Abstract

Mycoviruses are very significant viruses, which are found to be infecting fungi. These Mycoviruses require the living cells of their hosts for replicate like the plant and animal viruses. The genome of Mycoviruses mostly consist of double stranded RNA (dsRNA) and least of Mycoviruses genome consist of positive, single stranded RNA (-ssRNA). Moreover, DNA Mycoviruses have been reported recently. These viruses have been detected in almost all fungal phylum but still most of the Mycoviruses remain unknown. Mycoviruses are important in a sense that they mostly remain silent and rarely develop symptom in their hosts. Some Mycoviruses have been reported which are causing irregular growth, abnormal pigmentation and some are involved in changing their host sexual reproduction. For the management of Plant diseases, the importance of Mycoviruses arises because of their most significant effect that is they reduced virulence of their host. Technically the reduced virulence is called hypovirulence. This hypovirulence phenomena has increased importance of Mycoviruses because it has the potential to reduce the crop losses and forests caused by their hosts which are plant pathogenic fungi. In this review, I explore different aspects and importance of Mycoviruses.

Keywords: Mycoviruses; Genome; Hypovirulence; Evolution

Introduction

Mycoviruses are infecting fungal species and present in latent stage in them and rarely causing diseases [1]. There are few Mycoviruses which are involved in causing considerable changes in their fungal hosts but the most obvious changes in their fungal hosts are irregular growth, abnormal pigmentation and mutated sexual reproduction [1-4]. The most important quality of Mycoviruses, which can be utilized to manage fungal disease, is the hypo virulence, which means the reduction of virulence of plant pathogenic fungi. This quality has nowadays attracted much attention because several fungal diseases of forests as well as crops can be managed [4,5]. Research on these Mycoviruses, over the last fifty years has increased our know how regarding Mycoviruses.

Moreover, their interaction with their plant pathogenic fungal hosts has also been explored [2]. The first report of interaction was between Hypovirus CHV1 and the chestnut blight fungus Cryphonectria parasitica. The fungi C. parasitica produced abnormal pigmentation and reduced growth upon infection by CHV1 virus. We can say, the Mycovirus CHV1 induced Hypovirulence in chest nut blight [4,6]. Later several fungal species were studied which were infected with Mycoviruses. The other important plant pathogenic fungi was F. graminearum which has been widely studied [7]. The Mycovirus FgV1 induce hypovirulence to F. graminearum [8]. Upon infection with FgV1, the fungi F. graminearum exhibited reduced vegetative growth, abnormal pigmentation and mycotoxin [7]. More important aspect of mycovirus FgV1 is that, it can be transmitted to other fungal species such as C. parasitica where it induce more severe hypovirulence that its own Mycovirus CHV1 [9].

History of Mycoviruses

As previously mentioned, the Mycoviruses are the viruses, which are found to be in association with the fungal species. The first report on Mycoviruses appeared in 1962 from Agaricus bisporus. These mushrooms found to have misshaped fruiting bodies and consequently reduction in yield [2]. These Mycoviruses shared some of the characteristics with animal and plant virus but also have the distinct characteristics such as they lack an extracellular route for infection, transmitted intercellularly only through cell division, sporulation, and cell fusion and absence of a movement protein, which is essential for the life cycle of animal and plant viruses. Taxonomists reported the genome of most Mycoviruses consists of double-stranded RNA (dsRNA), while the genome of about 30% of Mycoviruses is a positive, single-stranded RNA (+ssRNA) [8]. The DNA Mycoviruses related to group Gemini virus have been recently reported for the first time [3]. Mycoviruses have been detected in all the major fungal phyla including Zygomycota, Ascomycota, Deuteromycota, Basidiomycota and Chytridiomycota. Most of the Mycoviruses remain unknown. Currently transcriptomic approaches have been widely used for identification and detection of several Mycoviruses.

Evolution of Mycoviruses

The classification of Mycoviruses is same as the other viruses developed by ICTV. They have been grouped into following seven linear dsRNA families;

- Chrysoviridae
- Endornaviridae
- Megabirnaviridae
- Quadirviridae
- Partitiviridae
- Reoviridae
- Totiviridae

Moreover, they have been classified into five linear positive-sense ssRNA families

- Alphaflexiviridae

*Corresponding author: Aqleem Abbas, College of Plant Science and Technology, HZAU Wuhan, China. Tel: 00862787396057; Fax: 00862787396057; E-mail: agdpath@gmail.com

Received December 19, 2016; Accepted December 29, 2016; Published December 31, 2016

Citation: Abbas A (2016) A Review Paper on Mycoviruses. J Plant Pathol Microbiol 7: 390. doi: 10.4172/2157-7471.1000390

Copyright: © 2016 Abbas A. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.
viruses have also been reported from the yeast Saccharomyces cerevisiae. Moreover, much of the research concerning Mycoviruses has dealt with current research has opened a gate by demonstrating that seven vic...intercellulary via hyphal anastomosis or spores. The transmission can also be utilized to explore the host ranges of several Mycoviruses. These techniques resemble to the human pathogen hepatitis E virus and Rubi like 3. For the origin of Mycoviruses two major hypothesis have been proposed 1. One of the hypothesis is called the "ancient coevolution hypothesis" which states that the origin of Mycoviruses is still remain a mystery, and reflects a long term coevolution. The other hypothesis is known as plant virus hypothesis, in contrast, which states that Mycoviruses originated relatively recently from the other plant viruses i.e. the original mycovirus was a plant virus that drifted from the plant to fungus within the same host plant 12. Still both the hypothesis are not convincing, so the origin of Mycovirus remains a mystery. There are other hypovirulence associated Mycoviruses such as a) Sclerotinia sclerotiorum hypoviruses b) Helminthosporium victoriae viruses c) Rosellinia necatrix viruses. These Mycoviruses have been detected and studied using reverse genetic approaches 1.5. These Mycoviruses have deficiency of extracellular phase, so researchers have investigated various transfection methods using the purified virus particles, full-length viral cDNA clones and in vitro RNA transcripts 14-16. These infection assays were helpful in identification of the viral and/or host factor(s), which are involved in symptom induction or virus replication of several Mycovirus host interactions. These techniques can also be utilized to explore the host ranges of several Mycoviruses. As previously mentioned, these Mycoviruses are transmitted intercellularly via hyphal anastomosis or spores. The transmission of viruses between different strains is inhibited by fungal vegetative incompatibility (vic). Vegetative incompatibility is one of key obstacle in the use of hypovirulent Mycoviruses used as biocontrol agents. The current research has opened a gate by demonstrating that seven vic genes which are present in five or six loci in fungal species C. parasitica played a role to incompatibility and also affect virus transmission 17. Moreover, much of the research concerning Mycoviruses has dealt with hypovirulence of plant pathogenic fungi but several dsRNA and ssRNA viruses have also been reported from the yeast Saccharomyces cerevisiae [18]. The most important viruses among them is Saccharomyces cerevisiae virus L-A (ScV-L-A) which has been well characterized.

Interaction of Mycoviruses with their Fungal Hosts

RNA Genome expression analysis revealed that there are several expression patterns of F. graminearum transcriptomes infected by four phylogenetically different Mycovirus [19]. Among these different Mycoviruses, the virus FgV3 and FgV4 did not cause any obvious changes in the phenotypes of their host. While the other viruses such as FgV1 and FgV2 which caused some obvious changes in the host phenotypes [19]. Moreover, the detailed study will finally enhance our knowledge of the interactions among these Mycoviruses and their fungal hosts. Mycoviruses are obligate intracellular parasites; they are involved in reprogramming of their host metabolism. They also involved in antiviral responses. There we can only know thier role in the life cycle of fungal host if we would be able to identify the important determinants which play their role in their interaction [20]. To identify these determinants currently scientist, use wide genome approaches particularly in studies of Mycoviruses of Cryphonectira, Fusarium graminearum and Sclerotinia sclerotiorum [19-22]. The results showed the expression level of viral genes differed between virus free and virus infected fungal isolates. Moreover, they are also found to be different among the viruses belong to different groups. Further, the results indicate that these Mycoviruses not only depend on various host factors but also on cellular processes and pathways such as related to cellular transport, metabolism, RNA processing and other RNA signaling.

In viruses of Yeast such as ScV-L-A, the host protein Mak3p which is an N-acetyl transferase is essential for the acetylation of major coat protein of that viruses and such acetylation is also very important for the virus assembly [18]. Quelling in fungi also termed as RNA silencing [23,24], has also been investigate with the fungi Neurospora crassa, and other reports are also found for C. parasitica and Aspergillus nidulans [24]. There is a large potential in the genome of Mycovirus because they consist of RNA, and thus quelling can protect their host from other Mycoviruses. The genes dcl2 and agl2 are very important for RNA-silencing for CHV1 infection in C. parasitica [24]. Some silencing-related genes (rdr1, dcl1, dcl2, and agl2) upon virus infection were also observed in Fusarium graminearum viruses-infected F. graminearum [19]. Many viruses have then devised a different strategy to suppress RNA silencing for example the p29 protein of Mycovirus CHV1 and the S10 gene product of Rosellinia necatrix Mycoviruses function as silencing suppressors [6,25]. The host genes that have been analyzed for biological function in mycovirus-host interactions are shown in Table 1.

Future Challenges in Studying Mycoviruses

Much of the early research on Mycoviruses has put them undesirable because they were attacking commercial mushrooms. Later they have been found to be considered beneficial when they were found to be act as biocontrol agents of fungal pathogens in the most economically important plants [3-5]. The first approach to manage diseases was carried out in the 1980s, the spores of fungi C. parasitica containing Hypovirus were artificially introduced into fungal populations to control chestnut blight. This approach completely became unsuccessful in orchards in eastern North America and in Europe [4]. The variation in efficacy resulted from the vegetative compatibility among fungal isolates or from the features of the hypoviruses [17]. These results suggests that the use of Mycoviruses as effective biological control agents may further require consideration of several factors including
both the host and virus properties. Recently the Sclerotinia sclerotiorum hypovirulence-associated DNA virus 1 was used to manage the rapeseed stem rot disease and this hypovirulence reduced the disease. The virus was applied as a suspension of virus-infected hyphal fragments or virus particles [3,5]. Several challenges are ahead in the use of hypovirulent strains to control plant pathogenic fungi. The challenges are as follows:

- Vegetative incompatibility, which inhibit the transmission of Mycovirus from a hypovirulent strain to a target strain
- The potential lack of fitness of the hypovirulent strain
- Most of the Mycoviruses do not significantly affect their fungal hosts. These suggest that these viruses may be adapted to living with their host for the long period of time. This kind of association might be helpful for both Mycovirus and its host
- The "killer phenomenon or killer hypothesis" is also a new phenomenon in the yeast. This is caused by combined presence of cytoplasmically inherited dsRNA virus and satellites or DNA virus-like elements (VLEs) [18]. Although these viruses do not induce symptoms in their hosts, they do substantially affect host biology

### Conclusion

- The scientists are struggling to understand the Mycoviruses but don’t know how to initiate infection so as to determine cause and effect of the Mycoviruses associated with their fungal hosts.
- The trans-infection methods and reverse genetic systems have been developed for several Mycoviruses. The future reverse genetic systems might help us to understand the molecular biology of Mycoviruses and used them as stable biological control agents or as virus based expression vectors.
- Moreover, the future studies are probably revealing the important clues of Mycoviruses which will be helpful in understanding their role in fungal hosts. Further the research on Mycoviruses and their fungal hosts will provide new insights into the largely dark matter of Mycoviruses

### Acknowledgements

I would like to dedicate this review to Dr. Dachong Jiang professor in the Department of Plant Pathology at the University of Huazhong Agricultural University, who did excellent work on Mycovirus research.

### References

1. Pearson MN, Beever RE, Boine B, Arthur K (2009) Mycoviruses of filamentous fungi and their relevance to plant pathology. Mol Plant Pathol 10: 115-128.
2. Ghabrial SA, Castón JR, Jiang D, Nibert ML, Suzuki N (2015) 50-plus years of fungal viruses. Virology 479-480: 356-68.
3. Jiang D, Fu Y, Ghabrial SA (2013) Mycoviruses: Chapter eight-Viruses of the plant pathogenic fungus Sclerotinia sclerotiorum. Adv Virus Res 86: 215-248.
4. Nuss DL (2005) Hypovirulence: Mycoviruses at the fungal-plant interface. Nat Rev Microbiol 3: 632-642.
5. Xie M, Jiang D (2014) New insights into Mycoviruses and exploration for the biological control of crop fungal diseases. Annu Rev Phytopathol 52: 45-68.
6. Craven M, Pawlyk D, Choi GH, Nuss DL (1993) Papain-like protease p29 as a symptom determinant encoded by a hypovirulence-associated virus of the chestnut blight fungus. J Virol 67: 6513-6521.
7. Chu YM, Jeon JJ, Yea SJ, Kim YH, Yun SH, et al. (2002) Double-stranded RNA mycovirus from Fusarium graminearum. Appl Environ Microbiol 68: 2529-2534.
8. King AM, Adams MJ, Leftkowitz EJ (2011) Virus taxonomy: Classification and nomenclature of viruses: Ninth Report of the International Committee on Taxonomy of Viruses: Elsevier.
9. Lee KM, Yu J, Son M, Lee YY, Kim KH (2011) Transmission of Fusarium boothii Mycovirus via proto-plast fusion causes hypovirulence in other phytopathogenic fungi. PLoS One 6: e21629.
10. Herrero N, Duemas E, Quesada-Moraga E, Zabalgoazcoa I (2012) Prevalence and diversity of viruses in the entomopathogenic fungus Beauveria bassiana. Appl Environ Microbiol 78: 8523-8530.
11. Roossinck MJ (2015) Metageneomics of plant and fungal viruses reveals an abundance of persistent lifestyles. Front Microbiol 5: 767.
12. Nibert ML, Ghabrial SA, Maisis E, Lesker T, Vainio EJ, et al. (2014) Taxonomic reorganization of family Partitiviridae and other recent progress in partitivirus research. Virus Res 188: 128-141.
13. Kwon SJ, Lim WS, Park SH, Park MR (2007) Molecular characterization of a dsRNA mycovirus, Fusarium graminearum virus-DK21, which is phylogenetically related to hypoviruses but has a genome organization and gene expression strategy resembling those of plant potyviruses. Mol Cell 23: 304-315.
14. Marzano SYL, Hobbs HA, Nelson BD, Hartman GL, Eastburn DM, et al. (2015) Transfection of Sclerotinia sclerotiorum with in vitro transcripts of a naturally occurring interspecies recombinant of Sclerotinia sclerotiorum hypovirus 2 significantly reduces virulence of the fungus. J Virol 89: 5060-5071.
15. Chen B, Choi GH, Nuss DL (1994) Attenuation of fungal virulence by synthetic infectious hypovirus transcripts. Science 264: 1762-1764.
16. Choi GH, Nuss DL (1992) Hypovirulence of chestnut blight fungus conferred by an infectious viral cDNA. Science 257: 800-803.
17. Choi GH, Dawe AL, Churbanov A, Smith ML, Mitgroom MG, et al. (2012) Molecular characterization of vegetative incompatibility genes that restrict Hypovirus transmission in the chestnut blight fungus Cryptophytophthora parasitica. Genetics 190: 113-127.
18. Wickner RB, Fujimura T, Esteban R (2013) Viruses and prions of Saccharomyces cerevisiae. Adv Virus Res 86: 1-36.
19. Lee KM, Cho WK, Yu J, Son M, Choi H, et al. (2014) A comparison of transcriptional patterns and mycological phenotypes following infection of Fusarium graminearum by four Mycoviruses. PLoS One 9:e100989.
20. Allen TD, Dawe AL, Nuss DL (2003) Use of cDNA microarrays to monitor transcriptional responses of the chestnut blight fungus Cryptophytophthora parasitica to infection by virulence-attenuating hypoviruses. Eukaryot Cell 2: 1253-1265.
21. Li H, Fu Y, Jiang D, Li G, Ghabrial SA, et al. (2008) Down-regulation of Sclerotinia sclerotiorum gene expression in response to infection with Sclerotinia sclerotiorum debilitation-associated RNA virus. Virus Res 135: 95-106.

22. Cho WK, Yu J, Lee KM, Son M, Min K, et al. (2012) Genome-wide expression profiling shows transcriptional reprogramming in Fusarium graminearum by Fusarium graminearum virus 1-DK21 infection. BMC Genomics 13: 173-188.

23. Son M, Lee KM, Yu J, Kang M, Park JM, et al. (2013) The hex1 gene of Fusarium graminearum is required for fungal asexual reproduction and pathogenesis and for efficient viral RNA accumulation of Fusarium graminearum virus 1. J Virol 87: 10356-10367.

24. Chang SS, Zhang Z, Liu Y (2012) RNA interference pathways in fungi: Mechanisms and functions. Annu Rev Microbiol 66: 305-323.

25. Zhnag DX, Spiering M, Nuss DL (2014) Characterizing the roles of Cryphonectria parasitica RNA-dependent RNA polymerase-like genes in antiviral defense, viral recombination and transposon transcription. PLoS One 9: e108653.

26. Sun Q, Choi GH, Nuss DL (2009) Hypovirus-responsive transcription factor gene pro1 of the chestnut blight fungus Cryphonectria parasitica is required for female fertility, asexual spore development, and stable maintenance of hypovirus infection. Eukaryot Cell 8: 262-270.

27. Márquez LM, Redman RS, Rodríguez RJ, Roossinck MJ (2007) A virus in a fungus in a plant: Three-way symbiosis required for thermal tolerance. Science 315: 513-515.

28. Gao K, Xiong Q, Xu J, Wang K, Wang K (2013) CpBir1 is required for conidiation, virulence and anti-apoptotic effects and influences hypovirus transmission in Cryphonectria parasitica. Fungal Genet Biol 51: 60-71.

29. Park SM, Choi ES, Kim MJ, Cha BJ, Yang MS, et al. (2004) Characterization of HOG1 homologue, CpMK1, from Cryphonectria parasitica and evidence for Hypovirus mediated perturbation of its phosphorylation in response to hypertonic stress. Mol Microbiol 51: 1267-1277.

30. Faruk MI, Eusebio-Cope A, Suzuki N (2008) A host factor involved in Hypovirus symptom expression in the chestnut blight fungus, Cryphonectria parasitica. J Virol 82: 740-754.

31. Soldevila AI, Havens WM, Ghabrial SA (2000) A cellular protein with an RNA-binding activity co-purifies with viral dsRNA from Mucovirus-infect Helminthosporium victoriae. Virol 272: 183-190.

32. Zhu W, Wei W, Fu Y, Cheng J, Xie J, et al. (2013) A secretory protein of necrotrophic fungus Sclerotinia sclerotiorum that suppresses host resistance. PLoS One 8: e53901.