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Major plant viruses: an overview

A.Saha[1]*, B. Saha[1] and D. Saha[2]
[1]Molecular Plant Pathology and Fungal Biotechnology Laboratory, Department of Botany; [2]Plant Biotechnology laboratory, Department of Biotechnology; University of North Bengal, Siliguri-734 013

Abstract

Plant viruses cause severe diseases leading to enormous crop loss. The present day viral researches of economic plants are centered on identification of virus, molecular characterization and management of viral diseases. Till date more than thousand viruses have been classified into several families. It is desirable to know about the different virus families along with their type genus and/or important genus. But due to an enormous volume of literature published on this aspect, it becomes difficult to study all of them. Hence the present review has highlighted the salient features of the major plant viruses which have been classified at the family level. Most of the virus families have been discussed with important/type genus of each family. Some viruses which could not be placed in any family have been grouped as 'no family'. Importance of molecular data, immunological data and data on protein configuration of coat proteins along with bioinformatics and its predictive power have been highlighted.

Keywords: Plant virus, virus classification, coat protein

Virus is an obligate parasite. It does not have inherent replication machinery which can replicate outside a living organism. Thus virus is unique. Plant viruses are those viruses which use higher plants as their obligate hosts and use the plants for their replication. Enormous losses of our crops have been reported due to viral attack (Pappu, 1997; Palukaitis *et al*., 1992; Hema and Prasad, 2004; Bateson and Dale, 1995; Espion *et al*., 1990; Robert and Lemaire, 1999; Lokhande *et al*., 1992). Presently, more than one thousand viruses are known (Jiskani, 2007). The nomenclature of virus and creation of new species is very important. The International Committee on Taxonomy of Viruses (ICTV) has suggested for creation of new genus if the molecular similarity is found less than 89% with the nearest species in case of geminivirus (ICTV, 2006). The present day viral researches of economic plants are centered on identification of virus, molecular characterization and management of viral diseases. Although it seems, the molecular characterization and nomenclature has taken central attention but to a beginner the knowledge of conventional techniques and classification rules are still important. To understand the whole scenario of role of virus in plant diseases the present review has been done with a view to proper understanding of a virus nomenclature.

More than thousand viruses have been classified into several families. All the families have been characterized by a type species. The virus families along with the type genus and/or important genus have been presented in the following lines. Among the different families mentioned some families are very important for their destructive role in economic crops. The other viruses although less important but they may provide some important information regarding viruses and their possible infecting capacity in continuously changing genotypes of our crops. Important families with salient molecular characters along with important plant diseases producing genus have been presented in the following lines. Most of the molecular informations given in the following lines have been presented from the ICTV reports. ICTV reports has summarized by Matthews, 1983a, 1985a,b. ICTV has published seven reports up to 2000 in Archives of Virology (Hull, 2002). The most recent report of ICTV has been edited by Fauquet *et al*., 2005.

Important families of plant virus:

Caulimoviridae: Members of Caulimoviridae are replicated by reverse transcription. All the viruses have circular DNA. The genome is discontinuous at specific sites. The members are divided into two groups: isometric particles containing *Caulimoviruses* and bacilliform particles containing *Badnaviruses*. *Cauliflower mosaic virus* (CaMV), the type member of the genus *Caulimovirus*, is one of the most common and important viruses of brassica crops in the world. CaMV has double-stranded DNA as their genetic material. This virus is wide spread in temperate regions wherever species of *Brassica* are grown (Sutic *et al*. 1999). CaMV has isometric particles about 50nm in diameter, composed of 420 capsid protein subunit and a circular double-stranded DNA genome which contains seven major ORFs (I to VII). Of these ORFs only the capsid protein (and/or its polyprotein precursor GAG), the polymerase polyprotein and the transactivator/ viroplasmin are essential for virus replication (Hohn and

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**Corresponding author.*
E-mail: asahanbu@yahoo.co.in

Futterer, 1997 and Kobayashi and Hohn, 2003) whereas the movement protein (MP) and the virion associated protein (VAP) are additionally required for induction of plant disease (Kobayashi *et al.*, 2002). Virus is replicated by the reverse transcription of an RNA intermediate (Haas *et al.*, 2002). Caulimoviruses have a restricted host range, usually one or two families. CaMV mainly infects members of Cruciferae and Solanaceae (Chenault *et al.* 1992). This virus induces a variety of systemic symptoms (Chlorosis, mosaic, vein clearing and stunting). On many cruciferous plants, particularly on various *Brassica campestris* and *B. oleracea* cultivars, often in mixed infection with *Turnip mosaic virus* (TuMV) (Shepherd, 1981). The virus is not transmissible by seed or pollen (Blanc *et al.*, 2001). The three viruses of genus '*Soybean chlorotic mottle virus-like*', '*Cassava vein mosaic virus-like*' and '*petunia vein clearing virus-like*' resemble genus *Caulimovirus* but their genome organizations are different. Two other genus '*Bodnavirus*' and '*Rice tungro bacilliform virus-like*' are in the group which contain bacilliform particles. Both the viruses are important in tropical agriculture.

Geminiviridae: The name of the family comes from geminate virus particles which contain the genome of the virus. Two incomplete icosahedra form the geminate particles (Kirthi *et al.*, 2002). The genome of the family is of circular ssDNA type (Rojas *et al.*, 2005). Geminiviridae and Circoviridae are the two families of plant viruses that have circular ssDNA. *Geminiviruses* constitute the largest, most diverse and economically important family of plant DNA viruses (Rojas *et. al,* 2005). They infect a broad range of plants and cause devastating crop diseases, particularly in tropical and subtropical regions of world (Mansoor *et al.*, 2006; Moffat, 1999 and Morales and Anderson, 2001). single-stranded DNA (*ss*DNA) genomes display high levels of genetic variability (Seal *et al.*, 2006). The family *Geminiviridae* is classified into four genera, *Begomovirus*, *Curtovirus*, *Topocuvirus* and *Mastrevirus*, based on their genome organization, host range and insect vectors (Faquet *et al.*, 2003). The largest genus of Geminivirus family is *Begomovirus*. *Begomovirus* have one or two genome components (designated as DNA-A and DNA-B) which infect dicots and are transmitted by *Bamisia tabaci*. A significant increase in the frequency and severity of *Begomovirus* diseases over the past 20 years have been well documented by Rashed, 2006. The DNA-A component of *Begomovirus* contains four genes (AC1, AC2, AC3 and AC4) on their c-sense strand and two genes (AV1 and AV2) on their v-sense strand. AC1 encodes Rep, replication initiator protein (Elmer *et.al,* 1988, Etessami *et al.*, 1991), AC2 gene encodes TrAP, transcription activator protein (Sunter and Bisaro, 1991, Hartiz *et al.*, 1999), AC3 encodes REn, Replication enhancer (Elmer *et al.*, 1988) and AC4 gene encodes C4 protein. AV1 gene encodes coat protein and AV2 encodes pre-coat protein. Similarly, the DNA-B component contains two ORFs which encode for proteins that assist in intra-cellular and inter-cellular viral movement- BC1/NSP (nuclear shuttle protein) and BV1/MP (movement protein) (Lazorawitz, 1999). The invariant TAATATT↓AC sequence, located in the intergenic regions, contains the initiation site (↓) of rolling circle DNA replication. Among the geminiviridae tomato leaf curl virus is one of the important virus which cause substantial loss of crops (Magar *et al.*, 2008). *Tomato leaf curl virus* (ToLCV) is a whitefly (*Bamisia tabici*) transmitted *Geminivirus* (family *Geminiviridae*, genus *Begomovirus*) causing destructive disease of tomato in many parts of India (Vasudeva and Sam Raj, 1984; Sastry and Singh, 1973; Muniyappa and Saikia, 1983; Saikia and Muniyappa, 1989; Harrison *et al.*, 1991; Reddy *et al.*, 2005; Kirthi *et al.*, 2002; Paximadis *et al.*, 2001; Ramappa *et al.*, 1998). Besides tomato *Begomovirus* infects variety of other plants including Kenaf (Paul *et al.*, 2006), *Dimorphotheca sinuta* (Raj *et al.*, 2007), Bimili jute (Raj *et al.*, 2007a), Bun ochre (*Urena lobata*)(Chatterjee *et al.*, 2007), *Mimosa invasa* (Koravich *et al.*, 2008), Bitter gourd (Rajinimala and Rabindran, 2007), *Datura stramonium* (Ding *et al.*, 2007), Papaya (Wu and Zhou, 2006), *Duranta repens* (Tahir *et al.*, 2006), Chilli (Shih *et al,* 2006), Methi (Raj *et al.*, 2001), common bean (Papayiannis *et al.*, 2007), *Ageratum conyzoides* (Wong *et al.*, 1993), potato (Garg *et al.*, 2001), pepper (*Capsicum annum*) (Strenger *et al.*, 1990) of India and other parts of the world. *Begomovirus* infected diseases are characterized by severe leaf curling, shrinking of leaves, stunted growth of the plants, yellowing of the veins (Chakraborty *et al.*, 2003). Jatropha (*Jatropha curcas* L.) an important biofuel producing plant is infected by JMIV. The disease cause stunted growth and several other symptoms. The disease cause low production of fruits which is used for extraction of biofuel (Rangaswamy *et al.*, 2005; Aswatha Narayana *et al.*, 2006).

Circoviridae: Like the geminiviridae this family also possesses genome of ss DNA but they possess much smaller circular DNA. The virus particle is also very small (approximately 20nm in diameter). Out of the two genus of the family only one genus (*Nanovirus*) infects plants. One of the species *Banana bunchy top virus* (BBTV) of *Nanovirus* is economically important. The icosahedral virus particle contains six or more circular ssDNA molecules of approximately 1 kb in size. Banana bunchy top disease is caused by BBTV, a multi-component, circular single-stranded DNA virus of the family Nanoviridae that is transmitted plant-to-plant by the aphid vector *Pentalonia nigronervosa*. The family Nanoviridae consists of aphid transmitted viruses with isometric virions, approximately 18–20 nm in size, and is divided into two genera; (BBTV is the only member of the genus), and Nanovirus. Nanovirus contain *Subterraneanclover stunt virus* (SCSV) (Boevink *et al.*, 1995), *Faba bean necrotic yellows virus* (FBNYV) (Katul, 1997 and 1998) and *Milk vetch dwarf virus* (MDV) (Sano *et al.*, 1998). Placement of *Coconut foliar decay virus* remains uncertain as only a single component of the virus has been described (Rohde *et al.*, 1990). The component described as satellitelike molecule associated with a geminivirus (Briddon *et al.*, 2006). The genome of BBTV has been reported to have at least six components of approximately 1100 nucleotides. The six components are DNA-R, DNA-S, DNA-C, DNA-M, DNA-N and DNA-U3 which encode a rolling-circle replication initiator protein [Rep], coat protein [CP], cell-cycle link protein [Clink]), movement protein [MP], nuclear shuttle protein [NSP]) and undetermined respectively (Vetten *et al*., 2005).

Reoviridae: The viruses of the family contain ds RNA. The most important part of the family is that some members of the family infect plants and those viruses also infect their vectors (invertebrate). All the three genera (*Fijivirus*, *Oryzavirus* and *Phytoreovirus*) which attack plants can be separated by their dsRNA segment number and particle size diameter. *Fijivirus* mostly attack monocotyledonous plants of poaceae and liliaceae. The third genus Phytoreovirus can attack both monocotyledonous and dicotyledonous plants. *Rice dwarf virus* (RDV) is a member of the genus *Phytoreovirus* of the family *Reoviridae*, which also includes animal *Reovirus*, *Orbivirus*, and *Rotavirus*. RDV replicates both in insects and in graminaceous plant cells, but it can be transmitted only by insects such as the leafhopper (*Nephotettix cincticeps* or *Resilia dorsalis*) (Suzuki *et al*., 1994). RDV does not induce neoplasia but induce stunted growth, develop characteristic chlorotic flecks, and fail to bear seeds. This virus is widespread among rice plants in southern China and other Asian countries. The RDV genome is composed of 12 double-stranded RNA segments, designated S1 to S12 in ascending order of their mobility on a polyacrylamide gel (Fujii-Kawata and Fuke, 1970). The complete sequences of all of these segments have been determined and 90% sequence similarity have been reported between a Japanese isolate (Uyeda *et al*., 1994) and a Chinese isolate (Zhang *et al*., 1997).

Partitiviridae: The plant infecting viruses of this family are commonly known as 'cryptic virus'. These viruses produce no symptoms or negligible symptoms. The viruses are characterized by non-enveloped bi-segmented dsRNA genome. The two plant infecting genera are *Alphacryptivirus* and *Betacryptovirus*. Plant cryptoviruses are associated with latent infections of their hosts. Pollen/seed transmission is the only means of virus dispersal. No cell-to-cell movement of the virus has been reported. The virus can only move when cell division takes place (Boccardo *et al*., 1987). One genus *Partitivirus* have been reported from fungi (Ghabrial *et al*., 2005).

No family: Varicosavirus genus could not be ascertained to any defined families and kept as no family. The type species is '*Lettuce big vein virus*'. Two ds RNA molecules are there in the genus and the shape of the virions are rods.

Rhabdoviridae: Rhabdoviruses are characterized by bacilliform to rounded structure enveloped by a membrane. The outer surface is characterized by glycoprotein spikes. The viruses are (-) strand RNA viruses. There are two well defined viral genera in the family although several plant rhabdoviruses could not be assigned to any genus due to inadequate data and information required for assigning a genus. All those viruses are kept in a group as 'unassigned Rhabdoviridae'. *Potato yellow dwarf virus* (PYDV) is a species of plant virus under the genus *Nucleorhabdovirus*. The virus was first identified in the USA by Barrus and Chupp (1922). The virus has several effects including stunted growth, dwarfing, apical yellowing, tuber cracking and malformation. PYDV has been transmitted artificially to species of the families Apocynaceae, Asteraceae, Brassicaceae, Fabaceae, Lamiaceae, Polygonaceae and Scrophulariaceae (Black, 1970; OEPP/EPPO, 1980). It occurred naturally during 1986-88 in Minnesota (USA) on the ornamental herbaceous plants *Mirabilis jalapa*, *Nicotiana alata*, *Tagetes erecta* and *Zinnia elegans*, causing severe stunting, chlorosis, vein yellowing and systemic vein and leaf necrosis (Lockhart, 1989). PYDV isolates can be distinguished by their serological reactions and their vector specificity. There are two serotypes: one transmitted by the leafhopper *Aceratagallia sanguinolenta* and another *Aceratagallia* sp. ("*Sanguinolenta yellow dwarf virus*"), the other by the leafhopper *Agallia constricta* ("*Constricta yellow dwarf virus*"). Both forms are transmitted by *Agalliota quadripunctata*. The California isolate is closely related to the sanguinolenta serotype (Falk & Weathers, 1983). Both serotypes have a long incubation period in their respective vector leafhoppers (at least 6 days), during which they multiply (Chiu *et al*., 1970). Nymphs, adult male and female insects transmit PYDV. *Leucanthemum vulgare* serves as the principal virus source for infecting potato crops. *Catharanthus roseus* is a natural host in California. PYDV is carried through tubers derived from infected plants. The virus is mechanically transmissible to seven species of tobacco (Falk *et al*., 1981).

Bunyaviridae: Bunyaviridae are characterized by spherical virions with glycoprotein spikes. The viruses are either of (-) strand RNA or in an ambisense arrangement [where both (-) and (+) strands of RNA are present]. Altogether three RNA segments are found. This is one of the large families. Most of the genus attack vertebrates and invertebrates. Only one genus (*Tospovirus*) attack plants and invertebrate vectors. Out of the three RNA segments of Tospovirus the largest one is of (-) strand and the other two are of ambisense type. Tomato spotted wilt (caused by *Tomato spotted wilt virus*) was first described in Australia in 1919. It is an important disease of several crops grown in temperate and subtropical regions of the world. TSWV infect approximately in 174 plant species (Zitter *et al*., 1989). The common hosts are tomatoes, peppers, celery, lettuce, eggplant, peanuts, pineapple, many legumes, many ornamentals, and many weeds such as field bindweed and curly dock. Symptoms of TSWV are numerous and varied. TSWV is transmitted from infected plants to healthy plants by at least nine species of thrips. Thrips transmit the virus in a persistent manner, which means that once the insect has picked up the virus, it is able to transmit the virus for the remainder of its life (Goldberg, 2000). There are significant differences in tospoviruses and their relationship with specific thrips species, so what is presented herein on TSWV is not applicable to all tospovirus-thrips interactions (Sherwood, 2003). The current understanding of the TSWV gene functions indicates that the NSm serves as a movement gene, NSs is a silencing suppressor and the glycoproteins contain determinants for thrips transmission. Management of TSWV has proven to be challenging due to the wide host range of both the virus and its vector, and emergence of resistance breaking strains. However, increased understanding of the biology, genetics, epidemiology and molecular biology of TSWV resulted in development of practical and effective integrated disease management programs for reducing the impact of TSWV in some crops (Pappu, 1997).

No family: Two genera *Tenuivirus* and *Ophiovirus* could not be placed in any family due to inadequate informations. These two genera have some similarities with the members of Bunyaviridae. Tenuivirus is spreaded by grass hoppers but the vector for *Ophiovirus* is unknown. *Tenuivirus* attack plants of the family Poaceae whereas the other genus can attack both monocotyledons and dicotyledons.

Bromoviridae: Members of this family contain tripartite (+) strand RNA. The viruses of the family are isometric with generally bacilliform in shape. Size varies in different genera. Five different genera are *Bromovirus, Cucumovirus, Ilarvirus, Alfamovirus* and *Oleavirus*. Among the genera *Cucumovirus* are most important as it has a wide host range. Largest number of plant species (approximately 1000 plant species) is infected by the virus (Kim *et al*., 2010). The genome of the virus consists of plus-sense single stranded three RNAs (RNA 1, RNA 2, and RNA 3) and a subgenomic RNA (RNA 4) which is encoded by the 3'-half of RNA 3 (Palukaitis *et al*., 1992) and which is involved in encapsidation (Suzuki *et al*., 1991). *Cucumber mosaic virus* (CMV) isolates are classified into two sub-groups, I and II, according to various converging criteria which include symptomatology, serology and nucleic acid homology etc. (Palukaitis *et al*., 1992). RNA 3 contains both the viral coat protein (CP) gene and movement protein gene involved in the cell-to-cell and long-distance movements (Davies and Symons, 1988). After mapping for the determination of CMV pathogenicity (Mossop and Francki, 1977), pseudorecombinants created by exchanging gel-eluted genomic RNAs revealed that each of the three genomic RNAs plays its determinant role by various host-strain interactions (Palukaitis *et al*., 1992). Asian strains of CMV have been placed in subgroup IB (Palukaitis and Zaitlin 1997). Several workers are working in elucidating the role of different proteins in different functions of the viral activities. *Alfalfa mosaic virus (AMV)* has a tripartite single-stranded genome. RNAs 1,2,3 and subgenomic RNA 4 are separately encapsidated into baciliform particles which are 18nm wide and have lengths characteristic of the RNA encapsided (about 56,43,35 and 35 nm respectively) (Thole *et al*. 1998). The genomic RNAs are not infective. Infection can start only in the presence of RNA 4 or its translation protein product (CP). AMV mostly infects herbaceous plants, but several woody species are included in the natural host range (Edwardson and Christie, 1997).

Comoviridae: *Comoviridae* are made up of two ssRNA of positive strand. Capsid proteins are very important. The capsid proteins are named for their functions. Encapsidation is only one feature of an extremely diverse array of structural, functional, and ecological roles played during viral infection and spread (Callaway *et al*., 2001). The capsid protein is multifunctional; in addition to having a role in encapsidation; it affects virus movement in plants (Kaplan *et al*, 1998), transmission, symptom expression, and host range (Shintaku and Palukaitis, 1990). *Comovirus, Fabavirus*, and *Nepovirus* are the three genera of the family. The capsid of Comovirus is made up of two proteins of different size. The capsid of *Fabavirus* are made up of two proteins of similar size but the capsid of *Nepovirus* are made up of a single protein. Cow pea mosaic virus of genus *Comovirus* is one of the important virus which infect *Vigna radiata*. Foliage turns yellowish green with areas of light and dark green tissue. Infected leaves are often stunted and frequently have a puckered appearance. Susceptible host species are *Datura stramonium, Glycine max, Gomphrena globosa, Nicotiana tabacum, Phaseolus vulgaris, Pisum sativum, Spinacia oleracea, Vicia faba, Vigna angularis, Vigna radiata, Vigna unguiculata* (Gomase and Kale, 2008; Gopinath *et al*., 2003).

Tombusviridae: The virus particles are in the size range of 30 to 35 nm in diameter. The viruses contain single species of RNA of positive ss type. Members have narrow host range. The eight genera are *Tombusvirus, Aureus virus, Avenavirus, Carmovirus, Machlomovirus, Necrovirus, Panicovirus* and *Dianthovirus*. Members either infect monocotyledons or infect dicotyledons but no virus attack both types of plants. *Tomato bushy stunt virus* (TBSV) RNA genome of approximately 4.8 kb, encodes five major open reading frames (ORFs) (Brunt *et al*., 1996). Viral replication require an ORF1and an ORF2 (Scholthof *et al*., 1995a). Coat protein and viral movement protein are encoded by ORF3 and ORF4 respectively. Cell to cell movement and symptom determination on certain host plants are controlled by ORF4 (Scholthof *et al*., 1995b). Product of ORF5 has a role in the induction of necrotic symptoms and in the long-distance spread of the virus, depending on the host. TBSV has been reported from tomato of Ireland, North and South America, Europe, Africa, and Japan (Ohki *et al*., 2005). TBSV has been divided on the basis of serological reactivity into three major strains. Because of serological reactivity and of the high sequence homology in their genomes, it was also proposed that *Petunia asteroid mosaic virus* and *Artichoke mottled crinkle virus* (AMCV) are also strains of TBSV (Luis-Arteaga *et al*., 1996).

Sequiviridae: The virus particle of 30nm size is made up of three different proteins of different sizes. Single positive ssRNA encodes poly proteins which after cleavage produce functional proteins. Two genera are *Sequivirus* and *Waikavirus* infect plants of limited importance.

Closteroviridae: The particles of different members of the family are flexuous and filamentous. The nucleic acid is linear (+) strand ss RNA. Depending on genus the nucleic acid may be monopartite or bipartite. The transmissions of the viruses are of different types. The viruses are generally restricting themselves in the phloem. The genera may be classified on the basis of transmission vectors like aphid-transmitted, mealy bug-transmitted and whitefly transmitted. *Closteroviridae* is represented by *Closterovirus* and *Crinivirus*. *Citrus tristeza virus* (CTV), an aphid-transmitted *Closterovirus*, has been the most important viral pathogen of citrus for the last ninety years. CTV has a huge destructive role and have been reported from almost all over the world (Harper *et al*., 2009). *Citrus tristeza virus* (CTV) has been reported from various Indian states also (Ahlawat and Raychaudhuri, 1988; Capoor, 1963; Narani *et al*. 1965; Vasudeva and Capoor, 1958). Vector specificity and reaction in differential hosts are the two criteria which have been followed to determine mild or severe strains in India (Capoor and Rao, 1967; Balaraman and Ramakrishnan, 1977; Capoor and Chakraborty, 1980). Among the seven aphid species reported as vectors of CTV, *Toxoptera citricidus* has been found to be the most efficient vector (Capoor and Rao, 1967).

Luteoviridae: 'Luteus' mean yellow in Latin. Most of the genus produce yellows type disease. Hence the name of the family is *Luteoviridae*. The members of the family contain (+) sense ss RNA. Three important genera are *Luteovirus*, *Poleovirus* and *Enamovirus*. Eleven viruses of family have not been assigned to any genus due to insufficient data availability for characterization. *Potato leafroll virus* (PLRV) of the genus *Polerovirus* infects potato crops worldwide (Robert & Lemaire, 1999). It is transmitted in a persistent manner by a limited number of aphid species like *Myzus persicae*; the most efficient and important vector (Harrison, 1984). Its natural host range is mainly restricted to a few solanaceous plants (*Solanum tuberosum*, *Physalis oridana*, *Datura stramonium* and *Lycopersicon esculentum* (Thomas, 1993). Moreover, a few plants of other families can be infected by PLRV, either experimentally (Harrison, 1984) or naturally (Lizarraga *et al*., 1996). Six main open reading frames (ORFs) numbered from 0 to 5 are there in the genome of the virus (Miller *et al*., 1997). Six different proteins (P0 to P5) are formed from the ORFs. P0 is essential for replication of the PLRV genome (Sadowy *et al*., 2001) and that P1 has a hydrophobic domain, thought to be involved in membrane attachment (Mayo & Ziegler-Graff, 1996). P2 is translated by a rarely occurring ribosomal frameshift from ORF1. P3, P4 and P5 being translated from a subgenomic RNA correspond to the major capsid protein (CP), the putative movement protein (MP) and a protein (of readthrough domain) which is translated by suppression of the ORF3 stop codon. Ashoub *et al*. (1998) identified two further putative ORFs encoding two proteins, P6 and P7, the roles of which remain unknown.

Potyviridae: Members of *Potyviridae* have flexuous particles 650-900 nm long and 11-15 nm in diameter. The genome is (+) sense ss RNA with a VPg (a genome-linked protein covalently bound to the 5'end) and with a 3' poly A portion. Inclusion bodies are found in all the hosts infected by the members of the family. Out of the six genera (*Potyvirus*, *Ipomovirus*, *Macluravirus*, *Rymovirus*, *Tritimovirus* and *Bymovirus*) *Potyvirus* is the largest and also the largest of plant viruses. Some economically important species are included in this family. Bean common mosaic virus was first reported in Russia in 1894 and has since been distributed worldwide (Agrios, 1988; Boss 1971, Hampton *et al*., 1983; Sherf and Macnab, 1986). *Bean common mosaic virus* (BCMV) on bean cause systemic mosaic, malformation of leaves and pods and rugosity of lower leaves, sometimes even necrosis. Viruses cause substantial loss (Hall, 1994). The virus is transmitted in non-persistent manner by insect vectors (e.g. *Acyrthosiphon pisum*, *Aphis craccivora*, *A. fabae* and *Myzus persicae*). It affects primarily the French bean (*Phaseolus vulgaris*) but also *Phaseolus* sp and faba bean (Bos, 1971; Sherf and Machnab, 1986; Smith, 1972). Mechanical inoculation and seed-transmission (in *P. vulgaris* up to 83%) have been reported by Brunt *et al*., 1996. *Papaya ring spot virus*, first described by Lindner *et al*. (1945), induces irregular mosaic patterns on leaves, ring on petioles and yellow ring on fruit (Shinde *et al*., 2005) of papaya where it is grown (Purcifull *et al*., 1984). The PRSV strains that infect papaya, designated as PRSV-P are distinct from the PRSV-W strain of cucurbits. Papaya trees infected with PRSV-P are stunted, produce deformed fruits with some ringspot, vein clearing, mottling, malformed leaves, streaks on fruit, stems and petioles (Kuan *et al*. 1999). Bateson *et al*. 1994 reported that PRSV-P evolved from PRSV-W, presumably by mutation. This was first indicated by the very close sequence similarity of the coat protein (CP)-coading region of P and W isolates. Another member of the genus *Potyvirus* is *Potato virus Y* (PVY). The isolates of PVY have been classified in three main strains: PVY^N, PVY^O and PVY^C (De Bokx and Huttinga, 1981). The virus can infect potato, tobacco, tomato and pepper as well as wild species, especially those in the *Solanaceae* family (Ellis *et al*., 1997). The serological classification of PVY isolates is a matter of discussion. Coat protein-directed polyclonal antibodies do not discriminate between PVY strains so monoclonal antibodies specific to O and N strains have been used to characterize selected PVY isolates (Gugerli and Fries, 1983; Hataya *et al*., 1998)

Conclusion

Although molecular data, immunological data and protein configuration of coat proteins are most important, bioinformatics is being increasingly used in virus classification due to its strongest predictive power. Bioinformatics is particularly important when information from several techniques is combined, including experimental confirmation of protein antigenicity predictions etc. (Gomase and Changbhale, 2007; Gomase *et al*, 2007). Sequence data of genome of different viruses are being available in the gene bank and all such sequences may be used to find out the closeness of the different isolates, species and genus of the viruses. Most importantly in several cases the sequence data have solved the problems of classification. Still several sequence data demand considerable reorganization of the classification.

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