Chapter 2
Viruses and Sub-Viral Agents

2.1 Introduction

Throughout the tropics the emerging, re-emerging and endemic plant pathogens are challenging our ability to safeguard plant health. Further globalization, climate change, increased human mobility and pathogen and vector evolution have contributed to increase the spread of invasive plant pathogens. Plant diseases including viruses and viroids are responsible for enormous losses worldwide ($30–50 billion annually) in cultivated and stored crops, and thus are a major impediment to effective food production and distribution. Virus and viroid diseases of short-lived vegetables and herbaceous annual crops (eg. tomato, capsicum, cucurbits, etc.) which are grown using true seed also show maximum infections. If viruses spread rapidly and infect a large population of the crop within few weeks or months, there will be maximum loss in yields. Even certain vegetable and fruit crops that are propagated vegetatively (potato, sweet potato, yam, citrus, apple, etc.) are particularly prone to damage by viruses, as infection tends to buildup in successive cycles of propagation. The emergence of a global community and the increasing numbers of plant viruses identified in the last two decades have increased the requirement for countries and regions to protect their farming systems from exotic viruses. The ProMED database (http://www.promedmail.org) is one of the global electronic reporting systems for detecting outbreaks of emerging infectious diseases and toxins, and these outbreak reports that has been generated since 1994. It is one of the most comprehensive plant emerging infectious disease database available (Anderson et al. 2004). Plant viruses including sub-viral agents and phytoplasmas were identified as the cause of 51 % of the emerging infectious diseases of plants that were recorded in the ProMED database during the period of 1996–2002 and it is likely that this trend will continue. The factors cited as responsible for emerging diseases caused by viruses included structure, genome organization and effective mode of spread. Tropical crops are affected by numerous viruses, the list includes those that are propagated vegetatively and also through true seed to various extents.

In this chapter basic information of viruses and sub-viral agents is briefly presented to realize their significance as an important category of plant pathogens.

K. S. Sastry, *Plant Virus and Viroid Diseases in the Tropics*,

DOI: 10.1007/978-94-007-6524-5_2,

2.2 Viruses

Plant viruses are infectious, intracellular and obligate pathogens that are too small to be seen with a light microscope, but despite their small size, they can cause lethal diseases in plants. The simplest viruses are composed of a small piece of nucleic acid, either RNA or DNA but not both, surrounded by a protein coat. The structure (morphology) of virus is given by its coat of proteins which surrounds the viral genome. As is the case with other organisms, viruses carry genetic information in their nucleic acid which typically specifies four or more proteins. All plant viruses are obligate parasites that depend on the cellular machinery of their hosts to reproduce. Viruses are not active outside of their hosts, and this has led some people to suggest that they are not alive. All types of living organisms including animals, plants, fungi, and bacteria are hosts for viruses, but most viruses infect only one type of host. Viruses cause many important plant diseases and are responsible for losses in crop yield and quality in all parts of the world (refer Chap. 3).

The beginnings of plant virology date back to the late 19th century, when Dutch microbiologist Martinus Beijerinck and Russian researcher Dmitrii Iwanowski were investigated the cause of a mysterious disease of tobacco. Subsequently, numerous scientists from around the world are responsible for the growth of the discipline of plant virology it occurs today. Some of the major developments in the history of plant virology are enumerated below.

1. Virus disease of plants was known long before the discovery of bacteria.

    i) Eupatorium yellow vein disease is the first record of viral disease by Japanese empress Koken in her poem in 752 AD.
    ii) Breaking of flower colour of tulips (as early as 1576).
    iii) Transmission of leaf variegations from the scion to the stock of woody plants (as early as 1700).

2. Tobacco mosaic was identified by Swietch in Holland during 1857.
3. In 1882, Adolph Mayer (1843–1942) described a condition of tobacco plants, which he called “mosaic disease” (“mozaïkziekte”). The diseased plants had variegated leaves that were mottled. Adolph Mayer (1886) was the first to point out that tobacco mosaic (TMV) is readily transmissible and infectious.
4. Iwanowski (1892) confirmed some of the results of Adolph Mayer. He demonstrated that the power to infect was lost if the sap was previously heated. He reported that infectiousness was retained even when sap was passed through bacteria proof filters indicating that the causal agent is different from bacteria.
5. In 1898, the Dutch microbiologist Martinus Beijerinck (1851–1931) repeated the experiments and became convinced that the filtered solution contained a new form of infectious agent. He observed that the agent multiplied only in cells that were dividing and he called it a contagium vivum fluidum (soluble living germ) and coined the word virus, which in Latin means toxin or poison.

6. Stanley (1935) crystallized tobacco mosaic virus with ammonium sulphate and concluded that the virus was an autocatalytic protein that could multiply within the living cells. For his discovery he was awarded the Nobel Prize.
7. Bawden and Pirie (1938) from TMV infected plants isolated a liquid crystalline nucleoprotein containing nucleic acid of the pentose type.
8. Kausche et al. (1939) saw virus particles for the first time with the electron microscope. They confirmed that TMV was rod shaped.
9. Bernal and Fankuchen (1941) were the first to study X-ray diffraction pictures of the crytallized virus. On the basis of pictures, Rosalind Franklin in 1955 discovered the full structure of the virus. In the same year, Heinz Fraenkel-Conrat and Robley Williams showed that purified tobacco mosaic virus RNA and its coat protein can assemble by themselves to form functional viruses, suggesting that this simple mechanism was probably the means through which viruses were created within their host cells.
10. Muller (1942): Williams and Wycoff (1944) developed as shadow casting technique with heavy metals which was useful for determining the overall size and shape of the virus particles.
11. Markham and Smith (1949) isolated *Turnip yellow mosaic virus* (TYMV) and showed that purified preparations contained two classes of particle, one an infectious nucleoprotein with about 35% of RNA, and the other an apparently identical protein particle that contained no RNA and that was not infectious.
12. Gierer and Schramm (1956) showed that the protein could be removed from the virus and that the nucleic acid carried the genetic information so that inoculating with the nucleic acid alone cause infection and could reproduce the complete virus.
13. Kassanis (1962) was the first to describe the satellite virus (Sv) which was found only in association with tobacco necrosis virus.
14. Doi et al. (1967) recognized MLO disease (Yellow Witches' broom). Ishiie et al. (1967) showed that the MLO bodies and the symptoms disappeared temporarily when the plants were treated with tetracycline antibodies.
15. In 1971, Diener identified that the potato spindle tuber disease was caused by a small (250–400 nucleotide long), single stranded circular molecule of infectious RNA which he called a viroid.
16. Davis and Worley (1973) observed motile, helical microorganisms associated with corn stunt disease and named it spiroplasma.

    More details about history of plant virology can be found in reviews by Scholthof (2001); Harrison (2009); Van der Want and Dijkstra (2006).

Disease and economic importance

Depending on the particular combination of virus and host, and on environmental conditions, a plant's response to infection may range from a symptomless condition (latent infection) to severe disease and subsequent plant death. In some cases, small necrotic or chlorotic spots called local lesions develop at the site of infection. In most cases, viruses cause systemic infection and spread throughout the whole plant. Typical leaf symptoms of viral diseases include mosaic patterns, chlorotic or necrotic lesions, yellowing, stripes or streaks, vein clearing, vein banding, and leaf rolling and curling. Symptoms on flower include deformation and changes in the color of the flowers including dramatic color mosaics called color breaking (e.g., tulip flower breaking). In fruit and vegetable crops, the general symptoms produced are mosaic patterns, stunting, discoloration or malformation, and chlorotic ringspots. Infected stems of plants, develop stem pitting and grooving or tumors in response to virus infection.

The symptoms induced by plant viruses lead to reduced crop quality and yield. The extent of these losses is demonstrated by the following three examples. *Cacao swollen shoot virus* (CSSV) (Bowers et al. 2001) is estimated to cause an annual loss of 50,000 tons of cocoa beans in Africa with an estimated value of $28 million dollars. In South east Asia, infection of rice with rice *tungroviruses* leads to an estimated annual loss of $1.5 billion dollars (Hull 2002). *Tomato spotted wilt virus* (TSWV) infects a wide variety of plants including tomato, peanuts, and tobacco (Sherwood et al. 2003), and the estimated annual losses due to infection by this virus worldwide are estimated at $1 billion dollars (Hull 2002; Thresh 2003).

The end result of virus infection is a reduction in plant growth, lower yield, inferior product quality, and economic loss to individuals who work in the plant industry. Most of the symptoms induced by viruses can also occur due to adverse environmental conditions or diseases caused by other plant pathogens (viroids, phytoplasmas). Because of this, correct diagnosis of viral diseases normally requires laboratory tests (Hull 2002).

Harrison (2009) narrated the development of plant virology in the twentieth century. These researchers independently described an unusual agent that caused mosaic disease in tobacco (Zaitlin 1998). What distinguished this agent from other disease-causing agents was its much smaller size compared to that of other microbes. This agent, later named *Tobacco mosaic virus* (TMV), was the first virus described and since then, a large number of diverse viruses have been found in plants, animals, humans, fungi, and bacteria. The current estimate of recognized viruses is 2284 of which about 1020 are plant viruses (King et al. 2012). The majority of the virus diseases which are affecting crop plants are responsible for heavy yield losses. Historically, viruses are perceived almost exclusively as a health threat to humans, livestock, and crop plants. However, recent progress in understanding virus-host interactions has transformed viruses into important molecular tools (gene vectors, regulatory elements of transcription and translation) of biomedicine and biotechnology. According to 9th ICTV report and subsequent online updates, there are 349 genera and 2284 virus species (King et al. 2012). Recently, Scholthof et al. (2011) have made a comprehensive review on the following top 10 ranking of plant viruses in the world. (1) *Tobacco mosaic virus* (TMV), (2) *Tomato spotted wilt virus* (TSWV), (3) *Tomato yellow leaf curl virus* (TYLCV), (4) *Cucumber mosaic virus* (CMV), (5) *Potato virus Y* (PVY), (6) *Cauliflower mosaic virus* (CaMV), (7) *African cassava mosaic virus* (ACMV), (8) *Plum pox virus* (PPV), (9) *Brome mosaic virus* (BMV) and (10) *Potato virus X* (PVX). In addition to these top ten viruses, there are other plant viruses of global economic importance e.g., *Citrus tristeza virus* (CTV), *Banana bunchy top virus* (BBTV), *Barley yellow dwarf virus* (BYDV), *Potato leaf roll virus* (PLRV), *Tomato bushy stunt virus* (TBSV) and *Rice tungro virus complex.*

Rybicki (2012) based on his rich experience in plant viruses, he has listed the following ten plant viruses in alphabetical order.

(1) *African cassava mosaic begomovirus* (ACMV) (Begomovirus complex)
(2) *Banana bunchy top nano virus* (BBTV)
(3) *Banana streak badna virus* (BSV)
(4) *Barley yellow dwarf disease* (BYDV) (Luteo virus complex)
(5) *Cucumber mosaic cucumovirus* (CMV)
(6) *Maize streak masterovirus* (MSV)
(7) *Maize dwarf mosaic/Sugarcane mosaic potyviruses* (MDMV/SCMV)
(8) *Rice tungro disease complex* (RTBV/RTSV)
(9) *Rice yellow mottle sobemovirus* (RYMV)
(10) *Sweet potato feathery mottle potyvirus* (SPFMV)

In addition to the above 10 viruses Rybicki (2012) has mentioned that tomato begomoviruses are worldwide especially in Asia. Even tospoviruses are also equally wide spread worldwide. In Brazil and some South American countries, begomoviruses are economically important in vegetable crops. In Asia, various potyviruses infecting vegetable crops are very important. In South east Asian countries Rice *tungro* virus complex is the major limiting factor for successful rice cultivation. In recent years *Tomato yellow leaf curl virus* and *Tomato torrado virus* transmitted by *Bemisia tabaci* and *Trialeurodes vaporariorium* respectively are causing heavy losses in tomato in majority of the countries.

Many of the above viruses occur in tropics and subtropics and inflict significant losses in crops like cassava, tomato and potato. For instance, plant viruses are being used to produce large quantities of proteins of interest in plants (Pogue et al. 2002) and to develop safe and inexpensive vaccines against human and animal viruses (Walmsley and Arntzen 2000; Canizares et al. 2005; Grasso and Luca 2010). Some plant viruses like TMV, PVX and *Brome mosaic virus* (BMV) have been exploited as model systems for varied purposes in plant biotechnology (Scholthof 2004; Ding et al. 2006).

More details about plant virus and viroid diseases can be found from the following sources: Hull (2002); Khan and Dijkstra (2002); Nayudu (2008); Mahy and Van Regenmortel (2008); Ahlawat (2010). The following websites will also provide more details of various aspects of plant virus and viroids viz., http://www.virology.net/garryfavwebplant.html, http://www.dpvweb.net, http://www.vegetablemdonline.ppath.cornell.edu/, http://www.actahort.org/, http://www.ncbi.nlm.nih.gov/ICTVdb/Ictv/fr-fst-g.htm, http://www.pk.uni-bonn.de/ppigb/, http://www.apsnet.org/edcenter/intropp/PathogenGroups/Pages/PlantViruses.aspx, http://www.pvo.bio-mirror.cn/refs.htm, http://www.isaaa.org/, http://www.q-bank.eu/Virus/. An overview of plant viruses with the basic concepts of virology like the structure of virus particles, genome, pathogenicity, replication, and other aspects are briefly presented here.

(a) Viral genome

Viruses are small enough to avoid our watchful eyes, hiding themselves in infected hosts for most of the time and only occasionally reveal their presence by causing symptoms. Plant viruses are a diverse group infecting hosts from unicellular plants to trees. Viruses are ultramicroscopic and have genomes, either ribonucleic acid (RNA) or deoxyribonucleic acid (DNA). The nucleic acid may be single stranded (ss) or double stranded (ds) and it may be linear or circular. Each plant virus consists of at least a nucleic acid and a protein. Some viruses consist of more than one size of nucleic acid and proteins, and some of them contain enzymes or membrane lipids. The majority of plant viruses possess single-stranded (ss), positive-sense RNA genomes, and these viruses are called positive-strand RNA viruses. Examples of the most economically important families of the positive-strand RNA viruses are *Bromoviridae, Secoviridae, Tymoviridae, Tombusviridae, Virgaviridae, Alphaflexiviridae, Betaflexiviridae, Closteroviridae, Luteoviridae*, and *Potyviridae*. Relatively few plant viruses, exemplified by the families *Bunyaviridae*, *Ophioviridae* and *Rhabdoviridae,* possess negative-sense RNA genomes. *Reoviridae, Partitiviridae, Endornaviridae* are the families of the double-stranded (ds) RNA viruses. There is only one family of the plant viruses with dsDNA genomes, the *Caulimoviridae* family or so-called *pararetroviruses*, and replication of these viruses involves an RNA intermediate. The ssDNA viruses are represented by the large and economically important family *Geminiviridae* and also *Nanoviridae*. These viruses possess ssDNA genomes, and they have a dsDNA intermediate in their life cycle (Hull 2002). The evolutionary relationships among the positive-strand, negative-strand, and dsRNA viruses, as well as the *pararetroviruses* and ssDNA viruses appear to be extremely distant if not absent. Most plant viruses (about 540) contain ssRNA, 40 contain dsRNA, 50 contain ssDNA and about 30 contain dsDNA (Agrios 2005). Based on 9th ICTV classification (King et al. 2012) genome nature and viruses (ssRNA, dsRNA, ssDNA, dsDNA) along with systematic position are presented in Table 2.1. Additions have been made as appears within the 2012 on line version (http://ictvonline.org/virusTaxonomy.asp).

The total genome size of plant viruses ranges from just over 1 kb for satellite viruses, which require helper virus for replication, and *Nanoviruses* (e.g., *Banana bunchy top virus*) to 28.9 kb for members of *Reoviridae* (*Sugarcane Fiji disease virus*). Nearly half of them are elongate (rigid rods or flexuous threads), and almost as many are spherical (isometric or polyhedral), with the remaining being cylindrical bacillus like rods.

Many plant viruses have segmented genomes, consisting of two or more distinct nucleic acid strands encapsidated in different sized particles made of the same protein subunits. Viruses with segmented genome include *Alfamoviruses*, *Bromoviruses*, *Bymoviruses*, *Comoviruses*, *Cryptoviruses*, *Dianthoviruses*, *Benyviruses*, *Hordeiviruses*, *Ilarviruses*, *Nepoviruses*, *Tenuiviruses*, *Tobraviruses*, *Reoviruses*, *Enamoviruses* and *Tospoviruses*. Mandahar (1989) have reviewed the multi component viruses. For example *Tobacco rattle virus* consists of 2 rods: a long one (195 by 25 nm) and a shorter one (43 by 25 nm). They are also called as multi-

Table 2.1 Nature of Genome, Families, Genera, and Species of Plant Viruses

Nature of genome	Family or unassigned genus	Genus	Type species
(+) sense ssRNA Viruses	*Potyviridae*	*Potyvirus*	*Potato virus Y*
		Rymovirus	*Ryegrass mosaic virus*
		Macluravirus	*Maclura mosaic virus*
		Tritimovirus	*Wheat streak mosaic virus*
		Ipomovirus	*Sweet potato mild mottle virus*
		Bymovirus	*Barley yellow mosaic virus*
		Poacevirus	*Triticum mosaic virus*
		Brambyvirus	*Blackberry virus Y*
		Unassigned genus	*Spartina mottle virus*
		Unassigned genus	*Tomato mild mottle virus*
	Secoviridae	*Sequivirus*	*Parsnip yellow fleck virus*
		Waikavirus	*Rice tungro spherical virus*
		Comovirus	*Cowpea mosaic virus*
		Fabavirus	*Broad bean wilt virus 1*
		Nepovirus	*Tobacco ringspot virus*
		Sadwavirus	*Satsuma dwarf virus*
		Cheravirus	*Cherry rasp leaf virus*
		Torradovirus	*Tomato torrado virus*
	Luteoviridae	*Luteovirus*	*Barley yellow dwarf virus-PAV*
		Polerovirus	*Potato leafroll virus*
		Enamovirus	*Pea enation mosaic virus-1*
	Tymoviridae	*Tymovirus*	*Turnip yellow mosaic virus*
		Marafivirus	*Maize rayado fino virus*
		Maculavirus	*Grapevine fleck virus*
	Tombusviridae	*Tombusvirus*	*Tomato bushy stunt virus*
		Carmovirus	*Carnation mottle virus*
		Alphanecrovirus	*Tobacco necrosis virus A*
		Machlomovirus	*Maize chlorotic mottle virus*
		Dianthovirus	*Carnation ringspot virus*
		Avenavirus	*Oat chlorotic stunt virus*
		Aureusvirus	*Pothos latent virus*
		Panicovirus	*Panicum mosaic virus*
	Bromoviridae	*Bromovirus*	*Brome mosaic virus*
		Alfamovirus	*Alfalfa mosaic virus*
		Cucumovirus	*Cucumber mosaic virus*
		Ilarvirus	*Tobacco streak virus*
		Oleavirus	*Olive latent virus 2*
	Closteroviridae	*Closterovirus*	*Beet yellows virus*
		Crinivirus	*Lettuce infectious yellows virus*
		Ampelovirus	*Grapevine leafroll-associated virus 3*
	Alphaflexiviridae	*Potexvirus*	*Potato virus X*
		Allexivirus	*Shallot virus X*
		Mandarivirus	*Indian citrus ringspot virus*

(continued)

Table 2.1 (continued)

Nature of genome	Family or unassigned genus	Genus	Type species
	Betaflexiviridae	*Carlavirus*	*Carnation latent virus*
		Capillovirus	*Apple stem grooving virus*
		Trichovirus	*Apple chlorotic leaf spot virus*
		Foveavirus	*Apple stem pitting virus*
		Vitivirus	*Grapevine virus A*
	Virgaviridae	*Tobamovirus*	*Tobacco mosaic virus*
		Tobravirus	*Tobacco rattle virus*
		Hordeivirus	*Barley stripe mosaic virus*
		Furovirus	*Soil-borne wheat mosaic virus*
		Pomovirus	*Potato mop-top virus*
		Pecluvirus	*Peanut clump virus*
	Unassigned genera	*Benyvirus*	*Beet necrotic yellow vein virus*
		Sobemovirus	*Southern bean mosaic virus*
		Idaeovirus	*Raspberry bushy dwarf virus*
		Umbravirus	*Carrot mottle virus*
(−) sense ssRNA Viruses	*Rhabdoviridae*	*Cytorhabdovirus*	*Lettuce necrotic yellows virus*
		Nucleorhabdovirus	*Potato yellow dwarf virus*
	Bunyaviridae	*Tospovirus*	*Tomato spotted wilt virus*
	Ophioviridae	*Ophiovirus*	*Citrus psorosis virus*
	Unassigned genera	*Tenuivirus*	*Rice stripe virus*
		Varicosavirus	*Lettuce big-vein associated virus*
dsRNA viruses	*Reoviridae*	*Phytoreovirus*	*Wound tumor virus*
		Fijivirus	*Fiji disease virus*
		Oryzavirus	*Rice ragged stunt virus*
	Partitiviridae	*Alphacryptovirus*	*White clover cryptic virus 1*
		Betacryptovirus	*White clover cryptic virus 2*
	Endornaviridae	*Endornavirus*	*Vicia faba endornavirus*
ssDNA Viruses	*Geminiviridae*	*Mastrevirus*	*Maize streak virus*
		Curtovirus	*Beet curly top virus*
		Topocuvirus	*Tomato pseudo-curly top virus*
		Begomovirus	*Bean golden mosaic virus*
	Nanoviridae	*Nanovirus*	*Subterranean clover stunt virus*
		Babuvirus	*Banana bunchy top virus*
dsDNA (Reverse transcribing viruses)	*Caulimoviridae*	*Caulimovirus*	*Cauliflower mosaic virus*
		Soymovirus	*Soybean chlorotic mottle virus*
		Cavemovirus	*Cassava vein mosaic virus*
		Petuvirus	*Petunia vein clearing virus*
		Badnavirus	*Commelina yellow mottle virus*
		Tungrovirus	*Rice tungro bacilliform virus*

partide viruses. However, there are many variations in the structure of the viral genomes. Viruses have one or more protein coats or capsids surrounding their perimeter. These capsid layers are composed of protein subunits and may be composed of the same type or different types of protein.

(b) Basic biology

Viruses are fundamentally different from other pathogens. Unlike all other living organisms, viruses are non-cellular. In contrast to cells, which multiply by dividing into daughter cells, viruses assemble from pools of their structural components. Mature virus particles are dormant; they come alive and reproduce only inside infected cells. In other words, viruses are obligate parasites that cannot be cultivated using any growth media suitable for bacterial, fungal, plant or animal cell types. All viruses lack protein-synthesizing and energy-producing apparatuses. As a rule, virus particles are immobile outside the infected host; they rely on the aid of other organisms (arthropods, nematodes, fungi) or the environment (water) for their dissemination. The plant virus stability outside of its host cell is variable. For example, TMV is stable for months to years whereas TSWV survives only for few hours.

Regarding the biological function of viral components, the infectivity of viruses is strictly the property of their genomic nucleic acid. The protein coat of a virus not only provides a protective sheathing for the nucleic acid of the virus, but also plays a vital role in determining vector transmissibility of a virus and the kinds of symptoms it causes. Protein itself has no infectivity, but its presence generally increases the infectivity of the nucleic acid. Among the various viral genes, one distinguishes those encoding for a structural protein, the coat protein, and those encoding for non-structural proteins such as the polymerase, the helicase, the movement protein, the transmission protein (helper component), or the protease, e.g., TMV genome.

Another important biological aspect in plant virology is of vector transmission. The mode of transmission is a useful characteristic of some groups of plant viruses. For example in the family *Potyviridae*, members of the largest genus (*Potyvirus*) are transmitted by aphids, while viruses in the genera *Rymovirus* and *Tritimovirus* are transmitted by mites of the genus *Abacarus* or *Aceria* respectively, and those in the genus *Ipomovirus* are transmitted by whiteflies and those in the genus *Bymovirus* by plasmodiphorids.

(c) Virus architecture

Viruses are the smallest among all known organisms. The shape and size of virions distinguish rod-shaped, filamentous, icosahedral, or large enveloped particles. On the other hand, viruses sharing the same shape and size are difficult to distinguish by their appearance. There is a simple structural principle that applies to virtually all viruses in their mature form. Virus particles (virions) are composed of two principal parts, the genome that is made of nucleic acid (4–5 % in viruses with rod or filamentous morphology, 15–45 % in case of icosahedral viruses), and a protective coat that is made of protein. A definite number of protein subunits present

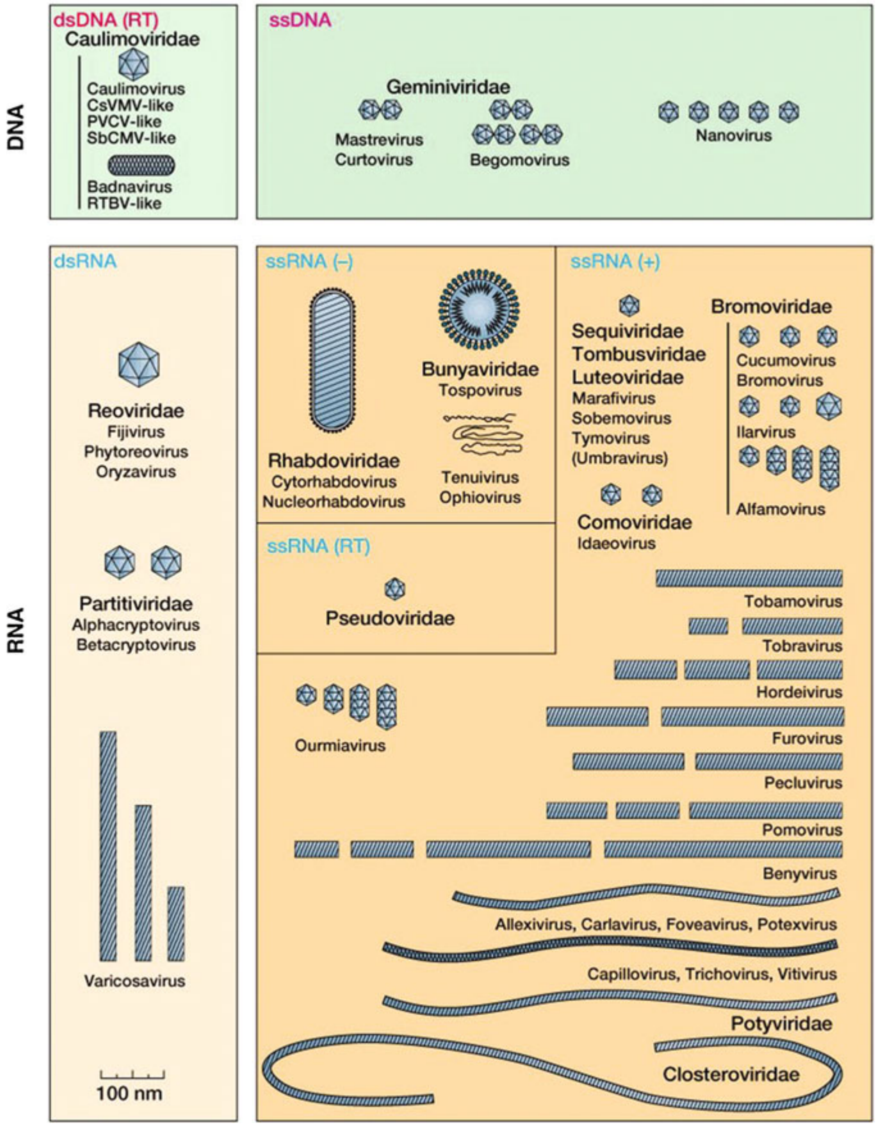

Fig. 2.1 Families and Genera of viruses infecting plants. *Courtesy* MHV van Regenmortel et al. eds., Virus Taxonomy: 7th Report of ICTV (Elsevier)

on surface of viruses are arranged spirally in the elongated viruses and packed on the sides of the polyhedral particles of the spherical viruses. In cross section, the elongated viruses appear as hollow tubes with the protein subunits forming the outer coat and the nucleic acid, also arranged spirally, embedded between the inner ends of two successive spirals of the protein subunits. In spherical viruses the visible shell consists of protein subunits, while the nucleic acid is inside the shell. The viral proteins consist of amino acids. The amino acid content and sequence for identical protein subunits of a given virus are constant, but vary for different viruses. In addition, some virus particles (*tospoviruses*, plant *rhabdoviruses*) are enveloped by an outer membrane containing lipids and proteins (lipoprotein membrane). The enveloped spherical tospoviruses are slightly pleomorphic and their diameter ranges 80–110nm. The protein coat of plant viruses (capsids) are assembled in accord with one of the two fundamental types of symmetry (Fig. 2.1). The first type of virion is helical (roughly elongated). The elongated viruses come in two major variants, rigid rods (e.g., *tobamoviruses*) and flexuous filaments (e.g., *potyviruses*). Over 50% of known plant viruses are rod shaped and the length of the particle is normally dependent on the genome, but it is usually between 300–500nm with a diameter of 15–20nm. Some of the filamentous viruses reach the length of ~2000nm (*Closteroviruses*). In both of these variants, the nucleic acid is highly ordered: it assumes the same helical conformation as the proteinaceous capsid. The second type of virus particle is icosahedral/roughly spherical (e.g., *Cucumoviruses*) and the general diameter will be 30nm. In cases where there is only a single coat protein, the basic structure consists of 60 T subunits, where T is an integer. Some viruses may have two coat proteins or associate to form an icosahedral shape particle. In icosahedral virions, the genomic nucleic acid forms a partially ordered ball inside the proteinaceous capsid. The smallest spherical virus is *Tobacco necrosis virus* (15 nm in diameter); *Nanoviruses* (18–20 nm in diameter). The diameter of plant *Reoviruses* and *Caulimoviruses* is 65–70 and 45–50 nm, respectively. For instance, small spherical viruses may be difficult to distinguish from each other and from plant ribosomes. The variations of this basic shape include bacilliform virions (e.g., Badnaviruses, 300–400 × 95 nm). In geminate particles, twin virions composed of two joined incomplete icosahedra (e.g., 18 × 30 nm) as seen in geminiviruses. The icosahedral and elongated virions alike can self-assemble in a test tube if the nucleic acid and protein subunits are incubated under proper conditions (Rao 2006; Atabekov et al. 2007). The particle morphology of some of the plant viruses is presented in Fig. 2.2.

Few viruses have their genome distributed in different particles (split genome) and accordingly they are divided into monopartite (e.g., *tobamoviruses, potexviruses*), bipartite (e.g., *tobraviruses, pecluviruses*), tripartite (e.g., *hordeiviruses*) or multipartite (e.g., *Alfamoviruses, Phytoreoviruses, Nanoviruses*). All the morphological components are essential for the infectivity of these viruses (Hull 2008).

The properties used to distinguish the viruses are the type of nucleic acid in the virus genome (single or double stranded DNA or RNA), the shape, size and number of their particles and the presence or absence of an envelope around the virus particles.

Viruses like *geminiviruses*, *badnaviruses* and *phyto rhabdoviruses* can be easily identified based on their characteristic virion morphology (Zechmann and Zelling 2009). The rigid, rod-shaped TMV particle is 300 × 18 nm and consists of an RNA genome of about 6,400 nucleotides encapsidated by 2,130 copies of the TMV coat protein.

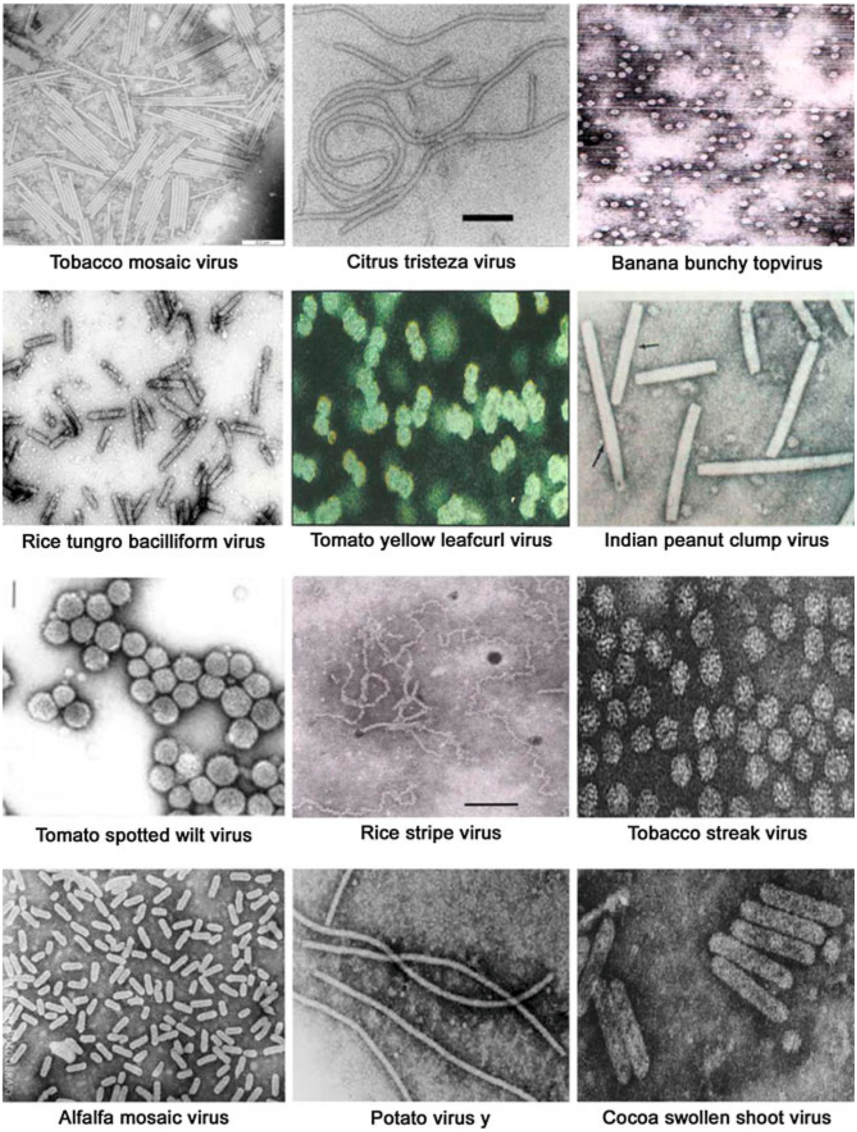

Fig. 2.2 Electron micrographs—particle morphology of different plant viruses. *Source* http://www.virology.net/big picture book of viruses

(d) Pathogenicity

Generally different viruses elicit similar symptoms, but the disease phenotype can provide only limited information for disease diagnosis. More specific and reliable methods of virus identification are based on various properties of the viruses like biological, physical, antigenic and molecular (Matthews 1993; Webster et al. 2004;

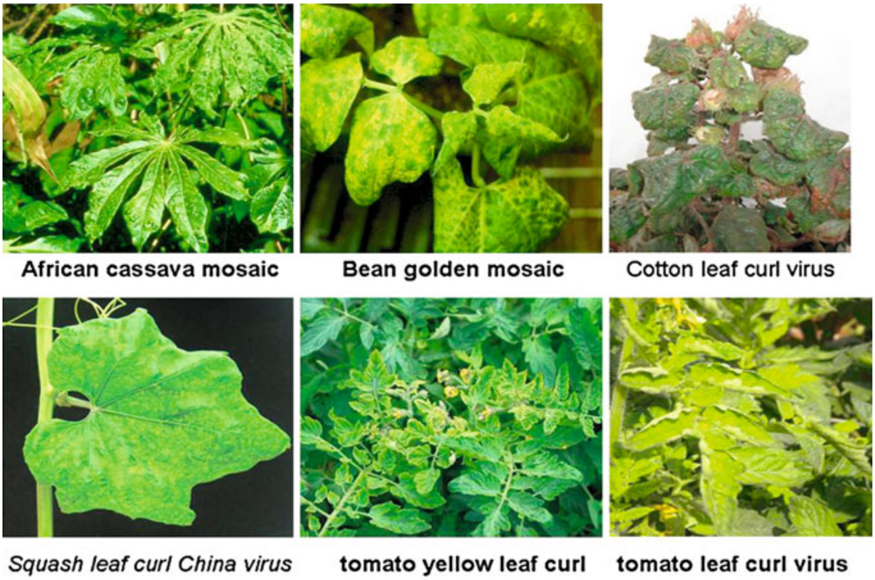

Fig. 2.3 Symptoms of diseases induced by certain begomoviruses. *Source* http://www.virology.net/big picture book of viruses

Nayudu 2008). Researchers during last four decades have precisely identifying the unknown viruses mainly based on their host range, physical properties and bioassays using indicator plants. Some plant genera, such as *Nicotiana tabacum* (tobacco), *Vigna sinensis* (cowpea), *Phaseolus vulgaris* cultivars (French bean) and *Chenopodium* species are hosts for a number of viruses. Since the responses of these plants to viral infections under greenhouse conditions are consistent and distinctive, they are commonly used as indicator plants (Nayudu 2008). In virus infected plants, two major types of responses are noticed. Local lesions, which are confined to inoculated leaves (local lesion hosts), and systemic infections which produce symptoms on leaves distant from the inoculation site (systemic hosts). Many plant viruses are transmissible to indicator plants by means of mechanical transmission or grafting. But for the past three decades plant viruses are identified and classified based on host and symptoms, particle morphology, physico-chemical properties, virus protein composition, virus NA sequence analysis, molecular tests and other factors (Murphy et al. 1995; van Regenmortel et al. 2000; Fauquet et al. 2005; King et al. 2012).
Plant viruses induce variety of systemic symptoms, sometimes they may be diagnostic useful to identify the causal virus. Symptoms induced by most prevalent *begomoviruses* and TSWV in tropics are given in Figs. 2.3 and 2.4.

In the tropics, the major fruit crops are banana, citrus, papaya, pineapple, grape, passion fruit and avocado which are affected by virus and viroid diseases. The symptoms of some of these diseases are shown in the Fig. 2.5. In some of the virus-host combinations, the flowers, fruits/parts will show viral symptoms viz.,

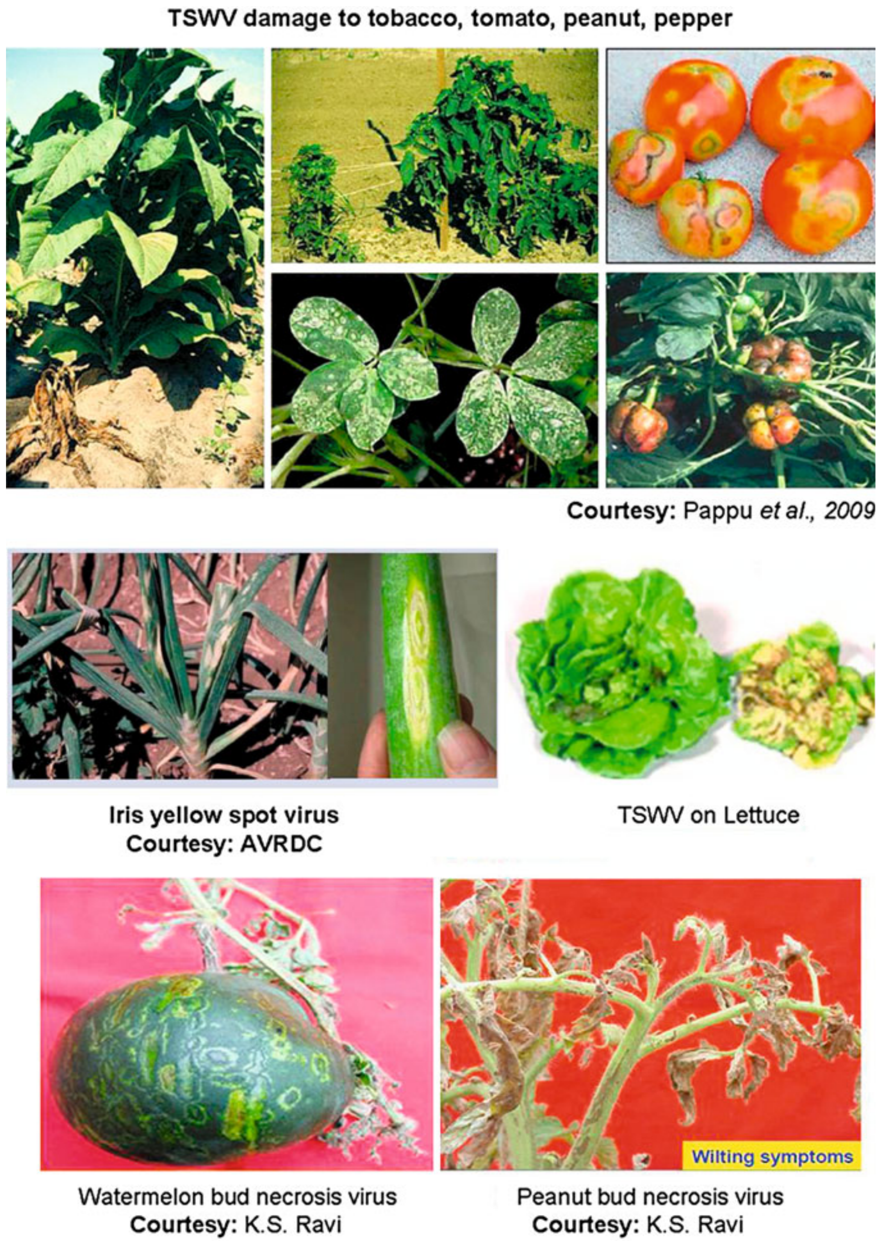

Fig. 2.4 Symptoms induced by TSWV on different crops

leaves with varied degrees of mosaic symptoms, ring spots, yellowing, reduced size, flower break/irregular colour streaks, fruits with reduced size, distortion, blistering and some times ring spot symptoms.

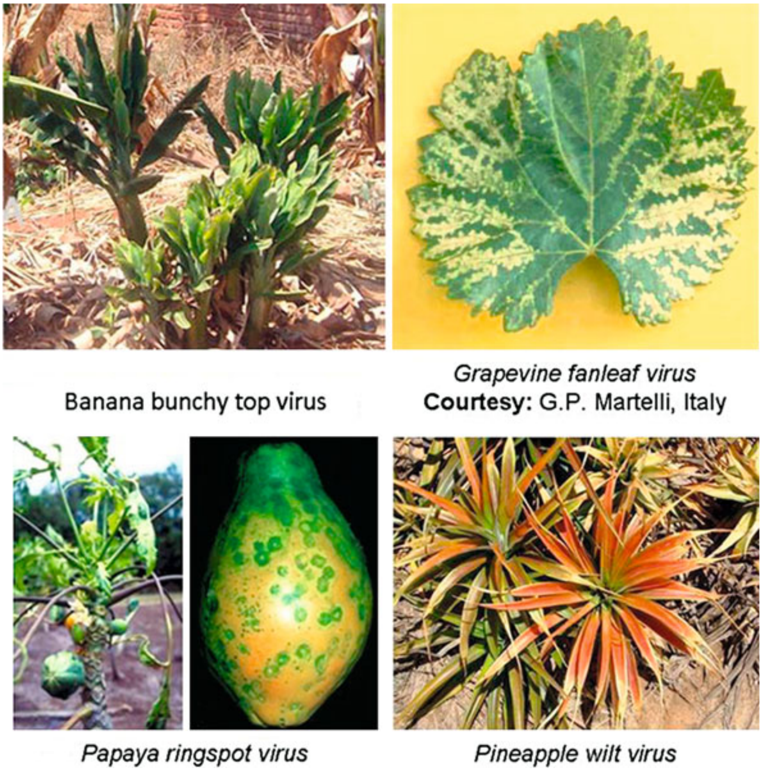

Fig. 2.5 Symptoms of virus diseases of fruit crops. *Source* www.virology.net/big picture book of viruses

After mechanical sap inoculation in host range studies, some plants may not show symptoms or virus multiplication for a period and the time interval is called "latency period" or "incubation period". After some time period, during which the virus will replicate to a critical concentration, but will not induce symptoms, as seen in *Carnation latent virus*. Whereas in some hosts at particular temperature, the symptoms will disappear temporarily, but after some period, the symptoms will be expressed as seen in *Pea leafroll virus* and *Prune dwarf virus*.

(e) Plant virus replication

The plant virus genome has the information for replication, assembly, movement, various interactions with its host etc. However, the genome of nearly 80% of plant viruses are made up of RNA. Most of the plant viruses are composed with ssRNA that is the same (positive-sense) polarity as the messenger RNAs of the cell (e.g., viruses belonging to families: *Potyviridae*, *Bromoviridae*, *Virgaviridae*, *Tombusviridae*, *Secoviridae*, *Luteoviridae*, *Tymoviridae*, *Closteroviridae*, *Alphaflexiviridae*, *Betaflexiviridae*) which follows the Baltimore strategy IV of virus genome replication and expression. There are some RNA viruses which are ssRNA of negative polarity (e.g., viruses belonging to families: *Rhabdoviridae*, *Bunyaviridae*, *Ophioviridae*). The basic mechanism of replication of positive sense RNA genome is that the virus encoded replicase synthesizes a complementary negative strand by using the positive strand as template and then new positive strands are synthesized from the negative strand template through semi conservative mode of replication. Synthesis of new RNA is from the 3’ and 5’ ends of the templates. Replication occurs in a replication complex that comprises the templates, newly synthesized RNA, the replicase and host factors. The positive and negative forms of the viral genome contain the signals that control both the specificity and timing of their replication. Sometimes the divided genome may be encapsidated either in single particle or morphologically distinct particles.

Viruses do not produce any kind of reproductive structures and they multiply by using host cell machinery. The life cycles start by penetration of the virion into the cell and to replication sites in the cell. Plant viruses are unable to penetrate the plant cuticle and cell wall, it is believed that the virion enters the cytoplasm of the cell passively through wounds caused by mechanical damage to the cuticle and cell wall or vector transmission. The next phase of virus infection is the partial or complete removal of the coat protein of the virion in the cytoplasm. In the next step, the cell mediates expression of the viral genome by providing a transcriptional apparatus and a translation apparatus.

Replication of single stranded RNA viruses starts with the entry of the virions in to the cell cytoplasm; the viral nucleic-acid is released from the coat protein and induces the viral RNA polymerase. This enzyme is being utilized for the synthesis of viral RNA as template and forms complimentary RNA. The initially synthesized RNA is not viral RNA but a mirror image of that RNA (complimentary copy). This complimentary RNA is temporarily connected to the viral strand and synthesizes double stranded RNA, later it synthesizes the progeny viral RNA which is a mirror image of negative strand. This cycle repeats for number of times and synthesizes more positive sense RNA strands. As soon as the progeny viral RNA is produced, some of these are translated to induce the protein molecules of viruses. When progeny virus RNA and virus protein sub-units have been produced, the RNA organizes the protein sub-units around it and the two are assembled together to form the provirion in the cytoplasm.

All viruses must direct the formation of at least three types of proteins: replication proteins that are essential for nucleic acid production, structural proteins that form the protein shell and other components (e.g., Vpg) contained in the virions, and movement proteins that mediate virus transport between plant cells (Hull 2002). The viral replication proteins combine with cellular proteins to produce a complex of proteins that manufactures multiple copies of the virus genome. These newly made genomes interact with the structural proteins to form new virions. The DNA genomes are replicated in the nucleus and RNA genomes in the cytoplasm of plant cells.

The next step in the virus replication cycle is movement of the virus into neighboring cells. There are two basic routes by which a virus moves through the plant to give full systemic infection i.e., cell to cell movement and long distance movement. Depending on the virus, the viral genome or the virions are transported into neighboring cells through small channels called plasmodesmata. Many viruses produce Movement Proteins (MP) that modify the plasmodesmata channels and facilitate viral movement into neighboring cells. The process of cell-to-cell movement is relatively slow: it takes from one to few hours for a virus to move to the next cell. The successful translocation of virus to entire plant, needs to enter in to the vascular system of the plant. The process of systemic or long-distance transport normally proceeds through the phloem sieve elements where viruses move passively with the flow of photosynthates. After quite rapid systemic spread of the virus (centimeters per hour) in the phloem, the virus moves from the phloem into surrounding cells where it reproduces and spreads by cell-to-cell movement. The time between initial infection of one or a few cells and systemic infection of the plant varies from few days to a few weeks depending on the type of virus, host plant and environmental conditions. Transmission of the virus from one plant to another completes the virus life cycle.

Some viruses have genome made up of dsRNA (e.g., viruses belonging to families: *Reoviridae*, *Partitiviridae*, *Endornaviridae*). Some of the plant viruses have genome that are composed of ssDNA (e.g., viruses belonging to families: *Geminiviridae*, *Nanoviridae*). There are very few plant viruses belonging to family: *Caulimoviridae* which have dsDNA genome. The genome may be either linear (e.g., tobamoviruses; cucumoviruses) or circular (e.g., caulimoviruses, geminiviruses, nanoviruses).

Since the virus replication steps vary for dsRNA, ssDNA and dsDNA viruses, more details can be obtained from reviews and references (Hull 2002, 2008; Mandahar 2006; Nayudu 2008; Laliberte and Sanfacon 2010).

(f) Plant-virus interactions

Plant viruses are capable of infecting virtually all species of cultivated and wild plants. Either mechanically or through vectors or both. However, host ranges of individual viruses vary from very narrow to very broad. For instance *Citrus tristeza virus* (CTV) infects only a few species in the *Citrus* genus, Similarly *Banana bunchytop virus* (BBTV) and *Cocoa swollen shoot virus* (CSSV) have limited host range, whereas CMV infects over 1000 species in 85 plant families. Even TSWV infects over 925 plant species, including both monocots and dicots, belonging to 70 botanical families. Because of the wide host range, the viruses like CMV, PVY and TSWV are worldwide in distribution and also have potential insect vectors. Susceptibility or resistance of plant species and cultivars to viruses is determined primarily by the plant genotype. Plants possess active and passive means of preventing virus infection. Passive defenses are due to the failure of the plant to produce one or more host factors required for virus reproduction and spread within the host. Active defenses include detection and destruction of the virus-infected cells due to the function of specific resistance genes in the plant. Normally, resistance genes are active only against a particular virus. In addition, plants possess a general defense system that is somewhat analogous to the animal immune system. The major difference between the two is that the immune system in animals targets a pathogen's proteins, whereas the plant defense system, which is called RNA silencing, detects and degrades viral RNAs (Wassenegger and Pelissier 1998).

On the other hand, in some of the plant viruses due to their inherent genetic differences and influence of the host and the environment, there will be synergistic or antagonistic effects due to multiplication of two or more related and unrelated viruses in the same host. The synergistic reaction will result into severe symptoms and heavy yield losses. To quote few examples viz., in Sub-Saharan Africa (SSA) the emerge of a new variant, EACMV-Ug is the result of recombination between two distinct viruses, namely *African cassava mosaic virus* (ACMV) and *East African cassava mosaic virus* (EACMV), and is responsible for epidemics in Uganda (Zhou et al. 1997; Otim-Nape et al. 1997). Another example is Corn lethal necrosis disease resulted from the combination of *Maize chlorotic mottle virus* with *Maize dwarf mosaic virus* (MDMV) (Uyemoto 1983). In Africa, severe Sweet potato virus disease (SPVd) which is due to infection of *Sweet potato chlorotic stunt virus* (SPCSV) and *Sweet potato feathery mottle virus* (SPFMV) (Nome et al. 2007). In general when a susceptible crop is infected by a single virus, the impact on yield losses will not be as great as when two viruses interact in the same host (Goldberg and Brakke, 1987). Due to a synergistic reaction increased seed transmission was noticed in certain virus-host combinations. For example seed transmission of *Southern bean mosaic virus* (SBMV) was 12% in cowpea but increased to 20% in the presence of *Cowpea chlorotic mottle virus* (CCMV) (Kuhn and Dawson 1973).

Almost all plant viruses can exhibit strainal variation and the strains may be mild, moderate or severe. The antagonism results due to mild strains which produces mild symptoms due to mild strains of plant viruses as seen in crops like tomato, potato, sweet potato, cucumber, soybean, citrus, passion fruit, cocoa and papaya and in these crops the cross protection aspect has been studied by different workers (Balaraman 1981; Fraser 1998; Tripathi et al. 2008; Zhou and Zhou 2012).

(g) Plant viruses as agents of agroterrorism

The majority of people are aware of bioterrorism with regard to introduction of severe strains of virus or insect vectors which transmit human and live stock viruses resulting in high mortality/devastation. There are also very few examples of viruses which are of crop devastating nature when a severe strain enters into a new country in which this particular virus was not previously known.

In recent years attention has been given to the threat posed by the deliberate introduction of plant pathogens that are not already present in a country, or of novel and particularly aggressive strains of pathogens already present. However, the risks are likely to be less than those posed by highly infectious viruses, or other pathogens of humans or livestock (Gewin 2003). Moreover, wind-borne plant pathogenic fungi seem to present a greater threat than plant viruses, which usually spread less rapidly and require an insect or fungus vector.

In certain countries of Africa and Asia in the earlier years, due to early infection of plant viruses, there was total financial shortage and partial food shortage for human and livelihood. On the other hand, the developed countries can compensate for any losses incurred by imports and purchase of food grains from elsewhere. There are very few opportunities for terrorists to exploit the ignorance of the general public on plant pathological issues. This makes it easy to provide misleading information and initiate unease and even panic or hysteria, especially by targeting fresh fruit or vegetable crops intended for immediate consumption.

Out of the two possibilities of bioterrorism, one possibility is to introduce particularly damaging strains of a plant virus or viruses that is/are already present, but having relatively benign effects. The scope for adopting this approach is apparent from the devastation caused by the recombinant strain of a *Cassava mosaic virus* that appeared naturally and is causing food shortages in large regions of East and Central Africa (Otim-Nape et al. 2000). Problems have also been caused by particularly virulent strains of *Citrus tristeza virus* (Bar-Joseph et al. 1981) and by novel strains of *Sugarcane mosaic virus* that seriously damage cultivars selected for their resistance to the strain(s) occurring previously (Thresh 1989). The chances for agro-terrorism is more in case of whitefly and thrips transmitted gemini and *tospoviruses* respectively, when introduced into a new areas. The last two viruses have very large number of new strains and variants as seen in case of TLCV in tomato, YVMV in okra, CoLCV in cotton and *tospoviruses* in vegetables. These two virus groups have very wide host-ranges. Even the vectors of this two viruses viz., whitefly and thrips have number of biotypes. Because of these factors wherever and whenever these viruses are introduced into new areas, there are maximum chances of causing epidemics if susceptible host is available. Clearly, considerable expertise will be required to select the most appropriate viruses for this approach and to develop suitable strains by selection from those occurring naturally, or following some sort of genetic manipulation.

The second possibility of agro-terrorism is the introducing an entirely new vector or a novel biotype of an existing vector, which will spread virus diseases and causes heavy losses. The consequence could be very damaging, as evident from the apparent ease with which the western flower thrips, the brown citrus aphid, and other aphids and the “B-biotype” of *B. tabaci* have become established recently in new areas. However, there is again a requirement for expertise, rearing facilities, an effective means of introduction and sufficient time for the vectors to become established and build up damaging populations.

The bio-safety measures and strict quarantine rules and regulations in each country, would certainly solved the problems that arise because of bioterrorism due to the entry of new virulent virus/viroid and insect vectors. Generally plant pathogens seem to pose a lesser threat than pathogens of humans and livestock. These agents would undoubtedly have a greater and more immediate impact on public sentiment, attitudes and actions, especially if reinforced by an effective propaganda campaign designed to initiate panic and an irrational behavior and response. The scope for this form of bioterrorism and the risks posed are discussed by Madden and Wheelis (2003).

2.2.1 Virus Classification

Classification or taxonomy of plant viruses is a method of categorization of viruses reported from different parts of the world and have two faces, systematic and nomenclature.

Classification is the arrangement of biological entities into taxonomic categories (taxa) on the basis of similarities and/or relationships, whereas *nomenclature* is the assignment of names to taxa according to international rules. To apply these (apparently) simple concepts to viruses, the Virology Division of the International Union of Microbiological Societies (IUMS) established, some 30 years ago, the International Committee for the Nomenclature of Viruses (ICNV), whose name was subsequently changed to the present International Committee on Taxonomy of Viruses (ICTV).

(a) The objectives of the ICTV are

(i) to develop an internationally agreed taxonomy for viruses,
(ii) to develop internationally agreed names for virus taxa, including species and subviral agents,
(iii) to communicate taxonomic decisions to the international community of virologists and
(iv) to maintain an index of virus names.

More details of the history of virus taxonomy can be obtained from the review articles of Gibbs (1969), Francki (1981), Matthews (1983), Martelli (1992), Mayo and Brunt (2007).

(b) Systematics and background information
When we consider plant virus classification, we should remember that it was the mid 1930s before the first plant virus was purified and characterized. Prior to this time, most plant virologists named a virus based on the host plant in which it was found and the type of major symptom that the virus caused in the plant. For example, TMV was first described in tobacco in which it induces a mosaic pattern in the leaves Virus names are usually shortened to an acronym, for example, tobacco mosaic virus is shortened to TMV, and tomato spotted wilt virus is shortened to TSWV. The names of many virus genera and families are derived from an important virus within the family. For example, the family name *Bromoviridae* is derived from *Brome mosaic virus* which is in this family.

As early as 1927 Johnson, drew attention to the need for a system of classification and nomenclature of plant viruses. In the following four decades, many schemes were introduced but none proved acceptable. Since little was known about the intrinsic properties of the viruses, great weight was placed on characters such as symptoms, host range, physical and chemical parameters.

After World War II, viruses were recognized as constraints for production throughout the world. Legume virus researchers were among the first to standardize the techniques for identifying the viruses (Bos et al. 1960). An International Working Group on Legume Viruses (IWGLV) was established in 1961 for the exchange of seeds, antisera and of information. The tentative list of viruses reported from naturally infected leguminous plants animated further worldwide assemblage of information in computerized form by the Australian Virus Identification Data Exchange project (VIDE). Its microfiche publication on VIDE viruses of legumes was soon followed by a printed version in 1983 (Boswell and Gibbs 1983). Similar books on viruses of plants in Australia (1988) and of tropical plants (1990) were succeeded by viruses of plants in 1996 which was also distributed on the internet and later contributed to the database of ICTV.

Within the structure of the ICTV, plant virus taxonomic matters are first handled by the Plant Virus Subcommittee (PVS) and there are similar subcommittees concerned with viruses of vertebrates, bacteria, invertebrates, and fungi. Plant virology is represented by the chairman of a subcommittee that itself consists of 19 study group chairs and eight other members. The study groups are concerned with particular taxa or groups of taxa (e.g., the *Potyviridae* Study Group). The subcommittee chair appoints the chair of the study groups, who then appoint study group members as is appropriate.

Ideas for taxonomic change, either creation or modification of plant virus taxa, or decisions about names of these taxa, usually originate in study group deliberations. These ideas are scrutinized by the Plant Virus Subcommittee, largely for their acceptability within the overall taxonomic scheme for plant viruses. If approved, the proposals are then submitted to the Executive Committee members who examine their acceptability in the context of all virus taxonomy. Approved proposals are then put to the membership of ICTV for a final vote as to their acceptability. After a favorable vote by ICTV, the proposals become part of the taxonomic scheme for viruses. These decisions are then published in Virology Division News in *Archives of Virology* and/or in the regular ICTV reports (e.g., van Regenmortel et al. 2000).

The president of the ICTV publishes a report every 3 years that has become the standard handbook on virus taxonomy. The latest 9th ICTV report is published by (King et al. 2012).

ICTV has been very active in the last 30 years, incrementally increasing the number of taxa and virus names from 369 in 1985 to 7,881 in 2004 (Martelli 1997). Not only have the numbers increased exponentially (more than 20-fold), but the complexity of virus nomenclature and taxonomy has become tremendously complicated and controversial. However, the overall stability of this virus classification, established in 1962 (Lwoff et al. 1962), is quite remarkable in that, for example, names of all genera and families established in the 1980s are still in use till 2011. The advancement with the most impact was the definition of a virus species (van Regenmortel et al. 1991; Mayo and Fauquet 2000), which still is not fully understood by most virologists.

Taxonomic decisions are taken by ICTV, which is authorized by statutes approved by the Virology Division of the International Union of Microbiological Societies (Mayo and Pringle 1998; Mayo and Horzinek 1998 and references therein).

Thus, decisions are subjected to representative international scrutiny. The ICTV is organized and advised by an Executive Committee that consists of 18 members: four officers, chairs of six subcommittees representative of each major branch of virology, and eight elected members.

(c) Nomenclature
Nomenclature is the assignment of names to taxa according to international rules. To apply these (apparently) simple concepts to viruses, the Virology Division of the IUMS established, some 30 years ago, the ICNV, whose name was subsequently changed to the present ICTV.

(d) Principles of nomenclature
The essential principles of virus nomenclature are to:

(i) aim for stability,
(ii) avoid or reject the use of names which might cause error or confusion and
(iii) avoid the unnecessary creation of names.

Nomenclature of viruses and sub-viral agents is independent of other biological nomenclature. Virus and virus taxon nomenclature are recognized to have the status of exceptions in the proposed International Code of Bio nomenclature (Bio Code).

The primary purpose of naming a taxon is to supply a means of referring to the taxon, rather than to indicate the characters or history of the taxon. The application of names of taxa is determined, explicitly or implicitly, by means of nomenclatural types. The name of a taxon has no official status until it has been approved by ICTV.

(e) Generating the ratified list of taxa
Using Taxonomic Proposals Management System (TPMS), it will be possible to generate a complete list of approved taxa at any time, and this will be possible either alphabetically or taxonomically. Accepted taxa also will be presented according to the order of presentation of virus taxonomy: dsDNA, ssDNA, rtDNA, rtRNA, dsRNA, ssNRNA, ssPRNA, SAT (Satellites), VIR (Viroids), UN (unassigned). Within each category, the families will be classified according to the order of presentation of the virus. Taxonomy species will be assigned to a genus and classified alphabetically within the genus. The species taxa should comprise at least one isolate but include as many as described.

(f) Rules about species
The definition of a virus species as a polythetic class means that all members of the species do not have a single defining property in common that is necessary and sufficient for class membership. It is also defined as a polythetic class of viruses that constitutes a replicating lineage and occupies a particular ecological niche. It is not appropriate, therefore, to search for an elusive, single property that would define a virus species.

Therefore, a virus species is defined as follows: *A virus species is a polythetic class of viruses that constitutes a replicating lineage and occupies a particular ecological niche* (van Regenmortel 1989, 1990).

(g) Construction of a species name

While dealing the virus taxonomy aspect, the names of orders, families, subfamilies, and genera are always printed in italics and the first letters of the names are capitalized. At its meeting in San Diego in March 1998, the Executive Committee of the ICTV decided to extend this practice to the names of species taxa to clearly indicate that the species name had been approved as the official, internationally recognized name (Pringle 1998).

The order name shall be a single word ending in… *virales*.
The family name shall be a single word ending in… *viridae*.
The subfamily name shall be a single word ending in… *virinae*.
The genus name shall be a single word ending in… *virus*.

(h) Latin and binomial nomenclature in virus taxonomy

When one talks about the virus species, the new ICTV rules demand that it be written "*Tobacco mosaic virus*", i.e. in italics and with a capital initial, whereas Dr. Bos, in his textbook, chose instead to use the name "*Tobacco mosaic tobamovirus*", i.e. a binomial name written in lower case Roman characters and without a capital initial.

The value of using italics is that it visibly reinforces the status of the corresponding species as a taxonomic entity, i.e., a formal, abstract class, distinct from the concrete viral objects that replicates and cause disease and that are written in Roman characters. Only if it is necessary to draw attention to the taxonomic position of the virus under study will it be necessary to refer to the official species name written in italics. Even then, the official name need be given only once, probably in the introduction or materials and methods sections (e.g., *Cucumber mosaic virus,* genus *Cucumovirus*, family *Bromoviridae*). In publications written in languages other than English, the use of italics for the English official species name would also indicate the alien nature of the term. In such publications, the common names of viruses will be those used in that language and not the English names. The use of italicized English instead of italicized Latin for the names of virus species reflects the emergence of English as the modern language of international scientific communication, and it also does away with the invidious task of having to coin new Latin names for all virus species (van Regenmortel 2000).

By introducing italicized virus species names, the ICTV in no way intended to replace the existing vernacular or common names of viruses written in Roman characters (van Regenmortel 2000; van Regenmortel and Fauquet 2002a). The viruses studied by virologists are concrete, disease-causing entities and not abstract classes, and they should continue to be referred to by their common, non-italicized names. As reiterated by Drebot et al. (2002), only the names of viral taxonomic classes are written in italics, not the names of viruses. In scientific articles, authors need to refer most of the time to the virus as a physical entity rather than as a member of a taxonomic class. Therefore, the common name written in Roman characters will most often be used; the species name, in italics, will appear only once for the purpose of taxonomic placement of the virus being discussed.

(i) A proposed binomial nomenclature for virus species

For many years, some plant virologists have been using an unofficial binomial system for referring to virus species (as well as to viruses). In this system, the italicized word *virus* appearing at the end of the current official species name is replaced by the genus name, which also ends in "-*virus*" (Gibbs 2000; Drebot et al. 2002). Thus *Tobacco mosaic virus* becomes *Tobacco mosaic tobamovirus* and *Cucumber mosaic virus* becomes *Cucumber mosaic cucumovirus*. The advantage of such a system is that inclusion of the genus name in the species name indicates relationships with other viruses and therefore provides additional information about the properties of the members of the species.

Such a binomial system for species names would also have the advantage of clearly distinguishing between the species name written in italics (*Tobacco mosaic tobamovirus*) and the common, non-italicized virus name, measles virus. At present, the distinction between the species name and the virus name in most cases relies only on typography (i.e., *Tobacco mosaic virus* versus tobacco mosaic virus), which can lead to confusion (van Regenmortel and Fauquet 2002a).

Whether nonlatinized binomials should become the official species names of viruses has been debated within the ICTV for many years (Bos 1999; van Regenmortel 2000; van Regenmortel et al. 2000; van Regenmortel 2001; Drebot et al. 2002; Bos 2002). Although most plant virologists have favored the use of binomials for many years (Albouy and Devergne 1998), to what extent human and animal virologists would find the system acceptable has not been known. As the ICTV strives to develop a universal system of nomenclature approved by all virologists (Mayo and Horzinek 1998; Mayo and Brunt 2007), it is bound to move cautiously before changing all the current, official names of virus species. Since very few virologists express their views on matters of taxonomy (van Regenmortel 2000), successive ICTV Executive Committees have always found it difficult to poll the representative opinion of virologists worldwide (Matthews 1983), and it is not clear what sort of democratic process would satisfy those who criticize ICTV decisions. During 2002, efforts were made to canvass virologists regarding their acceptance of a binomial system of species names; the results of two ballots showed that a sizeable majority (80–85 %) of the 250 virologists who expressed an opinion were in favor of a binomial system (van Regenmortel and Fauquet 2002b; Mayo 2002). The new ICTV Executive Committee established at the 12th International Congress of Virology, held in Paris in July 2002, decided the introduction of binomial names of virus species. A list of current virus species names, together with their binomial equivalents, can be found on ICTV net (available from: URL: http://www.danforthcenter.org/ILTAB/ICTVnet/). The details of the 1st to 9th ICTV reports furnishing the number of approved orders, families, subfamilies, genera, and virus species are furnished in the Table 2.2.

Table 2.2 Virus taxa dealt in different ICTV reports

ICTV report	International Congress of Virology held at	Number of approved 'families, sub families, groups/genera and species	References
First	Helsinki, 1968	43 families and groups	Wildy (1971)
Second	Budapest, 1971 and Madrid, 1975	47 families and groups	Fenner (1976)
Third	The Hague, 1978	50 families and groups	Matthews (1979)
Fourth	Strasbourg, 1981	54 families and groups	Matthews (1982)
Fifth	Sendai, 1984, Edmonton, 1987, and Berlin, 1990	2420 viruses belonging to 73 families or groups	Francki et al. (1991)
Sixth	Glasgow, 1993	1 order, 50 families, 9 subfamilies, 164 genera and more than 3,600 virus species	Murphy et al. (1995)
Seventh	Jerusalem, 1996	3 orders, 63 families, 9 subfamilies, 240 genera, 1550 species	van Regenmortel et al. (2000)
Eighth	Sydney, 1999 and Paris, 2002	3 orders, 73 families, 11 subfamilies, 289 genera and 1898 species	Fauquet et al. (2005)
Nineth	2011	6 orders, 87 families, 19 subfamilies, 349 genera; and 2284 species	King et al. (2012)

ICTV IXth report

The current ICTV IXth report lists 2284 species distributed amongst 349 genera, 19 sub-families, 87 families and six orders. More details are provided in Part II about the unassigned viruses that provides information on a number of viruses that have not yet been classified but which are probably representatives of new genera and/or families (King et al. 2012). The 9th report is being published both as a book and also online. ICTV expects to make regular updates to keep the online version in step with the latest taxonomic decisions (see http://ictvonline.org/virusTaxonomy.asp). Only the list of plant viruses included in the ICTV IXth report (King et al. 2012) is presented in the following Table 2.3.

Each genus contains a type species (the representative used in defining the genus) and often a number of other species. For each species, authors have been asked to provide details of a single isolate, a characterized virus that is

Table 2.3 9TH ICTV Classification of plant viruses

Order	Family	Subfamily	Genus	Type species	Species
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	0	*Barley yellow striate mosaic virus*
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	0	*Broccoli necrotic yellows virus*
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	0	*Festuca leaf streak virus*
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	1	*Lettuce necrotic yellows virus*
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	0	*Lettuce yellow mottle virus*
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	0	*Northern cereal mosaic virus*
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	0	*Sonchus virus*
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	0	*Strawberry crinkle virus*
Mononegavirales	*Rhabdoviridae*		*Cytorhabdovirus*	0	*Wheat American striate mosaic virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Datura yellow vein virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Eggplant mottled dwarf virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Maize fine streak virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Maize Iranian mosaic virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Maize mosaic virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	1	*Potato yellow dwarf virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Rice yellow stunt virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Sonchus yellow net virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Sowthistle yellow vein virus*
Mononegavirales	*Rhabdoviridae*		*Nucleorhabdovirus*	0	*Taro vein chlorosis virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Andean potato mottle virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Bean pod mottle virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Bean rugose mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Broad bean stain virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Broad bean true mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	1	*Cowpea mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Cowpea severe mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Glycine mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Pea green mottle virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Pea mild mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Quail pea mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Radish mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Red clover mottle virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Squash mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Comovirus*	0	*Ullucus virus C*
Picornavirales	*Secoviridae*	*Comovirinae*	*Fabavirus*	1	*Broad bean wilt virus 1*
Picornavirales	*Secoviridae*	*Comovirinae*	*Fabavirus*	0	*Broad bean wilt virus 2*
Picornavirales	*Secoviridae*	*Comovirinae*	*Fabavirus*	0	*Gentian mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Fabavirus*	0	*Lamium mild mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Apricot latent ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Arabis mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Arracacha virus A*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Artichoke Aegean ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Artichoke Italian latent virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Artichoke yellow ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Beet ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Blackcurrant reversion virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Blueberry leaf mottle virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Cassava American latent virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Cassava green mottle virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Cherry leaf roll virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Chicory yellow mottle virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Cocoa necrosis virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Crimson clover latent virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Cycas necrotic stunt virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Grapevine Anatolian ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Grapevine Bulgarian latent virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Grapevine chrome mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Grapevine deformation virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Grapevine fanleaf virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Grapevine Tunisian ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Hibiscus latent ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Lucerne Australian latent virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Melon mild mottle virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Mulberry ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Myrobalan latent ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Olive latent ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Peach rosette mosaic virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Potato black ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Potato virus U*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Raspberry ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	1	*Tobacco ringspot virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Tomato black ring virus*
Picornavirales	*Secoviridae*	*Comovirinae*	*Nepovirus*	0	*Tomato ringspot virus*
Picornavirales	*Secoviridae*		*Cheravirus*	0	*Apple latent spherical virus*
Picornavirales	*Secoviridae*		*Cheravirus*	1	*Cherry rasp leaf virus*
Picornavirales	*Secoviridae*		*Cheravirus*	0	*Stocky prune virus*
Picornavirales	*Secoviridae*		*Sadwavirus*	1	*Satsuma dwarf virus*
Picornavirales	*Secoviridae*		*Sequivirus*	0	*Carrot necrotic dieback virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Picornavirales	*Secoviridae*		*Sequivirus*	0	*Dandelion yellow mosaic virus*
Picornavirales	*Secoviridae*		*Sequivirus*	1	*Parsnip yellow fleck virus*
Picornavirales	*Secoviridae*		*Torradovirus*	0	*Tomato marchitez virus*
Picornavirales	*Secoviridae*		*Torradovirus*	1	*Tomato torrado virus*
Picornavirales	*Secoviridae*		Unassigned	0	*Black raspberry necrosis virus*
Picornavirales	*Secoviridae*		Unassigned	0	*Strawberry latent ringspot virus*
Picornavirales	*Secoviridae*		Unassigned	0	*Strawberry mottle virus*
Picornavirales	*Secoviridae*		*Waikavirus*	0	*Anthriscus yellows virus*
Picornavirales	*Secoviridae*		*Waikavirus*	0	*Maize chlorotic dwarf virus*
Picornavirales	*Secoviridae*		*Waikavirus*	1	*Rice tungro spherical virus*
Tymovirales	*Alphaflexiviridae*		*Allexivirus*	0	*Garlic mite-borne filamentous virus*
Tymovirales	*Alphaflexiviridae*		*Allexivirus*	0	*Garlic virus A*
Tymovirales	*Alphaflexiviridae*		*Allexivirus*	0	*Garlic virus B*
Tymovirales	*Alphaflexiviridae*		*Allexivirus*	0	*Garlic virus C*
Tymovirales	*Alphaflexiviridae*		*Allexivirus*	0	*Garlic virus D*
Tymovirales	*Alphaflexiviridae*		*Allexivirus*	0	*Garlic virus E*
Tymovirales	*Alphaflexiviridae*		*Allexivirus*	0	*Garlic virus X*
Tymovirales	*Alphaflexiviridae*		*Allexivirus*	1	*Shallot virus X*
Tymovirales	*Alphaflexiviridae*		*Lolavirus*	1	*Lolium latent virus*
Tymovirales	*Alphaflexiviridae*		*Mandarivirus*	1	*Indian citrus ringspot virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Alstroemeria virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Alternanthera mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Asparagus virus 3*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Bamboo mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Cactus virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Cassava common mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Cassava virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Clover yellow mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Commelina virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Cymbidium mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Daphne virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Foxtail mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Hosta virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Hydrangea ringspot virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Lettuce virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Lily virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Malva mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Mint virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Narcissus mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Nerine virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Opuntia virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Papaya mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Pepino mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Phaius virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Plantago asiatica mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Plantago severe mottle virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Plantain virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Potato aucuba mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	1	*Potato virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Schlumbergera virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Strawberry mild yellow edge virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Tamus red mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Tulip virus X*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*White clover mosaic virus*
Tymovirales	*Alphaflexiviridae*		*Potexvirus*	0	*Zygocactus virus X*
Tymovirales	*Betaflexiviridae*		*Capillovirus*	1	*Apple stem grooving virus*
Tymovirales	*Betaflexiviridae*		*Capillovirus*	0	*Cherry virus A*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Aconitum latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*American hop latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Blueberry scorch virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Cactus virus 2*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Caper latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	1	*Carnation latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Chrysanthemum virus B*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Cole latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Coleus vein necrosis virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Cowpea mild mottle virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Dandelion latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Daphne virus S*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Elderberry symptomless virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Garlic common latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Helenium virus S*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Helleborus net necrosis virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Honeysuckle latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Hop latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Hop mosaic virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Hydrangea latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Kalanchoë latent virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Ligustrum necrotic ringspot virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Lilac mottle virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Lily symptomless virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Melon yellowing-associated virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Mulberry latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Muskmelon vein necrosis virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Narcissus common latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Narcissus symptomless virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Nerine latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Passiflora latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Pea streak virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Poplar mosaic virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Potato latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Potato virus M*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Potato virus P*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Potato virus S*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Red clover vein mosaic virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Shallot latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Sint-Jan's onion latent virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Strawberry pseudo mild yellow edge virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Sweet potato chlorotic fleck virus*
Tymovirales	*Betaflexiviridae*		*Carlavirus*	0	*Verbena latent virus*
Tymovirales	*Betaflexiviridae*		*Citrivirus*	1	*Citrus leaf blotch virus*
Tymovirales	*Betaflexiviridae*		*Foveavirus*	1	*Apple stem pitting virus*
Tymovirales	*Betaflexiviridae*		*Foveavirus*	0	*Apricot latent virus*
Tymovirales	*Betaflexiviridae*		*Foveavirus*	0	*Grapevine rupestris stem pitting-associated virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Tymovirales	*Betaflexiviridae*		*Foveavirus*	0	*Peach chlorotic mottle virus*
Tymovirales	*Betaflexiviridae*		*Tepovirus*	1	*Potato virus T*
Tymovirales	*Betaflexiviridae*		*Trichovirus*	1	*Apple chlorotic leaf spot virus*
Tymovirales	*Betaflexiviridae*		*Trichovirus*	0	*Apricot pseudo-chlorotic leaf spot virus*
Tymovirales	*Betaflexiviridae*		*Trichovirus*	0	*Cherry mottle leaf virus*
Tymovirales	*Betaflexiviridae*		*Trichovirus*	0	*Grapevine berry inner necrosis virus*
Tymovirales	*Betaflexiviridae*		*Trichovirus*	0	*Peach mosaic virus*
Tymovirales	*Betaflexiviridae*		Unassigned	0	*African oil palm ringspot virus*
Tymovirales	*Betaflexiviridae*		Unassigned	0	*Banana mild mosaic virus*
Tymovirales	*Betaflexiviridae*		Unassigned	0	*Cherry green ring mottle virus*
Tymovirales	*Betaflexiviridae*		Unassigned	0	*Cherry necrotic rusty mottle virus*
Tymovirales	*Betaflexiviridae*		Unassigned	0	*Sugarcane striate mosaic-associated virus*
Tymovirales	*Betaflexiviridae*		*Vitivirus*	1	*Grapevine virus A*
Tymovirales	*Betaflexiviridae*		*Vitivirus*	0	*Grapevine virus B*
Tymovirales	*Betaflexiviridae*		*Vitivirus*	0	*Grapevine virus D*
Tymovirales	*Betaflexiviridae*		*Vitivirus*	0	*Grapevine virus E*
Tymovirales	*Betaflexiviridae*		*Vitivirus*	0	*Heracleum latent virus*
Tymovirales	*Betaflexiviridae*		*Vitivirus*	0	*Mint virus 2*
Tymovirales	*Tymoviridae*		Unassigned	0	*Poinsettia mosaic virus*
Tymovirales	*Tymoviridae*		*Maculavirus*	1	*Grapevine fleck virus*
Tymovirales	*Tymoviridae*		*Marafivirus*	0	*Bermuda grass etched-line virus*
Tymovirales	*Tymoviridae*		*Marafivirus*	0	*Blackberry virus S*
Tymovirales	*Tymoviridae*		*Marafivirus*	0	*Citrus sudden death-associated virus*
Tymovirales	*Tymoviridae*		*Marafivirus*	0	*Grapevine Syrah virus 1*
Tymovirales	*Tymoviridae*		*Marafivirus*	1	*Maize rayado fino virus*
Tymovirales	*Tymoviridae*		*Marafivirus*	0	*Oat blue dwarf virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Tymovirales	*Tymoviridae*		*Marafivirus*	0	*Olive latent virus 3*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Anagyris vein yellowing virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Andean potato latent virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Belladonna mottle virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Cacao yellow mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Calopogonium yellow vein virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Chayote mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Chiltepin yellow mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Clitoria yellow vein virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Desmodium yellow mottle virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Dulcamara mottle virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Eggplant mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Erysimum latent virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Kennedya yellow mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Melon rugose mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Nemesia ring necrosis virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Okra mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Ononis yellow mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Passion fruit yellow mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Peanut yellow mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Petunia vein banding virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Physalis mottle virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Plantago mottle virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Scrophularia mottle virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	1	*Turnip yellow mosaic virus*
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Voandzeia necrotic mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Tymovirales	*Tymoviridae*		*Tymovirus*	0	*Wild cucumber mosaic virus*
Unassigned	*Avsunviroidae*		*Avsunviroid*	1	*Avocado sunblotch viroid*
Unassigned	*Avsunviroidae*		*Elaviroid*	1	*Eggplant latent viroid*
Unassigned	*Avsunviroidae*		*Pelamoviroid*	0	*Chrysanthemum chlorotic mottle viroid*
Unassigned	*Avsunviroidae*		*Pelamoviroid*	1	*Peach latent mosaic viroid*
Unassigned	*Bromoviridae*		*Alfamovirus*	1	*Alfalfa mosaic virus*
Unassigned	*Bromoviridae*		*Anulavirus*	1	*Pelargonium zonate spot virus*
Unassigned	*Bromoviridae*		*Bromovirus*	0	*Broad bean mottle virus*
Unassigned	*Bromoviridae*		*Bromovirus*	1	*Brome mosaic virus*
Unassigned	*Bromoviridae*		*Bromovirus*	0	*Cassia yellow blotch virus*
Unassigned	*Bromoviridae*		*Bromovirus*	0	*Cowpea chlorotic mottle virus*
Unassigned	*Bromoviridae*		*Bromovirus*	0	*Melandrium yellow fleck virus*
Unassigned	*Bromoviridae*		*Bromovirus*	0	*Spring beauty latent virus*
Unassigned	*Bromoviridae*		*Cucumovirus*	1	*Cucumber mosaic virus*
Unassigned	*Bromoviridae*		*Cucumovirus*	0	*Gayfeather mild mottle virus*
Unassigned	*Bromoviridae*		*Cucumovirus*	0	*Peanut stunt virus*
Unassigned	*Bromoviridae*		*Cucumovirus*	0	*Tomato aspermy virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*American plum line pattern virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Apple mosaic virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Asparagus virus 2*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Blackberry chlorotic ringspot virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Blueberry shock virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Citrus leaf rugose virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Citrus variegation virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Elm mottle virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Fragaria chiloensis latent virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Humulus japonicus latent virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Lilac leaf chlorosis virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Lilac ring mottle virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Parietaria mottle virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Prune dwarf virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Prunus necrotic ringspot virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Spinach latent virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Strawberry necrotic shock virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	1	*Tobacco streak virus*
Unassigned	*Bromoviridae*		*Ilarvirus*	0	*Tulare apple mosaic virus*
Unassigned	*Bromoviridae*		*Oleavirus*	1	*Olive latent virus 2*
Unassigned	*Bunyaviridae*		*Tospovirus*	0	*Groundnut bud necrosis virus*
Unassigned	*Bunyaviridae*		*Tospovirus*	0	*Groundnut ringspot virus*
Unassigned	*Bunyaviridae*		*Tospovirus*	0	*Groundnut yellow spot virus*
Unassigned	*Bunyaviridae*		*Tospovirus*	0	*Impatiens necrotic spot virus*
Unassigned	*Bunyaviridae*		*Tospovirus*	0	*Tomato chlorotic spot virus*
Unassigned	*Bunyaviridae*		*Tospovirus*	1	*Tomato spotted wilt virus*
Unassigned	*Bunyaviridae*		*Tospovirus*	0	*Watermelon silver mottle virus*
Unassigned	*Bunyaviridae*		*Tospovirus*	0	*Zucchini lethal chlorosis virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Aglaonema bacilliform virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Banana streak GF virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Banana streak MY virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Banana streak OL virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Banana streak VN virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Bougainvillea chlorotic vein banding virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Cacao swollen shoot virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Canna yellow mottle virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Citrus yellow mosaic virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	1	*Commelina yellow mottle virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Dioscorea bacilliform AL virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Dioscorea bacilliform SN virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Gooseberry vein banding associated virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Grapevine vein clearing virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Kalanchoë top-spotting virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Pineapple bacilliform CO virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Pineapple bacilliform ER virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Piper yellow mottle virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Rubus yellow net virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Schefflera ringspot virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Spiraea yellow leaf spot virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Sugarcane bacilliform IM virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Sugarcane bacilliform MO virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Sweet potato pakakuy virus*
Unassigned	*Caulimoviridae*		*Badnavirus*	0	*Taro bacilliform virus*
Unassigned	*Caulimoviridae*		*Caulimovirus*	0	*Carnation etched ring virus*
Unassigned	*Caulimoviridae*		*Caulimovirus*	1	*Cauliflower mosaic virus*
Unassigned	*Caulimoviridae*		*Caulimovirus*	0	*Dahlia mosaic virus*
Unassigned	*Caulimoviridae*		*Caulimovirus*	0	*Figwort mosaic virus*
Unassigned	*Caulimoviridae*		*Caulimovirus*	0	*Horseradish latent virus*
Unassigned	*Caulimoviridae*		*Caulimovirus*	0	*Lamium leaf distortion virus*
Unassigned	*Caulimoviridae*		*Caulimovirus*	0	*Mirabilis mosaic virus*
Unassigned	*Caulimoviridae*		*Caulimovirus*	0	*Strawberry vein banding virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Caulimoviridae*		*Caulimovirus*	0	*Thistle mottle virus*
Unassigned	*Caulimoviridae*		*Cavemovirus*	1	*Cassava vein mosaic virus*
Unassigned	*Caulimoviridae*		*Cavemovirus*	0	*Sweet potato collusive virus*
Unassigned	*Caulimoviridae*		*Petuvirus*	1	*Petunia vein clearing virus*
Unassigned	*Caulimoviridae*		*Solendovirus*	0	*Sweet potato vein clearing virus*
Unassigned	*Caulimoviridae*		*Solendovirus*	1	*Tobacco vein clearing virus*
Unassigned	*Caulimoviridae*		*Soymovirus*	0	*Blueberry red ringspot virus*
Unassigned	*Caulimoviridae*		*Soymovirus*	0	*Cestrum yellow leaf curling virus*
Unassigned	*Caulimoviridae*		*Soymovirus*	0	*Peanut chlorotic streak virus*
Unassigned	*Caulimoviridae*		*Soymovirus*	1	*Soybean chlorotic mottle virus*
Unassigned	*Caulimoviridae*		*Tungrovirus*	1	*Rice tungro bacilliform virus*
Unassigned	*Closteroviridae*		*Ampelovirus*	0	*Grapevine leafroll-associated virus 1*
Unassigned	*Closteroviridae*		*Ampelovirus*	1	*Grapevine leafroll-associated virus 3*
Unassigned	*Closteroviridae*		*Ampelovirus*	0	*Grapevine leafroll-associated virus 5*
Unassigned	*Closteroviridae*		*Ampelovirus*	0	*Little cherry virus 2*
Unassigned	*Closteroviridae*		*Ampelovirus*	0	*Pineapple mealybug wilt-associated virus 1*
Unassigned	*Closteroviridae*		*Ampelovirus*	0	*Pineapple mealybug wilt-associated virus 2*
Unassigned	*Closteroviridae*		*Ampelovirus*	0	*Pineapple mealybug wilt-associated virus 3*
Unassigned	*Closteroviridae*		*Ampelovirus*	0	*Plum bark necrosis stem pitting-associated virus*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Beet yellow stunt virus*
Unassigned	*Closteroviridae*		*Closterovirus*	1	*Beet yellows virus*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Burdock yellows virus*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Carnation necrotic fleck virus*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Carrot yellow leaf virus*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Citrus tristeza virus*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Grapevine leafroll-associated virus 2*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Mint virus 1*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Raspberry leaf mottle virus*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Strawberry chlorotic fleck-associated virus*
Unassigned	*Closteroviridae*		*Closterovirus*	0	*Wheat yellow leaf virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Abutilon yellows virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Bean yellow disorder virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Beet pseudoyellows virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Blackberry yellow vein-associated virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Cucurbit yellow stunting disorder virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Lettuce chlorosis virus*
Unassigned	*Closteroviridae*		*Crinivirus*	1	*Lettuce infectious yellows virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Potato yellow vein virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Strawberry pallidosis-associated virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Sweet potato chlorotic stunt virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Tomato chlorosis virus*
Unassigned	*Closteroviridae*		*Crinivirus*	0	*Tomato infectious chlorosis virus*
Unassigned	*Closteroviridae*		Unassigned	0	*Alligatorweed stunting virus*
Unassigned	*Closteroviridae*		Unassigned	0	*Grapevine leafroll-associated virus 7*
Unassigned	*Closteroviridae*		Unassigned	0	*Little cherry virus 1*
Unassigned	*Closteroviridae*		Unassigned	0	*Megakepasma mosaic virus*
Unassigned	*Closteroviridae*		Unassigned	0	*Mint vein banding-associated virus*
Unassigned	*Closteroviridae*		Unassigned	0	*Olive leaf yellowing-associated virus*
Unassigned	*Endornaviridae*		*Endornavirus*	0	*Oryza rufipogon endornavirus*
Unassigned	*Endornaviridae*		*Endornavirus*	0	*Oryza sativa endornavirus*
Unassigned	*Endornaviridae*		*Endornavirus*	0	*Phaseolus vulgaris endornavirus*
Unassigned	*Endornaviridae*		*Endornavirus*	1	*Vicia faba endornavirus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Abutilon mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*African cassava mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Ageratum enation virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Ageratum leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Ageratum yellow vein Hualian virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Ageratum yellow vein Sri Lanka virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Ageratum yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Alternanthera yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Bean calico mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Bean dwarf mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Bean golden mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	1	*Bean golden yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Bhendi yellow vein mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Bitter gourd yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Boerhavia yellow spot virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cabbage leaf curl Jamaica virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cabbage leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Chayote yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Chilli leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Chino del tomate virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Clerodendron golden mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Corchorus golden mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Corchorus yellow spot virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Corchorus yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cotton leaf crumple virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cotton leaf curl Alabad virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cotton leaf curl Bangalore virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cotton leaf curl Gezira virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cotton leaf curl Kokhran virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cotton leaf curl Multan virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cowpea golden mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Croton yellow vein mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Cucurbit leaf crumple virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Desmodium leaf distortion virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Dicliptera yellow mottle Cuba virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Dicliptera yellow mottle virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Dolichos yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*East African cassava mosaic Cameroon virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*East African cassava mosaic Kenya virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*East African cassava mosaic Malawi virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*East African cassava mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*East African cassava mosaic Zanzibar virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Erectites yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Eupatorium yellow vein mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Eupatorium yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Euphorbia leaf curl Guangxi virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Euphorbia leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Euphorbia mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Hollyhock leaf crumple virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Honeysuckle yellow vein Kagoshima virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Honeysuckle yellow vein mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Honeysuckle yellow vein virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Horsegram yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Indian cassava mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Ipomoea yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Kudzu mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Lindernia anagallis yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Ludwigia yellow vein Vietnam virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Ludwigia yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Luffa yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Macroptilium mosaic Puerto Rico virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Macroptilium yellow mosaic Florida virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Macroptilium yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Malvastrum leaf curl Guangdong virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Malvastrum leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Malvastrum yellow leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Malvastrum yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Malvastrum yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Malvastrum yellow vein Yunnan virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Melon chlorotic leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Merremia mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Mesta yellow vein mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Mimosa yellow leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Mungbean yellow mosaic India virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Mungbean yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Okra yellow crinkle virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Okra yellow mosaic Mexico virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Okra yellow mottle Iguala virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Okra yellow vein mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Papaya leaf curl China virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Papaya leaf curl Guandong virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Papaya leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pedilenthus leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pepper golden mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pepper huasteco yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pepper leaf curl Bangladesh virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pepper leaf curl Lahore virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pepper leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pepper yellow leaf curl Indonesia virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pepper yellow vein Mali virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Potato yellow mosaic Panama virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Potato yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Pumpkin yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Radish leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Rhynchosia golden mosaic Sinaloa virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Rhynchosia golden mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Senecio yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida golden mosaic Costa Rica virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida golden mosaic Florida virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida golden mosaic Honduras virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida golden mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida golden yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida micrantha mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida mottle virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida yellow mosaic China virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida yellow mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida yellow mosaic Yucatan virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida yellow vein Madurai virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida yellow vein Vietnam virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sida yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Siegesbeckia yellow vein Guangxi virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Siegesbeckia yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*South African cassava mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Soybean blistering mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Soybean crinkle leaf virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Spilanthes yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Squash leaf curl China virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Squash leaf curl Philippines virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Squash leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Squash leaf curl Yunnan virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Squash mild leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sri Lankan cassava mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Stachytarpheta leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sweet potato leaf curl Canary virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sweet potato leaf curl China virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sweet potato leaf curl Georgia virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sweet potato leaf curl Lanzarote virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sweet potato leaf curl Spain virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Sweet potato leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tobacco curly shoot virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tobacco leaf curl Cuba virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tobacco leaf curl Japan virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tobacco leaf curl Yunnan virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tobacco leaf curl Zimbabwe virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato chino La Paz virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato chlorotic mottle virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato curly stunt virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato golden mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato golden mottle virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Arusha virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Bangalore virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Bangladesh virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl China virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Comoros virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Guangdong virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Guangxi virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Gujarat virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Hsinchu virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Java virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Joydebpur virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Karnataka virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Kerala virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Laos virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Madagascar virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Malaysia virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Mali virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Mayotte virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl New Delhi virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Philippines virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Pune virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Seychelles virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Sinaloa virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Sri Lanka virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Sudan virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Taiwan virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Uganda virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl Vietnam virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato mild yellow leaf curl Aragua virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato mosaic Havana virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato mottle Taino virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato mottle virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato rugose mosaic virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato severe leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato severe rugose virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Axarquia virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl China virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Guangdong virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Indonesia virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Kanchanaburi virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Malaga virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Mali virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Sardinia virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Thailand virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl Vietnam virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow margin leaf curl virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow spot virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Tomato yellow vein streak virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Vernonia yellow vein virus*
Unassigned	*Geminiviridae*		*Begomovirus*	0	*Watermelon chlorotic stunt virus*
Unassigned	*Geminiviridae*		*Curtovirus*	0	*Beet curly top Iran virus*
Unassigned	*Geminiviridae*		*Curtovirus*	1	*Beet curly top virus*
Unassigned	*Geminiviridae*		*Curtovirus*	0	*Beet mild curly top virus*
Unassigned	*Geminiviridae*		*Curtovirus*	0	*Beet severe curly top virus*
Unassigned	*Geminiviridae*		*Curtovirus*	0	*Horseradish curly top virus*
Unassigned	*Geminiviridae*		*Curtovirus*	0	*Pepper curly top virus*
Unassigned	*Geminiviridae*		*Curtovirus*	0	*Spinach curly top virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Bean yellow dwarf virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Chloris striate mosaic virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Digitaria streak virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Eragrostis streak virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	1	*Maize streak virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Miscanthus streak virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Panicum streak virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Setaria streak virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Sugarcane streak Egypt virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Sugarcane streak Reunion virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Sugarcane streak virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Tobacco yellow dwarf virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Urochloa streak virus*
Unassigned	*Geminiviridae*		*Mastrevirus*	0	*Wheat dwarf virus*
Unassigned	*Geminiviridae*		*Topocuvirus*	1	*Tomato pseudo-curly top virus*
Unassigned	*Luteoviridae*		*Enamovirus*	1	*Pea enation mosaic virus-1*
Unassigned	*Luteoviridae*		*Luteovirus*	0	*Barley yellow dwarf virus-MAV*
Unassigned	*Luteoviridae*		*Luteovirus*	0	*Barley yellow dwarf virus-PAS*
Unassigned	*Luteoviridae*		*Luteovirus*	1	*Barley yellow dwarf virus-PAV*
Unassigned	*Luteoviridae*		*Luteovirus*	0	*Bean leafroll virus*
Unassigned	*Luteoviridae*		*Luteovirus*	0	*Rose spring dwarf-associated virus*
Unassigned	*Luteoviridae*		*Luteovirus*	0	*Soybean dwarf virus*
Unassigned	*Luteoviridae*		*Polerovirus*	0	*Beet chlorosis virus*
Unassigned	*Luteoviridae*		*Polerovirus*	0	*Beet mild yellowing virus*
Unassigned	*Luteoviridae*		*Polerovirus*	0	*Beet western yellows virus*
Unassigned	*Luteoviridae*		*Polerovirus*	0	*Carrot red leaf virus*
Unassigned	*Luteoviridae*		*Polerovirus*	0	*Cereal yellow dwarf virus-RPS*
Unassigned	*Luteoviridae*		*Polerovirus*	0	*Cereal yellow dwarf virus-RPV*
Unassigned	*Luteoviridae*		*Polerovirus*	0	*Chickpea chlorotic stunt virus*
Unassigned	*Luteoviridae*		*Polerovirus*	0	*Cucurbit aphid-borne yellows virus*
Unassigned	*Luteoviridae*		Polerovirus	0	*Melon aphid-borne yellows virus*
Unassigned	*Luteoviridae*		Polerovirus	1	*Potato leafroll virus*
Unassigned	*Luteoviridae*		Polerovirus	0	*Sugarcane yellow leaf virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Luteoviridae*		Polerovirus	0	*Tobacco vein distorting virus*
Unassigned	*Luteoviridae*		Polerovirus	0	*Turnip yellows virus*
Unassigned	*Luteoviridae*		Unassigned	0	*Barley yellow dwarf virus-GPV*
Unassigned	*Luteoviridae*		Unassigned	0	*Barley yellow dwarf virus-RMV*
Unassigned	*Luteoviridae*		Unassigned	0	*Barley yellow dwarf virus-SGV*
Unassigned	*Luteoviridae*		Unassigned	0	*Chickpea stunt disease associated virus*
Unassigned	*Luteoviridae*		Unassigned	0	*Groundnut rosette assistor virus*
Unassigned	*Luteoviridae*		Unassigned	0	*Indonesian soybean dwarf virus*
Unassigned	*Luteoviridae*		Unassigned	0	*Sweet potato leaf speckling virus*
Unassigned	*Luteoviridae*		Unassigned	0	*Tobacco necrotic dwarf virus*
Unassigned	*Nanoviridae*		*Babuvirus*	0	*Abaca bunchy top virus*
Unassigned	*Nanoviridae*		*Babuvirus*	1	*Banana bunchy top virus*
Unassigned	*Nanoviridae*		*Babuvirus*	0	*Cardamom bushy dwarf virus*
Unassigned	*Nanoviridae*		*Nanovirus*	0	*Faba bean necrotic stunt virus*
Unassigned	*Nanoviridae*		*Nanovirus*	0	*Faba bean necrotic yellows virus*
Unassigned	*Nanoviridae*		*Nanovirus*	0	*Milk vetch dwarf virus*
Unassigned	*Nanoviridae*		*Nanovirus*	0	*Pea necrotic yellow dwarf virus*
Unassigned	*Nanoviridae*		*Nanovirus*	1	*Subterranean clover stunt virus*
Unassigned	*Nanoviridae*		Unassigned	0	*Coconut foliar decay virus*
Unassigned	*Ophioviridae*		*Ophiovirus*	1	*Citrus psorosis virus*
Unassigned	*Ophioviridae*		*Ophiovirus*	0	*Freesia sneak virus*
Unassigned	*Ophioviridae*		*Ophiovirus*	0	*Lettuce ring necrosis virus*
Unassigned	*Ophioviridae*		*Ophiovirus*	0	*Mirafiori lettuce big-vein virus*
Unassigned	*Ophioviridae*		*Ophiovirus*	0	*Ranunculus white mottle virus*
Unassigned	*Ophioviridae*		*Ophiovirus*	0	*Tulip mild mottle mosaic virus*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Alfalfa cryptic virus 1*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Beet cryptic virus 1*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Beet cryptic virus 2*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Beet cryptic virus 3*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Carnation cryptic virus 1*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Carrot temperate virus 1*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Carrot temperate virus 3*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Carrot temperate virus 4*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Hop trefoil cryptic virus 1*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Hop trefoil cryptic virus 3*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Radish yellow edge virus*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Ryegrass cryptic virus*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Spinach temperate virus*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*Vicia cryptic virus*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	1	*White clover cryptic virus 1*
Unassigned	*Partitiviridae*		*Alphacryptovirus*	0	*White clover cryptic virus 3*
Unassigned	*Partitiviridae*		*Betacryptovirus*	0	*Carrot temperate virus 2*
Unassigned	*Partitiviridae*		*Betacryptovirus*	0	*Hop trefoil cryptic virus 2*
Unassigned	*Partitiviridae*		*Betacryptovirus*	0	*Red clover cryptic virus 2*
Unassigned	*Partitiviridae*		*Betacryptovirus*	1	*White clover cryptic virus 2*
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Apple dimple fruit viroid*
Unassigned	*Pospiviroidae*		*Apscaviroid*	1	*Apple scar skin viroid*
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Australian grapevine viroid*
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Citrus bent leaf viroid*
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Citrus dwarfing viroid*
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Citrus viroid V*
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Citrus viroid VI*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Grapevine yellow speckle viroid 1*
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Grapevine yellow speckle viroid 2*
Unassigned	*Pospiviroidae*		*Apscaviroid*	0	*Pear blister canker viroid*
Unassigned	*Pospiviroidae*		*Cocadviroid*	0	*Citrus bark cracking viroid*
Unassigned	*Pospiviroidae*		*Cocadviroid*	1	*Coconut cadang–cadang viroid*
Unassigned	*Pospiviroidae*		*Cocadviroid*	0	*Coconut tinangaja viroid*
Unassigned	*Pospiviroidae*		*Cocadviroid*	0	*Hop latent viroid*
Unassigned	*Pospiviroidae*		*Coleviroid*	1	*Coleus blumei viroid 1*
Unassigned	*Pospiviroidae*		*Coleviroid*	0	*Coleus blumei viroid 2*
Unassigned	*Pospiviroidae*		*Coleviroid*	0	*Coleus blumei viroid 3*
Unassigned	*Pospiviroidae*		*Hostuviroid*	1	*Hop stunt viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Chrysanthemum stunt viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Citrus exocortis viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Columnea latent viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Iresine viroid 1*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Mexican papita viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Pepper chat fruit viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	1	*Potato spindle tuber viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Tomato apical stunt viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Tomato chlorotic dwarf viroid*
Unassigned	*Pospiviroidae*		*Pospiviroid*	0	*Tomato planta macho viroid*
Unassigned	*Potyviridae*		*Brambyvirus*	1	*Blackberry virus Y*
Unassigned	*Potyviridae*		*Bymovirus*	0	*Barley mild mosaic virus*
Unassigned	*Potyviridae*		*Bymovirus*	1	*Barley yellow mosaic virus*
Unassigned	*Potyviridae*		*Bymovirus*	0	*Oat mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Potyviridae*		*Bymovirus*	0	*Rice necrosis mosaic virus*
Unassigned	*Potyviridae*		*Bymovirus*	0	*Wheat spindle streak mosaic virus*
Unassigned	*Potyviridae*		*Bymovirus*	0	*Wheat yellow mosaic virus*
Unassigned	*Potyviridae*		*Ipomovirus*	0	*Cassava brown streak virus*
Unassigned	*Potyviridae*		*Ipomovirus*	0	*Cucumber vein yellowing virus*
Unassigned	*Potyviridae*		*Ipomovirus*	0	*Squash vein yellowing virus*
Unassigned	*Potyviridae*		*Ipomovirus*	1	*Sweet potato mild mottle virus*
Unassigned	*Potyviridae*		*Ipomovirus*	0	*Ugandan cassava brown streak virus*
Unassigned	*Potyviridae*		*Macluravirus*	0	*Alpinia mosaic virus*
Unassigned	*Potyviridae*		*Macluravirus*	0	*Cardamom mosaic virus*
Unassigned	*Potyviridae*		*Macluravirus*	0	*Chinese yam necrotic mosaic virus*
Unassigned	*Potyviridae*		*Macluravirus*	1	*Maclura mosaic virus*
Unassigned	*Potyviridae*		*Macluravirus*	0	*Narcissus latent virus*
Unassigned	*Potyviridae*		*Macluravirus*	0	*Ranunculus latent virus*
Unassigned	*Potyviridae*		*Poacevirus*	0	*Sugarcane streak mosaic virus*
Unassigned	*Potyviridae*		*Poacevirus*	1	*Triticum mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Algerian watermelon mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Alstroemeria mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Alternanthera mild mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Amaranthus leaf mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Amazon lily mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Angelica virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Apium virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Araujia mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Arracacha mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Artichoke latent virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Potyviridae*		*Potyvirus*	0	*Asparagus virus 1*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Banana bract mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Basella rugose mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Bean common mosaic necrosis virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Bean common mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Bean yellow mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Beet mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Bidens mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Brugmansia suaveolens mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Butterfly flower mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Calanthe mild mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Canna yellow streak virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Carnation vein mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Carrot thin leaf virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Carrot virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Celery mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Ceratobium mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Chilli ringspot virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Chilli veinal mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Chinese artichoke mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Clitoria virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Clover yellow vein virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Cocksfoot streak virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Colombian datura virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Commelina mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Cowpea aphid-borne mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Potyviridae*		*Potyvirus*	0	*Cowpea green vein banding virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Cypripedium virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Daphne mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Dasheen mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Datura shoestring virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Diuris virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*East Asian Passiflora virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Endive necrotic mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Euphorbia ringspot virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Freesia mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Fritillary virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Gloriosa stripe mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Groundnut eyespot virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Guinea grass mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Hardenbergia mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Helenium virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Henbane mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Hibbertia virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Hippeastrum mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Hyacinth mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Iris fulva mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Iris mild mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Iris severe mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Japanese yam mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Johnsongrass mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Kalanchoë mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Potyviridae*		*Potyvirus*	0	*Konjac mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Leek yellow stripe virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Lettuce mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Lily mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Lycoris mild mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Maize dwarf mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Malva vein clearing virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Meadow saffron breaking virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Moroccan watermelon mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Narcissus degeneration virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Narcissus late season yellows virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Narcissus yellow stripe virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Nerine yellow stripe virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Nothoscordum mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Onion yellow dwarf virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Ornithogalum mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Ornithogalum virus 2*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Ornithogalum virus 3*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Papaya leaf distortion mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Papaya ringspot virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Parsnip mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Passiflora chlorosis virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Passion fruit woodiness virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pea seed-borne mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Peanut mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pennisetum mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pepper mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pepper severe mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pepper veinal mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pepper yellow mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Peru tomato mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pfaffia mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pleione virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Plum pox virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Pokeweed mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Potato virus A*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Potato virus V*
Unassigned	*Potyviridae*		*Potyvirus*	1	*Potato virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Ranunculus leaf distortion virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Ranunculus mild mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Ranunculus mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Rhopalanthe virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sarcochilus virus Y*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Scallion mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Shallot yellow stripe virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sorghum mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Soybean mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Spiranthes mosaic virus 3*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sugarcane mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sunflower chlorotic mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sunflower mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sweet potato feathery mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sweet potato latent virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sweet potato mild speckling virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sweet potato virus 2*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sweet potato virus C*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Sweet potato virus G*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Telfairia mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Telosma mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Thunberg fritillary mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tobacco etch virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tobacco vein banding mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tobacco vein mottling virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tradescantia mild mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tropaeolum mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tuberose mild mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tuberose mild mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tulip breaking virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Tulip mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Turnip mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Twisted-stalk chlorotic streak virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Vallota mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Watermelon leaf mottle virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Watermelon mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Wild potato mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Wild tomato mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Wisteria vein mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Potyviridae*		*Potyvirus*	0	*Yam mild mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Yam mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Yambean mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Zantedeschia mild mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Zea mosaic virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Zucchini yellow fleck virus*
Unassigned	*Potyviridae*		*Potyvirus*	0	*Zucchini yellow mosaic virus*
Unassigned	*Potyviridae*		*Rymovirus*	0	*Agropyron mosaic virus*
Unassigned	*Potyviridae*		*Rymovirus*	0	*Hordeum mosaic virus*
Unassigned	*Potyviridae*		Rymovirus	1	*Ryegrass mosaic virus*
Unassigned	*Potyviridae*		Tritimovirus	0	*Brome streak mosaic virus*
Unassigned	*Potyviridae*		*Tritimovirus*	0	*Oat necrotic mottle virus*
Unassigned	*Potyviridae*		*Tritimovirus*	0	*Wheat eqlid mosaic virus*
Unassigned	*Potyviridae*		*Tritimovirus*	1	*Wheat streak mosaic virus*
Unassigned	*Potyviridae*		Unassigned	0	*Spartina mottle virus*
Unassigned	*Potyviridae*		Unassigned	0	*Tomato mild mottle virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Arabidopsis thaliana Art1 virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Arabidopsis thaliana AtRE1 virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Arabidopsis thaliana Evelknievel virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Arabidopsis thaliana Ta1 virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Brassica oleracea Melmoth virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Cajanus cajan Panzee virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Glycine max Tgmr virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Hordeum vulgare BARE-1 virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Nicotiana tabacum Tnt1 virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Nicotiana tabacum Tto1 virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Oryza australiensis RIRE1 virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Oryza longistaminata Retrofit virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Solanum tuberosum Tst1 virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Triticum aestivum WIS-2 virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Zea mays Hopscotch virus*
Unassigned	*Pseudoviridae*		*Pseudovirus*	0	*Zea mays Sto-4 virus*
Unassigned	*Pseudoviridae*		*Sirevirus*	0	*Arabidopsis thaliana Endovir virus*
Unassigned	*Pseudoviridae*		*Sirevirus*	1	*Glycine max SIRE1 virus*
Unassigned	*Pseudoviridae*		*Sirevirus*	0	*Lycopersicon esculentum ToRTL1 virus*
Unassigned	*Pseudoviridae*		*Sirevirus*	0	*Zea mays Opie-2 virus*
Unassigned	*Pseudoviridae*		*Sirevirus*	0	*Zea mays Prem-2 virus*
Unassigned	*Pseudoviridae*		Unassigned	0	*Phaseolus vulgaris Tpv2-6 virus*
Unassigned	*Reoviridae*	*Sedoreovirinae*	*Phytoreovirus*	0	*Rice dwarf virus*
Unassigned	*Reoviridae*	*Sedoreovirinae*	*Phytoreovirus*	0	*Rice gall dwarf virus*
Unassigned	*Reoviridae*	*Sedoreovirinae*	*Phytoreovirus*	1	*Wound tumor virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Fijivirus*	1	*Fiji disease virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Fijivirus*	0	*Garlic dwarf virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Fijivirus*	0	*Maize rough dwarf virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Fijivirus*	0	*Mal de Rio Cuarto virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Fijivirus*	0	*Nilaparvata lugens reovirus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Fijivirus*	0	*Oat sterile dwarf virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Fijivirus*	0	*Pangola stunt virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Fijivirus*	0	*Rice black streaked dwarf virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Oryzavirus*	0	*Echinochloa ragged stunt virus*
Unassigned	*Reoviridae*	*Spinareovirinae*	*Oryzavirus*	1	*Rice ragged stunt virus*
Unassigned	*Tombusviridae*		*Aureusvirus*	0	*Cucumber leaf spot virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Tombusviridae*		*Aureusvirus*	0	*Johnsongrass chlorotic stripe mosaic virus*
Unassigned	*Tombusviridae*		*Aureusvirus*	0	*Maize white line mosaic virus*
Unassigned	*Tombusviridae*		*Aureusvirus*	1	*Pothos latent virus*
Unassigned	*Tombusviridae*		*Avenavirus*	1	*Oat chlorotic stunt virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Ahlum waterborne virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Angelonia flower break virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Bean mild mosaic virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Calibrachoa mottle virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Cardamine chlorotic fleck virus*
Unassigned	*Tombusviridae*		*Carmovirus*	1	*Carnation mottle virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Cowpea mottle virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Cucumber soil-borne virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Galinsoga mosaic virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Hibiscus chlorotic ringspot virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Honeysuckle ringspot virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Japanese iris necrotic ring virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Melon necrotic spot virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Nootka lupine vein clearing virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Pea stem necrosis virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Pelargonium flower break virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Saguaro cactus virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Soybean yellow mottle mosaic virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Turnip crinkle virus*
Unassigned	*Tombusviridae*		*Carmovirus*	0	*Weddel waterborne virus*
Unassigned	*Tombusviridae*		*Dianthovirus*	1	*Carnation ringspot virus*
Unassigned	*Tombusviridae*		*Dianthovirus*	0	*Red clover necrotic mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Tombusviridae*		*Dianthovirus*	0	*Sweet clover necrotic mosaic virus*
Unassigned	*Tombusviridae*		*Machlomovirus*	1	*Maize chlorotic mottle virus*
Unassigned	*Tombusviridae*		*Necrovirus*	0	*Beet black scorch virus*
Unassigned	*Tombusviridae*		*Necrovirus*	0	*Chenopodium necrosis virus*
Unassigned	*Tombusviridae*		*Necrovirus*	0	*Leek white stripe virus*
Unassigned	*Tombusviridae*		*Necrovirus*	0	*Olive latent virus 1*
Unassigned	*Tombusviridae*		*Necrovirus*	0	*Olive mild mosaic virus*
Unassigned	*Tombusviridae*		*Necrovirus*	1	*Tobacco necrosis virus A*
Unassigned	*Tombusviridae*		*Necrovirus*	0	*Tobacco necrosis virus D*
Unassigned	*Tombusviridae*		*Panicovirus*	0	*Cocksfoot mild mosaic virus*
Unassigned	*Tombusviridae*		*Panicovirus*	1	*Panicum mosaic virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Artichoke mottled crinkle virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Carnation Italian ringspot virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Cucumber Bulgarian virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Cucumber necrosis virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Cymbidium ringspot virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Eggplant mottled crinkle virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Grapevine Algerian latent virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Havel River virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Lato River virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Limonium flower distortion virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Moroccan pepper virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Neckar River virus*
Unassigned	*Tombusviridae*		Tombusvirus	0	*Pelargonium leaf curl virus*
Unassigned	*Tombusviridae*		Tombusvirus	0	*Pelargonium necrotic spot virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Petunia asteroid mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Tombusviridae*		*Tombusvirus*	0	*Sitke waterborne virus*
Unassigned	*Tombusviridae*		*Tombusvirus*	1	*Tomato bushy stunt virus*
Unassigned	*Tombusviridae*		*Unassigned*	0	*Maize necrotic streak virus*
Unassigned	*Tombusviridae*		*Unassigned*	0	*Pelargonium line pattern virus*
Unassigned	Unassigned		*Benyvirus*	1	*Beet necrotic yellow vein virus*
Unassigned	Unassigned		*Benyvirus*	0	*Beet soil-borne mosaic virus*
Unassigned	Unassigned		*Cilevirus*	1	*Citrus leprosis virus C*
Unassigned	Unassigned		*Emaravirus*	1	*European mountain ash ringspot-associated virus*
Unassigned	Unassigned		*Emaravirus*	0	*Fig mosaic virus*
Unassigned	Unassigned		*Idaeovirus*	1	*Raspberry bushy dwarf virus*
Unassigned	Unassigned		*Ourmiavirus*	0	*Cassava virus C*
Unassigned	Unassigned		*Ourmiavirus*	0	*Epirus cherry virus*
Unassigned	Unassigned		*Ourmiavirus*	1	*Ourmia melon virus*
Unassigned	Unassigned		*Polemovirus*	1	*Poinsettia latent virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Blueberry shoestring virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Cocksfoot mottle virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Imperata yellow mottle virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Lucerne transient streak virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Rice yellow mottle virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Ryegrass mottle virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Sesbania mosaic virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Solanum nodiflorum mottle virus*
Unassigned	Unassigned		*Sobemovirus*	1	*Southern bean mosaic virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Southern cowpea mosaic virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Sowbane mosaic virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Subterranean clover mottle virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	Unassigned		*Sobemovirus*	0	*Turnip rosette virus*
Unassigned	Unassigned		*Sobemovirus*	0	*Velvet tobacco mottle virus*
Unassigned	Unassigned		*Tenuivirus*	0	*Echinochloa hoja blanca virus*
Unassigned	Unassigned		*Tenuivirus*	0	*Maize stripe virus*
Unassigned	Unassigned		*Tenuivirus*	0	*Rice grassy stunt virus*
Unassigned	Unassigned		*Tenuivirus*	0	*Rice hoja blanca virus*
Unassigned	Unassigned		*Tenuivirus*	1	*Rice stripe virus*
Unassigned	Unassigned		*Tenuivirus*	0	*Urochloa hoja blanca virus*
Unassigned	Unassigned		*Umbravirus*	0	*Carrot mottle mimic virus*
Unassigned	Unassigned		*Umbravirus*	1	*Carrot mottle virus*
Unassigned	Unassigned		*Umbravirus*	0	*Groundnut rosette virus*
Unassigned	Unassigned		*Umbravirus*	0	*Lettuce speckles mottle virus*
Unassigned	Unassigned		*Umbravirus*	0	*Pea enation mosaic virus-2*
Unassigned	Unassigned		*Umbravirus*	0	*Tobacco bushy top virus*
Unassigned	Unassigned		*Umbravirus*	0	*Tobacco mottle virus*
Unassigned	Unassigned		*Varicosavirus*	1	*Lettuce big-vein associated virus*
Unassigned	*Virgaviridae*		*Furovirus*	0	*Chinese wheat mosaic virus*
Unassigned	*Virgaviridae*		*Furovirus*	0	*Japanese soil-borne wheat mosaic virus*
Unassigned	*Virgaviridae*		*Furovirus*	0	*Oat golden stripe virus*
Unassigned	*Virgaviridae*		*Furovirus*	0	*Soil-borne cereal mosaic virus*
Unassigned	*Virgaviridae*		*Furovirus*	1	*Soil-borne wheat mosaic virus*
Unassigned	*Virgaviridae*		*Furovirus*	0	*Sorghum chlorotic spot virus*
Unassigned	*Virgaviridae*		*Hordeivirus*	0	*Anthoxanthum latent blanching virus*
Unassigned	*Virgaviridae*		*Hordeivirus*	1	*Barley stripe mosaic virus*
Unassigned	*Virgaviridae*		*Hordeivirus*	0	*Lychnis ringspot virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Virgaviridae*		*Hordeivirus*	0	*Poa semilatent virus*
Unassigned	*Virgaviridae*		*Pecluvirus*	0	*Indian peanut clump virus*
Unassigned	*Virgaviridae*		*Pecluvirus*	1	*Peanut clump virus*
Unassigned	*Virgaviridae*		*Pomovirus*	0	*Beet soil-borne virus*
Unassigned	*Virgaviridae*		*Pomovirus*	0	*Beet virus Q*
Unassigned	*Virgaviridae*		*Pomovirus*	0	*Broad bean necrosis virus*
Unassigned	*Virgaviridae*		*Pomovirus*	1	*Potato mop-top virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Brugmansia mild mottle virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Cucumber fruit mottle mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Cucumber green mottle mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Frangipani mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Hibiscus latent Fort Pierce virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Hibiscus latent Singapore virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Kyuri green mottle mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Obuda pepper virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Odontoglossum ringspot virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Paprika mild mottle virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Pepper mild mottle virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Rehmannia mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Ribgrass mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Sammons's Opuntia virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Streptocarpus flower break virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Sunn-hemp mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Tobacco latent virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Tobacco mild green mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	1	*Tobacco mosaic virus*

(continued)

Table 2.3 (continued)

Order	Family	Subfamily	Genus	Type species	Species
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Tomato mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Turnip vein-clearing virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Ullucus mild mottle virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Wasabi mottle virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Youcai mosaic virus*
Unassigned	*Virgaviridae*		*Tobamovirus*	0	*Zucchini green mottle mosaic virus*
Unassigned	*Virgaviridae*		*Tobravirus*	0	*Pea early-browning virus*
Unassigned	*Virgaviridae*		*Tobravirus*	0	*Pepper ringspot virus*
Unassigned	*Virgaviridae*		*Tobravirus*	1	*Tobacco rattle virus*

Source King et al. (2012)

representative of the species as a whole. Some sub-groups (SGs) are working to define official "type isolates" for each species; probably this is a desirable goal although it has not been adopted as ICTV policy.

(j) ICTV on the internet

A plan to develop a universal virus database was first discussed around 1990 and led to the development of ICTV data base. The known properties of virus isolates and species were encoded and "translated" for the user in natural language text. Enormous efforts were made to maintain and develop this database and to link with other important databases on biological taxonomy, publications, sequences etc. This was managed by the Virus Data Subcommittee of ICTV and relied heavily on the energy and commitment of Cornelia Buchen-Osmond. The database contains a wealth of important information but it has proved difficult to sustain funding and personnel at a time when taxonomic information is expanding rapidly.

In recent years, ICTV has also had a web presence providing lists of the currently recognized taxa and information on the Executive Committee, Subcommittees and Study Groups. Templates and other information to assist in writing and submitting taxonomic proposals have also been provided. For some years, this was hosted by Fauquet at the Danforth Center, St Louis, but since 2008 the Virus Data subcommittee has overseen the development and maintenance of an official ICTV website (http://www.ictvonline.org) that now provides a central point of reference for all ICTV matters. A separate website (http://www.talk.ictvonline.org) is used to host taxonomic proposals and allows for comment and discussion to which all virologists are invited to contribute.

2.3 Sub-Viral Agents

2.3.1 Viroids

A group of diseases resembling those caused by viruses are now known to be due to viroids. Viroids are circular, single stranded, non-coding RNAs that are able to infect certain plants. The infectious RNAs cause a number of economically important plant viroid diseases (Hadidi et al. 2003; Flores et al. 2005; Flores and Owens 2008). In 1971 Diener, for the first time used the term 'viroid' after studying the molecular nature of potato spindle tuber pathogen.

Viroids have not been found in man or animal although several diseases have been considered to be caused by viroid-like agents. Plant viroids are similar to some plant viruses in that they contain an RNA genome, but they differ from RNA plant viruses in two key ways. First, viroids are composed of "naked" RNAs, that is, they lack a protein coat. Second, they cannot specify any proteins in spite of the fact that they are made of RNA. The RNA genome of viroids is a small, circular molecule that contains between 246 and 375 nucleotides. Even though viroids do

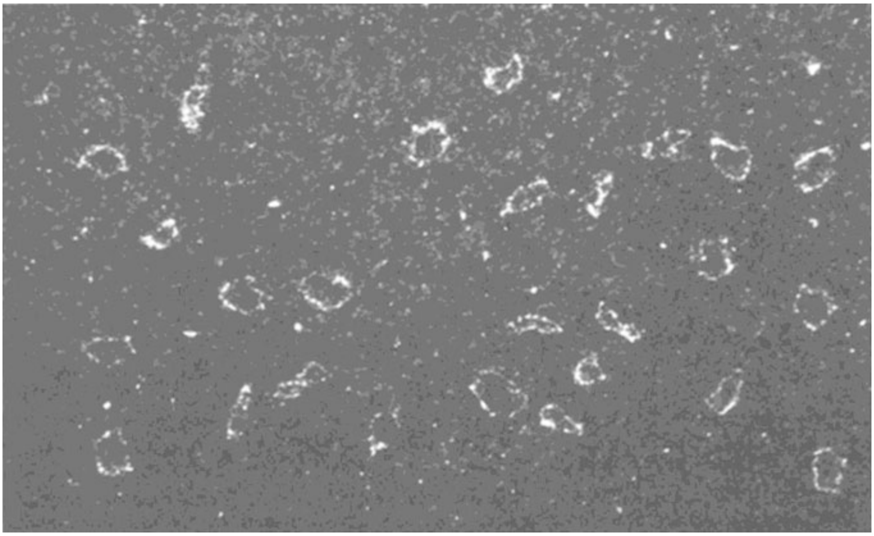

Fig. 2.6 Electro micrographs in dark-field illumination of viroids as relaxed circles. Magnification is 185,000. *Courtesy* (Riesner et al. 1983)

not produce their own proteins, they are capable of using the host cell machinery to reproduce their RNA and move into other cells to infect the whole plant (Fig. 2.6).

For many years prior to the discovery of viroids, the diseases caused by them were classified as plant virus diseases. One reason for this confusion is that the types of symptoms induced by viroids in plants are similar to those induced by plant viruses. These symptoms can be visualized by listing the imaginative names given to some viroids (note that viroids are named in a manner similar to plant viruses, but that the name ends in "d"): *Potato spindle tuber viroid* (PSTVd), *Apple scar skin viroid* (ASSVd), *Avocado Sunblotch viroid* (ASBVd), and *Pear blister canker viroid* (PBCVd). Despite their small size, the economic effects of viroids can be devastating.

PSTVd is the first viroid disease to be studied by number of plant pathologists. In 1923, its infectious nature and ability to spread in the field led Schultz and Folsom (1923) to group potato spindle tuber disease with several other 'degeneration diseases' of potatoes. Only in 1971 Diener, observed that the molecular properties of its causal agent, PSTVd, were fundamentally different than those of conventional plant viruses and for the first time Diener coined the term 'viroid' which means 'virus-like'.

(a) Geographic distribution

Among economically important viroid diseases, *Citrus exocortis viroid* (CEVd) is present in most of the citrus-growing areas where susceptible rootstock is used and is widespread in S. America (especially Brazil and Argentina), Australia and the

Mediterranean region (especially Spain) but is of limited occurrence in the USA, N. Africa and certain Asian countries. *Coconut cadang-cadang viroid* (CCCVd) is limited to the central eastern Philippines (Quezon, Bicol provinces, Samar provinces and Biliran). In many avocado-growing countries including Australia, Israel, Peru, South Africa, USA and Venezuela, ASBVd is recorded. PSTVd is common in the potato-growing regions of northern and north eastern USA and to an unknown extent in the USSR and South Africa. In some of the Asian countries like India, PSTVd is reported in very low incidence. Even viroid diseases affecting perennial woody fruit crops like grapes, pome and stone fruits and also in vegetatively propagated ornamental plants like chrysanthemum, viroid diseases are reported to a limited extent in certain tropical countries. The primary factor for increase and rapid spread of viroid diseases is the international exchange of plant germplasm and also the latent infections (asymptomatic).

(b) Host range and transmission

Depending on the viroid, the host range is either wide or narrow; for example the host range of CEVd is largely confined to *Rutaceae* and some species in the *Solanaceae* (potato, tomato, petunia) and some *Compositae* members. PSTVd has wide host range and can replicate in about 160 primarily solanaceous hosts, while only two members of the family *Lauraceae* are known to support ASBVd replication. *Hop stunt viroid* (HSVd) has a particularly wide host range that includes herbaceous species as well as woody perennials. On the other hand, CCCVd is confined to members of *Palmae* (*Arecaceae*). Viroids spread to other plants through vegetative propagation, mechanical contamination, pollen and seed.

All viroids are mechanically transmissible, and most of them are naturally transmitted from plant to plant by farm implements, pruning tools clothing and human hands. Individual viroids vary greatly in their ability to infect different plant species. Many natural hosts are either vegetatively propagated or crops that are subjected to repeated grafting or pruning operations. PSTVd, ASBVd, and *Coleus blumei-1 viroid* (CbVd-1) are vertically transmitted through pollen and/or true seed, but the significance of this mode of transmission in the natural spread of disease is unclear.

Seed transmission has been demonstrated for many but not all viroids and pollen-borne transmission is also known to occur in tomato. Reports of seed transmission of *Chrysanthemum stunt viroid* (CSVd) are contradictory; Monison et al. (1973) presented evidence for seed transmission, where as Hollings and Stone (1973) reported that CSVd is not seed transmitted. Vertical transmission has been demonstrated for ASBVd for Avocado. Vertical transmission has been demonstrated for ASBVd in avocado and PSTVd in tomato and pepino. Doubtful reports of aphid transmission of *Tomato planta macho viroid* (TPMVd) and PSTVd is reported (De Bokx and Pirone 1981; Salazar et al. 1995).

Commonly used techniques for the experimental transmission of viroids include the standard leaf abrasion methods developed for conventional viruses, ‘razor slashing’ methods in which phloem tissue in the stern or petiole is inoculated via cuts made with a razor blade previously dipped into the inoculum, and, in the case

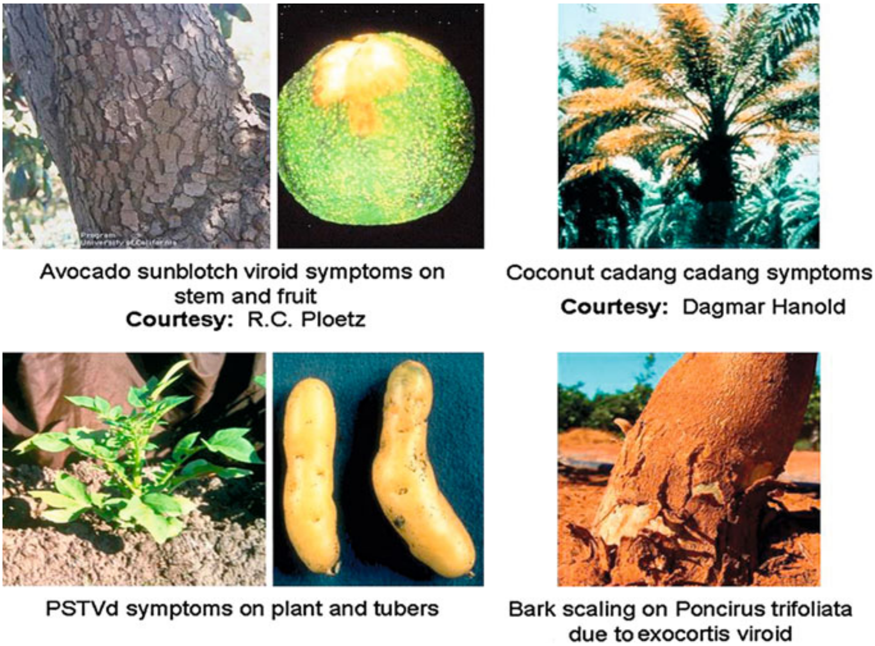

Fig. 2.7 Symptoms of viroid diseases. *Source* http://www.virology.net/big picture book of viruses

of CCCVd, high-pressure injection into folded apical leaves. Viroids can also be transmitted by either plant transformation or 'agroinoculation' during which a modified *Agrobacterium tumefaciens.* Ti plasmid is used to introduce full-length viroid-complementary DNA into the potential host cell. Under field conditions in general, contaminated cutting knives and tractor wheels also aid in the spread of viroid diseases. Identification of the molecular mechanism(s) that determine viroid host range remains an important research goal.

(c) Symptomatology

Stunting and leaf epinasty (a downward curling of the leaf lamina) are considered the classic symptoms of viroid infection. Other commonly observed symptoms are vein clearing, veinal discoloration or necrosis, and the appearance of localized chlorotic/necrotic spots or mottling in the foliage. Symptoms may also be expressed in flowers, on bark, on fruits and on tubers. The viroid-infected plants may be abnormally shaped, discolored (Fig. 2.7). For more photographs of symptoms associated with specific viroid diseases, see Hadidi et al. (2003) and the disease compendia series of the American Phytopathological Society for specific crops (APS Press).

Viroid infection of certain citrus rootstock/scion combinations may result in tree dwarfing. Viroid infections are often latent and rarely kill the host. It is

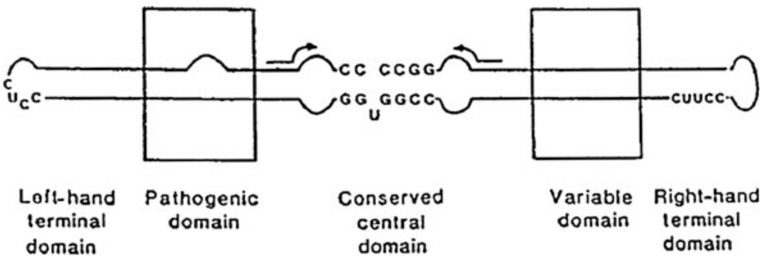

Fig. 2.8 The general structure and organization of viroids (Based on Keese and Symons 1985). *Courtesy* Randles and Ogle

estimated that more than 30 million coconut palms in the Philippines have died due to CCCVd.

Viroid infections are also accompanied by a number of cytopathic effects like chloroplast and cell wall abnormalities, the formation of membranous structures in the cytoplasm, and the accumulation of electron-dense deposits in both chloroplasts and cytoplasm. Metabolic changes include dramatic alterations in growth regulator levels.

(d) Molecular biology

Viroids are small, circular, noncoding RNAs and are the smallest self-replicating genetic units known. Without encoding proteins and requirement for helper viruses, these small RNAs contain all the information necessary to mediate intracellular trafficking and localization, replication, systemic trafficking, and pathogenicity. All or most of these functions likely result from direct interactions between distinct viroid RNA structural motifs and their cognate cellular factors. Viroid RNAs are rich in structural motifs that likely are involved in the diverse biological functions necessary to establish infection. Therefore, viroids will allow investigation of the many aspects of RNA–protein interactions to achieve specific biological functions. The multi-functionality of some viroid motifs is of exceptional value for investigating the structure–function relationships of RNAs in greater detail.

(e) Genome structure

The majority of the plant viroids reported today, have been sequenced. Despite their differences in sequences, certain domains have been recognized as common to all of them. These are also indicated in Fig. 2.8. The central conserved domain has been used as the basis for grouping viroids.

Intensive studies are made to understand viroid replication process. We know that viroid RNA does not code for any protein. The replication mechanism involves RNA polymerase II, an enzyme normally associated with synthesis of messenger RNA from DNA, which instead catalyzes "rolling circle" synthesis of new RNA using the viroid's RNA as template. Some viroids are ribozymes, having catalytic properties which allow self-cleavage and ligation of unit-size genomes from larger replication intermediates.

The complete sequences of nearly 29 distinct viroid species plus a large number of sequence variants have been determined (Table 2.4). All are single-stranded circular RNAs containing 246–401 unmodified nucleotides. Theoretical calculations and physicochemical studies indicate that PSTVd and related viroids assume a highly base-paired, rod-like conformation *in vitro* (Fig. 2.8). Pair wise sequence comparisons suggest that the series of short double helices and small internal loops that comprise this so-called 'native' structure are organized into five domains whose boundaries are defined by sharp differences in sequence similarity. The five structural domains termed are: central(C), variable(V), pathogenic(P), and terminal left and right (T_L and T_R) respectively (Keese and Symons 1985). The 'central domain' is the most highly conserved viroid domain and contains the site where multimeric PSTVd RNAs are cleaved and legated to form circular progeny. The 'pathogenicity domain' contains one or more structural elements which modulate symptom expression, and the relatively small 'variable domain' exhibits the greatest sequence variability between otherwise closely related viroids. The two 'terminal domains' appear to play an important role in viroid replication and evolution. Although these five domains were first identified in PSTVd, ASSVd and related viroids also contain a similar domain arrangement.

(f) Replication

The lack of protein-coding capacity of viroids entails that their replication mechanism is much more host-reliant than that of RNA viruses, which at least encode a subunit of the RNA-dependent RNA polymerase catalyzing initiation and elongation of viral strands.

Viroid RNA does not code for any protein. The replication mechanism involves RNA polymerase II, an enzyme normally associated with synthesis of messenger RNA from DNA, which instead catalyzes "rolling circle" synthesis of new RNA using the viroid's RNA as template. Some viroids are ribozymes, having catalytic properties which allow self-cleavage and ligation of unit-size genomes from larger replication intermediates.

Based on the site of viroid replication in the cell, the viroids are classified into two families, the *Pospiviroidae* and the *Avsunviroidae*. Intriguingly, viroids have evolved the ability to replicate in two cellular organella, the nucleus (family *Pospiviroidae*) and the chloroplast (family *Avsunviroidae*). Viroid replication proceeds through an RNA-based rolling-circle mechanism with three steps catalysed by: (i) host deoxyribonucleic acid (DNA)-dependent RNA polymerases redirected to accept RNA templates, (ii) processing enzymes or, in the family *Avsunviroidae*, hammerhead ribozymes and (iii) RNA ligases. When infecting a cell, the viroid RNA must travel to its replication organelle, with the resulting progeny moving cell-to-cell through plasmodesmata and reaching distal parts through the phloem.

Table 2.4 Officially recognized viroid species (VIII Report, ICTV)

Genus[a]	Species	Variants[b]	Length(nt)	Natural host(s)	Emerging hosts
Family *Pospiviroidae*					
Pospiviroid	Potato spindle tuber (PSTVd)	109	341–364	Potato	tomato, avocado
	Chrysanthemum stunt (CSVd)	19	348–356	chrysanthemum	
	Citrus exocortis (CEVd)	86	366–475	citrus, tomato	tomato
	Columnea latent (CLVd)	17	359–456	*Columnea*, *Brunfelsia*, *Nemathanthus*	tomato
	Iresine (IrVd)	3	370	*Iresine*	
	Mexican papita (MPVd)	6	359–360	*Solanum cardiophyllum*	
	Tomato apical stunt (TASVd)	5	360–363	tomato	tomato
	Tomato chlorotic dwarf (TCDVd)	2	360	Uncertain (tomato?)	tomato
	Tomato planta macho (TPMVd)	2	360	tomato	
Hostuviroid	Hop stunt (HSVd)	144	294–303	citrus, grapevine, *Prunus* spp.	hop, cucumber
Cocadviroid	Coconut cadang–cadang (CCCVd)	8	246–301	coconut palm	African oil palm, other monocots
	Coconut tinangaja (CTiVd)	2	254	coconut palm	
	Citrus bark cracking (CBCVd)	6	284–286	citrus	
	Hop latent (HLVd)	10	255–256	hop	
Apscaviroid	Apple scar skin (ASSVd)	8	329–333	apple, pear	
	Apple dimple fruit (ADFVd)	2	306	apple	
	Apple fruit crinkle (AFCVd)[c]	29	368–372	apple	
	Australian grapevine (AGVd)	1	369	grapevine	
	Citrus bent leaf (CBLVd)	24	315–329	citrus	
	Citrus dwarfing (CDVd)	53	291–297	citrus	
	Grapevine yellow speckle 1 (GYSVd-1)	49	365–368	grapevine	
	Grapevine yellow speckle 2 (GYSVd-2)	1	363	grapevine	
	Pear blister canker (PBCVd)	18	314–316	pear, quince	

(continued)

Table 2.4 (continued)

Genus[a]	Species	Variants[b]	Length(nt)	Natural host(s)	Emerging hosts
Coleviroid	*Coleus blumei*-1 (CbVd-1)	9	248–251	*Coleus*, *Mentha* spp.	
	Coleus blumei-2 (CbVd-2)	?	295–301		
	Coleus blumei-3(CbVd-3)	3	361–364	*Ocimum basilicum, Melissa officinalis*	
Family *Avsunviroidae*					
Avsunviroid	Avocado sun blotch (ASBVd)	83	239–251	avocado	
Pelamoviroid	Chrysanthemum chlorotic mottle (CChMVd)	21	397–401	chrysanthemum	
	Peach latent mosaic (PLMVd)	168	335–351	peach, nectarine	
Elaviroid	Eggplant latent (ELVd)	9	332–335	eggplant	

[a] Names of viroid genera are derived from those of the respective type species (listed first)
[b] Sequences available online from the Subviral RNA Database. [http://subviral.med.uottawa.ca]
[c] Provisional species (not officially recognized)
Source Subviral RNA Database [http://subviral.med.uottawa.ca]

(g) Movement

Limited information is available about the pathways and mechanism of viroid movement inside the host plant. The viroids after entering in a potential host cell, it has to move to either the nucleus (*Pospiviroidae*) or chloroplast (*Avsunviroidae*) before beginning replication. Available data suggest that PSTVd enters the nucleus as a ribonucleo protein complex formed by the interaction of cellular proteins with specific viroid sequence or structural motifs. Ding et al. (1997) have observed that PSTVd moves from cell to cell via plasmodesmata and this movement is mediated by a specific sequence of structural motif. VirPl, a bromodomain-containing protein isolated from tomato, has a nuclear localization signal and hinds to the terminal right domain of PSTVd. Proteins such as TFIIIA and ribosomal protein L5 that bind to the loop E motif may also be involved in viroid transport into the nucleus (Flores and Owens 2008).

To establish a systemic infection, viroids leave the initially infected cell-moving first from cell to cell and then long distances through the host vasculature. Long-distance movement of viroids occurs in the phloem where it follows the typical source-to-sink pattern of photoassimilate transport. Viroid movement in the phloem almost certainly requires formation of a ribonucleoprotein complex, possibly involving a dimeric lectin known as phloem protein 2 (Pp-2), the most abundant protein in phloem exudate.

(h) Diagnosis of viroid diseases

In the earlier years, biological methods have been used in detecting the viroids based on the reaction on diagnostic host plants. Since this test takes long time the scientists have switched over to molecular tests. Nucleic acid based techniques are the one that can help in reliable and rapid detection of viroids. Early molecular detection methods involved a combination of native and denaturing polyacrylamide gel electrophoresis that relies on the circular properties of the viroid RNA molecule to resolve it from other plant RNAs (Schumacher et al. 1986). This method is not as useful for the identification of specific viroids, as several viroids may have the same electrophoretic mobility.

Molecular method (dot-blot hybridization) is quite useful for viroid detection and is reliable for viroids of known sequence and very sensitive. However this method cannot be relied upon to detect new viroids where sequence information is unavailable. A number of reverse transcription-polymerase chain reaction (RT-PCR) protocols have been developed for detection of different viroids, including real-time RT-PCR (Shamloul et al. 1995; Hadidi et al. 1997; Boonham et al. 2004; Bagherian et al. 2009). Through microarray and macroarray technology a number of viroid diseases in different crop plants were identified (Agindotan and Perry 2008). Even tissue print immuno assay or tissue blot immuno binding were also used for viroid diagnosis (Hadidi et al. 1991; Hurtt and Podleckis 1995). The dot-blot hybridization techniques are widely used for the detection of viroid diseases in different crops (Podleckis et al. 1993).

2.3.1.1 Viroid Classification

The structural and functional properties, as well as their evolutionary origin of viroids differ fundamentally from those of viruses, posing specific problems for the classification of these sub viral pathogens. Rules concerned with the classification of viruses shall also apply to the classification of viroids.

Viroids can be classified into two major families, the *Pospiviroidae* and the *Avsunviroidae*, based on where the viroid replicates in the cell (Tabler and Tsagris 2004). Viroids in the *Pospiviroidae* family replicate in the nucleus while viroids in the *Avsunviroidae* family replicate in the chloroplast.

Pospiviroidae is further subdivided into three subfamilies: *Pospiviroinae* (from PSTVd), *Apscaviroinae* (from *Apple scar skin viroid*, ASSVd), and *Coleviroinae* (from *Coleus blumei viroid 1*, CbVd1). The subfamily *Pospiviroinae* contains three genera: *Pospiviroids* (from PSTVd), *Hostuviroids* (from *Hop stunt viroid*, HSVd), and *Cocadviroids* (from *Coconut cadang-cadang viroid*, CCCVd). The *Apscaviroinae* and *Coleviroinae* subfamilies each contain one genus, *Apscaviroids* and *Coleviroids*, respectively. The *Avsunviroidae* family contains three genera: *Avsunviroids* (from ASBVd) and *Pelamoviroids* (from *Peach latent mosaic viroid*, PLMVd) (Flores et al. 1998), and *Elaviroid* (from *Eggplant latent viroid* ELVd).

The formal endings for taxa of viroids are the word "viroid" for species, the suffix "-viroid" for genera, the suffix "-viroinae" for sub-families (should this taxon be needed) and "-viroidae" for families. For example, the species *Potato spindle tuber viroid* is classified in genus *Pospiviroid,* and the family *Pospiviroidae*. The list of recognized viroid species and their properties are provided in the Table 2.4.

More details about viroids can be obtained from the articles of Diener (1979, 1999); Flores (2001); Hadidi et al. (2003); Flores et al. (2005); Hammond and Owens (2006); Flores and Owens (2008).

2.4 Phytoplasma

During the past 35 years it has become apparent that yellows and witche's broom type of diseases are caused by agents similar to mycoplasmatales (Pleuro pneumonia-like organisms) and not due to viruses. The first report is by Doi et al. (1967) who discovered mycoplasmas-like bodies (MLO) in the phloem sieve elements of yellows-infected plants. They also observed that tetracyclines induced temporary remission of symptoms. Since then about 200 different plant species in 59 families are demonstrated to be affected by phytoplasma (Bertaccini and Duduk 2009; Rao et al. 2011). In recent years MLO diseases are renamed as phytoplasma diseases. The phytoplasma infected plants exhibit growth of adventitious shoots, chlorosis without spotting; clearing of the veins, growth stimulation of normally dormant axillary buds; malformation, stunting and the transformation of floral structures into green leaf like structures known as phyllody (Fig. 2.9).

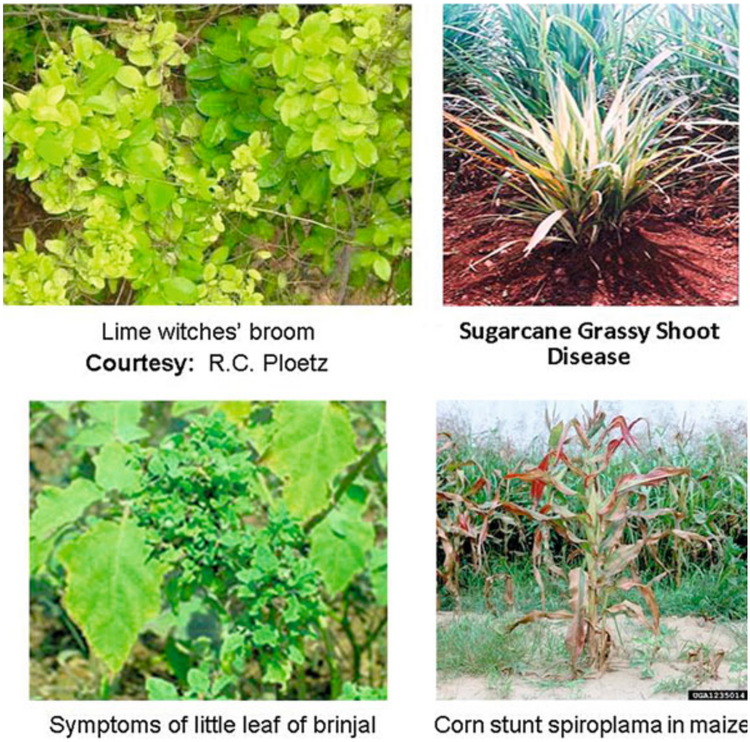

Fig. 2.9 Some important phytoplasma and spiroplasma infected plants. *Source* http://www.virology.net/big picture book of viruses

The diseases associated with phytoplasmas have been divided into the following four types: Aster yellows (elongation of internodes, leaf yellowing); Stolbour (apical dwarfing, stunting, leaf roll, epinasty, wilting, virescence); Witches' broom (proliferation of axillary shoots) and decline (degeneration). The morphology and structure of phytoplasma are similar to true mycoplasmas of animals and are usually spheroidal to ellipsoid, ranging from 70 to 1100 nm diameter with some elementary bodies of 50–10 nm. They are bounded by single unit triple-layered membrane, devoid of rigid cell wall and are highly pleomorphic (Cousin et al. 1970). In some cases irregularly tubular to filamentous structures are also noticed. They have cytoplasm and central nuclear areas comprised of a loose net work of double stranded DNA strands or more rarely a distinct nucleotide (Nasu et al. 1970). Ribosomes which are 10–15 nm in their size are either scattered throughout or clustered about the periphery of the cell and are smaller than host ribosomes (Hirumi and Maramorosch 1969). Vacuoles, which are only occasionally found in filamentous bodies, are frequently encountered in the large globular bodies (Fig. 2.10).

Table 2.5 Some of the major taxonomic groups and the candidatus species that belong to phytoplasma

16Sr group	Group name	Species
16SrI	Aster yellows	Ca. Phytoplasma asteris
	Japanese hydrangea phyllody	Ca. Phytoplasma japonicum
16SrII	Peanut witch's broom	Ca. Phytoplasma aurantifolia
16SrIII	X-disease	Ca. Phytoplasma pruni
16SrIV	Coconut lethal yellowing	Ca. Phytoplasma palmae
		Ca. Phytoplasma castaneae
		Ca. Phytoplasma cocosnigeriae
16SrV	Elm yellows	Ca. Phytoplasma ulmi
	Rubus stunt	Ca. Phytoplasma rubi
	Jujube witche's broom	Ca. Phytoplasma ziziphi
16SrVI	Clover proliferation	Ca. Phytoplasma trifolii
16SrVII	Ash yellows	Ca. Phytoplasma fraxini
16SrVIII	Luffa witch's-broom	Ca. Phytoplasma luffae
16SrIX	Pigeon pea witch's broom	Ca. Phytoplasma phoenicium
16SrX	Apple proliferation	Ca. Phytoplasma mali
	Pear decline	Ca. Phytoplasma pyri
	European stone fruit yellows	Ca. Phytoplasma prunorum
	Spartium witche's broom	Ca. Phytoplasma spartii
16SrXI	Rice Yellow Dwarf	Ca. Phytoplasma oryzae
16SrXII	Stolbur	Ca. Phytoplasma solani
	Australian grapevine yellows	Ca. Phytoplasma australiense
16SrXIII	Mexican periwinkle virescence	Undefined
16SrXIV	Bermuda grass white leaf	Ca. Phytoplasma cynodontis
16SrXV	Hibiscus witch's-broom	Ca. Phytoplasma brasiliense

The phytoplasma bodies have been reported in the sieve elements of the phloem and less often phloem parenchyma and parenchyma cells near the problem (Doi et al. 1967; Worley 1970), in phloem companion cells or cortical parenchyma (Cousin et al. 1970). However electron micrographs by several workers have shown that the bodies are capable of the deformation required to press through sieve pores. In the infected plants blockage of movement of the energy storage compounds like sugars from leaves to roots could account for the progressive decline and often death. Phytoplasma diseases are not transmissible to plants by mechanical inoculation, but they are transmitted to healthy plants by grafting diseased material or by using dodder. Natural spread is by insect vectors usually leaf-hoppers, although in few cases psyllids and planthoppers are also responsible. The leafhopper vectors are have a very long incubation period which ranges from 10 to 45 days and they are viruliferous throughout their life after incubation period. In some cases transovarial transmission was also noticed. Phytoplasma diseases were detected by nucleic acid based techniques like dot-blot hybridization assay and PCR. Even some success is achieved by Dienes stain for the detection of phytoplasmal infection. In tropical countries the phytoplasma diseases are

Fig. 2.10 Phytoplasmas (*arrows*) in the phloem cells of *Catharanthus roseus L.* (bar = 0.5 µ). *Courtesy* Rita Musetti, and Maria Augusta Favali

economically important and some of them are: Rice yellow dwarf, Sugarcane white leaf, Coconut lethal yellowing, Coconut root-wilt, Sandal spike, Cotton virescence, Tomato big bud, Pear decline, and Bois noir phytoplasma diseases of grapes (Table 2.5).

In recent years the phytoplasma is grouped under bacillus and is considered along with bacterium. Hence more details about diagnosis, epidemiology and management measures of phytoplasma are not dealt in this text book. However more information on phytoplasma and the diseases they cause can be obtained from review and text book chapters (Varma and Ahlawat 1994; Randles and Ogle 1997; Lee et al. 2000; Cousin and Boudon-Padieu 2002; Seemuller et al. 2002; Bertaccini and Duduk 2009).

2.5 Spiroplasma

Some of the yellows type of diseases which were earlier grouped under phytoplasma were identified to be due to spiroplasma organisms. The genus *Spiroplasma* has been placed in the family *Spiroplasmataceae,* under the order *Mycoplasmatales* (Skripal 1974). They are pleomorphic cells that vary in shape from spherical or slightly ovoid, 100–250 nm or larger in diameter and 3–25 µm in length. They often seem attached to spherical structures called blebs. They do not have true cell wall and are bounded by a single triple layered unit membrane. Although spiroplasmas are morphologically distinguish able from mycoplasmas, they are very similar in most respects. They can be easily cultured on nutrient media and they produce mostly helical forms in liquid media. For the first time, the name 'Spiroplasma' was proposed for the corn stunt organism by Davis and Worley (1973). They etiology of the term is as follows: Spiro (Greek noun 'Speira') meaning coil and Greek noun 'plasma' meaning something formed or molded to denote shape or form. The movement exhibited by the helical filaments is yet another characteristic divergent from members of the class mollicutes. The helical filaments are motile, moving by a slow undulation of the filament and probably by a rapid rotary or 'screw' motion of the helix (Brownian movement).

The common diseases caused by spiroplasmas are citrus stubborn, corn stunt, Bermuda grass white leaf, *Opuntia tunamonstrosa* witche's broom and aster yellows. Most of these spiroplasmas are cultured and they require sterol for their growth. The spiroplasmas have ribosomes consisting of RNA and a coil of DNA as their genome. Most probably they multiply by binary fission. They are resistant to penicillin; however, tetracyclines, erythromycin, amphotericin and neomycin inhibit these organisms. Serology and polyacrylamide gel electrophoresis are commonly used to find out the inter relationships of cultured spiroplasmas.

2.6 Other Sub-Viral Agents

2.6.1 Satellite Viruses

Satellite viruses are defined as sub-viral agents lacking genes that could encode the enzymes needed for their replication and they cannot cause infection by themselves. Instead, they must always be associated with certain typical viruses (helper viruses) because they depend on the latter for multiplication and plant infection. Satellite viruses often reduce the ability of the helper viruses to multiply and cause disease i.e., satellite viruses act like parasites of the associated helper viruses. Therefore, their multiplication depends on the co-infection of a host cell with a helper virus. A satellite virus is genetically distinct from its helper virus by virtue of having a nucleotide sequence substantially different from it, although some satellites share short sequences often at the termini of their RNA, with their helper viruses. Satellite viruses are not classified by species or genera because they are not a homogeneous group of agents and information on their properties (e.g., nucleotide sequence) is in sufficient to deduce their evolutionary origins.

For the convenience, satellite viruses are divided into two major categories:

(1) "Satellite viruses" (resembling *Tobacco necrosis satellite virus*) and the examples are Single-stranded RNA satellite viruses, Subgroup 1: *Chronic bee-paralysis satellite virus,* Subgroup 2: *Tobacco necrosis satellite virus.*

(2) "Satellite nucleic acid" is divided into (1) Single-stranded satellite DNAs, e.g., Alphasatellites, *Tomato leaf curl virus satellite DNA,* Betasatellites. (2) Double-stranded satellite RNAs, e.g., *Saccharomyces cerevisiae M virus satellite, Trichomonas vaginalis T1 virus satellite.* (3) Single-stranded satellite RNAs, e.g., Subgroup 1: Large satellite RNAs: *Arabis mosaic virus large satellite RNA, Bamboo mosaic virus satellite RNA, Chicory yellow mottle virus large satellite RNA, Grapevine Bulgarian latent virus satellite RNA, Grapevine fanleaf virus satellite RNA, Myrobalan latent ringspot virus satellite RNA, Tomato black ring virus satellite RNA, Beet ringspot virus satellite RNA,* Subgroup 2: Small linear satellite RNAs: *Cucumber mosaic virus satellite RNA, Cymbidium ringspot virus satellite RNA, Pea enation mosaic virus satellite RNA, Groundnut rosette virus satellite RNA, Panicum mosaic virus small satellite RNA, Peanut stunt virus satellite RNA, Turnip crinkle virus satellite RNA, Tomato bushy stunt virus satellite RNA B10, Tomato bushy stunt virus satellite RNA B1,* Subgroup 3: Circular satellite RNAs or "virusoids": *Arabis mosaic virus small satellite RNA, Cereal yellow dwarf virus-RPV satellite RNA, Chicory yellow mottle virus satellite RNA, Lucerne transient streak virus satellite RNA, Solanum nodiflorum mottle virus satellite RNA, Subterranean clover mottle virus satellite RNA, Tobacco ringspot virus satellite RNA, Velvet tobacco mottle virus satellite RNA.*

The genomes of satellites range upward from 359 nucleotides in length for *Satellite Tobacco Ringspot Virus* RNA (STobRV). Satellite viral particles should not be confused with satellite DNA. The aspect of plant virus satellites has been reviewed by Francki (1985) and Roossinck et al. (1992).

2.6.2 Defective Interfering Particles (DI Particles)

DI Particles are virus particles which contains genomes that are grossly altered genetically, usually by significant deletion of essential functions, but which nevertheless retain critical replication origins and packaging signals, allowing for amplification and packaging in co-infections with complimenting wild-type helper virus. These particles usually display a replication advantage relative to wild-type virus, resulting from increases in the copy number or efficiency of replications origins. DI particles actively inhibit replication of wild-type virus, presumably by competing for limiting essential replication factors. Study of DI particles has provided significant insight into the viral replication in particular structure and function of replication origins (Condit 2007). The DI genome is replicated only in a cell that is infected with infectious virus of the type from which the DI genome was generated as this is needed to supply replicative enzymes and structural proteins.

The production of subgenomic DNA, so-called defective interfering DNA, (DI DNA) has been observed in all geminivirus genera (Frischmuth and Stanley 1993). DI DNA generally have one or more parts of a genome deleted. It is assumed that the production of DI DNA is due to intramolecular recombination, and most DI DNAs have short sequence duplication at the deletion border. Characteristically, DI DNAs contain only viral derived sequences. They are dependent for their replication and movement on the parental virus and interfere with viral proliferation in transgenic plants (Frischmuth and Stanley 1993). Besides these virus derived DI DNAs are generally small DNA molecules described as satellite. Even nano virus like DNAs have been found in geminivirus infected plants. One of the examples of geminivirus group is *Cotton leafcurl virus* (CLCuV) infected with a small DNA molecule (designed as DNAI) related to nano viruses has been identified (Mansoor et al. 1999). More information on DI Particles can be obtained from Huang (1973).

2.7 Conclusions

The tropical zone has nearly 169 countries out of the total 270 countries of the world covering nearly 62.5 % of our planet. Besides the fungal, bacterial and insect pests, even the virus and virus-like diseases also cause extensive yield losses. Plant virus is basically a tiny bundle of genetic material-either DNA or RNA carried in a shell called viral coat or capsid which is made up of protein called capsomeres. Apart from the virus diseases, the viroid diseases also cause catastrophic yield losses of the crops. The viroids are low molecular weight, covalently closed circular RNA molecules and are distinguished from viruses by the absence of protein coat, lack of mRNA activity and by the homogenous structure, structural transitions and hydrodynamic behavior of their RNA molecules. Even the satellite viruses and DI particles cause diseases in plants. The identification of the etiological agent is most important and we have sufficient information on the particle morphology genomic composition, epidemiology and transmission mode for the majority of the virus diseases. Well established sero-diagnosis and molecular techniques are available for accurate identification of virus and virus-like pathogens. Since 1968, attempts have been made to classify plant viruses by a number of research workers. At present the ICTV in the 9th report which was updated in 2012, has a total of 87 families, 349 genera, and 2284 species. Similarly the viroids are also identified and classified into two families viz., *Pospiviroidae* and *Avsunviroidae*. Since the etiological agents and their epidemiological and pest risk analysis data is available for some of the diseases, progress on the management measures against the major virus diseases have been developed and these details are provided in Volume 2 of this series.

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Plant Virus and Viroid Diseases in the Tropics
Volume 1: Introduction of Plant Viruses and Sub-Viral Agents, Classification, Assessment of Loss, Transmission and Diagnosis
Sastry, K.S.
2013, XXV, 361 p., Hardcover
ISBN: 978-94-007-6523-8