International Journal of Plant & Soil Science

17(2): 1-11, 2017; Article no.IJPSS.33722
ISSN: 2320-7035

Prevalence of Viruses Infecting Sorghum in Nigeria- A Review

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Authors' contributions

This work was carried out in collaboration between all authors. Author BM designed the study, wrote the protocol and wrote the first draft of the manuscript. Authors MDA and BDK managed the analyses of the study. Author OOB managed the literature searches. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2017/33722
Editor(s):
(1) Nasima Junejo, Department of Forest Production, Faculty of Forestry, Universiti Putra Malaysia, Selangor, Malaysia.
Reviewers:
(1) Md. Belal Hossain, Sher-e-Bangla Agricultural University, Bangladesh.
(2) M. Ali Sevik, University of Ondokuz Mayis, Turkey.
Complete Peer review History: http://www.sciencedomain.org/review-history/19910

Review Article

Received 26th April 2017
Accepted 9th June 2017
Published 7th July 2017

ABSTRACT

Viruses infecting sorghum are widely distributed in Asia and Africa and are of economic importance. In recent years, apparent virus disease incidence has increased, probably due to changes in agricultural practices associated with the introduction of hybrids and new varieties that are being developed and released continuously. The first virus disease described on sorghum in the world was *Sugarcane mosaic virus* (SCMV). Nigeria is one of the leading sorghum producing countries in the world and most of its populace in the northern part depend on sorghum as their primary staple food and so far, seven viruses have been identified on sorghum in Nigeria: *Maize mosaic virus* (MMV), *Maize stripe virus* (MSpV), *Maize streak virus* (MSV), *Sugarcane mosaic virus* (SCMV), *Guinea grass mosaic virus* (GGMV), *Sorghum mosaic virus* (SrMV) and *Maize dwarf mosaic virus* (MDMV). This calls for proper molecular characterization and deployment of management strategies of the diseases the viruses incite. Future research needs are discussed.

Keywords: Virus; sorghum; prevalence; epidemiology; management; Nigeria.

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1. INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench), belongs to the grass family, *Poaceae*. The *Sorghum* spp. originated in northern Africa and can grow in arid soils and withstand prolonged drought. Its cultivation then spread throughout Africa and Asia and to the Americas and Australia [1,2]. Different types of *S. bicolor* are recognized including grain sorghums, sweet sorghums, and grass sorghums [3,4]. *S. bicolor* is known by a variety of names, including milo or milo-maize in the United States, dura in Sudan, great millet and guinea corn in West Africa, kafir corn in South Africa, Mtama in eastern Africa, and jowar in India [3,5]. Sorghum has been the most staple crop in the semi-arid region of Africa, and other parts of the world, both in terms of production and total land area put to cultivation. It is the world's fifth most important cereal crop after wheat, rice, maize, and barley [3,6,7,8]. The world sorghum production was estimated as 69 million metric tonnes and Africa is the leading producing continent with production estimate of 29 million metric tonnes. Nigeria was ranked third world's largest producer after USA and Mexico [9]. In Nigeria, the crop ranks first among all other cereal crops cultivated in the Savannah zone between latitude 8° and 14° N and it is the second most important cereal crop in the country [8,10]. The crop is usually grown and confined to areas where there is high temperature. It possesses wide adaptability to different biotic and abiotic stresses of the environment, including the erratic nature of rainfall found in the areas of its production in Nigeria, typically in areas where the climate is also suitable for cotton and groundnut production [3,1,8]. The crop is used for human consumption and as feed for livestock. It is dried, stored and later used for a variety of food such as tuwo, akamu, flakes, chin-chin, and biscuits [11,7].

The potential yield and quality of the crop is lowered by many insect pests and diseases, which attack the crop from the time of planting to storage. The viruses infecting sorghum documented in Nigeria are, *Maize mosaic virus* (MMV), *Maize stripe virus* (MSpV), *Maize streak virus* (MSV), *Sugarcane mosaic virus* (SCMV), *Guinea grass mosaic virus* (GGMV), and *Sorghum mosaic virus* (SrMV) and *Maize dwarf mosaic virus* (MDMV) [12,13,11,14,15,16]. The loss in grain yield to viruses depends on the virus and the stage at which the crop is infected, with earlier infections resulting in greater loss [17].

2. MAIZE MOSAIC VIRUS (MMV)

MMV is the causal organism of maize mosaic disease. It was first discovered in Hawaii in 1921 and then other countries including Nigeria. It may cause a significant crop loss when environment is favourable for its dissemination [18]. The virus occurs worldwide but is of developing countries importance [19,20] and it was the first rhabdovirus described on plants [21]. It belongs to the family Rhabdoviridae, genus Nucleorhabdovirus. It is an RNA containing virus, single-stranded and unipartite with a molecular weight of c. 4.2 ×106 Daltons [22]. The large genome part is 12.54 kb. The particle is bullet-shaped, enveloped with a clear modal length of 22 nm and width of 90 nm. The sedimentation coefficient is 774 S and the density is 1.18 g cm-3 in sucrose [23,11,24]. The genome replicates in the nuclei while the coat protein (mRNA) is probably translated in the cytoplasm. The virus has several strains. The synonyms include; Zea mays virus and Sorghum chlorosis virus [11] The virus infection process starts after its vector, *Peregrinus maidis* Ashmead, acquired the virus, which passes through the nervous system of the insect and the injected in the host plant [25]. The distinguishing symptoms of the disease are discontinuous interveinal chlorotic streaks or mosaic on sheath and stalk, stunting and severe yield loss [19,23]. Initial symptoms on sorghum are chlorotic streaks between the veins, which later may turn necrotic [26]. In severe infections, the leaves turn chlorotic and plants become severely stunted. Panicles on such plants contain very few seeds [7]. MMV is transmitted persistently by the leafhopper, *P. maidis*, the virus can be acquired in less than 15 minutes and optimum acquisition requires 24 hours. The latent period in the vector varies between 9 to 12 days. Transmission can occur in as short a period as 15 minutes but transmission efficiency increases with length of inoculation access period 24 hours [27,23,11]. Nymphs appear to be more efficient vectors than adults [27]. The virus is retained when the insect moults and multiplies in the vector [28] but intermittently transmitted [29]. It is not transmitted congenitally to the progeny of the vector, not transmitted mechanically, not by contact between plants. It is also not seed or pollen- transmitted [23,11,24,7]. MMV can be detected by double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) [28,26] or immunosorbent electron microscopy. Light microscopy may be used to identify MMV-distinctive intracellular inclusions in stained epidermal strips [30]. MMV occurs

worldwide in moist and irrigated lowlands in tropical and subtropical areas such as Australia, Caribbean Islands, Cote d'Ivoire, Costa Rica, Fiji, India, Kenya, Mauritius, Madagascar, Mozambique, Mexico, Nigeria, Peru, Spain, Tanzania, Trinidad and USA [19,23,11]. The virus occurs mainly in the Northern and Southern Guinea Savannah zone of Nigeria but absent in the Sahel and Sudan Savannah zones [13,11]. The natural hosts include *Rottboellia exaltata* L., *R. Cochinchinensis* (Lour) Clayton, *Setaria vulpiseta* (Lam.) Roem and Schult., *S. Verticilliforum* Dumort *Z. mays* L., and *S. bicolor* (L.) Moench. *Z. mays* is the best assay propagation and maintenance host [27,23,11]. In Nigeria, the most susceptible sorghum varieties are land races: Fara--fara, Kaura, Guinea and Chad [13,11]. MMV can lead total crop loss of up to 100%, making a virus of high economic importance [19]. MMV occurrence is mostly severe where the environmental conditions favour the survival of its vector, *P. maidis*. The most effective way of managing MMV is achieved through the use of resistant varieties; since some varieties resistant to MMV have been identified [19].

3. MAIZE STREAK VIRUS (MSV)

Maize streak disease is caused by the *Maize streak virus* (MSV). The disease was first reported in South Africa in the early 1900s by Fuller and remains a major constraint to maize production in most regions of sub-Saharan Africa [31]. He first named the disease as 'mealie variegation' and it was renamed as maize streak by [32] in a demonstration that the disease agent was transmitted by leafhopper *Balclutha*, subsequently named *Cicadulina mbila* Naude. It is probably the most destructive viral disease of maize [33,34,35]. MSV belongs to the genus *Mastrevirus*, family *Geminiviridae*. The virion is geminate and not enveloped. It is 18 nm in diameter and 30 nm in length. The genome consists of single-stranded DNA circular and unipartite, with molecular weight of 7.1×10^5 Da [36,37]. The coat protein subunit of MSV is reported to be a single species of molecular weight 28,000 Da [38]. Particles of the virus sediment as two components in sucrose solution [39]. However, one could be a damaged particle as majority of geminiviruses are one component [23]. The virus replicates in the nuclei and does not depend on the helper virus. The peculiar symptom of the disease is chlorosis, white streaking and lesions [40,23,41]. MSV is transmitted persistently by twenty-two known species of *Cicadulina* leafhoppers, of which eighteen occur in Africa [42]. Among which are: *Cicadulina mbila* Naude, *C. arachidis* China, *C. bipunctella* China, *C. triangula* Ruppel, *C. similis* China, *C. latens* Fennah, *C. niger* Ghauri and *C. parazeae* Ghauri [32,43,44,23]. The virus does not multiply in the vector and it is not transmitted congenitally to the progeny of the vector. It is also not transmitted mechanically as well as contact between plants. There is also no seed or pollen transmission [40,23]. Experimentally, MSV or its cloned genomic DNA is transmissible to germinating maize seedlings by vascular puncture inoculation (VPI) [45,46]. Experimental transmission is also possible using cloned virus and delivery by a procedure called 'Agroinfection' or 'Agroinoculation' [47,48,49,50,51]. [50] used agroinfection to rapidly screen for MSV resistance in various maize genotypes. MSV can be detected using ELISA test kits and PCR [52,53]. A PCR-RFLP technique is being employed in differentiating the strains of MSV [54]. MSV is known to infect a wide range of indigenous grass species in Africa in addition to various cereal crops, including wheat, oat, sugarcane, millet, rice, barley, rye and sorghum [55,56,23,52]. Among the susceptible weed grasses, *Axonopus compressus* (Sw.) Beauv., *Brachiaria lata* (Schumach) Hubbard and *Setaria barbata* (Lam.) Kunth are the ones most likely to perpetuate MSV between maize plantings in West Africa [57]. Maize streak is predominantly a disease of maize in Africa although it has also been reported from south and south-east Asia. MSV occurs extensively throughout Africa [58,59, 34] from Sudan to South Africa and from east to west coasts, and also occurs on the adjacent of islands of Madagascar, Mauritius, Reunion, Sao Tome and Pricipe, and in Egypt [60] and Yemen [61]. It has also been reported to infect maize in Nigeria in Kaduna, Ibadan, Mokwa, Jos and Zaria by [62]. Outbreaks of the disease are infrequent, although severe epidemics can result in considerable yield loss. Outbreaks of maize streak have been associated with drought and irregular rain in west Africa [58,23,52]. MSV causes yield loss in infected crops. Depending on the time of infection and the mode of resistance of the variety, yield loss ranges from 24 – 100% [63,64,65,66]. Host-plant resistant remains one of the most promising methods of controlling MSV in crop plants since there are available resistant varieties [67], although there are other viable means of managing the disease, which include cultural practices aimed at reducing the number of vectors and use of insecticides are all available [58].

4. MAIZE STRIPE VIRUS (MSPV)

Maize stripe virus (MSpV) is another virus infecting maize and sorghum and its occurrence is confined to tropical and subtropical countries. The virus causes significant yield loss [68,23]. It belongs to the genus *Tenuivirus*. It is a single-stranded RNA containing virus with flexuous filaments 3-4 nm wide or spiral shaped filament formed from coils of 3 nm filaments [23,11]. The virus contains 5.2 per cent nucleic acid, 94.8 per cent but no lipid. Genome consists of RNA; single-stranded; linear; of five parts; largest (or only) genome part the largest 9.12 kb; the second largest 3.58 kb; the third largest 2.38 kb; the fourth largest 2.23 kb and the fifth largest 1.32 kb [23]. The virus has sedimentation ranging between 51 and 70 S by sucrose gradient centrifugation. RNA constitutes 5.2% of the virion and the capsid has a weight of 32.7 kDa [69]. When MSpV infects a plant, the virus particle is found in the mesophyll, phloem and cytoplasm. Inclusions present in infected cells are unusual in shape, amorphous, semi-opaque and filamentous electron dense laminated aggregates [11]. The striking symptoms of the disease are chlorotic stripes, bands in leaves, stunting and lack of panicle formation. The symptoms intensity diminishes as the sorghum plants get older and infected plants suffer reduced growth and sometimes die within a short period of time [70,23]. MSpV is transmitted persistently by the planthopper, *P. maidis* Ashmead (Homoptera: Delphacidae). It is not mechanically transmissible. After acquisition, the virus undergoes a latent period of at least 10 days in the vector. Transovarial passages from females to their progeny and replication in the vector have been demonstrated [11]. It is not transmitted by contact, seed or pollen [69,23,11]. The virus can be detected using MSpV antisera and characterized by means of PCR [60,71]. The epidemiology of MSpV is strongly linked the ability of its vector's population, which changes from time to time. The vector *P. maidis* travels long distances to disseminate the virus [7]. The virus spread in Australia, Botswana, Guadeloupe, India, Kenya, Mauritius, Mozambique, Nigeria, Peru, Philippines, Reunion, Sao Tome, Principe, USA and Venezuela [23,11]. The virus occurs in the Northern Guinea Savannah, and to a little extent, in Southern Guinea and Sudan Savannah ecological zones of Nigeria [11]. The virus naturally infects *Rottboellia cochinchinensis* (Lour) Clayton*, Brachiara deflexa* Hubbard*, Hordeum vulgare* L.*, Hyperrhenia dissolute* (Nees ex steud) Clayton*, Secale creale* L.*, Setaria* spp., *S. bicolor* (L.) Moench *and Z. mays* L. [69,23,11]. [11] reported that the most susceptible sorghum varieties are land races in Nigeria were Chad, Fara-fara, Guinea and Kaura and that the virus is more prevalent in research fields than farmers' fields. Loss of 70 – 93% head weight was reported to be caused by MSpV on sorghum [72]. The virus is being managed through the use of resistant varieties, removal of alternate hosts from farm areas and control of *P. maidis,* the vector of the virus [59].

5. SORGHUM MOSAIC VIRUS (SrMV)

Sorghum mosaic virus (SrMV) is one of four assigned species of potyviruses that infect graminaceous plants. It was originally thought to be a strain of *Sugarcane mosaic virus* but was later discovered to be an independent species [73]. It is a member of genus *Potyvirus,* family *Potyvirdae*. The common strains of SrMV were originally identified as strains of SCMV and were named SCMV strains H, I and M. They are presently denoted as SrMV-SC-H, SrMV-SC-I and SrMV-SC-M respectively [74,75,76,77]. SrMV resembles SCMV more closely than MDMV and is least similar to *Johnson Grass Mosaic Virus* (JGMV), the other species of gramineous potyviruses. Its virions are flexuous rod-shaped, 13 nm in diameter, and 750 nm long [77]. The buoyant density is 1.35 g cm^{-3} in CsCl. It is a positive-sense monopartite single-stranded RNA-containing virus which encodes for a single protein of about 350 kDa [78,79,80]. It produces mosaic and red-leaf symptoms in sorghum. It also incites mosaic, dwarfism, yellow-green streaks which later changed into reddish-brown necrotic streaks and stripes, thereafter, extensive reddish-brown necrosis of leaves followed [23,7]. SrMV is transmitted in a non-persistent manner by aphid *Dactynotus ambrosiae* Thomas [77]. Mechanical transmission is used in greenhouse and laboratory experiments. Seed transmission has not been reported [80]. Serological methods suing triple antibody sandwich ELISA (TAS ELISA) have been used in detecting SrMV [15, 16]. The virus was characterized by PCR and the genome was fully characterized [81,82]. SrMV infection may result in yield loss ranging from 21 – 46% [82]. The virus is most commonly introduced into sugarcane fields by planting of infected cuttings. Sorghum and maize adjacent to ratooned crops of sugarcane are most vulnerable to infection by the virus. Spread and incidence of the disease are higher in the sub-tropics than tropical areas, probably due to

seasonal migrations of aphids as weed populations' change. It is found in USA, India and Nigeria [15]. It occurred in the two of the major producing states, Kaduna and Kano States in Nigeria [16]. Spread and incidence of mosaics are higher in the sub-tropics than tropical regions, perhaps because of seasonal migration of aphids as weed populations change; Plants in the young growing stages are the most susceptible [80]. Among the most promising methods of controlling SrMV is the use of resistant varieties. The resistant genes against SrMV are available and can be deployed to sorghum varieties preferable to a particular country or region [83].

6. SUGARCANE MOSAIC VIRUS (SCMV)

Sugarcane mosaic virus (SCMV) was first reported in *Saccharum* spp. The virus occurs worldwide, infecting majorly sorghum and maize [7]. It belongs to genus *Potyvirus* family *Potyviridae*. [23]. The virus has a filamentous flexuous measuring between 730-755 nm long and 13 nm wide. It also has a sedimentation coefficient of 148-176 *S* and buoyant density of 1.3327 g cm^{-3} in CsCl. The virion is found in mesophyll, cytoplasm and Golgi apparatus [23]. The symptoms induced by this virus include mosaic, necrosis, ringspots, leaf reddening and stunting. The natural hosts of the virus are *Saccharum* spp., *S. bicolor* (L.) Moench*, Panicum* spp., *Eleusine* spp., *Setaria* spp., *Z. mays* L. and *S. halepense* (Linn.) Pers. [23,84]. It is transmitted in a non-persistent manner by some aphid species such as *D. ambrosiae* Thomas, *Rhopalosiphum maidis* Fitch, *Hysteroneura setariae* Thom*, Toxoptera graminum* (Rond.) and a number of aphid species in a non-persistent manner [85,23]. [100] reported that *Myzus persicae* Sulzer, transmits SCMV in a range of 15-45% with a mean of 29%; likewise, *Aphis gossypii* Glover gave a range of 10-30% with a mean of 19%; whereas *Schizaphis graminum* Rondai transmitted SCMV in a range of 55-85% with a mean of 72%. The virus is transmitted mechanically, by seed and grafting [23]. DAS-ELISA was used to detect SCMV from infected sorghum plants [16]. SCMV has been detected and characterized by RT-PCR [86]. Aphids population played a great role in the spread of SCMV. Although, the aphids do transmit the viruses only for short distances after its acquisition, implying the significant of infected plants in the neighbouring field before transmission can occur [87]. It is probably distributed worldwide: Australia, India, Iran, Japan, Philippines, Kenya, Mali, Malawi, Nigeria, Cameroon, Congo, Egypt, South Africa and United States of America [23,79,88]. The virus control is achieved by the use of much available resistant genes such as SCMV*1* and SCMV*2* [89,90].

7. GUINEA GRASS MOSAIC VIRUS (GGMV)

Guinea grass mosaic virus (GGMV)` was first discovered in Cote'd Ivoire on *Panicum maximum* by [91]. It belongs to the family *Potyviridae*. It is a filamentous single stranded RNA-containing virus, 815 nm long and 15 nm wide. The virus is found in all parts of the host plant and produces pinwheel inclusion bodies [91,11]. The thermal inactivation point is 50-60℃, longevity *in vitro,* 1-2 days at 25℃, while the dilution end point is log_{10} 2-4. It has a sedimentation density 148-176 *S* and density of 1.3327 g cm^{-3} in CsCl [23,11]. The distinguishing symptoms of the virus infection are dwarfing and light green mosaic [91]. The virus is transmitted in a non-persistent manner by the following aphids: *Hysteroneura setariae* Thom*, Rhopalosiphum maidis* Fitch and *T. graminum* (Rond.) [23,11]. Electron microscopy was employed to detect and characterize the virus. [91]. Polyclonal antibody has been developed and used for the detection of GGMV [7]. It has been reported in Brazil, Columbia, Cote d'Ivoire, Nigeria, and Australia. Its natural hosts include *Panicum maximum* Jacq*., Pennisetum americannum* (L.) Schum, and *Z. mays* L. [23,11]. The virus like other viruses, can be controlled by developing resistant varieties and farmers are also encouraged to adopt the cultural practices that minimize viral diseases, for instance*,* the modification of planting dates and the removal of alternate and collateral hosts on which the virus and the vector can multiply [19,79].

8. MAIZE DWARF MOSAIC VIRUS (MDMV)

Maize dwarf mosaic virus (MDMV) is the most important virus disease of sorghum worldwide and one of the most widespread Potyviruses infecting maize and sorghum in developing countries [1,7]. (MDMV) is a member of genus *Potyvirus*, family *Potyviridae*. It was first reported in *Z. mays* L., from Ohio, U.S.A [92,93,23]. It was previously included as a strain of sugarcane mosaic virus, but later shown to be an independent member of the Potyvirus group [94].

The virus has flexuous filamentous particles *c.* 750 nm long and 13 nm in diameter containing single-stranded RNA. A sedimentation coefficient of 176 ± 5 *S*, buoyant density in CsCl of 1.3421 [94]. The symptoms of the virus infection vary with the host genotype, virus strain and temperatures. Time of infection also influence symptom expression, which is greatest with infection at the two- to three-leaf stage [1]. The distinguishing symptoms of the disease are systemic mosaic, red leaf, red stripe and necrosis of leaves, plant stunting, delayed flowering, and reduction in head length, number of heads, seed size, number of seeds per head and grain yield [95,1,96,23]. It is transmitted by the Greenbug (*Schizaphis graminum* Rondai) *Rhopalosiphum maidis*, R. padi, *M. persicae*, and *A*. *craccivora* in a non-persistent manner [94,1]. It is transmissible mechanically, but not transmitted by contact between plants. It is also transmitted by seed [94,23,79]. Triple antibody sandwich ELISA (TAS-ELISA) and RT-PCR have been used in the detection of MDMV [97,16]. It infects numerous species in the Gramineae, and induces the formation of cytoplasmic, cylindrical (pinwheel and scroll) inclusions in host cells. Different sorghum and maize cultivars are readily infected. Systemic mosaic and/or necrosis are produced [94]. MDMV virus dissemination relies on two main factors; availability of Johnson grass and aphid population [98]. The virus spreads widely in China, Thailand, Korea, South Africa, USA, India, Cote d'Ivoire, Burkina Faso, Mali, Ethiopia, Cameroon and Nigeria [23,79,16]. MDMV infection have been reported to cause 100% yield loss in sorghum [1]. Altering vector behaviour with light, sticky traps, pheromone traps, and the planting of disease-tolerant or – resistant varieties that reduce virus multiplication can improve virus disease management, especially MDMV [1,79]. Pathogen-derived resistance (PDR) has been developed for MDMV-B (SCMV-MDB) involving the CP gene introduced into maize to provide cross-protection/resistance to MDMV-A as well as to MDMV-B [99].

9. WEED HOSTS OF SORGHUM VIRUSES

Many weed species were shown to harbour plant virus either as alternative or alternate hosts. Some of the weeds found to serve as reservoir to viruses infecting sorghum, include *Rottboellia exaltata* L., *R. cochinchinensis* (Lour) Clayton, *Setaria vulpiseta* (Lam.) Roem and Schult and *S. Verticilliforum* Dumort, the afore-mentioned weed plants were found to be host of MMV [23,11,27]. While *Axonopus compressus* (Sw.) Beauv., *Brachiaria lata* (Schumach) Hubbard, and *Setaria barbata* (Lam.) Kunth were shown to host MSV [57]. For MSpV, its hosts are *Rottboellia cochinchinensis* (Lour) Clayton, *Brachiara deflexa* Hubbard, *Hordeum vulgare* L., *Hyperrhenia dissolute* (Nees ex steud) Clayton, *Secale creale* L., *Setaria.* [69,23]. The natural weed hosts of the SCMV are *Panicum* spp., *Eleusine* spp., *Setaria* spp., and *Sorghum halepense* (Linn) Pers. [23,84]. The natural hosts of GGMV are: *Panicum maximum* Jacq. and *Pennisetum americannum* (L.) [23]. Determining the distribution of wild graminaceous weed hosts and the vectors of the viruses is very essential for good management of the viral disease [79].

10. CONCLUSION

Prevalence of viruses infecting sorghum in Nigeria is factual, and many of the viruses reported to infect the crop in other parts of the world are yet to be identified in the country. To properly manage the diseases incited by these viruses, there is need to carry out more intensive surveys across the country, particularly the leading sorghum producing zones, in order to ascertain the status of the previously detected viruses and to detect new ones that are not yet detected, if present. Detailed molecular characterization of the viruses detected should also be conducted, as well as, epidemiology and weed hosts of the viruses should be studied. This is to enable the development of comprehensive management strategy of the viruses on sorghum in Nigeria for sustainable sorghum production.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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