al.* (2004), so salient points from their paper are here summarized, in anticipation that a similar mode of transmission may exist for TBSV.

TBSV has a restricted host range, mainly infecting *Solanum esculentum* M., *Petunia* sp., *Phaseolus vulgaris* L., *Capsicum* spp., *Nicotiana* spp., *Solanum* sp., *Dahlia* spp., *Dianthus barbatus* L., etc., (Alegbéjo, 2015). Various symptoms have been associated with TBSV infections, curling of leaves, with youngest leaves exhibiting tip necrosis from systemic infection. Tomato fruit yields can be greatly reduced by TBSV infections, and infected plants may be stunted with lateral shoot proliferation, which accounts for the name of the virus.

Control measures for TBSV are often limited to removal of infected plants. Genetic transformation has been explored engineer TBSV virus resistance (Rubino & Russo, 1995 and Rubio *et al.,* 1999), but the efficacy of this approach has yet to be tested under field conditions.

***Tomato aspermy virus* (TAV; genus *Cucumovirus*, family *Bromoviridae*)**

Tomato aspermy virus has a tripartite positive-sense single-stranded RNA messenger genome, designated RNAs 1 (3, 41 kb), 2 (3.07 kb) and 3 (2.21 kb), which are encapsidated in isometric 28 nm particles (Palukaitis & Garicia-Arenal, 2003 and ICTV, 2021). TAV has been reported in many countries, but particularly in Nigeria, causing significant yield losses. Chrysanthemum and tomato are the best-known natural hosts of TAV, but *Capsicum annuum* and cucumber have also been reported as natural hosts (Schmelzer *et*

al., 1977). Various symptoms have been associated with TAV infections, leaf mottling, stunted growth, malformation and small and seedless fruit (Raj *et al.*, 2011). Aphids (*Aphis gossypii* and *Myzus persicae*) readily transmit the virus in a non-persistent manner (Rivarez *et al.*, 2021), and it can also be transmitted by dodder and the sap of infected plants (Raj *et al.*, 2009).

***Alfalfa mosaic virus* (AMV; genus *Alfamovirus*, family *Bromoviridae*)**

Alfalfa mosaic virus occupies a monotypic genus, and is a single-stranded RNA virus of positive polarity with a non-enveloped capsid. The icosahedral symmetry of the capsid is round to elongated, of length 30 to 57 nm. AMV is multipartite, composed of four particles of diameter 18 nm. The genetic material of the virus includes three single linear strands (RNA1, RNA2 and RNA3), and a subgenomic strand (RNA4) which is obtained by transcription of the negative-sense strand of RNA3. RNA1 and RNA2 encode the proteins required for replication, RNA 3 is necessary for synthesis of the protein responsible for cell-to-cell movement, and RNA 4 encodes the capsid.

AMV infects more than 400 plant species, including several vegetable and woody crops. The virus is widely distributed, and is most common in in India, Iran, Bangladesh, and Pakistan (Damiri, 2014). Disease incidence ranges from 80 to 100%.

Various symptoms have been associated with AMV infections, including blotchy white and bright yellow mosaic on infected leaves, and plants infected by the virus at young stages display stunted growth with misshapen and blotchy fruit (Kenyon *et al*., 2014).

AMV is vectored by the green peach aphid (*Myzus persicae*) and at least 14 other aphid species are known to transmit the virus. AMV can also be transmitted through seeds, and by mechanical inoculation. Naturally, AMV has a restricted crop host range. The virus mainly infects vegetables and some legumes, including *Capsicum* spp., *Solanum esculentum* L., and *Nicotiana* spp. AMV infections cause significant crop losses, reduce host winter survival, and facilitate infections of affected plants by other viruses (Damiri, 2014).

***Tomato torrado virus* (ToTV; genus *Torradovirus*, family *Secoviridae*)**

Secoviridae includes viruses transmitted by insects or nematodes, nine of which are known to infect tomatoes. These viruses have mono- or bi-partite ssRNA genomes, of lengths 9 to 13.7 kbp packaged in icosahedral virions (ICTVdB, 2006). Several viruses from this group have been reported, including *Tomato black ring virus* (nepovirus) and *Tomato torrado virus* (torradovirus). Various symptoms have been associated with TBRV infections, including chlorotic and/or necrotic leaf ring spots, and was associated with eight satellite RNAs, but no assessment of economic losses due to TBRV has been carried out (Rymelska *et al*., 2013). ToTV has been reported to occur in many countries, since its discovery in 2007 in tomatoes from Spain exhibiting systemic necrosis or blight symptoms (Verbeek, 2013). ToTV has been reported in South Africa (Moodley *et al.*, 2019a, b) and Colombia (Verbeek, 2013), which were the first reports of the virus in the Afrotropical and Neotropical ecoregions. ToTV is transmitted by the whiteflies *T. vaporariorum* and *B. tabaci* (Moodley *et al*., 2019a, b).

***Pepino mosaic virus* (PepMV; genus *Potexvirus*, family *Flexiviridae*)**

Pepino mosaic virus is a filamentous virus, whose particles are 700 nm long and 11 nm wide. It has a positive ssRNA of 6450 nucleotides, and the genome encodes five proteins (Cotillon *et al.*, 2002). PepMV was first reported in tomato in 1999, when it appeared in crops in Germany, the Netherlands, and the United Kingdom (Van der Vlugt *et al.* 2002). In tomato, fruit marbling symptoms are considered as the most important causes of tomato production losses due to this virus (Hanssen and Thomma, 2010). PepMV is present in major tomato-growing areas of the Mediterranean region, and has been reported in United States of America and Mexico (Ling and Zhang, 2011), South Africa (Carmichael *et al.*, 2011), and Spain and Morocco, and causes significant economic losses in Europe and America (Van der Vlugt *et al.*, 2002). The virus spreads readily in tomato crops, being mechanically transmitted by horticultural workers who become contaminated when handling infected plants (Hanssen and Thomma, 2010). PepMV is also transmitted by plant-to-plant contact, by the greenhouse whitefly (*Trialeurodes vaporariorum*) and bumble-bees (*Bombus impatiens*), and through water in hydroponic crops (Noël *et al.*, 2014). Seed transmission can occur at low rates (0.026%) (Van der Vlugt *et al*., 2002), when the seed is not adequately disinfected. PepMV has been naturally isolated from infected plants including pear melon (*Solanum muricatum*) and tomato. Infection of other crops, such as eggplant, tobacco and potato, has been achieved only with artificial inoculation methods. Indexing for the virus can be achieved using sensitive plants such as *Datura metel, D. stramonium, Nicotiana glutinosa, N. occidentalis, N. benthamiana; Solanum lycopersicum* and *Solanum* spp. (Van der Vlugt *et al*., 2002 and Davino *et al.*, 2008).

Various symptoms have been associated with PepMV infections, including bright yellow angular spots on host plant leaves, and minor deformities sometimes develop on host growing points, similar to

hormonal damage or growth arrest. Infected plants can also show necrotic lesions, spots on leaves and stems, and become dwarfed and deformed, and the virus can cause flower abortion. The skin of fruit of some infected host varieties can have irregular discoloration or mottling (Van der Vlugt *et al*., 2002).

***Pepper mild mottle virus* (PMMoV; genus *Tobamovirus*, family *Virgaviridae*)**

Pepper mild mottle virus is a single-stranded RNA virus (Yoon *et al.*, 2006), with wide geographical occurrence, including India, Iran, Pakistan, Sri Lanka, and Bangladesh (Ahmad *et al.*, 2015). When young plants become infected with this virus, significant yield and fruit quality losses result. *Pepper mild mottle virus* incidence ranges from 20 to 80%, and yield losses can be 50 to 100% (Martínez-Ochoa *et al.*, 2003).

Various symptoms have been associated with PMMoV infections, including leaf mottling, mosaic, chloroses and malformations, stunted growth, and small and deformed fruit (Güldür and Çaglar, 2006). PMMoV is highly infectious, and it is spread by seed, rather than by insects (Rialch *et al*., 2015). This virus can survive on infected host debris and in soil, as inoculum for subsequent crops (Lamb *et al.*, 2001). *Capsicum* spp. are the primary PMMoV hosts, but 24 *Solanaceae* species and other *Chenopodiaceae*, *Cucurbitaceae*, *Labiatae*, and *Plantaginaceae* can be infected by PMMoV (Güldür and Çaglar, 2006).

Life Cycles of Rna Viruses Within Host Plants

Viruses are acellular parasites with polynucleotide genomes, which code for at least one protein involved in replication. Once inside each host cell, this protein induces virus multiplication (Astier *et al.*, 2001). The viruses are naturally transmissible by vegetative propagation, or, more often, are transmitted by vectors. In the laboratory, viruses can also be transmitted through wounds deliberately inflicted on host leaves, or by grafting. In host plant cytoplasm, the capsid protein (CP) enveloping the virus genome is detached (decapsidation), releasing the virus RNA. The viral genome can be directly translated into proteins using the host plant's ribosomes. The recognition protein at the 5' end of the viral RNA (e.g. in *Potyvirus*) enables recognition of the host protein eukaryotic translation initiation factor 4E (eIF4E), which is involved in initiating translation of messenger RNAs into proteins. As a result of the interaction between the recognition protein (VPg) and eIF4E, a polyprotein is synthesized, for which the multiple functions of each protein have been described (Quenouille *et al.*, 2013). A protein is also synthesized from a reading frame shift in the coding part of another protein (Chung *et al.*, 2008). The virus genome is then replicated via the RNA-dependent RNA polymerase protein complex, allowing the virus to multiply and accumulate in the host plant. Multiple virions are obtained following encapsidation of copies of the viral genome, and are then transported through plasmodesmata to move from cell to cell. Virus infection can then become systemic when virions travel through the host plant conducting vessels. At this stage in the infection cycle, vectors feeding on infected leaves can acquire the virus, and transmit it from plant to plant, initiating new infection cycles (Figure 11).

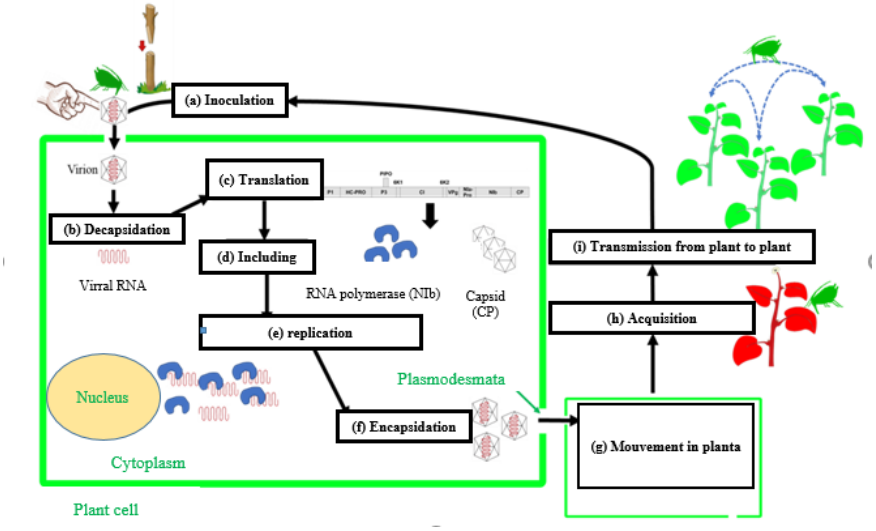

Figure 11. Life cycle of RNA viruses. (a) Inoculation of virions into a plant cell by mechanical inoculation, a vector, or grafting. (b) Decapsidation, which releases the virus RNA into the cell cytoplasm. (c) Translation of the RNA into a polyprotein, which is then cleaved into functional proteins, (d) including the RNA-dependent RNA polymerase (NIb) and the capsid (CP). (e) Replication of virus RNAs by virus-dependent RNA polymerases. (f) Encapsidation of virus RNAs to form new virions capable of infecting new cells via plasmodesmata, or all plant organs systemically (g). An aphid can then feed on an infected plant (in red), acquire the virus (h) and then transmit it from plant to plant (i)

Major Insect Vectors of Rna Viruses

Transmission is an essential event for the survival of viruses, and there are different for dissemination of plant viruses. They are transmitted to plants via insects and other living organisms. Arthropods that are major transmitters of plant viruses include aphids, beetles, thrips, leafhoppers, whiteflies, mealy bugs, and mites (Whitfield *et al.*, 2015 and Sarwar, 2020), and the major documented genera of virus vectors include *Aphis, Macrosiphum, Myzus, Macrosiphum, Acyrthosiphon* (subfamily *Aphidinae*) (Bragard *et al.*, 2013). Figure (12) illustrates insect vectors of plant viruses.

In Burkina Faso, four main insect vectors of RNA viruses have been identified on tomato. These are *Aphis gossypii, Bemisia tabaci, Aphis craccivora* and *Thrips tabaci* (Kere, 2016). However, there is no information about these insect vector mediated inoculations on tomato in this country.

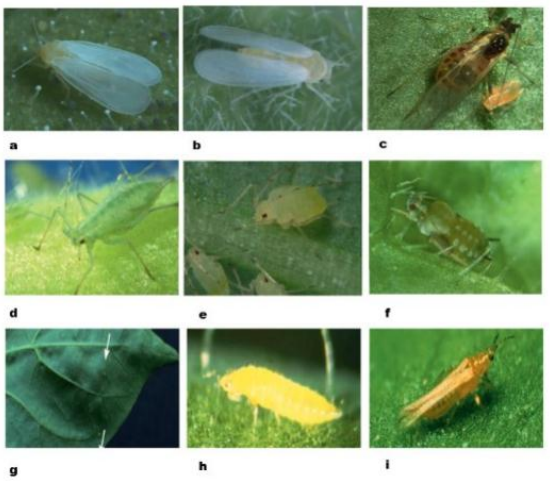

Figure 12. Arthropod vectors of virus. (a) *Trialeurodes vaporariorum*, (b): *Bemisia tabaci*, (c): The green peach aphid *Myzus persicae*, (d): *Macrosiphum euphorbiae*, (e): *Aulacorthum solani*, (f): *Aphis gossypii*, (g): Two eggs of *Frankliniella occidentalis* visible under the leaf, (h): A larva of *Frankliniella occidentalis* walks on the underside of this leaflet, (i): Adult *F. occidentalis* (Blancard *et al.*, 2012)

CONCLUSION

Numerous RNA viruses are known to cause economically important tomato diseases. These diseases are generally the most severe and difficult to manage, due to the frequency of epidemics and absence of effective curative control methods. Studies on tomato viruses in Burkina Faso have concentrated on DNA viruses. Therefore, the need to investigate tomato RNA viruses becomes important. Some RNA viruses, including PVX, PVY, ToMV, PVMV, TSWV and CMV reported to occur in Burkina Faso, need to be assessed in tomato growing areas, with attention on their occurrence, epidemiology, crop yield effects, management, molecular characterization, and function. Among these six RNA viruses, only PVMV, CMV, TSWV have been identified on tomatoes in Burkina Faso. This low representation of RNA viruses could be explained by the limited surveys that have been carried out with appropriate diagnostic methods. Detection methods most widely used in Burkinabe research have been serological tests (ELISA), which have limitations that can distort results. The actual diversity of RNA viruses in Burkina Faso be greater than the three RNA viruses identified on tomato to date. Implementation of effective control strategies requires accurate knowledge of the diversity of the RNA viruses in Burkina Faso. This present review provides relevant and up-to-date information regarding the major RNA viruses that cause economic losses in tomato crops in Burkina Faso, and outlines information on other RNA viruses that have been shown to cause diseases of minor impact. However, other RNA viruses that have caused serious damage and epidemics in tomato in other countries could threaten production in Burkina Faso. Information relating to identification and management of these potential pathogens is relevant for this country.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declares that NO generative AI technologies such as Large Language Models, etc have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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