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Emerged Plant Virus Disease in Ethiopian Agriculture: Causes and Control Options

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Abstract

Many plant virus diseases that have either newly emerged or expanded their distribution in the last two decades are causing tremendous crop losses to Ethiopian agriculture. The eight most significant of these are maize lethal necrosis (MLN), sweet potato virus (SPV), tobacco bushy top (TBT), tomato yellow leaf curl, legume stunt, faba bean necrotic yellows and stunt, enset leaf streak and cabbage mosaic diseases. MLN, SPV and TBT diseases are caused by synergistic interaction of at least two viruses while others are caused by single virus infection. Insect vectors transmit all the causal viruses. Five of the viruses involved namely Chickpea chlorotic stunt virus, Enset leaf streak virus, Ethiopian tobacco bushy top virus, Faba bean necrotic stunt virus and Faba bean yellow leaf virus are described and reported for the first time from Ethiopia. These new viruses have likely co-evolved with their hosts in Ethiopia. On the other hand, viruses previously known elsewhere such as Maize chlorotic mottle virus may have been introduced to the country by either germplasm import, seed trade or other means. If the causal virus and its mode of field spread are understood, disease control practices used elsewhere can be adapted and recommendation can be made accordingly. However, for efficient and sustainable management based on integrated approach, local studies on epidemiological parameters are necessary.

Introduction

Among the plant pathogens, viruses are considered second only to fungi with respect to economic losses in crops worldwide. Virus-like symptoms of crop plants in Ethiopia were first reported some 50 years ago (Stewart and Dagnachew, 1967) whereas systematic laboratory-based research started in late 1970s at Ambo Plant Protection Research Center. A review by Abraham and Assefa (2000) documented the earlier studies on virus and virus-like diseases of crop plants in Ethiopia. Many of the virus diseases described therein such as yellow dwarf of wheat and barley, streak of maize and mosaic of pepper and tomato are well established in the agricultural system and continue to negatively affect crop production. On the other hand, several virus diseases which have either emerged as new or increased their incidence in the last two decades continue to incur huge crop losses. The use of modern molecular technologies in the diagnosis and identification of such established or newly emerged virus diseases has led to detailed understanding of the genetic structure of causal viruses and helped in generating useful information to devise ways for their management. Subsequently, about 70 distinct viruses have so far been identified as causing plant diseases in Ethiopia while many more are expected to be revealed in years to come.

Emerging diseases are defined as the ones that have appeared in a population for the first time, or that may have existed previously but are rapidly increasing in incidence or geographic range in the past 20 years causing considerable damage (Castillo et al. 2015, Damstegt, 1999). Worldwide, the number of newly emerged plant disease epidemics has dramatically increased in the last few decades. A critical appraisal of emerging infectious plant disease globally by Aronson et al (2004) indicated that among plant pathogens, viruses make up close to half (47%) of newly emerged plant diseases followed by fungi (30%), bacteria (16%), phytoplasma, nematodes and others taking the remaining 7%. An existing virus when conditions are favorable or when they are introduced into a new area or by new viruses / virus strains or a new vector species or biotype may cause such emerging plant virus disease. Ethiopia is no exception to this and a number of newly emerged crop virus diseases are taking a heavy toll in national agricultural production. This paper describes the top eight most significant virus diseases that have newly emerged or increased their importance in the last two decades in Ethiopia with emphasis on their causal agents, economic importance and options for their control. The virus diseases selected are maize lethal necrosis disease, sweet potato virus disease, tomato yellow leaf curl, tobacco bushy top, chickpea stunt, faba bean necrotic yellows and stunt, enset leaf streak and cabbage mosaic. Specific properties of the causal viruses such as particles morphology, genome structure and methods of transmission are presented in Table 1.

Newly emerged virus diseases of major significance

Maize lethal necrosis disease

The most important disease affecting maize in Ethiopia currently is maize lethal necrosis (MLN) caused by synergistic interaction of two unrelated viruses. In Ethiopia, the disease is caused by double infection of *Maize chlorotic mottle virus* (MCMV, genus *Machlomovirus*, family *Tombusviridae*) and *Sugarcane mosaic virus* (SCMV, genus *Potyvirus*, family *Potyviridae)* (Mahuku et al., 2015). Among the two causal viruses, the new and the most important component is MCMV since SCMV is known to commonly occur on maize in Ethiopia for long time causing mild mosaic symptom (Lencho et al. 1997). Major symptoms of MLN include drying of leaves, premature plant death, failure to tassel, sterility in male plants, malformed or no ears and premature drying or rotting of cobs. High yield losses in maize due to MLN ranging from 50 to 90% have been reported (Niblett and Claflin, 1978) and this can reach 100% where the disease pressure is high. Single infection of maize with one of these viruses causes mild symptoms and does not cause MLN. Insect vectors transmitting the virus under field condition are thrips and beetles for MCMV and aphids for SCMV (Brunt et al. 2000). Low level of transmission through maize seeds has been reported for both MCMV and SCMV (Brunt et al. 2000).

In Africa, MLN has first been reported in 2011 in Kenya where it was reported to cause an extensive to complete yield losses to farmers (Wangai et al. 2012). The disease is first reported in Ethiopia in 2014 seasons causing various levels of damage ranging from low infection rate to total crop failure in some maize fields in rift valley area in East Shewa Zone in Oromia Region (Mahuku et al. 2015). Subsequent surveys revealed that the disease is widespread and has caused a total crop failure forcing farmers to replace maize with other crops in many areas of Oromia and SNNP regions (Fentahun et al. 2017, Guadie et al, 2018, Demissie et al. 2016). Because both viruses are known to be seed-transmitted at low rate, the Ethiopian Ministry of Agriculture had decided maize seeds produced for sowing in 2014/5 growing seasons from MLN infected areas not to be distributed for sowing in next season unless they are tested for and confirmed to be free of MCMV so that possible virus spread to virus-free areas with infected seeds and insect vectors is avoided. Despite initial attempts, the decision was not enforced due to practical difficulties and the disease unfortunately has rapidly spread to nearly all major maize growing areas establishing itself as a major production constraint. The distribution and economic importance of MLN in the country however still varies with Oromia and SNNP regions being the most affected, and Amhara, Tigray and Benshangul-Gumuz regions being of much lesser prevalence and incidence (Demissie et al. 2016, Fentahun et al. 2017, Guadie et al. 2018). Many MLN positive maize samples in Ethiopia were also shown to be infected with a polerovirus named Maize yellow mosaic virus (Guadie et al. 2017), although the role of this virus in symptom enhancement is not clear.

Since no single method can efficiently control MLN, research efforts are underway in Ethiopia to devise integrated management options. These include screening for resistant genotypes, the use of virus-free seeds and seeds treated with chemicals for vector control,

and cultural practices like rogueing of infected plants early in the season and removal of alternate hosts and volunteer plants. Some introduced maize varieties released in Kenya as MLN resistant are found to be promising under field condition and thus being verified under controlled greenhouse inoculation. Creating awareness of stakeholders in integrated MLN management is also essential.

Sweet potato virus disease

Sweet potato virus disease (SPVD) caused by dual infection of aphid-transmitted *Sweet potato feathery mottle virus* (SPFMV, genus *Potyvirus*, family *Potyviridae*) and whitefly-transmitted *Sweet potato chlorotic stunt virus* (SPCSV, genus *Crinivirus*, family *Clostroviridae*) is the most serious disease of sweet potato in Africa since 1940s. Single infection of any of the two viruses only causes milder symptoms and does not cause SPVD. The disease has not been reported in Ethiopia until the last decade. For example, Alemu (2004) reported a high incidence of SPFMV in some fields mainly from Wolayita zone but did not encounter SPCSV and thus suggested the absence of SPVD in the country. Few years later however, symptoms resembling those of SPVD were observed in some research and farmers' fields in southern Ethiopia (Abraham et al. 2010). The unusually high infection rates of what appeared to be SPVD in 2006/7 cropping seasons in particular forced the national research system to temporarily stop the distribution of 16 improved sweet potato varieties released over a period of a decade due to fear of further dissemination to farmers' fields where similar disease has not been reported. Follow up laboratory studies confirmed that most of the symptomatic sweet potato germplasm resources maintained in research fields at Awassa and Wondo Genet in southern Ethiopia had a high incidence of SPFMV and SPCSV, for the first time confirming the occurrence of the two components of SPVD (Abraham, 2010). A more comprehensive survey for SPVD that covered farmers' fields in most of the main sweet potato growing areas indicated that both SPFMV and SPCSV (Tesfaye et al. 2011) are prevalent in most zones of southern Ethiopia.

With the high prevalence and incidence in sweet potato fields in southern Ethiopia, the disease is already undermining food security in the affected areas with 47.8% - 92.6% yield reduction witnessed in susceptible genotypes under experimental conditions (Shiferaw et al. 2016). Thus, efforts are being made to provide farmers with affordable ways of management. Evaluation of 25 sweet potato genotypes for resistance by Shifereaw et al. (2016) indicated that thirteen introduced germplasms and one Ethiopian cultivar were found virus tolerant, high yielder and with good stand establishment. These promising genotypes are planted across the environments to further verify their resistance to sweet potato viruses (Shifereaw et al., 2016). Virus-free vines generated from tissue culture and tested as virus-free are being used to grow in higher altitude areas that are free of insect vectors to manage the disease in southern Ethiopia. While such initiatives are encouraging, they are currently done only in limited scale and due attention should be given by the concerned bodies to scale up the activities to have a meaningful positive impact in sweet potato production.

Tomato yellow leaf curl disease

Tomato yellow leaf curl disease (TYLC) is a major constraint of tomato production worldwide caused mainly by whitefly transmitted begomoviruses collectively called Tomato yellow leaf curl virus-like viruses (Aunpam and Malathi, 2003). Although TYLC has been recorded in 1970s as important tomato disease in the rift valley area based on symptomatology, the disease however was not reported in large scale surveys of tomato virus diseases done in 1980s and 1990s in Ethiopia in which mosaic causing viruses such as tobamoviruses and potyviruses have been reported as prevalent (Agranovisky and Anisimoff, 1986; Hiskias et al. 1999). Laboratory analysis of tomato samples with a disease resembling TYLC collected in Melkasssa area in central rift valley in 2003 for the first time revealed the association of a begomovirus identified as *Tomato yellow leaf curl Mali virus* (TYLCMLV) (Shih et al. 2006). A follow up PCR-based survey in 2009 indicated that TYLC occurred in epidemic proportion on tomato in some parts of the rift valley areas with a high incidence of (up to 95%) (Wada et al. 2014). The disease was particularly severe in fields at Upper Awash, Merti, Melkasa and fields along the road from Mojo to Zwai along with high whitefly population. This work thus revealed the emergence of TYLC as a major tomato virus disease causing serious losses in the fields of Rift Valley areas and that measures for its management are necessary. Further molecular studies of the complete genome of seven TYLCMLV isolates revealed the occurrence of two distinct sequence variants of TYLCMLV that may be considered as two strain groups that differ in 7% nucleotide sequence across the virus genome.

The epidemic of TYLC in the affected areas is consistently associated with the high population of the whitefly vector (*Bemsia tabaci)*. It is indicated that the warmer environmental conditions together with more intensive monoculture in the Rift Valley may have provided favorable condition for population increase of its whitefly vector. In other countries, the emergence of TYLC is believed to be associated with the global expansion of the B biotype of *B. tabaci* (Aunpam and Malathi, 2003). Hence, biotyping of whitefly population in affected tomato fields can provide useful information. It should be noted that the whitefly (*B. tabaci*) is also shown to transmit *Tomato mild mottle virus* (Abraham et al. 2012a), an ipomovirus known to be widespread in tomato fields in Ethiopia (Hiskias et al. 1999), raising further concern on the importance of the whitefly in tomato virus diseases epidemiology.

Controlling TYLC is a demanding task that can only be successful by integrated implementation of several management strategies including cultural practices like crop rotation, the use of host-free period, insecticidal control of the insect vector and obtaining transplants from virus-free areas and when available, along the use of resistant varieties (Anupam and Malathi, 2003). In Mali, for example a host-free period of two months has been reported to be successful for managing begomovirus infections of tomato (Pfeiffer et al. 2011). Whereas practices used elsewhere can be adapted to control TYLC, local studies on its integrated management based on adequate understanding of the epidemiological parameters including alternate hosts, vector pressure and appropriate planting date are necessary for efficient and sustainable management.

Tobacco bushy top disease

A new virus-like disease of tobacco (*Nicotiana tabacum*) first observed in 2006 cropping seasons in Bilate commercial farm during a general virus survey rapidly became widespread in the region resulting in drastic reduction (up to 60 %) in harvestable leaf yield. Diseased plants showed symptoms of stunted growth, leaf distortion and curling. Early formation of lateral shoots on which other shoots were produced resulted in infected plants showing the characteristic bushy top appearance. The symptoms resemble what is known to be characteristic of the tobacco bushy top disease (TBT) first reported in Zimbabwe in 1958 where it caused severe damage (Gates et al. 1962). In Zimbabwe, TBT is caused by a mixed infection of *Tobacco bushy top virus* (TBTV, genus *Umbravirus*) and *Tobacco vein distorting virus* (TVDV, genus *Polerovirus*, Family *Luteoviridae*). Due to striking similarity in symptoms, it was initially suspected that the same causal agents are involved in bushy top disease of tobacco in Ethiopia. In the contrary however, it was revealed that the disease is caused by a novel combination of a new umbravirus, *Potato leaf roll virus* (PLRV) and a new satellite RNA (Abraham et al., 2014).

In experimental host range study (Abraham et al. 2014), the disease was transmitted to Virginia tobacco causing disease identical to that in the field. In addition, many other solanaceous species including *N. occidentalis, N rustica, N. tabacum* (cv. Xanthi & Samsun), *N. hesperis, N. clevelendi* and *Solanum lycopersicum* (tomato) were infected by artificial inoculation. Among the weed samples collected from tobacco fields, the three agents were detected in *Nicandra physaloides* samples collected in both 2009 and 2011. All the three agents are efficiently transmitted from bushy top-diseased tobacco by field-collected red tobacco aphid (*Myzus persicae nicotiane*) to healthy tobacco plants including Virginia variety and several other plant species (Abraham et al. 2014). Hence, this aphid which is also the most common insect in tobacco fields in Ethiopia, is very likely responsible for the field spread of the disease. PLRV is required for transmission of all the viral agents by the aphid.

Experiences of tobacco bushy top disease management from countries like China and Zimbabwe shows that no single method can result in complete control of the disease and that integrating the various components is necessary to minimize the loss due to the disease. Since the disease is spread in similar way, the same approach can be adapted to manage the disease. The options include the use of insecticide to control the aphid vectors, employing cultural practices like avoiding planting and seedbed preparation during the time with high aphid pressure, suitable adjustment in crop calendar (intercrop period between the tobacco crops) and safe distance between seedbed and standing crops reducing primary infection sources like weeds and volunteer tobacco crops and early rouging of infected plants, and if available, using disease resistant varieties. In China for example, the use of insecticides alone resulted in 61% control efficiency whereas integrated approach using insecticides and cultural practices increased the efficiency to 86.9%.

Chickpea stunt disease

Stunt is considered the second most important chickpea disease in Ethiopia after fungal wilt and root rot disease and causes a yield loss as high as 30% (Hulluka and Tadesse, 1994). Serology-based surveys in late 1990's suggested that Beet western yellows virus (BWYV) is the main cause of stunting and yellowing diseases of chickpea, lentil and faba bean (Abraham et al. 2000, Tadesse et al. 1999). A more detailed molecular investigation on viruses associated with chickpea stunt and faba bean yellows in Ethiopia however revealed that stunt is predominantly caused by a new polerovirus for which the name Chickpea chlorotic stunt virus (CpCSV) has been coined (Abraham et al. 2006). In the same work, it was shown that the virus naturally infect lentil, grasspea and fenugreek causing yellowing and/or reddening symptoms. The virus is found to be transmitted by *Aphis craccivora* and its host range and complete genomic sequence have been described (Abraham et al. 2006).

Since its discovery in Ethiopia, CpCSV is reported from many countries including Eritrea, Sudan, Syria, Morocco, Egypt, Tunisia, Azerbajan, Australia, China, Yemen and Iran (Abraham et al. 2009, Makkouk and Kumari, 2009). A study also indicated that there are at least two CpCSV strains that differ considerably in their symptomatology, serology, nucleotide sequence and their geographical distribution within East and North Africa and West Asia (Abraham et al. 2009). The existence of serological cross reaction between CpCSV and other legume poleroviruses such as BWYV has been implicated as a possible reason for the previous misidentification of CpCSV as BWYV (Abraham et al. 2006).

In a legume virus survey conducted in 2007 growing season in northern Ethiopia (Gojam, Gonder, Tigray, Wello and Shewa regions), most of the 128 chickpea and lentil fields had stunt symptoms resembling those caused by viruses with incidence ranging from trace up to 80%. The highest prevalence and incidence of chickpea stunt was recorded in Western Tigray with incidence as high as 80% recorded in Shire area (Adane Abraham and Bedasso Jebessa, unpublished data). This contrasts with earlier reports where incidence of chickpea stunt disease is usually not more than 30% (Hulluka and Tadesse, 1994) and shows that chickpea stunt has become more important economically. CpCSV is also found to be the most prevalent virus serologically detected in 105 out of 125 (84%) of the fields. The reported high prevalence, incidence and expansion of geographical distribution of stunt in chickpea and other legumes caused by CpCSV suggests that its economic importance has increased in the last decade. Thus, concerted efforts should be made to manage the disease.

In addition to CpCSV, another new virus causing stunting and yellowing in lentil in Ethiopia has been described using molecular methods and a tentative name Lentil stunt virus is given (Abraham et al. 2008). Other viruses rarely associated with legume stunt disease hence of minor economic importance in Ethiopia include Bean leaf roll virus, Chickpea chlorotic dwarf virus and Faba bean necrotic yellows virus and Soybean dwarf virus (Abraham et al. 2000, Abraham et al. 2008. Tadesse et al. 1999).

As a newly discovered virus, little research attention was given in Ethiopia and elsewhere to the management of stunt caused by CpCSV. However, since the virus might have existed as a causal agent of chickpea stunt long before its discovery, previously identified sources of resistance for stunt (Hulluka and Tadesse, 1994) might be useful. In addition, the virus is persistently transmitted by aphids like many other luteoviruses and control options used for them such as seed treatment and planting date adjustment (Makkouk and Kumari, 2001; Makkouk and Kumari, 2009) can be adapted. Nevertheless, targeted research to identify sources of resistance and other integrated management in Ethiopian condition is required to stop this expanding disease.

Faba bean necrotic yellows and necrotic stunt disease

Necrotic yellows and necrotic stunt represent faba bean diseases caused by three closely related nanoviruses (*genus Nanovirus, family Nanoviridae*). Necrotic yellows was first reported in early 1989 from faba bean in Syria (Katul *et al.*, 1993), causing huge losses in affected areas. In Ethiopia, it was reported in lentil and faba bean with the causal agent identified as *Faba bean necrotic yellows virus* (FBNYV) (Tadesse *et al*., 1999; Abraham et al. 2000). In faba bean, leaves become thick and brittle and show interveinal chlorotic blotches starting from the leaf margins, which becomes necrotic and kills the plants within 5–7 weeks. In other legumes, the nanoviruses cause yellowing and stunting symptoms very similar to luteoviruses with the exception of grasspea on which severe stunting and bunchy top leaves are observed (Abraham and Lencho, 2000).

Earlier, serological studies suggested that FBNYV caused necrotic yellow disease of faba bean in Ethiopia (Franz et al. 1996, Tadesse et al. 1999, Abraham et al. 2000). Detailed molecular studies at genome level however later revealed that most faba bean nanovirus isolates from Ethiopia were genetically distinct from typical FBNYV isolates from other countries, by over 25% in total nucleotide sequences difference (Grigoras et al. 2010). Based on molecular criteria, these isolates predominant in Ethiopia were thus considered to belong to a distinct species for which the name Faba bean necrotic stunt virus (FBNSV) has been proposed (Grigoras et al. 2010). Further molecular analysis of large number of Ethiopian nanovirus isolates (Abraham et al. 2012b) revealed that in addition to FBNSV, two more distinct nanovirus species, comprising typical FBNYV identical to that found in countries like Syria and a novel species tentatively named Faba bean yellow leaf virus (FBYLV) exist in Ethiopia in limited proportion of samples. FBYLV is thus a tentative new nanovirus species so far reported only from Ethiopia. FBNSV, on the other hand, is reported from few more countries including Morocco, Azerbajan and Iran (Abraham et al. 2010).

The three nanoviruses have similar mode of field spread and thus can be managed more or less in the same way. Thus, the integrated virus management practices found effective for faba bean necrotic yellows virus in Egypt (Makkouk & Kumari, 2009) can be recommended for FBNSV in Ethiopia. These consist of seed treatment with imidacloprid before planting, judicious application of insecticide for vector control, planting at an appropriate time to avoid peak number of viruliferous aphids, planting to provide high-

density crop stand, and planting with resistant genotypes, where available. Attempts to obtain faba bean genotypes resistant to FBNSV from local accessions in Ethiopia as well as from international sources by field screening with supplementing artificial inoculation has not been successful as all accessions were highly susceptible (Abraham and Bedasso, unpublished data).

Enset leaf streak disease

Leaf streak disease, also causing severe stunting of enset (*Ensete ventricosum*) plants, has been reported in different parts of Ethiopia in 1990's. The association of a bacilliform DNA virus has been reported with the disease (Tessera et al. 1995). Preliminary yield loss assessment of two enset clones in natural stands showed that there is very high reduction in the fresh yield (93-98%), pseudostem circumference (74-77%) and height (64-73%) (Tessera et al, 2009). However, apart from suggested badnavirus etiology at genus level (Quimo and Tessera, 1996, Williams and Matile-Ferrero, 1999), the precise identity of the causal virus species remained unknown.

Recently, from enset with leaf streak disease, a virus resembling the badnavirus reported earlier (Tessera et al. 1995) by having bacilliform particles has been isolated and further characterized using molecular tools including rolling circle amplification, inverse PCR and nucleotide sequencing (Abraham et al. 2018). The virus particles decorated at medium level using Banana streak virus OL antibodies indicating their serological relationship. Sequence analysis of its circular dsDNA genome showed that the virus is genetically most closely related to Sugarcane bacilliform Guadaloupe D virus recently reported from sugarcane with 73.6% overall nucleotide identity. Based on molecular criteria, the virus is sufficiently distinct from others that it should be considered a new species in genus *Badnavirus* for which the name Enset leaf streak virus (ELSV) is suggested. The virus was also detected in 6 out of 40 randomly collected enset samples using virus specific primers in PCR suggesting that ELSV is fairly widely distributed. Banana streak OL virus (BSOLV), the most common banana virus in Africa, was not detected in any of enset samples while several banana samples were positive (Abraham et al. 2018).

Mealybugs which are known to be the main vectors of badnaviruses may also contribute to the field spread of the virus from infected to healthy plant. In Ethiopia, two species of mealybugs, *Cateanococcus ensete* and *Planaococcus ficus* are reported to be associated with enset (Williams and Matile-Ferrero, 1999). Hence, the potential of these mealybugs in transmitting ELSV should be investigated.

Since enset is vegetatively propagated, tissue culture in combination with heat and chemotherapy can assist in obtaining virus-free enset to minimize possible loss due to the virus. Similar approach has been successfully implemented for related vegetatively propagated crops like banana and plantain. In recent years, efforts are being made by research institutions in Ethiopia to provide growers with large quantity of tissue culture-derived disease-free enset seedlings of improved varieties to boost production (Abraham, 2009). Badnaviruses however are known to be integrated to host genome and there is evidence of the same in ELSV-enset pathosystem (Abraham et al. 2018). Thus, a reliable

virus-testing procedure discriminating integrated and episomal viral sequences is necessary.

Cabbage mosaic disease

Cabbage (*Brassica oleracea var. capitata*) is an important leafy vegetable crop grown widely in Ethiopia. About 70% of leafy vegetables consumed in Addis Ababa are supplied by small scale farmers living in the city of which cabbage locally named *tiqur gomen* is the most widely cultivated. A virus-like disease of cabbage with symptoms including mosaic, leaf distortion, a striking yellowing and veinal chlorosis, stunted growth and leaf deformation severely reducing yield and impair quality of cabbage has been observed by the author in fields in Addis Ababa since 2011. In a survey conducted in 2016 and 2017 in 21 farms, the disease was recorded in nearly all cabbage fields with incidence often reaching 100%. The symptoms were more severe in black stemmed varieties locally called Tikur gomen. When 108 samples collected from suspected cabbage samples were tested by double antibody sandwich ELISA for three viruses, *Turnip mosaic virus* (TuMV) was observed in all field while some also had mixed infection of TuMV and *Cauliflower mosaic virus* (CaMV) (Abraham and Guadie, unpublished data). The result was confirmed by reverse transcriptase-PCR and sequencing of TuMV genes product of ca. 1kb with selected cabbage samples which indicated that TuMV is indeed the causal agent of the disease. From the results, the Ethiopian TuMV isolate had 97% nucleotide identity with UK1isolates (from United Kingdom). This is the first report of virus disease infecting these crops in Ethiopia. The cabbage aphid (*Brevicoryne brassicae*) which is known to transmit the disease is also observed in many fields. The high incidence, the magnitude of losses in yield and marketability of cabbage due to TuMV calls for further information on its distribution and importance in other parts of the country and the need for devising immediate control measures.

TuMV has wide host range and is efficiently transmitted in a nonpersistent manner by several aphid species, most notably the green peach aphid (*Myzus persicae*) and the cabbage aphid (*Brevicoryne brassicae*). Cultural practices like removing TuMV-infected plant debris and eradicating infected plants around fields can help to reduce virus inoculum and hence spread. The application of a straw mulch to seed beds, to deter aphids from landing and feeding, ensuring that individual crop species are grown separately, destroying when possible all weeds, both in the crops and in their immediate vicinity are some of the control methods recommended. As a non-persistently transmitted virus, the use of insecticides is unlikely to completely control TuMV but might help to reduce aphid populations and reduce the rate of virus spread. Sources of resistance for TuMV have been found and used in other countries and could be looked after in Ethiopian cultivars.

Factors Deriving Virus Disease Emergence

An authoritative study on the factors deriving the global emergence of plant virus diseases revealed that, introduction from other countries makes up 71%, followed by change in vector population (16%), weather (5%), recombination (5%) and farming techniques (3%) (Aronson et al. 2004). Humans are known to be largely responsible for virus introduction directly or indirectly. Directly, humans contribute by introducing 1) a new virus or virus strain often linked to the movement of seeds or vegetative propagated materials due to germplasm movement or seed trade, 2) a new vector species or biotype (e.g. aphids, whiteflies, thrips and whiteflies) along with such materials, 3) a new crop or new vulnerable genotype during crop diversification. The weak quarantine system in which virus inspection is not done using reliable and sensitive techniques like ELISA and PCR may have contributed to the situation. Humans can also indirectly contribute by inducing changes in agronomic practices due to agricultural modernization by planting monocultures or exotic crops, by introducing agricultural practices like irrigation that enhance virus spread, or by excessively relying on chemical control enhancing vector resistance to insecticide. In addition to humans, viruses can be introduced to a country via aerial vectors across borders as many can fly long distances. Finally, seasonal or long-term changes in climate can enhance virus spread.

Possible Origin of the Causal Viruses

It is known that several exotic pathogens and insect pests have entered into Ethiopia during the past decades (Kumsa et al. 2009) but no information exists on intercepted viruses probably due to the fact that our quarantine system is unable to effectively detect viruses. Thus, one can only speculate about the possible origin of the specific viruses discussed above. MCMV is probably introduced with maize seeds from the Americas to Eastern Africa including Ethiopia from which further spread within the country is facilitated by ubiquitous aerial vectors and infected seeds. The finding of limited genetic diversity among isolates of MCMV from different geographic locations and hosts (Fentahun et al. 2017, Mahuku et al. 2015, Guadie et al. 2018) seems to support this suggestion. The widespread occurrence of SCMV, the presence of susceptible maize cultivars and environmental conditions favoring the vectors may have aggravated the development of MLN. Sweet potato viruses are very likely introduced from Eastern Africa with vegetative planting materials introduced for research purposes, further being disseminated in the country with virus-infected cuttings of released varieties. The likely route for the incursion of TYLCMLV is inadvertent introduction of infected tomato seedlings and fruits or seedlings from nearby African countries, as it is the case for the international movement of other TYLCV-like viruses. Among the viruses newly described in Ethiopia, CpCSV is found to be genetically most closely related to Groundnut rosette assistor virus (GRAV) (Abraham et al. 2006) while ETBTV is most closely related to Groundnut rosette virus (GRV) (Abraham 2014). These two groundnut viruses are known to be endemic to Africa causing a devastating groundnut rosette disease. Naidu et al. (1999) suggested that the groundnut rosette disease agents including GRAV and GRV have coevolved with indigenous plants other than groundnut in Africa

and later infected groundnut when it was introduced in the 16th century. CpCSV, ETBTV and the two groundnut viruses have overlapping geographical distributions in Africa. Therefore, it is possible that the CpCSV and GRAV on one hand, and ETBTV and GRV on the other, have common ancestors in Africa, perhaps in Ethiopia, from which they have diverged by adaptation to different hosts. ELSV appears to have specific adaptation to enset and hence may have co-evolved with the host in Ethiopia. TuMV is found in most places where brassica crops are grown but a recent study based on hundreds of genome sequences from isolates collected worldwide suggested that the virus probably originated in Germany and spread to other parts of the world via southern Europe (Yasaka et al. 2017).

Challenges in Virus Management and Ways Forward

It is clear from the foregoing account that considerable progress has been made in recent decades in diagnosis and identification of the causal agents of economically important crop virus diseases in Ethiopia. The ultimate goal of applied virus research is however to generate and adapt technologies to control the diseases and prevent economic losses. Unfortunately, the national agricultural research system is lagging behind in providing suitably large-scale virus control measures that are effective and affordable for use by farmers. This can be partly attributed to the challenging nature of research on virus disease management which involves selecting the best measures for each virus–crop combination and production system and sensibly integrating the various options. The basis for this is the knowledge of the epidemiology of the specific virus disease in a given agroecosystem typically generated by field-based research data, an area currently ignored. Such work is demanding and needs committed and well-organized research groups with adequate number of trained personnel, facilities and institutional set up. Due to lack of such prerequisites, research in virus epidemiology is currently very weak and available information is patchy and fragmented often lacking continuity. Consequently, the overall research effort has been inadequate compared to the magnitude of the virus disease problems the country is facing.

At present, only few researchers are involved in crop virus research on full time basis. These researchers on the other hand face a diverse array of challenges ranging from poor system of acquiring the necessary inputs and facilities to technical issues including absence of resistance genes in host plants, lack of expertise to identify and seasonally monitor major insect vectors, and inability to elucidate the contribution of alternate hosts, crop residues or seeds to inadequate information on virus ecosystems with the consequent inability to forecast epidemics. Furthermore, even if effective control package of a disease is developed, it is difficult to ensure their adoption on a sufficiently large scale due to the inability of the farmers to deploy and adopt the research findings due to unaffordable cost and knowledge gaps. This is compounded with the limitation in the capacity and resources available for extension services to implement specific recommendations. This shows that the complex task of managing important virus diseases and preventing the introduction of new ones was not given the attention it

deserves and that concerted effort of all stakeholders is needed to address the problem. Initiating a grand nationally coordinated research program on integrated management of major newly emerged virus diseases and allocating the necessary resources for its effective implementation can be a good step in addressing the problem. In conclusion, all the stakeholders in the country should discuss, devise and implement an effective and affordable management options to prevent huge crop losses being incurred currently by newly emerged economically important virus diseases at the same time preparing to avoid future damages.

Table 1. Properties of the virus) associated with the newly emerged diseases in Ethiopia

Disease	Causal Virus	Particle shape and size (nm)	Genome type and size	Natural transmission
Maize lethal necrosis	*Maize chlorotic mottle virus*	isometric, 30	ssRNA, ~4.5 kb	thrips, beetle, seed
	Sugarcane mosaic virus	filamentous, 750	ssRNA, ~10 kb	aphids, seed
Chickpea stunt	*Chickpea chlorotic stunt virus*	isometric, 28	ssRNA, ~5.9 kb	aphids
Faba bean necrotic yellows or stunt	*Faba bean necrotic stunt virus; faba bean necrotic yellows virus; faba bean yellow leaf virus*	isometric, 18	ssDNA, multipartite, ~8 kb	aphids
Tobacco bushy top	*Ethiopian tobacco bush top virus*	isometric, 25	ssRNA,~ 4.3 kb	aphids
	Potato leaf roll virus	isometric, 25	ssRNA, ~6 kb	aphids
	satRNA	isometric, 25	ssRNA, ~0.6 kb	aphids
Enset leaf streak	*Enset leaf streak virus*	bacilliform, 30x150	dsDNA, ~7.2 k b	mealybugs, propagule
Cabbage mosaic	*Turnip mosaic virus*	filamentous, 750	ssRNA, ~10 kb	Aphids
	Cauliflower mosaic virus	isometric, 52	dsDNA, ~8 kb	Aphids
Sweet potato virus	*Sweet potato feathery mottle virus*	filamentous, 750	ssRNA, ~10 kb	Aphids, propagule
	Sweet potato chlorotic stunt virus	filamentous, 900	ssRNA, ~17 kb, bipartite,	whitefly, propagule
Tomato yellow leaf curl	*Tomato yellow leaf curl Mali virus*	isometric, twin, 20x38	ssDNA, ~2.7 kb	Whitefly

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