Mushtaq, S., Shafiq, M., Abid, M.A, Rana, S., Yaqub, M.S., & Haider, M. (2019). A review on wheat streak mosaic virus (WSMV) disease complex. *World Journal of Biology and Biotechnology, 4*(1), 29-33.
DOI: https://doi.org/10.33865/wjb.004.01.0205

(Online)
ISSN2522-6754
2019
(Print)
ISSN 2522-6746
WORLD JOURNAL OF BIOLOGY AND BIOTECHNOLOGY
Volume: 04
www.sciplatform.org
Issue: 01

A REVIEW ON WHEAT STREAK MOSAIC VIRUS (WSMV) DISEASE COMPLEX

[a] Sehrish Mushtaq*, [a] Muhammad Shafiq, [a] Muniba abid, [a] Muhammad A. Rana, [b] Shazia Yaqub, [a] Muhammad S. haider
[a] Institute of Agriculture Sciences, University of the Punjab, Lahore, Pakistan,
[b] Institute of Food Science and Nutrition University of Sargodha, Sargodha, Pakistan.
*Corresponding email address: sherry.a143@gmail.com

ABSTRACT

Wheat is one of the most important staple food crop .*Wheat streak mosaic virus* (WSMV) was first time reported in Nebraska in 1922 as "yellow mosaic". Since then, although sporadic in its appearance and severity, wheat streak mosaic has caused losses throughout North America, Europe, North Africa and Russia. The disease was probably present in other counties, but was not detected. WSM symptoms are characterized by a yellow leaf streaking or stippled pattern and stunting, head sterility, low test weights, and poor tillering and it is a seed born or mite born disease. WSMV is transmitted by eriophyid mite in both semi persistent and circulative manners. Mostly WSMV infects the crops belonging to family Graminae or Poaceae (wheat, barley) and other alternate host of the WSMV are the grassy weeds or green bridge where wheat curl mite (WCM) over winters and lay eggs in the absents of the host. Wheat production in the Great Plains is also threatened by the newly discovered wheat viruses including *Wheat mosaic virus* and *Triticum mosaic virus* (TriMV). Both viruses closely match the life cycle of WSMV and are transmitted by WCM. Genome of WSMV contains positive sense ssRNA virions and one polyprotein. The tritimovirus which is approximately of 10kb in size.

Key word: Potyviridae, tritimoviruses, erysiphoid mite*, Aceria tosichella*, Aetiology, wheat streak mosaic virus, USA.

INTRODUCTION

Potyvirus that belongs to family *Potyviridea* and this genus contains more than 100 known species. These viruses are usually 720-850 nm long and could be transmitted by mechanical means as well as through aphids. *Rymovirus* and *Tritimovirus* both genus are 680-750nm longs. One of the main characteristic of this family is formation of cylindrical inclusion (CI) bodies in virus infected cell, and they are unique for the diversity of these inclusion bodies (Barnett, 2012). These CI bodies appear as pin wheel when cut in transverse section and unusually clusters of virion aggregates are formed inside cells by virus encoded proteins and consider as most important phenotypic criteria for the identification of virus of family *Potyviridae*. As a result of potyvirus infection in plant cells, certain changes has been reported i.e., disruption of cell organelles, expansion of cytoplasm induced by virus, membrane proliferation and cell wall deposits. Some groups of potyviruses induced amorphous cytoplasmic inclusion bodies while few other form nuclear inclusions (Nia or Nib)(Carr *et al.*, 2018). WSMV belongs to genus Ryomovirus that lies in the plant virus family *Potyviridae* (Tatineni *et al.*, 2010). This classification of viruses belongs to family *Potyviridae* is based on the vector and Host genotypes.

Etiology and distribution of WSMV: Wheat streak mosaic virus (WSMV) is a serious disease of wheat (*Triticum aestivum* L.) in the Great Plains region of the United States, Canada, Jordan, Eastern Europe and Russian Federation and many other wheat producing countries (Brakke, 1971; Börner *et al.*, 2015). The disease is caused by wheat streak mosaic virus (WSMV) of the genus *Tritimovirus* in the family *Potyviridae* (Tatineni *et al.*, 2010). WSMV is economically significant virus causing substantial yield losses among those viruses that infect wheat in United States (Mirik *et al.*, 2011). Wheat virus, *Triticum mosaic virus* was found in Kansas and Nebraska and WSMV is the type member of this genus (Wosula *et al.*, 2016). In contrast, TriMV was reported by (Seifers *et al.*, 2009) and its genome has revealed that it is a member of the family *Potyviridae*. However, TriMV encodes several proteins having only 18 to 41% amino acid similarity with the other proteins of family *Potyviridae* (Tatineni *et al.*, 2009).

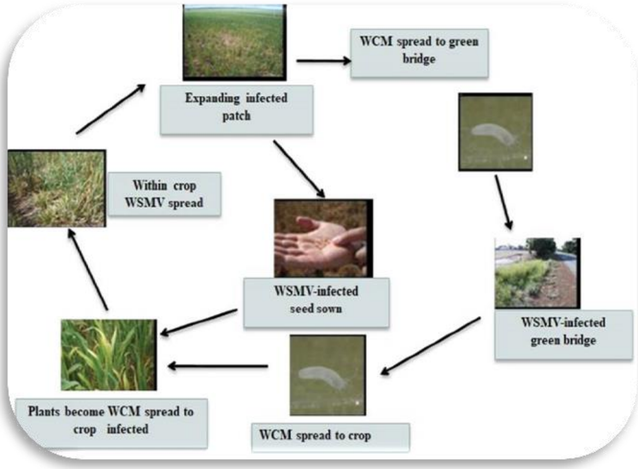
Physical properties and morphology of virus: The virus is described as non-enveloped, filamentous, 700 nm long (Brakke, 1971). The genome of WSMV contains 9,384 nucleotide, monopartite, positive sense ss RNA that encodes a polyprotein of 3,035 amino acid residues (Knoell, 2018). Morphologically virion particles of WSMV are flexuous element with helical symmetry. *Tritimovirus* also have one major structural protein capsid protein and one molecule of VP g which are covalently bounded to the 5' prime end of the genome. Other association of Virion with nucleic acid is not yet reported (Miras *et al.*, 2017).

Agricultural importance of WSMV: Wheat streak mosaic virus (WSMV) is a widely prevailing and important virus in small grain production systems worldwide (Ito *et al.*, 2012). Yield loss in individual fields due to WCM can be severe (near 100%), If early infection occurs on susceptible varieties (Coutts *et al.*, 2014). Depending on the variety, 25 to 80% yield loss has been recorded in Montana (Ito, 2011).WSMV is consistently present in north central Montana (Golden Triangle) where approximately 40% of all wheat, primarily winter wheat, in Montana is produced. The disease can be severe in the northeastern portion of the state that grows primarily spring and durum wheat.

Host range of WSMV: Oat, Barley, Proso millet, Rye, Corn, Sorghum, Downy chess, Barnyard grass and all plant belonging to *Poaceae* family are the host for the WCM. Grassy weed hosts of WSMV and the WCM are prevalent in the Great Plains region and include wild oat, cheat, downy brome, jointed goat grass, green foxtail and Persian darnel (Ito *et al.*, 2012). It is believed that neither WSMV nor WCM survive on broadleaf plants (Skoracka *et al.*, 2018). Grassy weeds can be important in the maintenance of the 'green bridge' due to their abundance in wheat fields in the Great Plains region. Summer annual grasses such as wild oat and green foxtail and volunteer wheat are more likely candidates to be 'green bridge' hosts during such period.

Emergence of new wheat viruses: In addition to WSMV, wheat production in the great plains is threatened by the newly discovered wheat viruses including *Wheat mosaic virus* (WMoV, formerly known as high plains virus, HPV) (figure 1) and *Triticum mosaic virus* (TriMV). Both viruses closely match the life cycle of WSMV and are transmitted by WCM. Co-infection of a single plant with multiple wheat viruses enhances symptom severity and potential yield loss (Tatineni *et al.*, 2010). WMoV was identified in Colorado, Idaho, Kansas and Texas in 1993 and 1994 first in corn, then in winter wheat (McMechan, 2016). Host range studies of WMoV in Kansas showed grassy weed hosts of WMoV closely matched WSMV, such as cheat, oat (*Avena sativa*), rye (*Secale cereale*), and green foxtail (Ito, 2011).

Figure 1: life cycle of wheat streak mosaic virus (WSMV).



Transmission and movement of WSMV: WSMV has three mechanisms to move from plant to plant: mechanical, seed, and the wheat curl mite vector. Mechanical transmission of the virus occurs when viruliferous plant sap enters a susceptible host through damage caused by human activities such as moving equipment, by herbivores, or from plants rubbing together (Richardson *et al.*, 2014). The primary transmission mechanism for WSMV is by the WCM, an eriophyid mite less than 0.3 mm in length with two pairs of legs (Price, 2015).The WCM prefers to feed on the upper leaf surface adjacent to the leaf sheath. Heavy infestations cause the leaf margin to curl inwards. WCM produce larger, more robust forms than normal in response to favorable temperatures, environmental conditions and food supply (Ito, 2011). WCM can overwinter at any stage of their life cycle inside the curled leaf and become active and reproduce during warm days in mid-winter. An adult WCM can survive winter temperatures of -15ºC to -20ºC for 2 days, and eggs can survive up to 8 days (Ito, 2011). WCM can survive in sub-freezing temperatures for 3 months. Mites lay 12 to 20 eggs, which leads to rapid increase of the mite populations. Mites migrate up the plant to the youngest leaves as their population increases (Navia et al., 2013).

Symptoms: WSM symptoms are characterized by a yellow leaf streaking or stripped pattern and stunting, head sterility, low test weights, and poor tillering (Ali, 2012). Early infection can be confused with nutrient deficiency, drought, root rots, and early stages of fungal foliar diseases. Symptoms commonly appear first on the edge of the field as the virus and vector, the wheat curl mite move into the crop from ditches and infected crops that are adjacent or upwind (figure 2 and 3).

Figure 2: Wheat curl mite (100 X magnification) b) WSMV infected plant showing yellowing and stunting (by Marcia Msmullen, NDSU) c) Yellow streaking and mottling symptoms on individual leave, bottom leaf is healthy (phot courtesy, NDSU Archives).

Figure 3: a) Pale green leaf streaks in young wheat leaves infected with WSMV. b) Bright yellow leaf streaks on older leaves caused by WSMV in late winter/early spring. c) Stunted, tufted, chlorotic Wheat plants infected with WSMV as young seedlings.

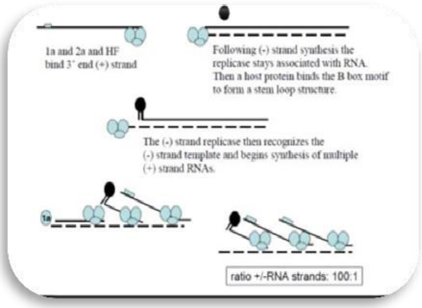
As the plant matures, the mites move to glumes and are carried by wind currents to a new host (Ito, 2011). This 'green bridge' occurs when susceptible hosts are present in or near a field between harvesting of one crop and the planting of the next crop.

Wheat streak mosaic virus is thought to be transmitted by WCM in a semi-persistent manner (De Oliveira, 2013), although recent data suggests it may be circulative In the case of WSMV (Bragard *et al.*, 2013), WCM can be viruliferous at all stages except the egg, with a minimum of 10 to 15 minutes of feeding on infected plant material. Transmission efficiency is high (84 to 92%) if the mites acquire the virus from wheat (Knoell, 2018). The mites remain viruliferous for up to 21 days (Miller *et al.*, 2012).Infections first appear at the margins of a field because of the movement of the virus's mite vector. Infections may occur in the winter, but symptoms often do not appear until the spring temperatures rise to above 10°C. Transmitted by a vector; a mite; wheat curl mite (WCM) *Aceria tulipae*; Eriophyidae. The virus is not transmitted congenitally to the progeny of the vector; transmitted by mechanical inoculation; not transmitted by contact between plants; transmitted by seed (very low levels).The HC-Pro of WSMV is required for vector transmission but dispensable for suppression of host defense mechanisms (Syller, 2012).

In general, early fall infection by WSMV appears in winter season. Wheat causes the most significant damage to yield and provides the greatest amount of inoculum for spread in the spring (Mulenga *et al.*, 2018). Fall infection is hard to diagnose because the symptoms may not be observed until temperatures warm up in the spring.

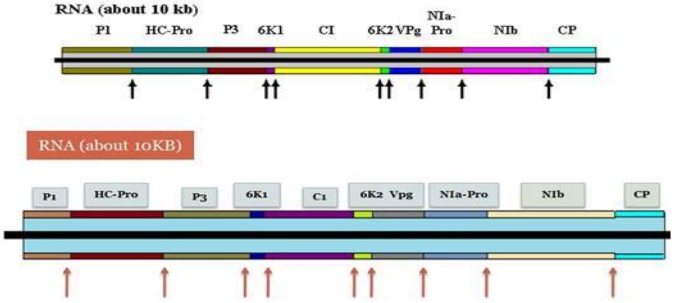
Organization of genome and its replication: The ssRNA Genome of *Tritimovirus* is approximately of 10kb in size. The WSMV genome contains one open reading frame (ORF) which is translated as a large polyprotein that is processed into one mature protein (P1,HC-Pro and NIa- Pro) by viral encoded proteinases (Lewsey *et al.*, 2018). The 5 prime- untranslated region (UTR) possibly has one molecule of VPg protein at the 5' terminus of the ssRNA strand the 3'prime-UTR ends in a polyadenylated tail which is of variable length (figure 4 and 5).

Figure 4: Replication process of positive sense ss RNA genome of WSMV



The WSMV replication process involves Viral RNA polymerase that copies plus-sense genomic RNA into complementary minus-sense RNA with help of Viral RNA polymerase (vRdRps and Certain Host proteins.

Figure 5: Genome organization of WSMV



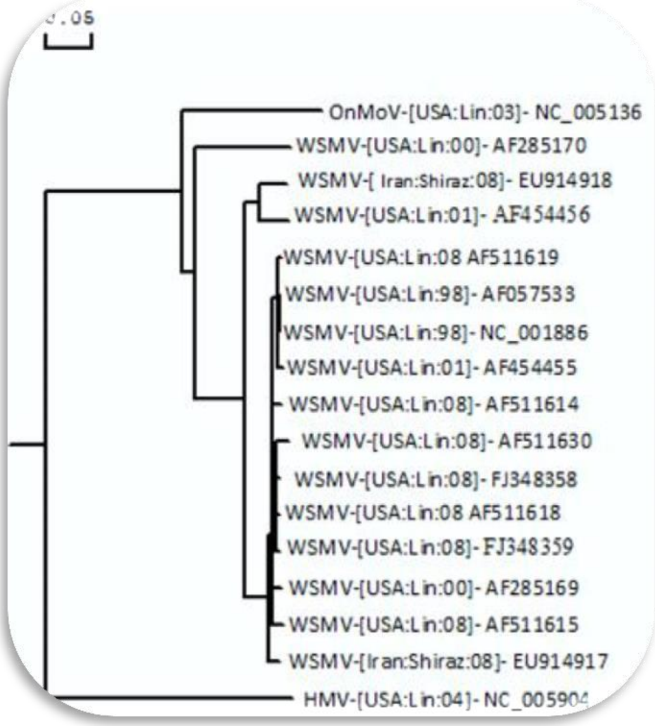
During replication new minus sense strand served as template for the newly synthesize positive sense strands. The newly synthesized strand has three fates either serve as template for the newly synthesize positive sense strands. The newly synthesized strand has three fates either serve as template for minus strand, might be packed as progeny of virions and may be translated into the protein (Miorin *et al.*, 2013). *Tritimoviruses* has genome similar to other species of family *Potyviridae* (monopartite) genome. Generally viral replication process starts in the cytoplasm of the plant cell and most of the *Tritimovirus* proteins are multifunctional as polyprotein and cleaved into ten different proteins as shown in figure 5. Some important functions of the WSMV proteins are described in table 1.

Proteins	Functions
P1 (35K)	N terminal protein or Proteinase protein that cleaves the poly proteins and helps RNA binding.
HC-Pro (52 K)	Helper component proteinase, this protein is proteinase enzyme that cleaves the poly protein and also a helper component of activity necessary for the insect transmission of the potyvirus.
P3 (50 K or 6K)	Activity is unknown
C1	Cylindrical inclusion proteins help in movement of virus.
Vpg (21K)	Virus encoded protein, or Primer for replication of virus, exact function is unknown but may be associated by the ability of RNA act as mRNA e.g. to be translated into protein.
Nla-Pro (27 K)	Nuclear inclusion protein is proteinase enzyme needed for cleaving the viral polyproteins at Gln (ser/Gly) bonds.
Nib (58 K & 71 K)	NIb, involved in replication of the virus, components of RNA polymerase of virus
Cp (30K)	Virus movement in plants and their interaction with insect vector for transmission and help in symptoms development

Table 1: Functions of some important ORF of the WSMV.

Phylogenetic analysis of WSMV species among *Tritimoviruses*: The maximum likely hood phylogram was based on nucleotide sequence alignment correspondence to WSMV-type nucleotides 7618-9384. WSMV (AF285170) has similarity with OnMoV (NC_005136) which are sister texa and clearly distinct from species of genus Rymoviruse. Wheat streak mosaic virus isolate WA94 polyprotein gene, complete cdsFJ348358 (USA:Lin:08) has maximum 99% identity with AF511618 (USA:Lin:08) and AF511630 (USA:Lin:08), AF285169 (USA:Lin:00) has 98% similarity with FJ348358 as shown in figure 6.

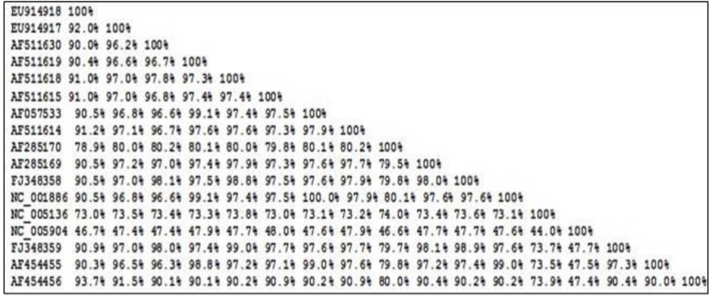
Figure 6: Phylogenetic analysis of nucleotide sequences of *Tritimoviruses* constructed in DNAMAN software by using multiple sequence alighnment and maximam likelihood method.



Phylogenetic relationship among different strains of WSMV showed that these virus strains has been isolated from Iran and USA respectively but most of the work had been done in University of Nebraska, 344 Keim Hall, Lincoln, NE 68583, USA. Mostly WSMV are present in Great Plains of United States, Canada, Jordan, Eastern Europe and Russian Federation and many other wheat producing countries (Navia *et al.*, 2013). This virus was first time identified in Nebraska as "yellow mosaic" in 1922. Since than it is spreading throughout the North America, Europe, part of Russia, and North Aftrica (McMechan, 2016).

All of the séquences use for the comparaison were collected from the GenBank NCBI. The maximum likely hood method was to construct phylogenetic dandrogram using DNAMAN software. Nucleotide sequence alignment correspondence to WSMV-type nucleotides 7618-9384. WSMV (AF285170) has similarity with On MoV (NC_005136) which are sister texa and clearly distinct from species of genus *Rymoviruse*. From multiple homology matrix sequence alignment DNAMAN software homology of sequence were confirmed. That was similar to these virus sequences of WSMV 99% FJ348358), WSMV 99% (AF511618) WSMV 98% (AF511630, AF285169), WSMV 90% (AF511630) as shown in figure 6 and 7.

Figure 7: Homology matrix of 17 sequences showed the similarity of different strains of WSMV among each other constructed by using Mega Align software



EU914918	100%																
EU914917	92.0%	100%															
AF511630	90.0%	96.2%	100%														
AF511619	90.4%	96.6%	96.7%	100%													
AF511618	91.0%	97.0%	97.8%	97.3%	100%												
AF511615	91.0%	97.0%	96.8%	97.4%	97.4%	100%											
AF057533	90.5%	96.8%	96.6%	99.1%	97.4%	97.5%	100%										
AF511614	91.2%	97.1%	96.7%	97.6%	97.6%	97.3%	97.9%	100%									
AF285170	78.9%	80.0%	80.2%	80.1%	80.0%	79.8%	80.1%	80.2%	100%								
AF285169	90.5%	97.2%	97.0%	97.4%	97.9%	97.3%	97.6%	97.7%	79.5%	100%							
FJ348358	90.5%	97.0%	98.1%	97.5%	98.8%	97.5%	97.6%	97.9%	79.8%	98.0%	100%						
NC_001886	90.5%	96.8%	96.6%	99.1%	97.4%	97.5%	100.0%	97.9%	80.1%	97.6%	97.6%	100%					
NC_005136	73.0%	73.5%	73.4%	73.3%	73.8%	73.0%	73.1%	73.2%	74.0%	73.4%	73.6%	73.1%	100%				
NC_005904	46.7%	47.4%	47.4%	47.9%	47.7%	48.0%	47.6%	47.9%	46.6%	47.7%	47.7%	47.6%	44.0%	100%			
FJ348359	90.9%	97.0%	98.0%	97.4%	99.0%	97.7%	97.6%	97.7%	79.7%	98.1%	98.9%	97.6%	73.7%	47.7%	100%		
AF454455	90.3%	96.5%	96.3%	98.8%	97.2%	97.1%	99.0%	97.6%	79.8%	97.2%	97.4%	99.0%	73.5%	47.5%	97.3%	100%	
AF454456	93.7%	91.5%	90.1%	90.1%	90.2%	90.9%	90.2%	90.9%	80.0%	90.4%	90.2%	90.2%	73.9%	47.4%	90.4%	90.0%	100%

Management of wheat streak mosaic virus disease: Management of viral disease is difficult and these diseases cannot be control by the use of chemicals. So the only way left is to control vector population and WSMV can be managed by the disturbance in the life cycle of WCM (De Oliveira, 2013). Destruction of all the residues of previous wheat crop before two weeks of planting is good practice to manage wheat curl mite. Surrounding weeds should be destroyed by tillage practices and with the use of herbicides, so that sources of virus inoculum and mite population can reduce. Crop rotation and early/late season crop sowing practices can also be used to reduce the population of mites.

REFERENCE

Ali, N., 2012. Molecular markers, cytogenetics and epigenetics to characterize wheat-thinopyrum hybrid lines conferring wheat streak mosaic virus resistance. University of Leicester.

Barnett, O. W., 2012. Potyvirus taxonomy. Springer science & Business Media.

Börner, A., F. C. Ogbonnaya, M. S. Röder, A. Rasheed, S. Periyannan and E. S. Lagudah, 2015. *Aegilops tauschii* introgressions in wheat. In: Alien introgression in wheat. Springer: pp: 245-271.

Bragard, C., P. Caciagli, O. Lemaire, J. Lopez-Moya, S. MacFarlane, D. Peters, P. Susi and L. Torrance, 2013. Status and prospects of plant virus control through interference with vector transmission. Annual review of phytopathology, 51: 177-201.

Brakke, M., 1971. Wheat streak mosaic virus. CMI/AAB descriptions of plant viruses, 48: 1-4.

Carr, J. P., R. Donnelly, T. Tungadi, A. M. Murphy, S. Jiang, A. Bravo-Cazar, J.-Y. Yoon, N. J. Cunniffe, B. J. Glover and C. A. Gilligan, 2018. Viral manipulation of plant stress responses and host interactions with insects in. Advances in virus research, 102: 177-197.

Coutts, B. A., M. Banovic, M. A. Kehoe, D. L. Severtson and R. A. Jones, 2014. Epidemiology of wheat streak mosaic virus in wheat in a mediterranean-type environment. European journal of plant pathology, 140(4): 797-813.

De Oliveira, C. F., 2013. Impact of wheat streak mosaic virus and triticum mosaic virus on transmission by *Aceria tosic*hella keifer (eriophyidae) and virus epidemiology in wheat.

Ito, D., 2011. Evaluation of susceptibility to wheat streak mosaic virus among small grains and alternative hosts in the great plains. Montana State University-Bozeman, College of Agriculture.

Ito, D., Z. Miller, F. Menalled, M. Moffet and M. Burrows, 2012. Relative susceptibility among alternative host species prevalent in the great plains to wheat streak mosaic virus. Plant disease, 96(8): 1185-1192.

Knoell, E. A., 2018. Transmission characteristics of triticum mosaic virus by the wheat curl mite aceria tosichella keifer and ecology of the wheat-mite-virus complex on field corn.

Lewsey, M., P. Palukaitis and J. P. Carr, 2018. Plant–virus interactions: Defence and counter-defence. Annual plant reviews online: 134-176.

McMechan, A. J., 2016. Over-summering ecology of the wheat curl mite (A*ceria tosic*hella Keifer).

Miller, A., P. Umina, A. Weeks and A. Hoffmann, 2012. Population genetics of the wheat curl mite (*Aceria tosichella* Keifer) in Australia: Implications for the management of wheat pathogens. Bulletin of entomological research, 102(2): 199-212.

Miorin, L., I. Romero-Brey, P. Maiuri, S. Hoppe, J. Krijnse-Locker, R. Bartenschlager and A. Marcello, 2013. Three-dimensional architecture of tick-borne encephalitis virus replication sites and trafficking of the replicated rna. Journal of virology, 87(11): 6469-6481.

Miras, M., W. A. Miller, V. Truniger and M. A. Aranda, 2017. Non-canonical translation in plant rna viruses. Frontiers in plant science, 8: 494.

Mirik, M., D. Jones, J. Price, F. Workneh, R. Ansley and C. Rush, 2011. Satellite remote sensing of wheat infected by wheat streak mosaic virus. Plant disease, 95(1): 4-12.

Mulenga, B. P., B. W. Brorsen, F. M. Epplin, C. M. Rush and F. Workneh, 2018. Economic threshold of wheat streak mosaic virus in the texas high plains.

Navia, D., R. S. de Mendonça, A. Skoracka, W. Szydło, D. Knihinicki, G. L. Hein, P. R. V. da Silva Pereira, G. Truol and D. Lau, 2013. Wheat curl mite, aceria tosichella, and transmitted viruses: An expanding pest complex affecting cereal crops. Experimental and applied ccarology, 59(1-2): 95-143.

Price, J. A., 2015. Ecology and epidemiology of wheat streak mosaic virus, triticum mosaic virus, and their mite vector in wheat and grassland fields.

Richardson, K., A. D. Miller, A. A. Hoffmann and P. Larkin, 2014. Potential new sources of wheat curl mite resistance in wheat to prevent the spread of yield-reducing pathogens. Experimental and applied acarology, 64(1): 1-19.

Seifers, D. L., T. Martin, T. L. Harvey, J. P. Fellers and J. Michaud, 2009. Identification of the wheat curl mite as the vector of triticum mosaic virus. Plant disease, 93(1): 25-29.

Skoracka, A., L. F. Lopes, M. J. Alves, A. Miller, M. Lewandowski, W. Szydło, A. Majer, E. Różańska and L. Kuczyński, 2018. Genetics of lineage diversification and the evolution of host usage in the economically important wheat curl mite, *Aceria tosichella* Keifer, 1969. BMC evolutionary biology, 18(1): 122.

Syller, J., 2012. Facilitative and antagonistic interactions between plant viruses in mixed infections. Molecular plant pathology, 13(2): 204-216.

Tatineni, S., R. A. Graybosch, G. L. Hein, S. N. Wegulo and R. French, 2010. Wheat cultivar-specific disease synergism and alteration of virus accumulation during co-infection with wheat streak mosaic virus and triticum mosaic virus. Phytopathology, 100(3): 230-238.

Tatineni, S., A. D. Ziems, S. N. Wegulo and R. French, 2009. Triticum mosaic virus: A distinct member of the family potyviridae with an unusually long leader sequence. Phytopathology, 99(8): 943-950.

Wosula, E., A. J. McMechan, C. Oliveira-Hofman, S. N. Wegulo and G. Hein, 2016. Differential transmission of two isolates of wheat streak mosaic virus by five wheat curl mite populations. Plant disease, 100(1): 154-158.

Date Published (D-M-Y): 15-04-2019