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Potential of Mycovirus in the Biological Control of Fungal Plant Pathogens: A Review

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ABSTRACT

Fungal pathogenic populations such as *Sclerotinia*, *Rhizoctonia* and *Fusarium* are ubiquitous and have broad range of host enabling them to cause a severe infection resulting in huge yield losses. Albeit the various tactics such as cultural, mechanical implemented to counteract the havoc, it still creates a formidable challenge to the researchers to keep the pathogenic population below threshold. From Eco-friendly sustenance perspective, Biological control can play a vital role in combination along with the other efficient tactics. In field condition various strains are available having two characters namely virulent and hypovirulent, the latter may exhibit hypovirulent nature genetically or due to the invasion of mycoviruses becomes hypovirulent. In both the cases are of interest to the researchers in studying the biological control exhibited by the mycoviruses. The biocontrol agents include Mycoviruses, which plays a significant role in infecting the virulent fungal pathogen by reducing their virulence giving to a phenomenon known as Hypovirulence. Their genome consist of mostly dsRNA and others include +ssRNA, -ssRNA and dsDNA. These studies in fungal and viral interaction can lead to the development of novel biological control strategies and help us to explore upto the molecular level.

Key words: Biological control, Hypovirulence, Mycoviruses, Virulent.

The first report of mycovirus was identified in that of dieback disease of *Agaricus bisporus*, a basidiomycete in 1948 in a mushroom house owned by the La France brothers of Pennsylvania (Sinden and Hauser, 1950). Mycoviruses are those viruses that infect fungi and multiply within it. They are also commonly known by the name fungal virus, mycophage and virus like particles (VLPs). Most mycoviruses have double-stranded RNA (dsRNA) as their genomes (Ghabrial, 1994) with exception in *Sclerotinia sclerotiorum* where a DNA virus was identified that may host both RNA viruses and DNA viruses (Liu *et al*., 2010; Liu *et al*., 2009; Yu *et al*., 2011). According to “ancient coevolution hypothesis” of mycovirus origin, mycovirus and fungi shares an ancient relationship reflecting a long-term coevolution (Botella *et al*., 2012; Roossinck, 2015a, 2015b). On contrary, the “plant virus hypothesis” suggests thatthese mycoviruses were assumed plant viruses that invaded from the host to the fungal pathogens indicating the phenomenon of viral transmission on the co-existence of fungus and the plants (Nibert *et al*., 2014). A peculiar difference occurring between the mycoviruses to other viruses is the absence of movement proteins genes for cell to cell in the mycoviruses (Sinha and Tarafdar, 2007; Kotakadi *et al*., 2012). Recent studies have uncovered the mechanism driving within its surrounding behind their significant suppression of the fungal pathogens. This became a limelight against the researcher’s objectives to emphasize their potential that can aid in reducing the devastating fungal diseases. Due to their potential as a biocontrol component against the ubiquitous fungal pathogens, many researchers were attracted towards their interaction and the hypovirulence associated phenomenon caused by the mycoviruses. Moreover, by this phenomenon our understanding towards diversity of mycoviruses, evolution and establishment of host-mycovirus system (i.e., *Cryphonectria parasitica,* hypovirus, *Helminthosporium victoriae*, *Sclerotinia sclerotiorum*-mycovirus, *Rosellinia necatrix*-mycovirus and *Fusarium graminearum*- mycovirus) will be enhanced and beneficial for studying virus-host interactions at the molecular level (Xie and Jiang, 2014; Wang *et al.*, 2015). Here in this review we highlight the various mycovirus identified in different fungal pathogens and their potential to reduce the virulent population.

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Taxonomy

Mycoviruses are recorded in almost all the groups of filamentous fungi including yeasts and oomycetes (Pearson *et al.,* 2009). The mycoviruses with RNA genomes are classified into 15 families, 22 Genera (ICTV, 2014) (Fig 1), 7 families (Chrysoviridae, Endornaviridae, Partitiviridae, Reoviridae, Totiviridae, Quadriviridae and Megabirnaviridae) containing double-stranded RNA (dsRNA) genomes encapsulated within capsid proteins and form rigid virus particles, 2 families (Metaviridae and Pseudoviridae) belonging to ss(+) RNA-RT, 1 family (Mycomononegaviridae) containing ss(-)RNA and 5 families (Alphaflexiviridae, Barnaviridae, Gammaflexiviridae, Hypoviridae and

Narnaviridae) contain single-stranded RNA (ss(+)RNA) as their genomes, of which Alphaflexiviridae and Gamma flexiviridae form filamentous particles and the rest four families do not form typical virus particles (Lin *et al*., 2012). The base sequence of ss(+) RNA are similar with that of mRNA and the RNA functions as a template for synthesis of protein (RNA-dependent RNA polymerase) while genome of ss(-) RNA mycoviruses are transcribed to positive sense by RNA replicase. The size of mycovirus varies species to species, the virus Chalara elegans RNA virus 1 (CeRV1) which infect *Thielaviopsis basicola* causal organism of black root rot carrot, gerbera etc can vary upto 5.31 kbp in length and has three ORFs (Park *et al*., 2005) whereas Cryphonectria hypovirus 1 (CHV1) measures upto 12.70 kbp in length having two ORFs (Allemann *et al*., 1999; Shapira *et al*., 1991).

Crossing the cellular membrane is the key step for the virus to infect the host. However, Mycoviruses are known to lack extracellular transmission, due to their larger size than the pores and the rigid cell wall of fungi hinders the entry of virus inside the host cell. Thereby, initiation of fungal infections by extracellular transmission makes it impossible to the mycovirus. Thus, extracellular transmission can be by far only be achieved in advanced protocols using protoplasts (Yphantis *et al.,* 1967). Transmission of mycoviruses occurs by intracellular movement *via* protoplasmic fusion (anastomosis) and sporulation (vertically). Horizontal transmission (anastomosis) is accomplished through hyphal fusion and cell division. Mycoviruses are mainly spread by vertical intracellular transmission through asexual or sexual spore formation, with asexual sporulation being the most efficient means of transmission (Coenen *et al*., 1997; Diepeningen *et al*., 2006 and Liu *et al.,* 2003). The interaction of the virus with fungus can be categorized as latent infection, Cryptic infection and beneficial interaction: Increased thermal tolerance and increased competitive ability by producing a killer protein (*Ustilago maydis*) and Hypovirulence and different effect can be initiated by the same mycovirus to the host which varies with ecological condition (Hyder *et al.,* 2013). Reproducible transfection protocols with purified rigid virus particles have been reported for some mycoviruses in the families' Reoviridae (Hillman *et al*., 2004), Megabirnaviridae (Chiba *et al.,* 2009), Totiviridae (Chiba *et al.,* 2013) and Partitiviridae (Sasaki *et al.,* 2007). The advanced technique has helped to clarify the relationship of virus–host interactions and virocontrol (Ghabrial and Suzuki, 2009).In biological control perspective, hypovirulence initiates the conversion of the virulent pathogen population to hypovirulent population through anastomosis. The process of anastomosis is controlled genetically in the presence of vegetative incompatibility genes. These *vic* genes restricts causes a hindrance for the transmission of hypovirulent associated dsRNA which eventually limits their effectiveness in biological control of fungal diseases. The presence of different Mating Types (MAT) in the population of fungus also complicates the process of transmission (Coppin *et al*., 1997; Milgroom and Hillman, 2011). When two incompatible strains come in contact, death of the cells follows, this phenomenon is referred to as vegetative incompatibility. It is controlled by several genes which limits the process of hyphal anastomosis. Vegetative compatibility is controlled by one to several nuclear genes that limit completion of hyphal anastomosis. The cells involved in anastomosis results to death when the colonies are not compatible and thus prevent the transfer of nuclei and organelles between incompatible strains. However, the virus may be transferred to the adjacent undamaged cells if the incompatibility reaction is slow. Vertical transmission enables spread of the virus within its host across longer distances and occurs through spores (conidia) produced by infected strains. The lower rate of spore production by the hypovirus-infected strains causes a negative impact. Transmission rate through conidial spores differs between the hypovirus subtype. Such as CHV1–721, CHV-1 Euro7 (CHV1-I) and CHV1- EP713 (CHV1-F1), the CHV1 hypovirus found in Europe is divided into five subtypes: CHV1-D, CHV1-E, CHV1-F1, CHV1-F2 and CHV1-I (Allemann *et al*. 1999). The percentage of the infection rate of mycovirus also varies host to host. Ihrmark *et al*., 2002 reported only 3% of conidia infected in *Hetrobasidion annosum* on contrary to 100% infection by *Cryphonectria parasitica* (Ding *et al*., 2007).

Recent reports have revealed another means of transmission i.e. extracellular transmission Yua *et al.* (2013) in an experiment reported a DNA mycovirus, Sclerotinia sclerotiorum hypovirulence-associated DNA virus 1 (SsHADV-1), which was found to be infectious to its host *Sclerotinia sclerotiorum*when applied extracellularly. The hyphae of virus free *S. sclerotiorum* are reported to be infected when infected host harbouring virus are isolated and grown on PDA (Potato Dextrose Agar) or sprayed on leaves of *Arabidopsis thaliana* and *Brassica napus*. It was also concluded that SsHADV-1 cancolonize and infect*Sclerotinia minor* and *Sclerotinia nivalis*but was ineffective for other colonies, such as *Botrytis cinerea*, belonging to the same family with *S. sclerotiorum*. The role of mycovirus in the host are well established by some key determinants and to identify these determinants, researchers employed wide genome approaches in certain fungal pathogen and reported that the expression of fungal genes differs with virus free and virus infected isolates and also among different viral groups.

Biological significance of mycovirus

Cryphonectria parasitica

The first report of chestnut blight disease in North America appeared in 1905 and located within the New York Zoological Gardens (Merkel, 1905). The disease is characterized by the damage of the tissues responsible for the growth of stem and roots and appearance of cankers eventually accompanied by girdling of the stem (Milgroom and Cortesi, 2004). In the early 1950s, it was found that chestnut trees

Table 1: General taxonomy of mycoviruses according to ICTV classification criteria, Virus Taxonomy 2014 Release.

Family	Genus	Genome
Alphaflexiviridae	Botrexvirus, Sclerodarnavirus	ss(+) RNA
Gammaflexiviridae	Mycoflexivirus	
Barnaviridae	Barnavirus	
Hypoviridae	Hypovirus	
Narnaviridae	Mitovirus, Narnavirus	
Chrysoviridae	Chrysovirus	dsRNA
Endornaviridae	Endornavirus	
Megabirnaviridae	Megabirnavirus	
Partitiviridae	Alpha; Beta; Gammapartitivirus; (unassigned)	
Quadriviridae	Quadrivirus	
Reoviridae	Mycoreovirus	
Totiviridae	Totivirus; Victorivirus	ss(+) RNA-RT*
Metaviridae	Metavirus	
Pseudoviridae	Hemivirus; Pseudovirus	
Unassigned	Rhizidiovirus	ssDNA
Mycomononegaviridae**	Unassigned	ss(-) RNA

Transmission and interaction of mycovirus with their host.

*Classification under consideration; **Family proposed by Ghabrial *et al.,* (2015).

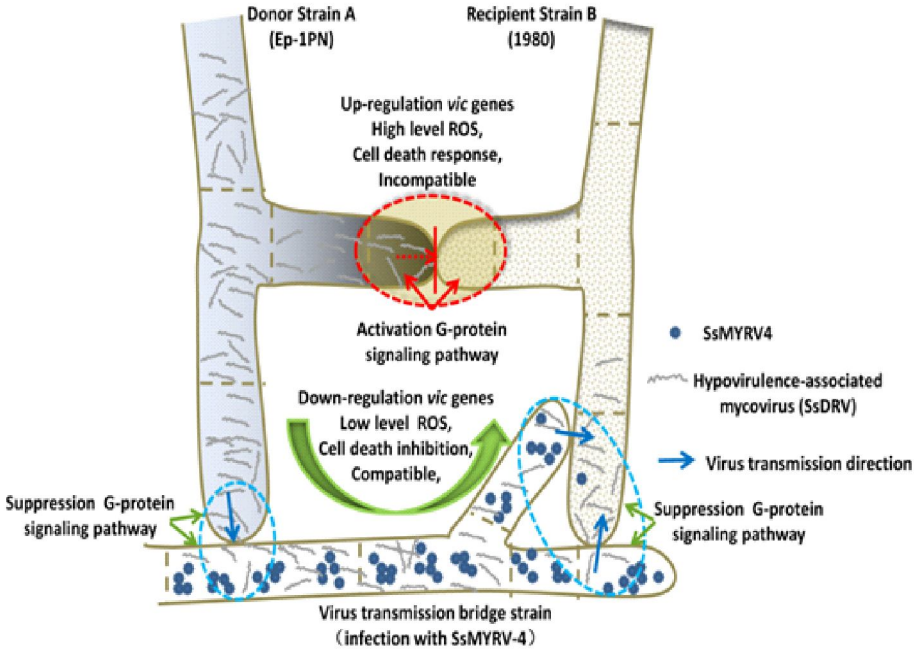


Fig 1: SsMYRV4-mediated enhancement of horizontal transmission between different VCGs. Effectively prevents and controls Sclerotinia diseases (Wu *et al.*, 2017).

infected by *C. parasitica* were not killed and the lesions on the stems healed with no outside influence. This report eventually led to the discovery and development of biological control of chestnut blight through hypovirulent strains of mycoviruses.The successful biological control of chestnut blight through hypovirulence has led to explore other mycoviruses to manage other severe fungal diseases and for successful management depends on the natural spread of viruses and the triple interaction (hypovirus, fungal pathogen and host) and environmental factors determined the success or failure. The phenomenon of hypovirulence was first observed in Italy in the 1950s in heavily infected chestnut stands that showed signs of recovery from the disease (Heiniger and Rigling, 1994). The biocontrol potential of hypovirulence was subsequently discovered by Grente (1965). Hypovirulent strains of phytopathogenic fungi and their associated mycoviruses are model systems to examine the mechanisms of fungal pathogenesis and might serve as or lead to biocontrol. The chemical management for this pathogen was not achievable by any molecules

combining with the cultural techniques. The most effective and promising way to counteract their presence is employing biological control namely hypovirulence in which virulent population of the pathogen are colonized with hypovirulent colonies. Henceforth, many researchers studied *in vitro* (Çeliker and Onoğur, 1998, 2009; Coşkun *et al*., 1999; Açıkgöz *et al.,* 2009; Akıllı *et al*., 2009; Döken *et al.,* 2009; Gürer *et al*., 2001) and *in vivo* (Çeliker and Onoğur, 2011; Aksoy *et al.,* 2005; Akıllı *et al.,* 2011) on the biological control of chestnut blight were conducted by different researchers. The host of *C. parasitica* includes *Castanea crenata, C. sativa, C. mollissima* etc and the mycovirus associated with the fungus has been reported to be from family Hypovirus *viz* Cryphonectria hypovirus 1-4 (CHV 1, CHV 2, CHV 3 and CHV 4) which have ss(+) RNA as their genome (Turina and Rostagno, 2007). The best known example of mycovirus exhibiting hypovirulence is CHV-1. The infected fungus are able to form only superficial cankers which the damage cause by its invasion is negligible and the colony of the isolates changes along with the morphology in the presence of the mycovirus. Other hypovirus have also been reported from different family such as Mycoreovirus 1 (MyRV-1) of family Reoviridae and Cryphonectria mitovirus 1 (CpMV1) (Suzuki *et al*., 2004; Hillman and Suzuki, 2004). The infected conidia are disseminated mostly by the same vector as normal conidia but some studies have also reported mites also play an important role in initiating hypovirulence (Bouneb *et al.,* 2016; Nannelli and Turchetti, 1999; Simoni *et al*., 2014). In recent studies two Croatian CHV1 strains (CR23 and M56/1) were selected as potential biocontrol agents. *In vitro* transfection of selected virus strains from hypovirulent to virus-free fungal isolates and subsequent inoculation of all virus/fungus combinations on stems of chestnut trees revealed that Croatian virus strain CR23 had an equally hypovirulent effect on the host as the strong French strain CHV1-EP71 (Krstin *et al*., 2016). The intensive study of the interaction between *C. parasitica* and CHV-1 have led to the exploration of its ability to affect its host aside from reduced hypovirulence which includes phenotypic symptoms such as reduced pigmentation and reduced sporulation which occurs due to interference in fungal signal transduction pathways (Choi *et al*., 1995; Larson *et al*., 1992; Park *et al.,* 2004).

Rhizoctonia solani

The fungus *Rhizoctonia solani* pathogen belonging to Basidiomyceteis a cosmopolitan pathogen and infects many cultivated crops. It is a heterogeneous assemblage of filamentous fungal taxa belonging to a group of fungi called the Mycelia Sterilia (Kumar *et al*., 2018). It is the causal organism of sheath blight of rice and has wide host range, it causes banded leaf in maize, rice and sorghum, damping-off in cotton, stem rot in green gram and soybean, sheath rot in sugarcane, heart rot in cabbage, black scurf in potato and leaf blights of fruits and plantation crops. The pathogen is also capable of causing root rot, collar rot, stem canker, crown rot, bud and fruit rots on a variety of susceptible agriculturally important causing considerable economic loss worldwide (Nagaraj *et al*., 2017). *Rhizoctonia solani* is a complex species comprising of least 13 related but distinct genetically anastomosis groups (AGs) (Carling *et al.,* 2002a).*Rhizoctonia solani* (AG-1 IA) is considered to cause rice sheath blight disease throughout tropical and subtropical rice growing areas and Binucleate *Rhizoctonia* isolates were associated with diseased potato plants (Tsror, 2010). Thirteen AGs of *R. solani* are currently known to exist and each AG can vary in host range and often geographic locations (Carling *et al.,* 2002b).The hypovirulence associated mycovirus in *Rhizoctonia solani* isolates have been studied intensively resulting in high degree of debilitating the virulent strains. The mycovirus associated with *Rhizoctonia solani* contains dsRNA as their genome ranging from 1.7 to 90 kb and belongs to family Endornaviridae, partiviridae andNarnaviridae can be commonly identified in the natural population of their fungal host (Bharathan *et al*., 2005; Bartholomau *et al*., 2016; Das *et al.,* 2016). Castanho and Butler (1978) first characterized dsRNA in *Rhizoctonia solani*. Three viruses have been reported in *Rhizoctonia solani* (AG-11A) isolates causing sheath blight of rice *viz*, RsRV1 (R. solani dsRNA virus 1, RsPV2 (*R. solani* partivirus 2) and RsRV- HN008 (R. solani RNA virus HN0008) (Zheng *et al.,* 2013; Zheng *et al*., 2014; Zhong *et al*., 2015). Another peculiar feature by the mycovirus associated with *R. solani* is the mixed infection by different types of virus on the same isolates (Li *et al*., 2018). Some other mycovirus were also reported from the fungal pathogen and were well characterized which included Rhizoctonia solani virus 717 belonging to genus Partitivirus (Supyani and Gutomo, 2014), *Rhizoctonia solani* endornavirus - RS002 (RsEV-RS002) associated with black scurf of potato (Das *et al.,* 2014). Some experiments also convey the interaction of virulent strain with other beneficial microorganisms which have proved a positive response and an efficient method in controlling the fungal pathogens. As we know the cosmopolitan nature of the soil borne pathogen *Rhizoctonia solani* which constitutes different pathogenicity from the genus ranging from high virulence to avirulence, strainof *Pseudomonas fluorescens* and fungus *Glomus mosseae* which are arbuscular mycorrhizal (AM) were inoculated in tomato plants infested by the virulent pathogen of *Rhizoctonia solani*. Plant growth and topological parameters were quantified and concluded that these combination of the microorganism had significantly reduced the fungal pathogen, the infected roots weakly developed and displayed dichotomous pattern (Gamalero *et al*., 2010). In crops like potato Soilborne pathogens are persistent and evoke a huge resistance for the proper development of the crop and initiation of the cultural and chemical practices have proven efficient yet not enough to combat the damages caused by the pathogen. Hence, some researchers conducted some combination methods of organic tactics to reduce the population to the threshold level or below. The amendment of *Bacillus subtilis* GB03 strain, hypovirulents

train of *Rhizoctonia solani* Rhs1A1andcompost recorded a positive impact on the virulent population of the pathogenic population. The biocontrol strains reduced the disease of stem and stolon canker, black scurf and common scab by 20-38%, 30-58% and 10-34% respectively, whereas the better performance was recorded in the combination treatment of both the biocontrol organism. Tuber yield of 11-37% was higher as compared to the rest of the treatments (Bandy and Tavantzis 1990;Brewer and Larkin 2005; Larkin and Tavantzis, 2013).

Sclerotinia sclerotiorum

Sclerotinia sclerotiorum (Lib.) de Bary is a cosmopolitan soil borne fungal pathogen having world-wide distribution. The pathogen has been known to infect more than 500 plant species and the disease caused by the fungal pathogen consists of different names such as white rot, white blight, *Sclerotinia* rot etc. and cause an annual loses of 60% (Dixit *et al.,* 2015: Mondal *et al.,* 2015). The characteristic feature of this pathogen is its ability to produce black resting structures known as sclerotia and white fuzzy growths of mycelium on the surface of the plant it infects. The pathogen is known to secrete oxalic acid which is considered as the pathogenicity factor and cell wall degrading enzymes which kills their host and uptake the nutrients from the dead tissues (Hegedus and Rimmer, 2005; Kim *et al.,* 2008; Williams *et al.,* 2011). In management perspective, advance cultural and several other techniques have been developed yet it does not show satisfactory performance, the pathogen still outruns the tactics. Recently, the genes for oxalic acid degrading enzymes were allowed to transform into the plants to enhance the resistance against the pathogen but the process is still a long way before the transgenics can be field evaluated (Dong *et al.,* 2008). To reduce the usage of chemical pesticides, alternative approaches need to be developed. Hypovirulence-associated mycoviruses have highly attracted much interest because of their potential for exploitation as biocontrol agents. Hypovirulence-associated mycoviruses that infect *S. sclerotiorum* have been reported from several mycovirusesfamily with either RNA genome or DNA genome. The first characterized DNA virus that infects a fungus is Sclerotinia sclerotiorum hypovirulence-associated DNA virus 1 (SsHADV-1). SsHADV-1 wasisolated from a hypovirulent strain, DT-8; of *S. sclerotiorum* from a diseased rapeseed plant (Yu *et al*., 2010).

Xie *et al.,* (2011) reported that a mycovirus after extracting from a hypovirulent strain SZ-150 of Sclerotinia sclerotiorum infecting rapeseed was closely related to CHV 3 in the family Hypoviridae and designated as Sclerotinia sclerotiorum hypovirus 1 (SsHV1). Mycovirus were also repoted from the members of the family *Partitiviridae* which have segmented double-stranded RNA (dsRNA) genomes. *Sclerotinia sclerotiorum* partitivirus 1 (SsPV1)belonging to genus partitivirus exhibited hypovirulence against its pathogenic host, *Sclerotinia sclerotiorum* strain WF-1 leading to damage of Cellular organelles like mitochondria and also Hypovirulence and strains of WF-1 and SsPV1 cotransmitted horizontally to different vegetative compatibility groups of *S. sclerotiorum* and interspecifically to *Sclerotinia nivalis* and *Sclerotinia minor* (Xiao *et al.,* 2014). Sclerotinia sclerotiorum botybirnavirus 2 (SsBRV2) with bipartite dsRNA genome and Sclerotinia sclerotiorum mitovirus 4 (SsMV4) with (+) ssRNA as their genome which are unrelated to each other were detected in a single hypovirulent strain of *S.sclerotiorum* AH16. When the virus free isolates were inoculated with the virions of the mycoviruses, hypovirulence against the pathogenic isolates was observed providing a concrete evidence of hypovirulence shown by SsBRV2 and SsMV4 against the isolates. The findings also revealed the first evidence whereby co-infection by two mycovirus infects a single strain (Ran *et al.,* 2016). Recently, a novel virus Sclerotinia sclerotiorum deltaflexivirus 2 (SsDFV2) was recorded in the hypovirulent strain of *Sclerotiniasclerotiorum* 228 in an infected rapeseed plant which was observed that this mycovirus can overcome the vegetative incompatibility transmission system. This provides us the first (+) ssRNA mycovirus to exhibit such kind of phenomenon where it can facilitate and enhance the biological of fungal pathogens by mycovirus (Hamid *et al.,* 2018). So far upto date, 24 *S. sclerotiorum* strains harboring mycovirus have been isolated, sequenced and intensively studied of which 19 mycoviruses were reported to contain (+) ssRNA as their genome namely Hypoviridae (Khalifa and Pearson, 2014a; Marzano *et al.,* 2015), Alphaflexiviridae (Xie *et al.,* 2006), Endornaviridae (Khalifa and Pearson, 2014b), Narnaviridae (Xie and Ghabrial, 2012; Khalifa and Pearson, 2014c; Xu *et al*., 2015) and Deltaflexiviridae (Li *et al.,* 2016).

***Fusarium* sp**

Fusarium is a filamentous fungal pathogen belonging to division Ascomycota, class Sordariomycetes, order hypocreales and family Nectriaceae. They are known to have a broad range of host causing many diseases including vascular wilt, damping off, corm rot etc. their host may include rice, wheat, horticultural crops, ornamental crops etc (Jadhav *et al*., 2019: Jain *et al*., 2014; Lin *et al*., 2014; Riad and Zeidan, 2015; Rusli *et al.,* 2015; Zhang *et al*., 2013). Despite of the innovative approaches to combat their infection below threshold till date there is lack of eco-friendly approaches for managing this fungal pathogenic population. However, a tactful emerging trend that has performed some satisfactory level is the introduction of hypovirulent strain against the virulent population. Mycovirus associated hypovirulence against *Fusarium* sp has been studied extensively at molecular level and have produced efficient result. Phylogenetic analysis provides that the mycoviruses associated with *Fusarium* sp recorded so farfalls under the family of Chrysoviridae, Hypoviridae, Partitiviridae and Totiviridae (Cho *et al*., 2013). In Indonesia hundred isolates of *Fusarium* from chili were collected in Boyolali, Central Java. Assay for virulence were conducted against hypovirulent isolates in apple, four isolates were found to be hypovirulent and based on the presence of viral RNA in one isolate mycovirus caused hypovirulence and the other

three hypovirulent traits were due to genetic factors (Supyani and Widadi, 2015). Another analysis from Iran reported that out of 33 isolates of *Fusarium graminearum* 12 isolates had three viral fragments measuring 0.9, 1.2, 3, 3.2 and 5 kb and the severity of the disease of the isolates containing dsRNA was significantly less than that of dsRNA free isolates on wheat (Aminian *et al.,* 2011). Mycovirus associated hypovirulence in *Fusarium* sp has also been reported from different strains recently which had showed its interaction with the hypovirulent strains reducing the population deliberately. These includes *Fusarium graminearum* virus 2 (Fgv1) isolated from *Fusarium graminearum* strain 98-8-60 (Yu *et al*., 2011), Fusarium graminearum virus 3 (FgV3) and Fusarium graminearum virus 4 (FgV4) from *F. graminearum* strain DK3 (Yu *et al*., 2009), Fusarium graminearum virus china 9(FgV-ch9) from *F. graminearum* isolate China-9 (Darissa *et al.,* 2012), Fusarium graminearum hypovirus 1 (FgHV1) from *F. graminearum* strain HN10 (Wang *et al*., 2012), *Fusarium graminearum* Hypovirus 2 (FgHV2) isolated from *F. graminearum* strain JS16 (Li *et al*., 2015), Fusarium graminearum mycotymovirus 1 (FgMTV1) of family Tymoviridae isolated from *F. graminearum* strain SX64 (Li *et al*., 2016), *Fusarium* poae dsRNA virus 2 (FpV2) and *F.poae* dsRNA virus 3 (FpV3), isolated from the plant pathogenic fungus, *F.poae* strain SX63 (Wang *et al.,* 2016), *Fusarium graminearum* alternavirus 1 (FgAV1), from the isolate AH11 of the phytopathogenic fungus *F. graminearum*. FgAV1 are placed in the family Alternaviridae, a newly proposed family and is the first report of mycovirus from Alternaviridae to infect *F. graminearum* (He *et al*., 2018).

CONCLUSION

The residues after pesticidal application have deliberately damaged the pristine nature of the environment harming the biology of the natural enemies, pollution at its highest peak, socio economic welfare of consumers and producers. Some pesticides can even reside in the soil for more than 10 years posing an insidious impact to the environment. Many tactics have been merged together to combat the situation and to minimize the usage of synthetic chemicals to maintain the pest population below threshold. Still, there need a lot of attention for improvement and efficacy of these various tactics. Fungal pathogens having broad range of host are present in almost all the habitats due to which creates a hindrance to employ suitable management practices efficiently. On the other hand, high usages of chemicals are encouraged out of compulsion. This cycle of initiation to counteract the population creates a hazard to the environment eventually. Therefore, for sustainable agriculture implementing biological control can change the scenario to the desired level. Mycovirus have been intensively studied at molecular level despite of the vegetative incompatibility groups present in the population which cause a barrier to employ them as a biocontrol tool. Their ability to destroy the virulent strains has highly attracted the researchers and with the advanced sophisticated protocols the drawbacks can be subdued.

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