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Genomics-led Insight into Potyvirus Family, Prevalence and Management

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ABSTRACT: *Potyvirus* is the largest genera with more than 200 viral species in *Potyviridae* family. *Potyvirus* is a major aphid-transmitted pathogen of potato and other solanaceous crops. *Potyvirus* infection causes severe yield loss in many crops. Potato virus Y (PVY) *Potyvirus* is the most studied virus that affects potato cultivation worldwide. PVY has infected around 495 plant species of 72 genera in 31 families. PVY is an RNA virus which mutate in higher rate. The complexity of the PVY strains is differentiated by their reactions against resistant genes and genome organization in potato. Mutation, recombination, migration, natural selection and genetic drift give birth to a pool of viruses which then are adapted to new niches. Aphid control and introduction of resistant cultivars is an eco-friendly way of maintaining the viral diseases. An insight into PVY genetic structure, variability and evolutionary changes will help to strategize PVY control. This article discusses *Potyvirus* genetic complexity, function of the viral proteins and disease control measures, with emphasis to Potyviral Y strain.

Keywords: *Potyvirus* family, Potyviral genome, Potato virus Y, Aphids, Polyprotein.

INTRODUCTION

Plant-virus interaction is a well-known area in the field of plant biology. Since time immemorial, viruses have been affecting a wide range of economically important plants like legumes, forages, fruits, vegetables and ornamentals. Large number of studies has been conducted to recognize the relationship between plants and viruses. Among all the known plant viruses, commonly studied are *Potyvirus*es of family *Potyviridae* which was first described in the early 1930s (El-Aziz, 2020). *Potyvirus* is one of the largest plant RNA virus groups with a positive sense RNA with size 9.7 kb and has been significantly affecting crops over the years globally. Economically important plants and many wild plants get affected by *Potyvirus* (Roossinck, 2012). *Potyvirus* is the largest genus of *Potyviridae* family and has more than 200 viral member species (White *et al*., 1987). The genera are characterized in terms of composition of their genome and its structure, similarity of their sequences and vector responsible of their transmission from plant to plant (Adams *et al*., 2011). A common trait shared among this class of plant viruses is scroll-shaped inclusion bodies ordinate inside the infected cell's cytoplasm (Edwardson, 1974). These inclusion bodies are called as cylindrical inclusion (CI) bodies. The CI bodies encoded by viral protein are of important phenotypic criterion for the viruses of the *Potyvirus* genus. Majority of the viruses in this family are aphid-transmitted and in a non-persistent manner while some are transmitted via seed and a few are possibly transmitted through mites and whiteflies (Shukla *et al*., 1989). The transmission of PVY occurs almost all over the world. PVY chiefly affects the crops of *Solanaceae* family such as potato, tomato, chili, and tobacco (Singh *et al*., 2008). Two other plant families affected by PVY are *Amaranthaceae* and *Chenopodiaceae* (White *et al*., 1987). Besides its increasing effect as a major plant virus, several different strains of PVY has been detected and studied.

Members of *Potyviridae* family. *Potyvirus* family has a large geographical distribution and it affects a wide range of plants. The type member Potato virus Y (PVY) of genus *Potyvirus* and family *Potyviridae* along with Potato virus A (PVA) and Potato leaf roll virus (PLRV) of the genus *Polerovirus* leads to a tremendous loss in potato production leading to a loss of about 90% crop yield. Another *Potyvirus* named Plum pox virus (PPV) is of economic importance which causes devastating diseases in stone fruits worldwide. Pepper veinal mottle virus (PVMV), a *Potyvirus*, has created havoc in Chilli yield loss in Africa (Alegbejo and Abo, 2002). Zucchini yellow mosaic *Potyvirus* (ZYMV) affect cucurbit plants in Mediterranean countries (El-Aziz, 2020). Bean common mosaic virus (BCMV), bean common mosaic necrosis virus (BCMNV), bean yellow mosaic virus (BYMV), cowpea aphid-borne mosaic virus (CABMV),

pea seed-borne mosaic virus (PSbMV), peanut mottle virus (PeMov) and soybean mosaic virus (SMV) affect legumes in Iran (Golnaraghi *et al*., 2004; Shahraeen *et al*., 2005; Esfandiari *et al*., 2006). Examples of some other *Potyvirus*es are Soybean mosaic virus (SMV), Turnip mosaic virus (TuMV) and Tobacco etch virus (TEV) (Bosque *et al*., 2014). There are many *Potyvirus*es in nature which affect wide range of plants. The complete list of the species under the genus *Potyvirus* are presented in supplementary Table 1.

Table 1: Potyviral polyproteins and their functions.

Sr. No.	Protein name	Size (k-Da)	Function
1.	P1	30-60	It is a protease. Helps in distinguishing the *Potyvirus*es from one another
2.	HC-Pro	56	It has multiple functions: Aphid transmission factor, gene silencing movement, self-cleaved protease
3.	P3	40+6	Helps in viral replication
4.	6K1		Plays important role in movement, Potyviral infection
5.	CI	70	It has various functions like movement, symptom development, replication
6.	6K2	6	It helps in anchoring to membranes, movement
7.	VPg Pro NIa	21+28	Plays important role in virus cycle, 5'end genome linked protein
8	NIa		VPg protease
9.	NIb	58	Helps in viral replication
10.	CP	30-36	Plays important role in aphid transmission, movement, virion assembly

Genomic structure of *Potyvirus*. The genus *Potyvirus* consist of monopartite genome with an exception to genus *Bymovirus* which has a bipartite genome (Revers and García, 2015). *Potyvirus* has a single stranded RNA with a flexible filamentous viron of about 680–900 nm long and 11–20 nm in diameter (Gibbs *et al*., 2020). Potyviral RNA consists of a single open reading frame (ORF) which encodes for major polyproteins processed by viral proteinases (Reverse and Gracia, 2015). The 5' end of genomic RNA of *Potyvirus* is flanked with a non-coding region (NCR) of less than 200 bp with a terminal protein (VPg) and acts as a translation enhancer. The 3' end is flanked with a 200 bp NCR with a polyA tail at its end (Reverse and Gracia, 2015). The central region of polyprotein in *Potyvirus* encodes for the mature viral proteins P3-6K1-CI-6K2-VPg and NIaPro-Nib-CP (Reverse and Gracia, 2015) which are processed by NIaPro proteinase (Adams *et al*., 2005) (Fig. 1).

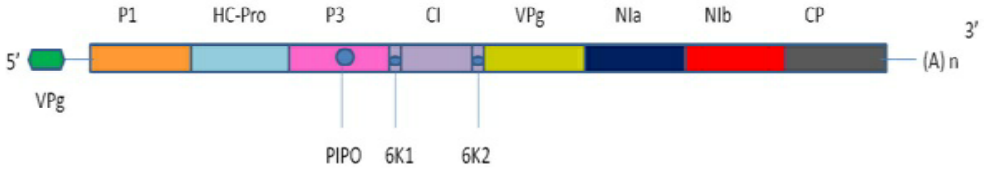

Fig. 1. Monopartite genome of *Potyvirus* and different types of viral protein encoded by the virus.

Function of different potyviral proteins. The proteins encoded by polyprotein gene of *Potyvirus* in sequence from N to C terminal are P1, HC-Pro, P3, 6K1, CI, 6K2, NIa, NIb and CP (Moya, 2009). A new potyviral protein P3N-PIPO (Pretty Interesting *Potyvirus* ORF) has been recognized in the potyviral genome (Wei *et al*., 2010). This protein gets generated in two ways either by ribosomal slippage which creates a +2 frameshift within the ORF of P3 or by incorporating an additional nucleotide at an extremely conserved $G_{1\text{-}2}A_{6\text{-}7}$ motif at the PIPO 5' end sequence (Olspert *et al*., 2015). All these potyviral proteins interact with several other viral encoded proteins, with host proteins in some other cases which allow *Potyvirus*es to carry out all its basic functions and fulfill their life cycle (Lacomme *et al*., 2017). The functions of different potyviral polyproteins are depicted in Table 1. A few of the polyproteins of the potyviral genome are discussed below.

P1 protein. The P1 protein, the first protein of the potyviral polyproteins, is a serine protease of about 30-60 kDa in size and has an important role in distinguishing the *Potyvirus*es from each other (Reverse and Gracia, 2015). P1 can elevate viral infection in RNA silencing deficient plants and has an independent role in RNA silencing suppression (Pasin *et al*., 2014). A new small ORF named PISPO in the P1 coding sequence of some *Potyvirus*es was identified recently which infects sweet potato (Clark *et al*., 2012).

HC-Pro. The second protein of the potyviral polyproteins is Helper component HC-Pro which is the most studied potyviral protein (Reverse and Gracia, 2015). The HC-Pro is present in the C-terminal of the potyviral polyprotein which is a self-cleaved protease (Carrington *et al*., 1989). It has been reported in many studies that this particular protein has multiple functions among which one specialized one is its ability of suppressing RNA silencing (Kasschau and

Carrington, 2001; Jay *et al*., 2011). Some recent studies reported that HC-Pro helps in stabilizing CP which is another polyprotein required for proper infectivity of *Potyvirus* (Valli *et al*., 2014). In addition to this, both the C and N terminals of this polyprotein have special functions. The C terminal performs the proteolytic activity whereas the N terminal helps in virus aphid transmission (Kasschau and Carrington, 2001).

P3, 6K1, and PIPO. P3, a 50 kDa polyprotein, is reported to be associated with a CI protein forming cylindrical inclusion bodies in the cytoplasm of infected cell (Rodrı´guez-Cerezo *et al*., 1993). The P3 also associates with the nuclear inclusions of NIb and NIa viral proteins (Langenberg and Zhang, 1997). The P3 has two hydrophobic regions of which one in the C-terminal region is responsible for the P3 ER targeting and has a role in viral replication (Eiamtanasate *et al*., 2007). The P3-6K1 junction affects the expression of symptoms revealing that 6K1 solely has some role in potyviral infection (Reverse and Gracia, 2015). The function of 25 kDa P3N-PIPO coding sequence was witnessed in Wheat streak mosaic virus before it was discovered (Choi *et al.*, 2005).

CI. The CI protein (71 kDa) forms inclusion bodies in the infected cell cytoplasm (Edwardson, 1974). The CI functions as ATPase and performs as RNA helicase in viral RNA replication (Ferna´ndez *et al*., 1997). For several resistance genes, the CI acts as virulence factor (Sorel *et al*., 2014). The CI interacts with three host factors, one is a translation initiation factor eIF4E (Tavert-Roudet *et al*., 2012), second one is a component of the chloroplastic photosystem I (PSI-K) (Jime´nez *et al*., 2006) and the last is a plant ortholog of a double stranded RNA-dependent protein kinase inhibitor (P58IPK) (Bilgin *et al*., 2003).

6K2 and NIa. NIa, being the largest potyviral protein, forms inclusion bodies with many *Potyvirus*es (Knuhtsen *et al*., 1974). NIa partially produces VPg and NIaPro (Dougherty and Dawn, 1991). When NIa is parted with VPg, it gets localized in the cytoplasm as well as in the nucleus of the infected cell (Cotton *et al*., 2009). But when NIa collaborates with 6K2–VPg–NIaPro product, VPg gets targeted to membranous factories where it plays a vital role in viral RNA replication (Wei and Wang, 2008). The VPg interacts with most of the viral proteins (Elena and Rodrigo, 2012). Nucleotide-binding motif is contained within VPg which when bound to the NIaPro domain and has ATPase activity preferably in *cis* position (Mathur and Savithri, 2012). The protease NIaPro domain in the potyviral polyprotein helps in the processing of the proteolytic C-terminal and central region, and NIaPro has DNase activity (Adams *et al*., 2005). Degradation of the host DNA by NIaPro might have some regulatory roles in the expression of host gene which are crucial for viral infection (Anindya and Savithri, 2004).

Nib. NIb polyprotein is a RNA dependent RNA polymerase and helps in the replication of the potyviral genome (Hong and Hunt, 1996). When NIb interacts with the host proteins eEF1A, PABP and Hsc70-3, it leads to the formation of functional replication complexes (Dufresne *et al*., 2008). The VPg protein is uridylated by NIb protein and the product generated is used to prime viral RNA synthesis (Anindya *et al*., 2005).

CP. The last polyprotein of the potyviral genome is the CP protein of 30 kDa and has a prime role in viral genome encapsidation (Reverse and Gracia, 2015). The potyviral virions which are flexuous and rod like in shape with diameter of about 11-13 nm and 680-900 nm in length are formed by about 2000 CP subunits arranged in helical structure (Adams *et al*., 2011). The central region of CP is highly conserved (Reverse and Gracia, 2015) and the N-terminal region of the CP protein is highly variable and disordered (Ksenofontov *et al*., 2013).

***Potyvirus* Evolution.** *Potyviridae* family members are characterized as picorna-like supergroup as they have similar genome expression strategy and have a well conserved set of proteins which are involved in replication and can lead to cassette evolution. Studies have been conducted to understand the evolutionary capacities of *Potyvirus*es adapting to their new host. RNA viruses have been characterized on basis of their higher mutation rate, shorter generation period and a very large size progeny population which together contributes to its higher evolutionary potential making them responsible for numerous emerging diseases (Elena *et al.,* 2011). Because of epistatic and pleiotropic effects of viral genome mutation, evolutionary constrains lead to host switching processes which further lead to the generation of trade offs for host adaptation (Elena *et al.,* 2011). When different lineages were sequenced, accumulation rate of mutation within the lineages was found to be similar but the mutation along the genome are not scattered and are specific within the evolutionary history (Reverse and Gracia, 2015). The switching events, recombination among lineages, radiation, host and geographical adaptations are considered as the causes of evolution within the *Potyvirus* family. Recombination within nearly identical, phenotypical and similar viral gemones can lead to the rise of new strains of virus with new level of virulence and symptom phenotypes. Recombinant events, partial duplication, point mutation and other important factors can help to elaborate the extravagant variability which is observed among the *Potyvirus*es.

***Potyvirus* Y (PVY).** Potato virus Y *Potyvirus* (PVY) is one of the important viral pathogens of potato. It is transmitted through aphids. PVY belongs to the genus *Potyvirus* and the family *Potyviridae*. The virus is rod-shaped flexuous filament of 680-900 nm long and 11-13 nm wide. PVY has been identified as a complex of different isolates of *Potyvirus*es (Tsedaley, 2015). PVY is a major virus of potato and it spreads easily and reduces crop yield up to 80% (El-Aziz, 2020). PVY infect other solaneceous crops such as tomato, pepper and tobacco.

PVY has a single stranded, positive sense RNA genome of approx. 9.7 kb. It shares a similar genetic makeup with other *Potyvirus* strains. Protein content in the virus particle is about 94%. Only two proteins, VPg and coat protein (CP), are found in the viral particles. Molecular weight of the CP is calculated to be 29.95 kDa (Tsedaley, 2015). It has a 5'- terminal genome-linked protein (VPg) and a 3' poly(A) tail (Murphy *et al*., 1990). The viral RNA encodes a single polyprotein precursor of 3,063 amino acids for a PVYN isolate, 3,061 amino acids for a PVYNTN isolate and 3,061 amino acids for a PVYO isolate (Tsedaley, 2015). The precursors are cleaved by three proteases (P1) encoded by virus into ten functional proteins (P1, HC-Pro, P3, 6K1, CI, 6K2, VPg, NIa-Pro, NIb and CP) and an additional peptide P3N-PIPO. PVY exists as complex of strains that can be differentiated based on their reaction towards a series of resistant genes in potato and their genome organization (Verma *et al*., 2015). A strain group that evoke hypersensitive response in potato which carries the *Ny* gene was named PVY O, whereas those that evoke hypersensitive response in potato that carries the *Nc* gene was named PVY C. Strains that did not evoke hypersensitive response towards *Ny* and *Nc* genes due to the presence of *Nz* gene was termed as PVY Z (Karasev *et al*., 2011). PVY N evokes hypersensitive response in presence of all the three resistant genes (Karasev and Gray, 2013). However, multiple recombinants have been discovered with part of PVY O and PVY N genome sequences. The most studied recombinants are PVY NTN (with three to four recombinant junctions), PVY N-Wi (with two recombinant junctions) and PVY N:O (with one recombinant junction) (Singh *et al*., 2008).

The original wild strain of PVY is PVY O, 'O' stands for ordinary. The PVY O strain causes mottling induces severe systemic mosaic, crinkle, leaf and stem necrosis in potato, and mild systemic mottling in tobacco (Rigotti and Gugerli, 2007). PVY N causes veinal necrosis on tobacco leaves but not on potato foliage (Singh *et al*., 2008). It causes mild molting in almost all potato cultivars (Rigotti and Gugerli, 2007). PVY C causes stipple streak. PVY E produces only mosaic and vein clearing in tobacco. Infection of PVY NTN in tobacco causes necrosis and some potato varieties has been seen to develop necrotic flecking and ring spot symptoms upon infection of PVYNTN. 'NTN' is employed for "n-tuber necrotic". The members of PVY are depicted in Table 2.

Table 2: Available strains of Potato virus Y *Potyvirus.*

Genotype or strain	N gene elicited in potato	Molecular structure	Year of first description of groups and variants of PVY
PVY C	Nc	Non-recombinant	1947
PVY O	Ny	Non-recombinant	1943
PVY N	None/unknown	Non-recombinant	1961
PVY E	None/unknown	R Parents: PVYNTN and PVY-NE11	1999
PVY Z/ PVYNTN	Nz (putative)	R Parents: PVYO and PVYN	1990
PVY N:O	None/unknown	R Parents: PVYO and PVYN	2002
PVY N-Wi	None/unknown	R Parents: PVYO and PVYN	1984
PVY NA-N	None/unknown	Non-recombinant	2003
PVY-NE11	None/unknown	R Parents: PVYN and unknown	2008

The PVYO, PVYN, and PVYC strains are found to be non-recombinant and they serve as parents for many recombinants, with PVYO and PVYN being the parents of majority of PVY isolates. Common recombinants of PVY detected in different geographical locations are PVYN:O, PVYN-Wi, PVYNTNa, PVYNTNb, PVY-NE11, PVYE , PVY-SYR-I, PVY-SYR-II and PVY-SYR-–III. Several rare recombinants found and reported once or twice are PVYN-Wi-156var, PVYN-Wi-261-4, PVY-SCRI-N, PVYFrN, PVY-Nicola, PVY-T13 and PVY-nnp. PVYNTNa belongs to the PVYZ strain, while PVYE shows a sophisticated recombinant structure with PVYNTNa and PVY-NE11 serving as parents. The positions of the main recombinant junctions (RJs) of different PVY strains are remarkably conserved. To track the evolution of different PVY strains, phylogenetic relationships between various virus recombinants are created. Phylogenetic studies of PVY recombinants is challenging due to limited number of whole genomes availability (Green *et al*., 2017).

PVY prevalence in north east of India. PVY is one of the most economically important viruses which cause huge yield loss throughout different potato growing areas in India. Compared to the other north-east Indian states, Assam has the highest area under potato cultivation (Mishra and Nath, 2016). PVY causes severe mosaic disease resulting in nearly 80% yield loss (Mishra and Nath, 2016). Despite the virulence of the PVY and large area affected by the virus, control measures for this aphid-transmitted virus of potato (Sigvald, 1984) are still in research and very limited information are available. The present documentation

on prevalence of the PVY and control measures will serve as a valuable resource for management of this virus in potato cultivation. Cultivation practices and chemical control of the virus are discussed later in this article. In short, restricting the virus from spreading and controlling the vector are two ways of managing the spread of PVY in potato fields (Mishra and Nath, 2016).

PVY detection. Symptoms of PVY vary depending on many factors, viz. PVY strain, and time of infection, host resistance and environmental conditions. Thus, these factors can be used to characterize and classify different PVY strains. ELISA is a commonly used PVY detection technique but it cannot detect infection in dormant leaves or in aphids, cannot distinguish some strains like PVYNTN and cannot detect these viruses in one step reaction. Molecular methods like PCR, PCR-ELISA, IC-PCR, RT-PCR, PC-PCR-ELISA, foluorogenic 5, nuclease RTPCR and isothermal NASBA amplification assay are consistently used for PVY detection. PCR technique helps to generate epidemiological data of PVY in field condition and to access the distribution of diseases in different parts of the world (Singh *et al*., 1998; Fakhrabad *et al*., 2012). The typical symptoms of aphid colonization, leaf curling and infection in fruits of capsicum species are presented in Fig. 2.

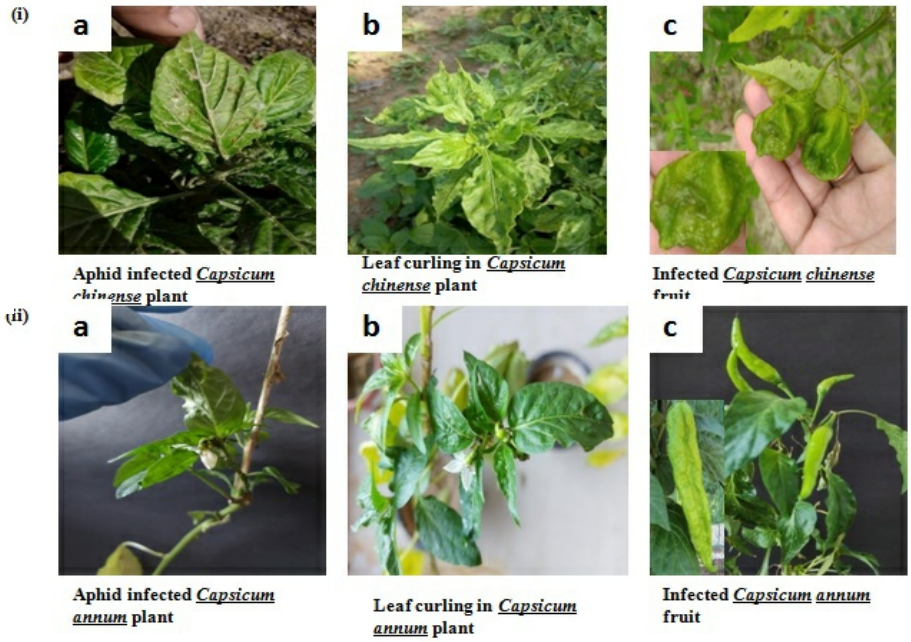

Fig. 2. PVY infection in (i) *Capsicum chinense* and (ii) *Capsicum annum*. (i) a: aphid colonization on *Capsicum chinense* leaves, (i) b: leaf curling, (i) c: infected *Capsicum chinense* fruit, (ii) a: aphid colonization on *Capsicum annum* leaves, (ii)b: leaf curling, (ii)c: infected *Capsicum annum* fruit.

Strategies for PVY disease control. Viruses are crucial and biologically intriguing from the agricultural point of view. In spite of the fact that viruses are simple genetic entities, the mechanisms by which viral disease symptoms arises and how plants resist these effects, are yet to be known to a large extent (Kang *et al*., 2005). Prior knowledge of the viral pathogen, its source of infection and mode of viral transmission are prerequisite to formulate its control measures (Stevens, 1983). One best way to prevent PVY infection is by avoiding introduction of virus into field. Once the virus is detected, immediate steps must be taken to control the spread of the virus. Spread of the virus can be controlled by different methods. Different strategies for managing PVY are discussed below.

Cultural control

Crop borders. Crop borders are one of the promising cultural methods for PVY control. Two different mechanisms are 'virus sink' effect and 'mechanical barrier' effect (Boiteau *et al*., 2009). Aphid fails to transmit PVY as it loses its virulence by the time it has probed the plants of the crop border, this effect is known as the 'virus sink' effect. 'Mechanical barrier' effect is where tall crops create a physical barrier around the field, hindering colonization of the aphids in potato crop (Boiteau *et al*., 2009).

Intercropping. Intercropping has advantages over the crop borders as this can be used in small fields without wasting any crop land. Intercropping acts as a mechanical barrier for aphids and acts as virus sink as the viruses tend to land on the associated crops. Intercropping limits the spread of PVY by reducing gaps in the crop canopy which is found to favour PVY spread (Davis *et al*. 2009).

Straw mulching. Straw mulching is one of the potent tools for reducing the spread of PVY. It minimizes the

occurrence of PVY by 30% (Kirchner *et al*., 2014). Straw mulching is effective against transmission of viruses by aphids in a number of crops, including vegetables (Summers *et al*., 2005), barley (Kendall, 1991), faba beans (Saucke, 2009) and organically grown potatoes (Saucke and Döring, 2004). Despite its efficacy, straw mulching is not extensively used in controlling PVY and other viruses in potato seed production because there are limited studies and reports on its response at the field scale. The studies so far have reported only field experiments at small scale where stronger virus inoculums were used for artificial disease inoculation.

Practicing a strict sanitation protocol. All planting and cutting equipments should be thoroughly disinfected before every use. PVY can be mechanically transmitted from healthy to infected plants via plant sap on tools and hands. Infected plants serve as a source of viral inoculums. Therefore, viral inoculums should be removed on a regular basis. Some common weed hosts of PVY like purslane, pigweed, nighshades and lambsquarters should be destroyed during the crop growing season to avoid viral infection (Kreitinger, 2021).

Organic control. Mineral oil treatment

Spaying of mineral oil on potato foliage is one way of controlling PVY to reduce transmission of PVY (Döring *et al*., 2007; Boiteau *et al*., 2009). Mineral oil lowers the acquisition and retention of PVY but contrasting results have also been reported (Hansen and Nielsen, 2021). Though the mechanism is not clear, it is assumed that mineral oil may affect virus particles with aphid stylet interactions or the behavior of aphids (Ameline *et al*., 2010). Pyrethroid, deltamethrin, pyrethroid and RU-15525 are other potent compounds that obstruct viral infection of healthy crops against beet mild yellowing virus (BMYV), potato virus Y (PVY) and sugar beet yellows virus (BYV) by *Myzus persicae* (Rice *et al*., 1983). Foliar spray of compost tea in potato is one of the best organic approaches to prevent potato late blight (Islam *et al*., 2013). The suitability of application of compost tea needs to be explored against PVY infection.

Anti-feedant compounds. Different types of aphids, namely green peach aphid, potato aphid and buckthorn aphid, colonizes and reproduces in plants and are efficient PVY vectors. Application of anti-feedant compounds such as 'Fulfill' and 'Beleaf' can control the spread of PVY by colonizing aphids.

RNA viruses exhibit a higher degree of genetic variability because of recombination, mutation, migration, genetic drift and natural selection. These viruses show one mutation per replication for each genome and it has the highest mutation rates among any group of organisms (Malpica *et al*., 2002). Recombination acts as a dominant force in shaping genetic makeup of an organism and their associated phenotypes (Posada *et al*., 2002), predominantly traced in the *Potyviridae* family and *Potyvirus* genus (Chare and Holmes, 2005). Migration of the genes i.e. gene flow from one population to another is one of the causes for evolution of RNA viruses (Moya *et al*., 2004). Natural selection events occur when a fit variant has the potential for their growth and survival in certain environment (Rubio *et al*., 2013). Genetic drift may occur in different phases of the virus life cycle such as transmission of virus between plants by vectors (Betancourt *et al*., 2008), movement of virus between plant cells (Li and Roossinck, 2004), and interaction between co-infecting viruses (Fraile *et al*., 1997). The evolution of new viruses has challenged the disease control in crops with huge economic yield loss every year. This comprehensive review on PVY genomic organization, function of potyviral proteins, the disease prevalence in north-east India, detection and control strategies of PVY will surely help the research community in designing experiments for crop improvement with PVY resistance, specifically in solanaceous crops. Andigena is a subspecies of potato (*Solanum tuberosum*) which is extensively grown in South America is mostly resistant to PVY (Dehdar *et al.,* 2016) and therefore can be used in intraspecific breeding programs for development of resistant potato lines against PVY.

CONCLUSION

Potyvirus causes huge amount of economic yield loss. *Potyvirus*es have a monopartite genome with an exception to genus Bymovirus which has a bipartite genome. Different proteins of the *Potyvirus* help in alleviating the viral infection. The viral RNA encodes a single polyprotein. PVY is a good example of RNA virus with high mutation rate and numerous recombinants. PVY exists as complex of strains that can be differentiated based on their reaction towards a series of resistant genes in potato and their genome organization. Extreme resistance and hyper-sensitive resistance are the two main types of resistance found in potato. Mutation, recombination, migration, natural selection and genetic drift are responsible for development of a vast pool of viral genomes that helps in adaptation of viral strains in new niches. Development of resistant cultivars is one of the economic and environment-friendly ways of controlling viral diseases. Aphid control is another best way in the management of PVY. This article provides a comprehensive understanding of PVY genetic structure, genetic variability and evolutionary changes and will help in developing management strategies against PVY infection and in establishing sustainable crop production globally and will aid in significant increase in crop yield and quality.

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Conflict of Interest. None.

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