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Plant Viruses and Human Health: An Assessment of Risks and Impacts

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ABSTRACT

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Received on: 05.01.2021 **Revised on:** 21.06.2021 **Published on:** 28.06.2021 Plant viruses are ubiquitous in nature, and humans and animals are often exposed to them in different ways. Some plant viruses show high persistence, but these viruses are currently thought to be immuno-restrictive, and plant and animal viruses have distinct limitations in terms of host specificity and disease. Therefore, plant viruses are not considered pathogens to vertebrates, including humans. However, many studies have shown the ability of plant viruses to circulate and replicate in insect populations, raising an important question: Can plant viruses cross kingdom boundaries? Do they harm human health? Although structural and functional similarities between some plant and animal viruses are well-documented, cross-border infections remain a problem. The current literature suggests the need for comprehensive, large-scale studies of interactions between plant and animal viruses, especially humans, to assess their potential for disease. The aim of this review is to examine the current understanding of the biology of plant viruses and their impact on human and animal health, and to highlight areas for further research.

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INTRODUCTION

Viruses that influence plants are plant viruses, which make a serious danger to agricultural and horticultural produce (Soosaar *et al.*, 2005). These are ultramicroscopic, acellular, mesobiotic entities that don't have the sub-atomic hardware to replicate without a host. The majority of plant viruses are made up of protein coats and nucleic acid. Tobacco mosaic virus (TMV) was the first reported virus. Ivanovski (1892) discovered that even after passing through Chamberland filter candles, the infectious qualities of mosaic disease-affected leaf sap remain intact. Beijerinck (1898) uncovered that the causative agent of Tobacco mosaic had the option to relocate and considered the separated irresistible substance a "Virus" and gave the expression "*Contagium vivum fluidum*". From that point forward, different plant viruses were found and classified into 3 orders, 22 families, 108 genera and 1019 species (WHO, 2015). Most plant viruses are transmitted through vectors. Plant infection by viruses has a few advantages too. They are utilized for designing viral vectors and as the wellspring of biomaterials and nanotechnology gadgets. The principal recorded use of plant viruses is to upgrade the magnificence of decorative plants. Plant viruses are likewise utilized for cross-protection, weed and



pest biocontrol, utilitarian genomic studies, genome altering, crop quality treatment blooming enlistment and so on. Aside from these benefits, these plant viruses are no less destructive to their hosts. In greater part of cases, viruses are harmful and cause serious diseases in crops which hamper the harvest quality and yield. The symptoms created by plant viruses are mosaic, chlorosis, putrefaction, leaf twist, leaf roll, vein clearing, mottle, crinkling, enation, rosetting, hindering, phyllody, puckering and so on.

Animal viruses, on the other hand, are typically referred to as viruses that infect animals. Such infections are caused by intracellular agents that totally depend on the host cell for propagation and afterwards pass on the host cell to contaminate other host cells. There are a variety of viruses that can infect various organs of the body, sometimes causing no symptoms at all and other times causing extremely dangerous symptoms. Other vertebrate viruses can infect humans, causing diseases like rabies, yellow fever and others (zoonotic infections). In this article, close relatedness between some plant virus and animal virus is examined momentarily.

The crossing point of plant infections and human well-being is an emerging field that features both the likely advantages and dangers related to these viruses. While generally seen as dangerous to farming, ongoing examination shows that plant viruses might have applications in medication, especially in immunization advancement and restorative protein creation.

Security and Biocompatibility

Plant viruses, for example, virions and virus-like particles (VLPs), are viewed as safe for people and animals, showing no replication in vertebrates. They are biodegradable and can be dispensed with from organic entities, making them appropriate for biotechnological applications (Nikitin *et al.*, 2016).

Environmental Effect

Plant viruses assume a pivotal part in biological system security, possibly forestalling excess of homogeneous plant populaces and advancing host adaptation. Their associations with hosts can prompt mutualistic connections, albeit the degree of these collaborations stays under investigation (Lefeuvre *et al.*, 2019).

Applications in Medicine

The potential of infectious plant virus clones in molecular breeding and as pharmaceutical production vectors is being investigated (Brewer *et al.*, 2018). Customary plant-based prescriptions are additionally being researched for their antiviral properties, especially with regard to COVID-19 (Prajapati *et al.*, 2020).

In spite of these promising applications, worries about the natural dangers of hereditarily changed plant viruses continue, requiring cautious biosafety assessments. In this context, this article explores the critical question: Are plant viruses harmful to human beings?

UNIFORMITY BETWEEN PLANT AND ANIMAL VIRUSES

Many similitudes exist between some animal and plant viruses. Quality succession correlations and protein examinations give more proof that transformative connections exist among animal and plant viruses, independent of the size of the molecule (isometric or bar molded) or whether they have a monopartite or multipartite genome. Tymoviridae, Bunyaviridae, Rhabdoviridae, Reoviridae families contain both plant and vertebrate viruses including human. Three genera (Fijivirus, Oryzavirus and Thytoreovirus) of the family Reoviridae infect the two plants and bugs (Keller and Jonard, 2004). Rotavirus of the family Reoviridae causes gastroenteritis in people (Choi et al., 2013). Essentially, Rabies infection, caused by viruses from the family Rhabdoviridae and infections such as Hantaan and Toscana, which belong to the family Bunyaviridae, are pathogenic to humans (Tordo et al., 2010; Kallio-Kokko et al., 2006).

A significant number of plant viruses that rely upon insect vectors for their duplication and sent by circulative transmission are gathered in families which likewise contain animal viruses. The structural and genetic similarities between the



cowpea mosaic virus (CPMV) of the Secoviridae family, the Coxsackie virus, the polioviruses and the Theiler's murine encephalomyelitis virus of the animal picornaviruses lend credence to the idea that these animal and plant viruses share a common ancestor (Lin et al., 2000; Koudelka et al., 2009). Some plant virus genera contrast from animalinfecting genera because of the presence of an additional quality that code for a development protein (Deom et al., 1992). For instance, under the family Rhabdoviridae, genera infectious to animals, Vesiculovirus, for example, Lyssavirus, Novirhabdovirus and Ephemerovirus vary from plant infecting genera like Nucleorhabdovirus and Cytorhabdovirus (Benitez-Alfonso et al., 2010). In view of RNA polymerases phylogeny, Hepatitis E virus, a human virus was gathered with a plant virus, *i.e.*, beet necrotic yellow vein virus (Koonin, 1991). Endogenous viral elements (EVE) near plant viruses having a place to the family Virgaviridae were seen in the genome of Aedes aegypti, Drosophila rhopaloa and Bombyx terrestris. EVE found in Aedes aegypti was the same as the tobamovirus genome. However, this Aedes aegypti isn't a bug vector for tobamovirus (Cui and Holmes, 2012). During the nectar collection process, there was a possibility that the insect would interact with the virus-infected plant. RdRp of +ve ssRNA and dsRNA infections contaminating the two - the insect and plant comprise of amino corrosive succession and three-dimensional construction which recommend the normal base of these viruses (Ng et al., 2008). Gibbs and Weiller (1999) detailed that few similitudes exist between the ssDNA genomes of circoviruses that infect vertebrates and the nanoviruses that contaminate plants. They likewise discovered some proof that a phytovirus switched hosts and contaminates a vertebrate and afterwards rejoins with a vertebrate-infecting virus. The purpose of this host switch is the openness of a vertebrate to the sap of a plant that is contaminated (Gibbs and Weiller, 1999).

The investigation of viruses uncovers interesting likenesses and contrasts among plant and animal viruses, testing conventional orders. Late exploration demonstrates that the two gatherings share normal developmental beginnings and hereditary highlights, recommending a more bound together comprehension of virology.

Normal Parentage and Hereditary Similitudes

Many plant and animal viruses have homologous qualities fundamental for viral replication, demonstrating a common transformative history (Dolja and Koonin, 2011). Quality arrangement correlations show huge developmental connections among plant and animal RNA viruses, no matter what their underlying differences are (Goldbach, 1987).

Systems of Transmission

Both plant and animal viruses can spread straightforwardly between cells; however the components for this movement contrast. Plant viruses use plasmodesmata because of inflexible cell walls, while animal viruses might frame virological neurotransmitters between cells (Ritzenthaler, 2011).

Transformative Elements

The development of these viruses can be credited to three situations: normal family, level exchange through vectors and equal advancement from related hereditary elements (Dolja and Koonin, 2011). The dynamic nature of viral evolution across various hosts is highlighted by this complexity.

Despite these resemblances, the distinct interactions between viruses and their respective hosts cause distinct evolutionary pressures, which in turn produce diverse behaviours and adaptations. This continuous examination keeps on reshaping how we might interpret viral scientific categorization and development.

DISSIMILARITY BETWEEN PLANT VIRUSES AND ANIMAL VIRUSES

There are numerous distinctions among plant and animal viruses which infer that a boundary is there which isolates these viruses either to animals or plants. The morphologies and genome designs of some plant and animal viruses show some uniqueness (Hogenhout *et al.*, 2008). The instruments utilized by plant and animal viruses for entry into the cell and for engendering from one cell





to another vary (Fereres and Raccah, 2009). For entry into the plant, plant viruses need to cross the inflexible cell wall. They enter through wounds created by insect-pests, through contaminated seeds and furthermore mechanically during a few horticultural practices. According to Lazarowitz (2007), some phytoviruses can be transmitted directly into the phloem or through aphids, whiteflies, mites, fungi and nematodes. Then, plasmodesmata aid in the spread of plant viruses from one cell to the next, requiring a movement protein that is encoded in the plant virus genome (Taliansky et al., 2008). Interestingly, different connections happen between cell receptors and animal virus before entry into the animal cell by endocytosis and combination (Klempner and Shapiro, 2004; Yamauchi and Helenius, 2013).

Rather than this multitude of contrasts plant viruses rely upon insect vectors for their transmission. A larger part of these bug vectors belongs to the order Hemiptera that incorporates thrips, planthoppers, whiteflies, aphids and leafhoppers (Hogenhout et al., 2008). These insect vectors transmit viruses and help virus families having a wide host range. Because of the presence of some particular protein, these phytoviruses likewise can contaminate invertebrate vectors. The vector cell permissivity relies upon the presence or absence of glycosylated protein G for Potato yellow dwarf virus and for Rice dwarf virus a P2 protein freak stops the virus contamination in the bug (Gaedigk et al., 1986; Tomaru et al., 1997). A plant virus by and large gets transmitted through bugs by two strategies: circulative transmission and non-circulative transmission. Plant viruses can repeat in their vectors which make them kind of infectious bugs. During this transmission cycle, some bugs show variation in their way of behaving which recommends that plant viruses might be irresistible for the bugs. For instance, the male taking care of conduct of Frankliniella occidentalis has been modified in light of Tomato spotted wilt virus (Stafford et al., 2011). Moreover, when Bemisia tabaci was infected by tomato yellow leaf curl virus, it brings about a decrease in bug's life span and fecundity (Rubinstein and Czosnek, 1997). This multitude of discoveries makes whether or not

some plant viruses further cross the realm line for section and replication in vertebrates. In the mark of reality, assuming the phylogenetic distance is considered among plants and bugs or warm-blooded animals; it shows up extremely challenging for viruses to cross the realm line first from plants to bugs than from plants to any well-evolved animals (Koonin, 2010; Roger and Simpson, 2009).

The dissimilarities among plant and animal viruses are established in their primary, useful and developmental attributes. Despite having some genetic elements in common, the infection and replication processes of these two types of viruses are vastly distinct.

Underlying Contrasts

Plant viruses frequently have unbending designs that work with development through plant cell walls by means of plasmodesmata, though animal viruses use more adaptable components, like virological neural connections, to spread between host cells (Ritzenthaler, 2011). The capsid proteins of plant and animal viruses show checked contrasts, mirroring their unmistakable transformative ways and host interactions (Dolja and Koonin, 2011).

Replication Systems

Animal DNA viruses ordinarily exploit cell apparatus for record and replication, frequently undermining cell pathways, while plant viruses have advanced extraordinary methodologies that line up with their host's cell architecture (Gutierrez and Martínez-Salas, 2001). The two assemblies have single-stranded RNA and DNA viruses, yet their transformative rates and populace elements can fluctuate fundamentally, with some plant viruses showing archaic origins (Gibbs *et al.*, 2010).

Conversely, the similarities in hereditary parts recommend a common transformative history, demonstrating that both plant and animal viruses might have developed from normal predecessors or through even trait transfer (Dolja and Koonin, 2011). This intricacy features the many-sided connection between viruses and their hosts across various natural realms.





EXPOSURE OF HUMANS AND ANIMALS TO PLANT VIRUSES

Humans and animals are exposed to plant viruses through the food varieties that are infected with plant viruses. Tobacco Mosaic virus infects around 150 plants including tomato, pepper and cucumber. A few plant viruses are likewise present in items which are delivered from plant sources. Colson et al. (2010) found 57% of the 28 pepper-based foods containing PMMoV RNA that could still infect health plants. Around 107 viral duplicates ml⁻¹ were additionally recognized in Tabasco sauce. It is reasonable to assume that phytoviruses may be present in our faeces because we consume these old times individuals foods. Since utilize conventional strategies for managing diseases. Through the ingestion of natural medication people can likewise be exposed to phytoviruses (ICTV, 2015). TMV is available in cigarettes as it is impervious to manufacturing processes (Smith, 1957) let alone its presence in raw chewing tobacco. Mean TMV RNA titer was viewed as 9.5log₁₀ RNA duplicates per cigarette and 3.8log₁₀ RNA duplicates ml⁻¹ in the spit of smokers (Balique et al., 2012). Smoking is extremely damaging and is another risk factor for exposure to phytoviruses (Bothwell, 1960; Chyle et al., 1971). These phytoviruses are likewise found in the climate including water, mists, hazes and soil (Rosario et al., 2009; Yolken et al., 2014). Tomato mosaic virus (ToMV) of family Virgaviridae was recognized in depleting the water of woods strands of New York (Jacobi and Castello, 1991) and in 140,000 year-old frigid ice in drill destinations of Greenland (Castello et al., 1999). In Slovenia, this ToMV was also found in irrigation systems. Melon necrotic spot virus has been found in water system set-ups in Spain (Gosalvez et al., 2003). Tomato bushy stunt virus and Cucumber green mottle mosaic virus were recognized from Thames and Yamuna separately and these viruses were pathogenic to healthy plants (Tomlinson and Faithfull, 1984; Vani and Varma, 1993). This indicates that these viruses may persist in the environment, thereby increasing their capacity for transfer and dispersal.

Exposure to plant viruses can fundamentally influence both human and animal well-being, essentially through zoonotic transmission and food pollution. Understanding these elements is pivotal for general well-being and agrarian practices.

Zoonotic Transmission from Animals

Numerous zoonotic infections start from animals, with warm-blooded animals like bats and trained species being key sources. Spillover risks increase as a result of increased human-animal interactions brought on by habitat loss and wildlife exploitation (Johnson *et al.*, 2020). Hepatitis E virus (HEV) represents this, as it may very well be communicated from pig to people, featuring the potential for getting humans diseased through consumption of contaminated meat (Goens and Perdue, 2004).

Plant Virus Effect on Herbivores

Phytoviruses, like the White clover mosaic viruses, can adjust plant qualities, influencing herbivore conduct. Infected plants might discharge different unpredictable mixtures, making them less appealing to herbivores, which could by implication impact biological system dynamics (van Mölken *et al.*, 2012).

The interaction between plant viruses and herbivores suggests a complex ecological balance that requires more research, despite the fact that zoonotic diseases typically receive the majority of the attention. Understanding these cooperations can illuminate methodologies to alleviate risks related to both human and animal exposure to viruses.

EVIDENCE OF PERSISTENCE OF PLANT VIRUSES IN MAMMALS INCLUDING HUMANS

Phytoviruses have been found in mammals, including humans, in a number of studies. Three days after feeding the cow infected cucumbers, Cucumber green mottle mosaic virus was discovered in the cow's dung in 1988 (van Dorst, 1988). Individuals from the family Luteoviridae, Secoviridae, Tymoviridae and Partitiviridae were tracked down in *Bat guano*. Likewise, some viruses





of the family Secoviridae, Geminiviridae, Partitiviridae, Luteoviridae, Tymoviridae, Nanoviridae and Tombusviridae were found in mouse, vole and rodent stools (Phan et al., 2011). By qRT-PCR, Pepper mild mottle virus was identified in 7 out of 15 waste examples from Chicken, 1 out of 10 from Geese and 1 out of 6 from cows, at titers up to 3.1log₁₀ duplicates mg⁻¹ (Hamza *et al.*, 2011). It was accounted that cows, jackasses and grass rodents lead to Rice yellow mottle virus (Sarra and Peters, 2003) and that sheep communicate the underground clover mottle virus (MCkirdy et al., 1998). Additionally, numerous viral pathogens have been isolated from gastroenteritis patients' faeces. These are Citrus tristeza virus, Tobacco mosaic virus, Tomato ragged stunt virus, Carnation mottle virus, Oat chlorotic trick virus, Melon necrotic spot virus, Maize chlorotic mottle virus, Grapevine speck virus, Eggplant mosaic virus, Pepper mild mosaic virus, Panicum mosaic virus and so forth (Zhang et al., 2006; Nakamura et al., 2009).

The proof of plant virus' persistence in well-evolved animals, including humans, is an emerging area of exploration. Certain plant viruses have mechanisms that allow them to survive in mammals, despite being traditionally associated with plants. These mechanisms may have an impact on health outcomes.

Transmission Instruments

Some plant viruses, for example, those in the Furoviruses and Bymoviruses groups, can be communicated by insect vectors and may make due in their bodies for expanded periods (Watson and Roberts, 1939). This proposes a potential for these viruses to enter mammalian frameworks through well-established orders of things or natural exposure. Because they facilitate the movement of viruses into host cells, which may include mammalian cells under certain conditions, viral coat proteins play a crucial role in transmission (Campbell, 1996).

Zoonotic Potential

Ongoing examinations demonstrate that specific microsporidian diseases, such as *Encephalitozoon intestinalis*, have been distinguished in warm-

blooded animals, suggesting zoonotic transmission pathways that could include plant viruses. Humans have been exposed to a variety of viral agents, some of which may have originated from plant sources, influencing immune responses and disease susceptibility, according to the evolutionary history of viruses (van Blerkom, 2003).

Wellbeing Suggestions

The circuitous proof connecting viral contaminations to diseases, for example, different sclerosis recommends that plant viruses could assume a part in comparable constant circumstances through relentless diseases or resistant intervened damage.

While the immediate proof of plant viruses in warmblooded animals stays restricted, the potential for transmission and well-being suggestions warrants further examination.

PRESENCE OF PHYTOVIRUSES IN HUMAN SAMPLES

A few bits of proof show that plant viruses are available in human examples. Tomato bushy stunt virus (TBSV) was refined and consumed by human workers in 1982. Symptoms of the infection were induced when their faeces were inoculated on Quinoa leaves (Tomlinson et al., 1982). During the 1950's-1970's, few investigations detailed that TMV is available in human lungs and uncovered that it plays a part in cellular breakdown in the lungs (Bothwell, 1960). TMV was retrieved from 15 out of 35 sputum examples and 1/4 thoracentesis liquids from smokers having respiratory diseases (LeClair, 1967) and furthermore in the lungs of smokers who handled or exposed themselves to tobacco leaves (Falk, 2011). Recently, tobacco plant DNA was found in the Bronchoalveolar Lavage of incubatorbound patients (Bousbia et al., 2010). Constant PCR was utilized and PMMoV was distinguished in waste examples of 22 (7.2%) out of 304 grown-ups (Colson et al., 2010). A connection was likewise seen between the presence of PMMoV in stools and a few clinical signs. As a matter of fact, in 39% of PMMoV-positive patients and in 13% of PMMoVnegative patients fever was recorded and in 39% of PMMoV-positive patients and in 7% of PMMoV-



negative patient's stomach torment was noticed. In any case, no particular relationship was uncovered between the presence of PMMoV and clinical side effects. These side effects might be because of the eating of an abundance of pepper or food items containing pepper. TMV RNA was additionally distinguished in 45% of smokers' spit tests while all non-smokers' salivation tests were found to be negative and cigarettes from different brands were tracked down TMV positive (Balique *et al.*, 2012).

The environmental routes by which these viruses can spread make the presence of phytoviruses in human samples a complicated matter. While direct proof of phytoviruses contaminating people is limited, their presence in water sources raises worries about possible circuitous openness.

Natural Presence of Phytoviruses

- Phytoviruses are many times tracked down in ecological waters, especially in streams and lakes, where they can endure because of their strength and high focuses in infected plants (Koenig, 1986).
- These viruses can be sent through debased water, particularly in regions lacking flying vectors, which might incorporate human openness through ingestion or contact with polluted water (Koenig, 1986).
- Studies have demonstrated that human enteric viruses, such as noroviruses, are prevalent in river and treated wastewater, suggesting that waterborne transmission routes could also facilitate the spread of phytoviruses (Maunula *et al.*, 2012).
- The location of viral genomes in water does not necessarily correspond to potential risk, accentuating the requirement for a cautious understanding of viral presence in human-related contexts (Gassilloud *et al.*, 2003).

While the immediate effect of phytoviruses on human well-being stays questionable, their ecological strength and potential for waterborne transmission warrant further examination concerning their epidemiological importance.

CONCLUSION

The cumulative evidence suggesting the potential of plant viruses as human pathogens warrants targeted research. Currently, there is no definitive information indicating that plant viruses are fatal to humans or animals. For a plant virus to be pathogenic to humans, it must be shown that the virus is capable of entering human cells, replicating in the cell and satisfying Koch's pathogenicity hypothesis.

Humans have been dealing with plant diseases for thousands of years, and our reliance on plants reinforces the widespread belief that these viruses are safe for humans. However, some plant viruses may still play a role in human disease. Although there is currently no clear evidence to classify plant viruses as human pathogens, their indirect negative effects on human health cannot be ruled out.

Overall, it is important to advance research in this area. Comprehensive studies are needed to provide clear evidence of the disease of plant viruses in humans and to better understand their general impact on public health.

Conflict of Interest

The authors declare no conflict of interest.

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