

REVIEW

Changing Dynamics in the Spread and Management of Banana *Xanthomonas* Wilt Disease in Uganda Over Two Decades

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ABSTRACT

Banana *Xanthomonas* wilt (BXW) is a destructive disease caused by *Xanthomonas vasicola* pv. *musacearum* (*Xvm*), a bacterium that indiscriminately infects all banana varieties grown in East and Central Africa (ECA). In this region, BXW was first reported in 2001 in Uganda and was projected to eliminate >90% of Uganda's banana crops (worth USD4 billion) if not controlled in less than 10 years. Lack of basic information led to application of control approaches that were based on similarity of BXW symptoms to those of Moko disease of banana. However, the approaches were unsuccessful and, in 7 to 9 years, BXW had covered six countries and threatened to wipe out the banana industry in ECA. However, BXW has been tamed to date, mainly due to relentless and systematic deployment of carefully crafted and packaged cultural control practices based on epidemiological information generated within target banana cropping ecosystems. In Uganda, the initial "top-down" communication approaches reached >85% of banana farming communities but did not mobilize the communities enough into

action; hence, only 30% impact in controlling BXW was registered. In contrast, participatory approaches mobilized farming communities into action and effectively controlled BXW at field and community levels to near eradication. The approaches effectively controlled BXW in Uganda and, consequently, in eastern Kenya, northern Tanzania, Rwanda, Burundi, and the Democratic Republic of Congo. This article reviews step-wise processes leading to success over the 2 decades and identifies critical research gaps. Deployment of resistant genotypes is urgently needed as a significant addition to the BXW management toolbox to create BXW-free banana cropping systems in ECA.

Keywords: banana (*Musa* spp.), banana *Xanthomonas* wilt (BXW), community participatory approaches, disease management, East and Central Africa, plant disease epidemiology, Uganda

Banana (*Musa* spp.) is the main food and cash crop for over 70 million smallholder farmers in East and Central Africa (ECA), with an annual production worth US\$4.3 billion, equivalent to approximately 6% of ECA's gross domestic product (Arvanitoyannis et al. 2008; FAOSTAT 2020; Kakuru et al. 2018; Nyombi 2013). Although the crop is important in ECA, the world's per capita consumption of banana is highest in Uganda at 220 to

400 kg/capita/year (Kabahenda et al. 2010; Kalyebara et al. 2006; PIBID 2007). The ability of banana to be amenable to a diversity of food, feed, and industrial uses places the crop strategically in transforming economies of some countries in ECA such as Uganda (Padam et al. 2014). Because alternative food security staples such as cassava (*Manihot* spp.) and sweetpotato (*Ipomoea* spp.) in ECA had been damaged by the emergence of devastating viral disease epidemics in the region since the late 1990s (Alabi et al. 2011; Alicai et al. 2007; Clark et al. 2012; Rey and Vanderschuren 2017; Thresh et al. 1997; Valverde et al. 2007), the pressure to sustain the region's food security system remained anchored on banana.

The productivity and ability of banana to support ECA food security, however, became severely constrained with the emergence of a highly destructive disease, banana *Xanthomonas* wilt (BXW) (Drenth and Kema 2021; Tushemereirwe et al. 2004). BXW destroyed entire household banana farms in some areas of East Africa because it successfully and indiscriminately infects all banana

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varieties grown in this region (Geberewold 2019; Karamura et al. 2008; Smith et al. 2008b). Currently, BXW is known only in Africa (Uganda, the Democratic Republic of Congo [DRC], Rwanda, Burundi, Kenya, Tanzania, and Ethiopia) (Mbaka et al. 2008; Ndungo et al. 2006; Niko et al. 2011; Ocimati et al. 2019; Tushemereirwe et al. 2003; Yirgou and Bradbury 1974). Prior to 2001, BXW was only historically known in and restricted to Ethiopia on a cultivated relative of banana, enset (*Ensete ventricosum*) (Yirgou and Bradbury 1968), and on banana (Yirgou and Bradbury 1974). In ECA, the disease soon became an epidemic, quickly destroyed banana plantations, caused close to 100% loss of production, and threatened people's livelihoods and the banana industry in the region (Kalyebara et al. 2006; Tripathi et al. 2009; Tinzaara et al. 2011).

Lack of information in the early 2000s led to application of ineffective control methods that were based on similarities between BXW and another bacterial wilt disease of banana, Moko disease (Blomme et al. 2011, 2017a; Lehmann-Danzinger 1987; Tushemereirwe et al. 2004). Unfortunately, these methods were ineffective and, consequently, BXW quickly spread to all major banana-growing regions in Uganda between 2001 and 2006 and, within only 9 years, the disease had spread across the six countries of the ECA (Ndungo et al. 2006; Niko et al. 2011; Tushemereirwe et al. 2003). Since then, with accumulated epidemiological information on the BXW, various control and management options have been developed and applied with varying success levels (Blomme et al. 2014; Kikulwe et al. 2019; Kubiriba et al. 2016; McCampbell et al. 2018; Smith et al. 2008a). Because Uganda's food security system was the first to be most severely affected by BXW, and being the first recorded BXW incidence outside Ethiopia (Tripathi et al. 2009; Tushemereirwe et al. 2004), the national agricultural research system in Uganda launched initial multipronged, rapid control strategies against BXW. Rapid rural appraisal and participatory approaches were mounted involving active participation of banana farming communities, local leaders, and government. Most of these strategies were scalable to the region (Blomme et al. 2014, 2017b; Gotor et al. 2022; Karamura et al. 2006; Kubiriba and Tushemereirwe 2014; Kubiriba et al. 2014; Mbabazi et al. 2021; Pagnani et al. 2021). Despite the success, resurgences of BXW were recorded where the disease had been successfully managed (Kubiriba et al. 2012b). Furthermore, there are reports that BXW is still spreading in areas of DRC (Blomme et al. 2014; Ocimati et al. 2019), partly because of not fully implementing recommended control and management strategies (Gotor et al. 2022). Recently, Mozambique was listed at high risk of BXW due to the abundance of Bluggoe (*Musa* ABB genotype), which is highly susceptible to insect-, bird-, and bat-vectored disease transmission (Ocimati et al. 2019). Therefore, there is no guarantee that BXW will not resurge or that its spread to new areas will be halted.

The aim of this review is to summarize information on achievements and experiences on BXW management in Uganda over the last two decades and how these provide a springboard for research and development efforts in relation to the BXW epidemic in ECA. This will enable stakeholders to identify areas of successful approaches for deployment at scale. We stimulate scholarship by identifying the most urgent research gaps as well as action points for regional governments on more effective management and possibilities of BXW eradication for sustainable banana production in ECA.

SYMPTOMS, TRANSMISSION, AND SPREAD OF BXW

Symptoms of BXW include progressive yellowing and wilting of leaves, premature and uneven ripening of fruit, and creamy-

yellowish bacterial oozes that appear 5 to 20 min after cutting diseased pseudostems (Tripathi et al. 2009; Tushemereirwe et al. 2004). These symptoms develop rapidly and the infected plants wilt and rot within 3 to 4 weeks under field conditions (Smith et al. 2008a). Under conditions of water stress, banana plants are physiologically weak and, hence, more vulnerable to BXW and express symptoms faster (Ochola et al. 2015).

BXW is transmitted by insects, birds, and bats during natural process of pollination by these agents (Buregyeya et al. 2014; Rutikanga et al. 2015; Ssekiwoko et al. 2006a; Tinzaara et al. 2006). Moreover, disease spread is promoted by repeated use of contaminated farm tools during crop husbandry practices, and using infected suckers as planting materials (Mwangi and Nakato 2007). The spread of BXW differs between cropping systems because farming practices in different areas may predispose the plants to BXW differently (Smith et al. 2008a). Over 90% of banana cultivars grown in Uganda belong to the subgroup of East African highland banana (EAHB, matooke, AAA-EA) compared with DRC where Kayinja (Pisang Awak, ABB) constitutes the main variety grown (Blomme et al. 2014). The flowers of Kayinja are sweeter and contain more nectar than the EAHB cultivars, which promotes more frequent visitations of airborne vectors to Kayinja (Kagezi et al. 2006; Mwangi and Nakato 2007). In contrast, EAHB cultivars are predominantly grown on a larger-scale plantation, characterized by intensive husbandry practices, which presents a greater risk of mechanical or tool-mediated spread of BXW (Drenth and Kema 2021; Karamura et al. 2013; Tinzaara et al. 2009; Tushemereirwe et al. 2006). Therefore, whereas in the less-managed Kayinja-based system, vector-mediated transmission is the dominant route, tool-mediated transmission is the main route of BXW transmission in the highly managed EAHB-based cropping system.

XANTHOMONAS VASICOLA PV. MUSACEARUM

Xanthomonas vasicola pv. *musacearum* (*Xvm*), previously designated as *X. campestris* pv. *musacearum* (Studholme et al. 2020), is a rod-shaped, aerobic, Gram-negative, flagelled, xylem-limited proteobacterium and the causative agent of BXW (Bradbury 1986; Smith et al. 2008a). Isolates of *Xvm* collected from various areas affected by BXW showed a high level of genetic homogeneity and close phylogenetic relationships (Aritua et al. 2007; Odipio et al. 2009). Observed close phylogenetic relationships within *Xvm* isolates in Uganda were strange, given the high level of severity of the disease in the field and rapidly spreading nature of the disease. It could possibly be explained by recent spread originating from a single introduction event of *Xvm*.

Using single-nucleotide polymorphism analysis, two major sublineages of *Xvm* (named sublineages I and II) were later identified (Wasukira et al. 2012). This was suggestive of two introductory events: one event represented by sublineage I (isolates from DRC and Rwanda) and another represented by sublineage II (isolates from Uganda, Tanzania, Burundi, and Kenya) (Wasukira et al. 2012). Using polymorphic multilocus number of tandem repeat analysis markers on a larger *Xvm* collection, 12 clusters were identified (Nakato et al. 2018a). Although most of the clusters were consistent with the sublineage classification suggested earlier by Wasukira et al. (2012), more diversity was observed in the clusters that were not assigned to any of the earlier reported sublineages (Nakato et al. 2018a). However, symptom expression does not differ significantly between sublineages because the *Xvm* diversity observable at a molecular level is not obvious phenotypically. Thus far, the management practices have not changed but may need to change for effective control of future BXW epidemics if the variants continue to become apparent.

INITIAL EFFORT FOR THE CONTAINMENT AND MANAGEMENT OF BXW

A “fire-fighting” strategy that never put out the fire. Because the BXW outbreak was abrupt and new in Uganda, and no epidemiological information was available on which to base action (Tushemereirwe et al. 2004), all of the initial methods of containment were in a “fire-fighting” mode, based on experiences of another banana bacterial wilt (Moko) disease control in Central America (Blomme et al. 2017a; Fegan and Prior 2006; Lehmann-Danzinger 1987; Munar-Vivas et al. 2010). Uganda government, through the Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), responded by constituting a task force in December 2001 to develop a strategy for disease eradication. This strategy emphasized massive creation of awareness and measures aimed at eradication of BXW by massive cutting and burying of infected banana stools (Fig. 1), quarantine, decapitation of male buds to block further vector transmission, and disinfection of farm tools used in the affected fields (Tushemereirwe et al. 2006). The strategy was administered in the two affected districts of central Uganda (Mukono and Kayunga), which temporality reduced disease incidence to <10%. However, due to high costs, limited awareness about the need for BXW control by the farming communities, and nonsystematic deployment of the measures, implementation of the strategy became unsustainable and soon BXW escalated into 11 new neighboring districts, necessitating a change of approach from disease “eradication” to “containment and management”.

Consequently, in 2003, the National Agricultural Research Organization (NARO) constituted another taskforce to formulate a more comprehensive research strategy for a country-wide containment of BXW. The strategy emphasized surveillance, generating scientific information and technologies for disease management, improving policies appropriate for control of BXW, and monitoring the impact of implementing these activities (Tushemereirwe et al. 2006). The development of BXW resistance was one of the key objectives under this strategy but this was only feasible in the long run (Tripathi et al. 2016, 2017, 2022).

Identifying sources of resistance to BXW in banana germplasm. Some banana cultivars such as Mbawazirume (AAA-EA), Nakitembe (AAA-EA), and M9 (AAA-EA hybrid), all of which belong to the EAHB group, can escape vectored BXW infection because they have persistent or semipersistent bracts on the male inflorescence (Mudonyi et al. 2019). Persistent flowers or bracts remain attached to the flower stalk (peduncle), leaving no room for insect contamination because there is no entry point left, whereas dehiscent inflorescences of other varieties create room for insect contamination (Fiaboe et al. 2010). In rare cases, cultivars such as Scambia (AAB) lack male buds (Kubiriba and Tushemereirwe 2014), which eliminates vector-mediated transmission. Deployment of such cultivars can only reduce the cost of cultural control of BXW, eliminating vectored BXW infection. However, these cultivars are susceptible to tool-mediated BXW infection. Thus, a more durable form of resistance is desired, and this can only be achieved through conventional or nonconventional breeding.

Early studies confirmed the inedible wild progenitor of banana, *Musa balbisiana* (BB genome), as a potential source of resistance among several tested *Musa* genotypes (Ssekiwoko et al. 2006c, 2015). In addition, Nakato et al. (2019) screened 72 banana accessions from the International Institute of Tropical Agriculture (IITA) germplasm collection, including male parents widely used in banana breeding programs. *M. balbisiana* was reconfirmed as resistant, while other genotypes were either tolerant or susceptible. This increases the possibility of using conventional breeding

to develop BXW resistance. Otherwise, the only current, feasible way to improve BXW resistance is using transgenic technology (Lorenzen et al. 2008; Shotkoski et al. 2010; Tripathi et al. 2016) or genome editing approaches (Tripathi et al. 2022). There-



Fig. 1. Some of the early methods of controlling banana *Xanthomonas* wilt (BXW) that were not sustainable. **A**, Massive uprooting and burying of BXW-infected plants into a ditch dug in the middle of the plantation. The banana plantation (background) had just undergone intensive pruning by tool-mediated removal of fresh leaf sheath from the base of the pseudostem, a practice known to enhance tool-mediated transmission of BXW (Photo taken by Dr. Guy Blomme in Rwanda). **B and C**, Banana farmers in Kayunga district, central Uganda in June 2002 undertaking massive destruction of banana plantations where BXW-infected plants had been identified during the very early stages of BXW epidemic. Part of the plantation that had just been cut down (**B**) and the same farmers disinfecting their hands by washing with JIK (sodium hypochlorite) (**C**). Kayunga is where the first record of BXW was made in Uganda and East and Central Africa (Photos taken by Jerome Kubiriba).

fore, IITA in collaboration with NARO and the African Agricultural Technology Foundation tested constitutive expression of a hypersensitive response-assisting protein (*Hrap*) gene and a plant ferredoxin-like protein (*pflp*) gene from sweet pepper (*Capsicum annuum*) (Chen et al. 2000; Lin et al. 1997). Both genes showed stable and specific resistance against BXW in banana (Nimusiima et al. 2015; Shotkoski et al. 2010; Tripathi et al. 2014, 2016, 2017, 2019). Currently, the most used biotechnology tools revolve around use of transgenes; however, with better understanding of the *Xvm* pathosystem (Wasukira et al. 2014), other tools such as gene editing may be used to develop BXW resistance in the future. For example, broad-spectrum disease resistance that has been developed in cotton through CRISPR/Cas9 genome editing of specific host-susceptibility genes has been demonstrated in banana against BXW and other diseases (Ntui et al. 2020; J. N. Tripathi et al. 2021; L. Tripathi et al. 2021, 2022).

Applying knowledge of disease etiology and epidemiology to manage BXW. Studies were designed to generate etiological and epidemiological information within the areas of disease outbreak. These included survival of the bacteria in the soil, refuse and hosts, disease spread dynamics, and possible ways to stop spread in new fields or within fields. This then formed a basis for development of cultural control practices for the management of BXW (Smith et al. 2008a; Tushemereirwe et al. 2006). Use of clean planting material was the first recommendation for BXW management in the early years of the epidemic in ECA, because it was thought to be a major means of limiting long-distance spread of the disease. The assumption at the time was that infected mats could not produce clean suckers and that a single infected plant on a mat meant that all plants of that mat were infected because they were all anatomically connected to the same corm (Tushemereirwe et al. 2004). Later, it was observed that corms of infected mats were not uniformly colonized by *Xvm* bacteria (Ocimati et al. 2015), suggesting a possibility of obtaining disease-free suckers from previously infected mats for establishment of new plantations, especially if BXW was not observed in the field for 10 to 12 months. Recently, *Xvm* infection was shown to induce organ-specific defence responses in banana plants (Mustafa et al. 2022), providing additional support to nonuniform bacterial colonization of tissues as well as differential responses to infection. The corm was postulated to be an important organ for ensuring disease-free lateral shoots (Mustafa et al. 2022; Ocimati et al. 2013; Ssekiwoko et al. 2006b).

Uneven colonization of banana corms by *Xvm* and the fact that most BXW infection starts from the shoot system and progresses slowly down to the corm (Ssekiwoko et al. 2006c) indicated a possibility to limit movement of *Xvm* into lateral shoots by timely removal of the diseased plants from the mat. This led to the emergence of a new technique of BXW management, named “single diseased stem removal” (SDSR) (Blomme et al. 2017b; Kikulwe et al. 2022; Kubiriba et al. 2014, 2016). In SDSR, only a BXW-diseased plant is aseptically removed at the soil level from the mat while leaving the other, symptomless plants on the same mat (Kubiriba et al. 2014).

Initially, the control of BXW included rouging of entire banana mats, including symptomatic and symptomless plants. Implementation of this practice became an extremely laborious process and most farmers in the severely affected areas did not adopt it (Bagamba et al. 2006; Mwangi 2007). Where it was practiced, it exposed land on steep slopes to soil erosion agencies (Niko et al. 2011). Moreover, it proved costly for the farmer to reestablish banana production because plantations take approximately 2 years to revert to previous production levels (Blomme et al. 2008). Therefore, early removal of flower-infected (symptomatic) pseudostems at the mat base (SDSR) at the onset of first floral symptoms prevented the disease from spreading to the rest of the plants on the mat

(Blomme et al. 2008; Kubiriba and Tushemereirwe 2014; Kubiriba et al. 2014). SDSR was successfully applied in Uganda, Kenya, and DRC and significantly reduced BXW incidence (Kubiriba and Tushemereirwe 2014; Kubiriba et al. 2014). The advantage of using SDSR is that there are no costs of uprooting or replanting the whole mat or the entire plantations, which allows the remaining uninfected plants to continue yielding harvestable fruit (Blomme et al. 2008; Kikulwe et al. 2022; Kubiriba et al. 2014). Therefore, SDSR has been essential in rehabilitating sections of plantations infected by BXW without the necessity of uprooting the entire plantation and planting afresh. Such local sections in banana plantations are characterized by an open space of newly planted or sprouted young shoots (Fig. 2).

Utilizing knowledge of disease transmission routes to control BXW. In addition to tool-mediated transmission, BXW is also spread by insects, birds, and bats from male buds of diseased plants to those of healthy plants (Kubiriba and Tushemereirwe 2014). Therefore, to tame the spread of BXW, early removal of male buds from banana plants using a forked stick eliminated the spread of the disease by vectors within or into new fields (Tinzaara et al. 2006). Tools used for pruning create wounds on diseased plants, pick up the sap with bacteria, and spread it to nondiseased plants (Mwangi and Bandyopadhyay 2006; Mwangi et al. 2007; Yirgou and Bradbury 1968). Live *Xvm* bacterial cells were recovered from knives and machetes up to 20 days after inoculation (Buregyeya 2010). Banana traders in Uganda travel over 300 km a day with nondisinfected tools, indicating possibilities of spreading BXW between banana-growing regions of Uganda. In one household, a single tool that is not disinfected with either sodium hypochlorite solution or flame is able to transmit BXW 20 days after inoculation (Buregyeya 2010). Recently, Ocimati et al. (2021) showed that a thorough washing of farm tools with cold water and different locally available laundry soaps that had no antibiotics and detergents, just like household bleach, eliminated all of the *Xvm* bacteria on farm tools.

The method of disposing of diseased plant materials is important in controlling BXW successfully; however, this depends on the longevity of pathogen in soil or debris. Initially, it was recommended that infected plant material be burned or buried immediately after rogueing (Blomme et al. 2008). This was based on the assumption that *Xvm* is easily spread from debris of infected plants, as is the case for *Fusarium wilt* disease of banana, caused by the fungal pathogen *Fusarium oxysporum* f. sp. *cubense*, which survives in the soil for more than 20 years (Stover 1962). However, burning colossal masses of fresh succulent banana tissues was not feasible and the effort of digging large, deep pits to bury the material was prohibitively labor intensive (Rutikanga et al. 2013; Smith et al. 2008a). Fortunately, studies also showed that *Xvm* did not survive beyond 35 days in soil or plant debris (Mwebaze et al. 2006). Consequently, farmers were advised to chop infected material into small fragments to accelerate both desiccation and decomposition (Kubiriba et al. 2014). The poor survival of *Xvm* in soil and plant debris also implied that banana can be replanted in fields that were previously infested by BXW after a fairly short period of time. Hence, a fallow period of at least 6 months following the destruction of entire mats was recommended in central Uganda agroecological conditions, whereas no fallowing is required where SDSR is more widely used as a means of inoculum removal.

ROLE OF LOCAL COMMUNITIES IN DEPLOYING BXW CONTROL PRACTICES

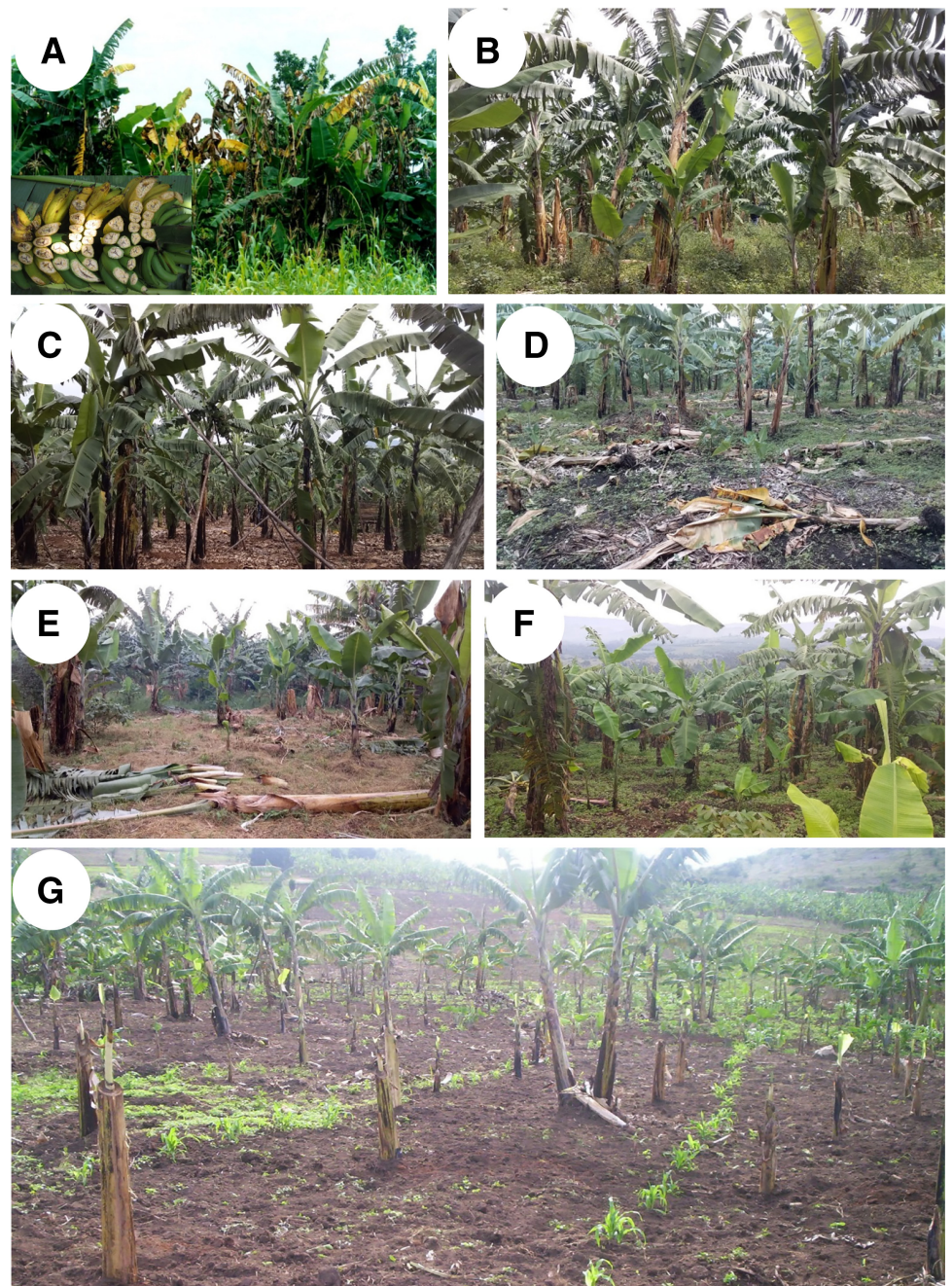
Use of participatory approaches for BXW control among the communities. An earlier action plan of 2001 aimed at eradicating BXW around the initial outbreak areas was top-down, denoting a

hierarchical system of government or management in which actions and policies are initiated at the highest level, and could not be sustained, while BXW persisted (Tushemereirwe et al. 2006). Indeed, where banana farming communities are the primary formulators of the methods, high rates of adoption are likely (Gold et al. 1993; Kikulwe et al. 2019; Tinzaara et al. 2019, 2021). Therefore, participatory approaches to proactively engage the banana farmers and other stakeholders in the community were used to improve BXW control. This involved facilitation of dialogue among the different stakeholders with the aim of developing and implementing an action plan to solve the problem (Supplementary Table S1). Because BXW was highly devastating and could also be spread by itinerant vectors able to fly several kilometres in a very short time, one infected farm or plant could act as source of inoculum for all banana farms in a community. Thus, it was considered a community prob-

lem instead of individual farmers' problem. It was emphasized that every member of the community had to control the disease to save other banana crops in the community.

Using community bylaws to enforce implementation BXW control measures. Due to an eradication campaign of cocoa trees infected with cocoa swollen shoot virus launched in 1946, the virus was largely under control by early 1960 and only resurfaced when the government stopped the campaign (Thresh and Owusu 1986). Similar campaigns were successfully implemented in controlling Citrus tristeza virus in Israel (Fishman et al. 1983) and banana bunchy top virus in Australia (Allen 1983). Legislation seems to have been one of the important components of the above successful programs. It mainly involved guidelines on movement of planting material from infected fields or from one region to another and required growers to destroy any diseased plants (Magnaye 1994).

Fig. 2. **A**, Unmanaged banana plantation with banana *Xanthomonas* wilt (BXW) leaf symptoms (inset: banana bunch showing uneven fruit ripening with blackening of fruit pulp) compared with **B and C**, managed plantations in Uganda in which no single diseased stem removal (SDSR) is done. Upon identification of BXW, infected plants are rogued by **D**, uprooting or **E**, cutting above soil level, which creates open spaces in the plantations, allowing new shoot growth after SDSR. Open spaces begin to fill again progressively; for example, **F**, which is 7 weeks after SDSR. **G**, In more severe BXW, many plants are eliminated, which creates much larger open spaces and allows intercropping while, at the same time, enforcing plantation reestablishment through replanting.



The governments in West Africa in the colonial era enforced these rules, though farmers were not happy with some of them (Thresh and Owusu 1986). In Australia and Honduras, however, farmers cooperated to organize an efficient system for detecting and destroying diseased plants and generally enforcing rules constituted by them.

In Uganda, compelling all banana farmers in the community to control BXW necessitated a “localized legislative mechanism”. One option was a law issued by central or local government, where everybody must comply or face dire consequences. Instead, communities formulated and enforced their own bylaws (Supplementary Table S2). The bylaws included a set of rules and penalties that compelled members of the community to meet regularly to discuss progress towards BXW control, effectively detect the disease in the fields, execute actions aimed at limiting its spread, and ensuring that the community members abided by the bylaws (Kubiriba and Tushemereirwe 2014). Implementation of community bylaws started in Ntungamo District (southwestern Uganda) in 2005, were adopted in Kyazanga-Lwengo District in 2006 (central Uganda), and, by 2014, all major banana-growing areas of Uganda had adopted the bylaws (Kubiriba et al. 2016).

Participatory surveillance for mapping and tracking BXW distribution and spread. Traditionally, crop disease outbreaks are mapped based on formal surveys and transects, which normally target only representative samples of disease outbreaks. Currently, frontline remote sensing tools coupled with machine learning methods have a significant role in crop monitoring and disease surveillance (Kreuze et al. 2022; Selvaraj et al. 2019, 2020). The devastating and fast-spreading nature of BXW dictated that control efforts could not ignore the presence of even one outbreak in the major banana-growing areas. To halt economic loss, a new system was devised to track all outbreaks in real time as they occurred in Uganda (Kubiriba and Tushemereirwe 2014), which consisted of the following: (i) massive and aggressive awareness creation through mass media, posters, and brochures, aimed at building capacity for the farming communities to identify the disease; (ii) farmers were urged to report to the nearest extension worker or via hotline telephone numbers indicated on posters and brochures; (iii) symptoms were described, as well as details of the location of the outbreak; (iv) a return call was made by the nearest trained extension officer or extension staff was sent to the location to verify and confirm the presence of the outbreak; and (v) data were continuously compiled into a database at NARL-Kawanda and used to generate disease distribution maps. This reporting system was key in showing the disease spread, supporting mobilization of the stakeholders for BXW control, and targeting the control measures in real time. However, it was heavily dependent on the vigilance of the farmers. Therefore, this was complemented by other reporting systems such as going public. At the time of the epidemic, disease mapping was based on the subcounty-generated information; fortunately, the current and more accurate GIS tools for disease mapping tools can provide accurate data on disease incidence (Kreuze et al. 2022; Selvaraj et al. 2019, 2020).

Going public and participatory monitoring and evaluation of BXW control. The aforementioned participatory surveillance system was backed up with another one, dubbed “going public” (Tushemereirwe et al. 2006). This was used to trace new BXW outbreaks in areas of southwestern Uganda, where >75% of Uganda’s banana crops are produced (Kalyebara et al. 2006). The team would go to public places such as open markets, trading centers, and places of worship to display posters of BXW symptoms in a way that the team would attract public attention. The public was then mobilized around the posters and sensitized about BXW symptoms and spread, and how it can be controlled. Meanwhile, records of at-

tendance, including the subcounties and villages participants came from, were taken. The participants were asked if they had ever observed similar symptoms in their localities. The occurrences were recorded and followed up for verification and mapped by district or national BXW control partners. Therefore, it was possible to map most new occurrence by engaging the public, instead of going to every household (Tushemereirwe et al. 2006).

The BXW control initiative used participatory monitoring and evaluation (M&E) which emphasizes involvement of target communities and stakeholders to facilitate the process. To execute participatory M&E, the community stakeholders, including farmers, were facilitated to select quantifiable and monitorable indicators, record data on them, and report to fellow farmers and village BXW taskforces regularly. Progress in BXW control observed by farmers and discussed at community level built farmers’ confidence that BXW can be controlled. This encouraged reluctant farmers to devote more efforts to BXW control. During community meetings, farmers were able to modify the recommended practices and also resolve the hindrances to BXW control peculiar to the community. The unique approach of involving farmers as key players in the management of a devastating plant disease burden proved effective because there is a great sense of personal and community responsibility for the outcomes of these efforts (Tinzaara et al. 2019).

STATUS OF BXW CONTROL AND MANAGEMENT (2005 TO 2018)

BXW control between 2005 and 2013. The above M&E systems were complemented with formal surveys with structured questionnaires and checklists between 2006 and 2018. Consequently, BXW prevalence decreased between 2005 and 2008 from higher than 75 to 45% in central Uganda, where the disease had become endemic (Tushemereirwe et al. 2006). In the areas between Lake Victoria basin and Mountain Rwenzori, BXW prevalence decreased from 55 to 24%, whereas it was reduced to <5% in the main banana-growing areas of the southwestern Uganda (Kubiriba and Tushemereirwe 2014). Apparently, BXW had been effectively controlled in the most important southwestern, Lake Victoria, and Mt. Rwenzori regions (Fig. 3) which, together, produce >80% of Uganda’s banana crops (Bagamba 2007; Gold et al. 1999; Katungi 2007; Nyombi 2013; Rubaihayo and Gold 1993; Tushemereirwe et al. 2006). Other banana-growing areas, grouped as endemic to the disease, still had high levels of BXW incidence; however, this did not affect the overall national banana production because they were not key in banana production. There was only a slight decrease in value of banana production at the national level against predicted BXW damage between 2003 and 2007 (Fig. 4).

However, in 2008, there was a resurgence of BXW with prevalence of up to 51% at the national level and, by 2010, it had spread to new areas with a 60% prevalence (Kubiriba et al. 2012b, 2014). Some of the reasons for the resurgence were (i) trained extension agents had been replaced by new, untrained staff; (ii) laxity and abandonment of the surveillance system; and (iii) lack of coherent institutional frameworks for organizing communities for BXW control, inadequate mobilization and sensitization of key stakeholder platforms along the production-consumption chain, and less effective surveillance methods (no application of digital tools) leading to untimely actions. Therefore, this information was the basis for the revision of the national BXW control strategy that was launched in 2013 (Kubiriba and Tushemereirwe 2014).

Controlling BXW under the revised national BXW strategy of 2013. The revised national BXW strategy aimed at reducing disease prevalence from 51% to <1% by the end of 2015. It was observed that the recommended cultural control practices were still

effective in controlling BXW, and the main challenge was mass mobilization of farmers to deploy them (Kubiriba and Tushemereirwe 2014). Therefore, the revised strategy of 2013 aimed at (i) aggressively and widely disseminating information on BXW spread and control, (ii) mobilizing communities for BXW control, (iii) supporting the development and implementation of legal instruments, and (iv) monitoring and evaluation of implemented BXW control activities.

Like the previous BXW control efforts, implementation of the 2013 control strategy was driven by participatory approaches, with modifications. Previously, awareness campaigns were based on information generated and spearheaded by the research teams, supported by inspectors at the MAAIF and production departments at

local governments (Bagamba et al. 2006). Under the 2013 BXW control strategy, information was picked from the participating communities as they implemented BXW control and packaged by the media houses that eventually disseminated it. Information was more focused on organization of stakeholders to control BXW: farmer mobilization and implementation of bylaws. It was anticipated that capturing information from farmers free of technical jargon and disseminating it through radio and newsprint would improve information access and be used for decision making by fellow farmer beneficiaries (Kubiriba et al. 2016).

Successful BXW control at the selected hotspots became obvious, with the value of giving confidence to the surrounding, less-affected communities that BXW can be controlled, as demonstrated

Fig. 3. Map of Uganda showing banana bacterial wilt (BBW) occurrence and control in major banana-growing areas of Uganda as of 2008.

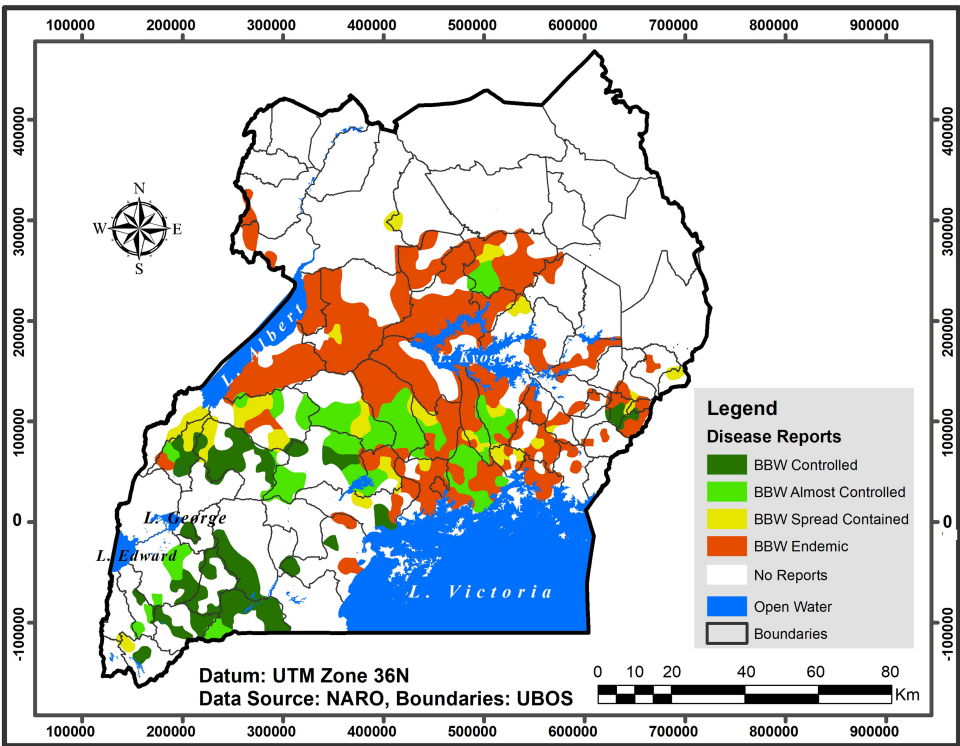
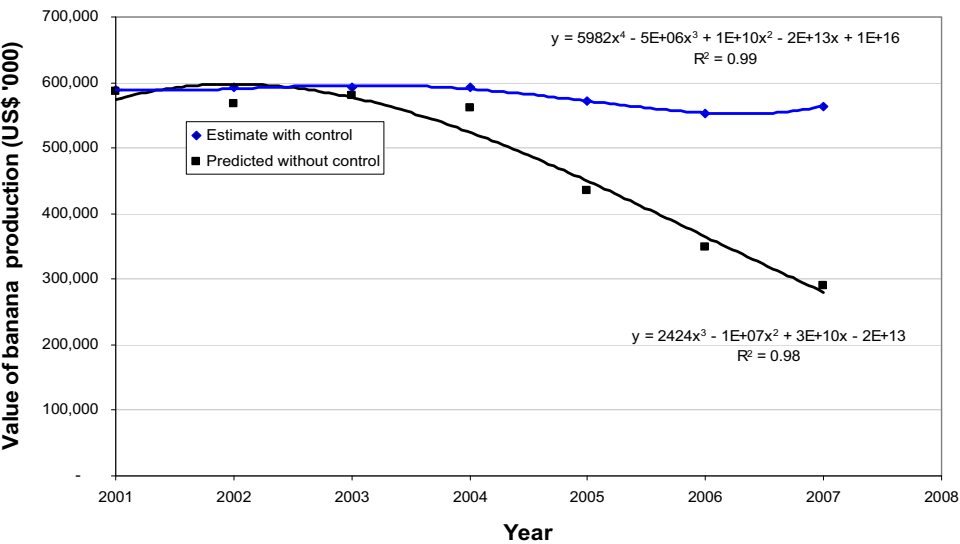


Fig. 4. Value of banana crops produced in Uganda during the banana *Xanthomonas* wilt epidemic: 2001 and 2007.



by hundreds of farmers (Kubiriba et al. 2016). Linking of farmers with networks of organizations and individuals which focused on getting more people to use the technologies for greater economic benefit (Bentley et al. 2006) was executed through field days (Kubiriba et al. 2016). Clearly, lessons were learned by peer farmers in how to drastically reduce BXW incidence through surveillance for diseased plants in a community and the significant contribution of administrative and political support through effective formulation and implementation of bylaws at subcounty level (Kubiriba et al. 2016).

Between 2006 and 2008, except for the southwestern region, which produced most banana crops, all other regions had 30% higher BXW prevalence (Fig. 5). During the time of BXW resurgence in 2010 and 2013, all regions, including the southwestern region, experienced >30% BXW prevalence and, by 2018, this was reduced to <5% BXW. This successful control of BXW in all banana-growing areas in Uganda resulted in weekly banana sales recovery to approximately 72% in 2018 (Fig. 5). The successes in the management of BXW could only be sustained with institutional support through key players at the community level.

TECHNOLOGY ADOPTION FOR EFFECTIVE CONTROL OF BXW

Many initiatives, innovations, and technologies that target small-holder farmers in sub-Saharan Africa struggle with adoption and scaling up, even when returns are proven in pilot studies (Franzel et al. 2001; Lynam and Twomlow 2014). Successful scaling up requires that the factors affecting adoption as well as the spaces or contexts that scaling up has to navigate are well understood, iteratively evaluated, and incorporated into the scaling-up process (Linn 2012). Key attributes of a successful scaling-up strategy include effective communication, peer learning, and strong leadership, altogether contributing to the quality of community participation (Gillespie 2004; Kolavalli and Kerr 2002; Ndah et al. 2015).

One of the key determinants of farmers' acceptance and adoption of the technology is the importance that end-users attach to the enterprise. Ndah et al. (2015) categorized this under conditions of the output markets at both village and regional level. This explains why, between 2005 and 2008, only banana farmers in the southwestern region of Uganda were able to keep BXW incidence below 5% (Kubiriba and Tushemereirwe 2014). It is in this region that banana fruit not only provide food security but also are key for daily income, and the region produces >75% of Uganda's banana fruit.

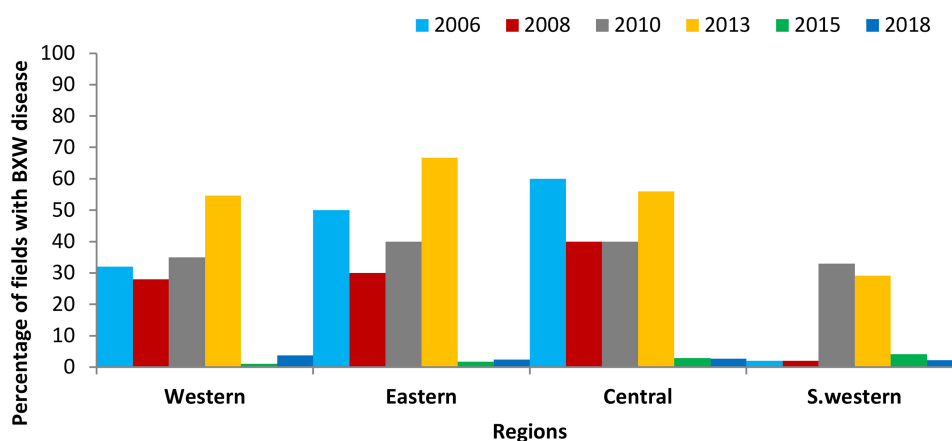
Characteristics of a technology are key in influencing farmers to adopt it. BXW control was based on epidemiology information generated within the ecological set up of the BXW outbreaks. The ease with which BXW insect-vectored or tool-mediated spread was blocked through timely removal of male buds with the right tools and disinfection of cutting tools (Blomme et al. 2008), short *Xvm* survival in the soil (Mwebaze et al. 2006), and nonuniform colonization of the corm and pseudostem (Ocimati et al. 2015) all contributed to development of a cultural management package that was significantly effective at controlling BXW. This package was suited to controlling a rapidly spreading and destructive epidemic, as demonstrated in the affected farming communities in Uganda and successfully applied across the banana-growing regions of ECA, with minor modifications (Blomme et al. 2017b, 2019; Kubiriba and Tushemereirwe 2014; Kubiriba et al. 2012a, b, 2014, 2016). Such a strategy could be applicable to any phytopathosystem of comparable epidemiology and etiology, provided the farming communities attach this value to the enterprise and the approach is participatory.

CONCLUSIONS AND FUTURE RESEARCH PERSPECTIVES

The challenges associated with plant disease threats of food security in developing countries are enormous (Jeger et al. 2021; Sherman et al. 2019) and the challenge is exacerbated when essential food staples such as banana are affected (Ristaino et al. 2021; Rizzo et al. 2021; Savary et al. 2019; Strange and Scott 2005). This demands careful and immediate application of approaches based on basic scientific and social science structures of the communities for ease of adoption (Garcia-Figuera et al. 2021; Mills et al. 2011). Over the last two decades, the most fundamental progress made in addressing BXW disease problem in ECA is that it can be controlled or eradicated. The rigor of interventions against BXW in Uganda represent a success story of disease management that is comparable with transgenic management of papaya ringspot disease in Hawaii (Gonsalves and Gonsalves 2014; Gonsalves et al. 2007). However, the success in combatting a threatening epidemic of BXW's magnitude hinges on the importance of informing farmers about the effectiveness and benefits of control strategies as opposed to emphasizing the risk posed by the disease (Milne et al. 2020). Hence, the following additional information is needed to guide further evidence-based efforts in controlling BXW.

First, *Xvm* bacterial isolates have not been sufficiently analyzed for their population biology. Whereas *Xvm* isolates show close phylogenetic relationships (Nakato et al. 2018b; Wasukira et al. 2012),

Fig. 5. Proportion of banana fields infected with banana *Xanthomonas* wilt (BXW) in the different regions of Uganda between 2006 and 2018.



there is no description of *Xvm* population genetics parameters. Population parameters such as haplotype diversities, gene flow, and population contraction or expansion indices are means of examining pathogen demographic trajectory that require profiling. Also, the sublineages may differ in their rate of evolution or direction and magnitudes of Darwinian selection pressures but this has not been investigated.

Second, uneven colonization of the corm by *Xvm* results in incomplete systemic movement of the bacteria and subsequent escape from BXW of some lateral shoots on the same corm as the infected banana plant (Blomme et al. 2017b; Mustafa et al. 2022; Ocimati et al. 2015). However, the mechanism for uneven colonization of the corm is unknown. One plausible hypothesis is that, upon entry into the corm, *Xvm* gets “weakened” to a level below the threshold required to induce disease in the lateral shoots. This possibility is supported by the finding that the corm is an organ highly responsive to *Xvm* attack when compared with other organs (Mustafa et al. 2022). The anatomical connectivity between corm, pseudostem, and “true stem” implies that *Xvm* may associate with the corm transiently to perpetually, depending on the point of inoculation. Further studies describing the anatomical assembly and physiological traits of the corm and associated *Xvm* histopathology are needed urgently.

Third, a link between the stage of plant growth and rate of BXW disease development is not well known, although the assumption is that disease progresses faster in younger than in older plants. Accordingly, depending on the developmental stage, banana plants may show varied speeds of *Xvm* systemic spread within the plant. This knowledge is important because a single banana plant lasts for 9 to 14 months between sprouting on the corm and its removal by harvesting mature fruit, which gives a broad window for the plant to become infected. Recently, the spread of *Xvm* within banana mats was shown to be influenced by the amount of inoculum and the physiological stage of the mother plant and attached suckers (Ocimati et al. 2022). Our unpublished observations show that there is a long delay of 8 to 12 weeks postinoculation with *Xvm* to the appearance of systemic BXW leaf symptoms when inoculations are made on the male banana buds. In contrast, faster development of systemic leaf (but not necessarily fruit) BXW symptoms was observed upon leaf inoculations with *Xvm*. In more than 200 mats for which the mother plants were inoculated and no SDSR was practiced, <7.5% of lateral shoots developed BXW compared with >95% that showed no BXW 40 weeks postinoculation, indicating the corm’s natural ability to limit disease progression into lateral shoots despite continuous *Xvm* loading from the infected mother (our unpublished observations). This topic requires extended studies.

Fourth, although methods of biocontrol for banana fungal and bacterial diseases could be feasible (Blomme et al. 2017a; Dadrasnia et al. 2020; Premabati and De Mandal 2020), application of these methods to the control of *Xvm* is still limited or underdeveloped. For example, bacteria antagonistic against *Xvm* showed a reduction in disease incidence on onset (Abayneh 2010). Also, endophytic bacterial isolates of *Burkholderia*, *Herbaspirillum*, and *Enterobacter* spp. isolated from banana in Uganda were shown to suppress *Xvm* (Were 2016). Consequently, suppression of *Xvm* by endophytes at the banana corm level was postulated to account for incomplete systemic spread of *Xvm* at the mat level (Blomme et al. 2017a; Karamura et al. 2016). However, empirical evidence supporting this hypothesis is still lacking. Of current interest, yet also not fully developed, is biocontrol of *Xvm* in banana using bacteriophages. The potential of bacteriophages as biocontrol agents against *Ralstonia solanacearum* (causative agent of Moko disease of banana) or various pathogenic species of *Xanthomonas* spp. has been shown (Domingo-Calap et al. 2022; Erdrich et al. 2022; Nakayinga et al. 2021; Ramírez et al. 2020; Romero-Suarez et al. 2012). However,

specific studies of bacteriophages against *Xvm* in banana are still limited or lacking. Previously, *Xvm* was shown to be unable to survive beyond 35 days in soil or plant debris (Mwebaze et al. 2006); however, whether this inability is enhanced by phaging activities of soilborne bacteriophages against *Xvm* or competing saprophytic microbes or other factors is an interesting topic for further study.

Fifth, the plethora of microbial communities associated with BXW-infested or healthy banana plants (plant microbiota or plant microbiome) require in-depth studies because healthy plants host taxonomically diverse and structured communities of microorganisms. These plant–microbiome associations have long coevolved to have a direct influence on rhizosphere functioning, plant development, and disease processes (Dastogeer et al. 2020; Gao et al. 2021; Trivedi et al. 2020). Apparently, the plant microbiome, now viewed as an extension of the host plant genome, can be modulated or enhanced for better plant health and productivity (Beck et al. 2022; Compant et al. 2019; Trivedi et al. 2020, 2022; Turner et al. 2013). Also, plant microbiome research has revolutionized our view of plant health, in which the classic disease triangle (host, environment, and pathogen) has expanded to include plant-associated microbial communities (Gao et al. 2021; Malacrino et al. 2022; Trivedi et al. 2020). Studies on the core banana microbiome show differences between plant compartments and soils but not genotypes (Birt et al. 2022), which opens up opportunities to manage banana diseases (Ali and Imran 2022; Malacrino et al. 2022). If the BXW-infected banana microbiome can be segregated between different parts, *Xvm* mobility and multiplication can be curtailed. However, although there are a few descriptions under conditions for banana *Fusarium* wilt fungal disease (Kaushal et al. 2020; Liu et al. 2019; Xue et al. 2015), there is a limitation in the analysis of scenarios under BXW disease. Other than showing that BXW-resistant transgenic banana plants have the same stable rhizosphere microbiome as nontransgenic plants (Nimusiima et al. 2015), how banana microbiome composition and modulation may contribute to the management of BXW is not well known. Alteration in and composition of the plant microbiome can be induced by climate change, which can subsequently modulate the disease development process (Trivedi et al. 2022). Generally, reports show that, whereas banana plants have benefited from the effects of climate change since 1961, this situation will be reversed in the future and, by 2050, all previous gains will be lost (Fernandez et al. 2022; Machovina and Feeley 2013; Varma and Bebbler 2019). Plant disease can be driven by climate change that modulates microbiomes and plant adaptation (Gao et al. 2021; Trivedi et al. 2022). Short-term (years to decades) adaptation of plants to climate change will be mainly driven by the plant microbiome whereas, in the long term (century to millennia), the adaptation of plants will be driven equally by ecoevolutionary interactions between the plant microbiome and its host (Gao et al. 2021; Trivedi et al. 2022). Therefore, urgent studies of the banana microbiome in relation to *Xvm* and BXW incidence are required as an alternative strategy for further management and eradication of this disease from banana farming communities of ECA.

Taken together, BXW has been largely controlled in Uganda by a package of cultural methods in the last two decades. However, complete BXW eradication and management is not guaranteed under this framework because of the need for continuous active involvement of farmers and supportive stakeholder community. These gains are applicable to the greater ECA where BXW is a problem, including Mozambique, which is currently at high risk of BXW (Ocimati et al. 2019). Banana microbiome modulation presents a new opportunity for BXW management because banana plants tend to establish compartment-specific microbiomes at an early age that persist to maturity (Birt et al. 2022). Moreover, a missing yet feasible alternative element in the management of BXW is the deploy-

ment of resistance, either introgressed from the wild *M. balbisiana* or by transgenic methods. Transgenic resistance against BXW in banana is available (Tripathi et al. 2016, 2017); however, it suffers legislative and political impediments in the region, including in Uganda. A promising alternative is to employ CRISPR/Cas9-mediated genome editing, which has shown promise and could deliver acceptable BXW-resistant banana varieties (Schaart et al. 2021; J. N. Tripathi et al. 2021; L. Tripathi et al. 2021, 2022). Urgent deployment of BXW resistance is paramount and would be a significant addition to the existing BXW control and management toolbox to create BXW-free banana cropping systems in ECA and enhancement of regional food security.

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LITERATURE CITED

- Abayneh, T. B. 2010. Evaluation of biological control agents against bacterial wilt pathogen (*Xanthomonas campestris* pv. *musacearum*) of ensete (*Ensete ventricosum*). Master of Science, Addis Ababa University, Addis Ababa, Ethiopia.
- Alabi, O. J., Kumar, P. L., and Naidu, R. A. 2011. Cassava mosaic disease: A curse to food security in sub-Saharan Africa. APSnet Features. <https://www.apsnet.org/edcenter/apsnetfeatures/Pages/cassava.aspx>
- Ali, S., and Imran, A. 2022. Plant disease management through microbiome modulation. Pages 113-150 in *Microbial Biocontrol: Sustainable Agriculture and Phytopathogen Management*, Vol. 1. A. Kumar, ed. Springer International Publishing, Cham, Switzerland.
- Alicai, T., Omongo, C. A., Maruthi, M. N., Hillocks, R. J., Baguma, Y., Kawuki, R., Bua, A., Otim-Nape, G. W., and Colvin, J. 2007. Re-emergence of cassava brown streak disease in Uganda. *Plant Dis.* 91:24-29.
- Allen, R. N. 1983. Spread of banana bunchy top and other plant virus diseases in time and space. Pages 51-59 in: *Plant Virus Epidemiology: The Spread and Control of Insect-Borne Viruses*. R. T. Plumb and J. M. Thresh, eds. Blackwell Scientific Publications, Oxford, U.K.
- Aritua, V., Nanyonjo, A., Kumakech, F., and Tushemereirwe, W. 2007. Rep-PCR reveals a high genetic homogeneity among Ugandan isolates of *Xanthomonas campestris* pv. *musacearum*. *Afr. J. Biotechnol.* 6:179-183.
- Arvanitoyannis, I. S., Mavromatis, A. G., Grammatikaki-Avgeli, G., and Sakellariou, M. 2008. Banana: Cultivars, biotechnological approaches and genetic transformation. *Int. J. Food Sci. Technol.* 43:1871-1879.
- Bagamba, F. 2007. Market access and Agricultural Production: The Case of Banana Production in Uganda. Ph.D. thesis, Wageningen University & Research, Wageningen, The Netherlands.
- Bagamba, F., Kikulwe, E., Tushemereirwe, W., Ngambeki, D., Muhangi, J., Kagezi, G., and Green, S. 2006. Awareness of banana bacterial wilt control in Uganda: 1. Farmers' perspective. *Afr. Crop Sci. J.* 14:157-164.
- Beck, A. E., Kleiner, M., and Garrell, A.-K. 2022. Elucidating plant-microbe-environment interactions through omics-enabled metabolic modelling using synthetic communities. *Front. Plant Sci.* 13:910377.
- Bentley, J. W., Priou, S., Aley, P., Correa, J., Torres, R., Equise, H., Quiruchi, J. L., and Barea, O. 2006. Method, creativity and CIALs. *Int. J. Agric. Resour. Governance Ecol.* 5:90-105.
- Birt, H. W. G., Pattison, A. B., Skarshewski, A., Daniells, J., Raghavendra, A., and Dennis, P. G. 2022. The core bacterial microbiome of banana (*Musa* spp.). *Environ. Microbiome* 17:46.
- Blomme, G., Dita, M., Jacobsen, K. S., Pérez Vicente, L., Molina, A., Ocimati, W., Poussier, S., and Prior, P. 2017a. Bacterial diseases of bananas and enset: Current state of knowledge and integrated approaches toward sustainable management. *Front. Plant Sci.* 8:1290.
- Blomme, G., Eden-Green, S., Mustafa, M., Nwauzoma, B., and Thangavelu, R. 2011. Major diseases of banana. Pages 85-119 in: *Banana Breeding: Progress and Challenges*. M. Pillay and A. Tenkouano, eds. CRC Press, Boca Raton, FL, U.S.A.
- Blomme, G., Jacobsen, K., Ocimati, W., Beed, F., Ntamwira, J., Sivirihauma, C., Ssekiwoko, F., Nakato, V., Kubiriba, J., Tripathi, L., Tinzaara, W., Mbolela, F., Lutete, L., and Karamura, E. 2014. Fine-tuning banana *Xanthomonas* wilt control options over the past decade in East and Central Africa. *Eur. J. Plant Pathol.* 139:271-287.
- Blomme, G., Ocimati, W., Sivirihauma, C., Lusenge, V., Bumba, M., and Ntamwira, J. 2019. Controlling *Xanthomonas* wilt of banana: Influence of collective application, frequency of application, and social factors on the effectiveness of the single diseased stem removal technique in eastern Democratic Republic of Congo. *Crop Prot.* 118:79-88.
- Blomme, G., Ocimati, W., Sivirihauma, C., Vutseme, L., Mariamu, B., Kamira, M., van Schagen, B., Ekboir, J., and Ntamwira, J. 2017b. A control package revolving around the removal of single diseased banana stems is effective for the restoration of *Xanthomonas* wilt infected fields. *Eur. J. Plant Pathol.* 149:385-400.
- Blomme, G., Turyagyenda, L., Mukasa, H., and Eden-Green, S. 2008. The effectiveness of different herbicides in the destruction of banana *Xanthomonas* wilt infected plants. *Afr. Crop Sci. J.* 16:103-110.
- Bradbury, J. F. 1986. *Guide to Plant Pathogenic Bacteria*. CAB International Mycological Institute, Farnham Royal, Slough, U.K.
- Buregyeya, H. 2010. Evaluation of the Contribution of Birds, Bats and Farm Tools in the Long Distance Transmission of Banana Bacterial Wilt. Masters' thesis, Makerere University, Kampala, Uganda.
- Buregyeya, H., Kubiriba, J., Tusiime, G., Kityo, R., Ssekiwoko, F., and Tushemereirwe, W. 2014. Role of birds and bats in long distance transmission of banana bacterial wilt in Uganda. *Int. J. Agric. Innovations Res.* 2:636-640.
- Chen, C., Lin, H., Ger, M., Chow, D., and Feng, T. 2000. The cloning and characterization of a hypersensitive response assisting protein that may be associated with the harpin-mediated hypersensitive response. *Plant Mol. Biol.* 43:429-438.
- Clark, C. A., Davis, J. A., Abad, J. A., Cuellar, W. J., Fuentes, S., Kreuze, J. F., Gibson, R. W., Mukasa, S. B., Tugume, A. K., Tairo, F. D., and Valkonen, J. P. T. 2012. Sweetpotato viruses: 15 Years of progress on understanding and managing complex diseases. *Plant Dis.* 96:168-185.
- Compant, S., Samad, A., Faist, H., and Sessitsch, A. 2019. A review on the plant microbiome: Ecology, functions, and emerging trends in microbial application. *J. Adv. Res.* 19:29-37.
- Dadransia, A., Usman, M. M., Omar, R., Ismail, S., and Abdullah, R. 2020. Potential use of *Bacillus* genus to control of banana diseases: Approaches toward high yield production and sustainable management. *J. King Saud Univ. Sci.* 32:2336-2342.
- Dastogeer, K. M. G., Tumpa, F. H., Sultana, A., Akter, M. A., and Chakraborty, A. 2020. Plant microbiome—An account of the factors that shape community composition and diversity. *Curr. Plant Biol.* 23:100161.
- Domingo-Calap, M. L., Bernabéu-Gimeno, M., Aure, C. M., Marco-Noales, E., and Domingo-Calap, P. 2022. Comparative analysis of novel lytic phages for biological control of phytopathogenic *Xanthomonas* spp. *Microbiol. Spectrum* 10:e02960-02922.
- Drenth, A., and Kema, G. 2021. The vulnerability of bananas to globally emerging disease threats. *Phytopathology* 111:2146-2161.
- Erdrich, S. H., Sharma, V., Schurr, U., Arsova, B., and Frunzke, J. 2022. Isolation of novel *Xanthomonas* phages infecting the plant pathogens *X. translucens* and *X. campestris*. *Viruses* 14:1449.
- FAOSTAT. 2020. FAO database. <https://www.fao.org/faostat/en/#home>
- Fegan, M., and Prior, P. 2006. Diverse members of the *Ralstonia solanacearum* species complex cause bacterial wilts of banana. *Australas. Plant Pathol.* 35:93-101.
- Fernandez, E., Do, H., Luedeling, E., Luu, T. T. G., and Whitney, C. 2022. Prioritizing farm management interventions to improve climate change adaptation and mitigation outcomes—A case study for banana plantations. *Agron. Sustain. Dev.* 42:76.
- Fiaboe, K., Vigheri, N., and Tinzaara, W. 2010. Scale and scope of the problems due to BXW in Eastern DRC (North and South Kivu and Province Oriental); an expert evaluation of existing information. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.
- Fishman, S., Marcus, R., Talpaz, H., Bar-Joseph, M., Oren, Y., Salomon, R., and Zohar, M. 1983. Epidemiological and economic models for spread and control of citrus tristeza virus disease. *Phytoparasitica* 11:39-49.
- Franzel, S., Coe, R., Cooper, P., Place, F., and Scherr, S. 2001. Assessing the adoption potential of agroforestry practices in sub-Saharan Africa. *Agric. Syst.* 69:37-62.
- Gao, M., Xiong, C., Gao, C., Tsui, C. K. M., Wang, M.-M., Zhou, X., Zhang, A.-M., and Cai, L. 2021. Disease-induced changes in plant microbiome assembly and functional adaptation. *Microbiome* 9:187.
- Garcia-Figuera, S., Grafton-Cardwell, E. E., Babcock, B. A., Lubell, M. N., and McRoberts, N. 2021. Institutional approaches for plant health provision as a collective action problem. *Food Secur.* 13:273-290.

- Geberewold, A. Z. 2019. Review on impact of banana bacterial wilt (*Xanthomonas campestris* pv. *musacerum*) in East and Central Africa. *Cogent Food Agric.* 5:1586075.
- Gillespie, S. 2004. Scaling up community-driven development: A synthesis of experience. World Bank Group, Washington, D.C.
- Gold, C. S., Karamura, E. B., Kiggundu, A., Bagamba, F., and Abera, A. M. 1999. Geographic shifts in the highland cooking banana (*Musa* spp., group AAA-EA) production in Uganda. *Int. J. Sustain. Dev. World Ecol.* 6: 45-59.
- Gold, C. S., Ogenga-Latigo, M. W., Tushemereirwe, W., Kashaia, I., and Nankinga, C. 1993. Farmer perceptions of banana pest constraints in Uganda: Results from a rapid rural appraisal. Pages 3-24 in: Res. Coord. Meet.: Biol. Integr. Control Highland Banana Plantain Pests Dis., Cotonou, Benin, 12-14 November 1991. C. S. Gold and B. Gemmil, eds. International Institute of Tropical Agriculture (IITA), Kampala, Uganda.
- Gonsalves, C., Lee, D. R., and Gonsalves, D. 2007. The adoption of genetically modified papaya in Hawaii and its implications for developing countries. *J. Dev. Stud.* 43:177-191.
- Gonsalves, C. V., and Gonsalves, D. 2014. The Hawaii papaya story. Pages 642-660 In: Handbook on Agriculture, Biotechnology and Development. Edward Elgar Publishing, Cheltenham, U.K.
- Gotor, E., Di Cori, V., Pagnani, T., Kikulwe, E., Kozicka, M., and Caracciolo, F. 2022. Public and private investments for banana *Xanthomonas* wilt control in Uganda: The economic feasibility for smallholder farmers. *Afr. J. Sci. Technol. Innovation Dev.* 14:135-146.
- Jeger, M., Beresford, R., Bock, C., Brown, N., Fox, A., Newton, A., Vicent, A., Xu, X., and Yuen, J. 2021. Global challenges facing plant pathology: Multidisciplinary approaches to meet the food security and environmental challenges in the mid-twenty-first century. *CABI Agric. Biosci.* 2:20.
- Kabahenda, M., Kapiriri, M., Egeru, A., Majaliwa, J., Isubikalu, P., Mukwaya, P., and Bukenya, M. 2010. Analysing agricultural science and technology innovation systems: A case study of the banana sub-sector in Uganda. Technical Centre for Agricultural and Rural Cooperation (CTA) and Regional Universities Forum for Capacity Building in Agriculture (RUFORUM), Makerere University, Kampala, Uganda.
- Kagezi, G., Kangire, A., Tushemereirwe, W., Bagamba, F., Kikulwe, E., Gold, C., Ragama, P., and Kubiriba, J., 2006. Banana bacterial wilt incidence in Uganda. *Afr. Crop Sci. J.* 14:83-91.
- Kakuru, M., Rietveld, A., Mbabazi, E., and Ajambo, S. 2018. Banana-based beverages in East and Central Africa-a money-maker for rural male and female value-chain actors? *Acta Hort.* 1196:229-236.
- Kalyebara, M., Ragama, P., Kikulwe, E., Bagamba, F., Nankinga, K., and Tushemereirwe, W. 2006. Economic importance of the banana bacterial wilt in Uganda. *Afr. Crop Sci. J.* 14:93-103.
- Karamura, E., Osiru, M., Blomme, G., Lusty, C., and Picq, C. 2006. Developing a regional strategy to address the outbreak of banana *Xanthomonas* wilt in East and Central Africa. In: Proc. Banana *Xanthomonas* Wilt Regional Preparedness and Strategy Development Workshop, Kampala, Uganda, 14-18 February 2005.
- Karamura, E., Turyagyenda, F., Tinzaara, W., Blomme, G., Molina, A., and Markham, R. 2008. *Xanthomonas* wilt of bananas in East and Central Africa. Pages 978-982 in: Diagnostic and Management Guide. Bioversity International, Rome, Italy.
- Karamura, E. B., Jogo, W., Rietveld, A., Ochola, D., Staver, C., Tinzaara, W., Karamura, D. A., Kubiriba, J., and Weise, S. 2013. Effectiveness of agro-ecological intensification practices in managing pests in smallholder banana systems in East and Central Africa. *Acta Hort.* 986:119-126.
- Karamura, G., Dennis, O., Julian, S., Jerome, K., and Eldad, K. 2016. Evaluation of a lateral flow device for in-field detection of banana *Xanthomonas* wilt and its application in tracking the systemicity of *Xanthomonas campestris* pv. *musacearum*. *Afr. J. Agric. Res.* 11:2250-2256.
- Katungi, E. M. 2007. Social Capital and Technology Adoption on Small Farms: The Case of Banana Production Technology in Uganda. University of Pretoria, Pretoria, South Africa.
- Kaushal, M., Swennen, R., and Mahuku, G. 2020. Unlocking the microbiome communities of banana (*Musa* spp.) under disease stressed (Fusarium wilt) and non-stressed conditions. *Microorganisms* 8:443.
- Kikulwe, E., Asindu, M., Ocimati, W., Ajambo, S., Tinzaara, W., Iradukunda, F., and Blomme, G. 2022. Scaling banana bacterial wilt management through single diseased stem removal in the Great Lakes Region. Pages 289-317 in: Root, Tuber and Banana Food System Innovations: Value Creation for Inclusive Outcomes. G. Thiele, M. Friedmann, H. Campos, V. Polar, and J. W. Bentley, eds. Springer International Publishing, Cham, Switzerland.
- Kikulwe, E. M., Kyanjo, J. L., Kato, E., Ssali, R. T., Erima, R., Mpiira, S., Ocimati, W., Tinzaara, W., Kubiriba, J., Gotor, E., Stoian, D., and Karamura, E. 2019. Management of banana *Xanthomonas* wilt: Evidence from impact of adoption of cultural control practices in Uganda. *Sustainability* 11:2610.
- Kolavalli, S., and Kerr, J. 2002. Scaling up participatory watershed development in India. *Dev. Change* 33:213-235.
- Kreuze, J., Adewopo, J., Selvaraj, M., Mwanzia, L., Kumar, P., Cuellar, W. J., Legg, J. P., Hughes, D. P., and Blomme, G. 2022. Innovative digital technologies to monitor and control pest and disease threats in root, tuber, and banana (RT&B) cropping systems: Progress and prospects. Pages 261-288 in Root, Tuber and Banana Food System Innovations. Springer, Cham, Switzerland.
- Kubiriba, J., Bagamba, F., Rockfeller, E., and Tushemereirwe, W. 2012a. The changing spread dynamics of banana *Xanthomonas* wilt (BXW) in Uganda. *Uganda J. Agric. Sci.* 13:53-60.
- Kubiriba, J., Erima, R., and Tushemereirwe, W. 2016. Scaling out control of banana *Xanthomonas* wilt from community to regional level: A case from Uganda's largest banana growing region. *J. Dev. Agric. Econ.* 8:108-117.
- Kubiriba, J., Karamura, E., Jogo, W., Tushemereirwe, W., and Tinzaara, W. 2012b. Community mobilization: A key to effective control of banana *Xanthomonas* wilt. *J. Dev. Agric. Econ.* 4:125-131.
- Kubiriba, J., Muthomi, J., Ndungo, V., Kwach, J., Erima, R., Rwomushana, I., Wilberforce, T., and Fina, O. 2014. Strategies for rehabilitation of banana fields infested with *Xanthomonas campestris* pv. *musacearum*. *J. Crop Prot.* 3:21-29.
- Kubiriba, J., and Tushemereirwe, W. 2014. Approaches for the control of banana *Xanthomonas* wilt in East and Central Africa. *Afr. J. Plant Sci.* 8:398-404.
- Lehmann-Danzinger, H. 1987. The distribution of Moko disease in Central and South America and its control on plantains and bananas. In: Improving Citrus and Banana Production in the Caribbean through Phytosanitation, 2-5 Dec 1986, St. Lucia.
- Lin, H.-J., Cheng, H.-Y., Chen, C.-H., Huang, H.-C., and Feng, T.-Y. 1997. Plant amphipathic proteins delay the hypersensitive response caused by harpin Pss and *Pseudomonas syringae* pv. *syringae*. *Physiol. Mol. Plant Pathol.* 51: 367-376.
- Linn, J. F., ed. 2012. Scaling up in Agriculture, Rural Development, and Nutrition, Vol. 19. International Food Policy Research Institute (IFPRI), Washington, D.C.
- Liu, Y., Zhu, A., Tan, H., Cao, L., and Zhang, R. 2019. Engineering banana endosphere microbiome to improve Fusarium wilt resistance in banana. *Microbiome* 7:74.
- Lorenzen, J., Tenkouano, A., Bandyopadhyay, R., Vroh, B., Coyne, D., and Tripathi, L. 2008. Overview of banana and plantain (*Musa* spp.) improvement in Africa: Past and future. *Acta Hort.* 879:595-603.
- Lynam, J., and Twomlow, S. 2014. A twenty-first-century balancing act: Smallholder farm technology and cost-effective research. Pages 324-354 in: New Directions for Smallholder Agriculture. P. B. R. Hazell and A. Rahman, eds. Oxford University Press, Oxford, U.K. <https://doi.org/10.1093/acprof:oso/9780199689347.003.0011>
- Machovina, B., and Feeley, K. J. 2013. Climate change driven shifts in the extent and location of areas suitable for export banana production. *Ecol. Econ.* 95:83-95.
- Magnaye, L. X. 1994. Virus diseases of banana and current studies to eliminate the virus by tissue culture. Pages 38-43 in: Towards Making Pest and Disease Management Relevant to Big and Small Banana Growers. Proc. 1st PPS-SMD Natl. Symp. Pests Dis. Philipp. 23-24 April 1993. Phytopathological Society Inc., Southern Mindanao Division, Davao City, Philippines.
- Malacrino, A., Abdelfattah, A., Berg, G., Benitez, M.-S., Bennett, A. E., Böttner, L., Xu, S., and Schena, L. 2022. Exploring microbiomes for plant disease management. *Biol. Control* 169:104890.
- Mbabazi, E. G., Kikulwe, E. M., Kyanjo, J. L., Mulumba, N., Kato, E., and Gotor, E. 2021. Has continued exposure to banana *Xanthomonas* Wilt worsened farmers' welfare over time? Evidence from banana-producing households in Uganda. *J. Agric. Sci.* 13:11-22.
- Mbaka, J. N., Maina, M., Nakato, V., and Auma, J. 2008. An outbreak of banana *Xanthomonas* wilt in banana orchards in Western Kenya. *Afr. J. Hortic. Sci.* 1:9-18.
- McCampbell, M., Schut, M., Van den Bergh, I., van Schagen, B., Vanlauwe, B., Blomme, G., Gaidashova, S., Njukwe, E., and Leeuwis, C. 2018. *Xanthomonas* wilt of banana (BXW) in Central Africa: Opportunities, challenges, and pathways for citizen science and ICT-based control and prevention strategies. *NJAS Wageningen J. Life Sci.* 86-87:89-100.
- Mills, P., Dehnen-Schmutz, K., Ilbery, B., Jeger, M., Jones, G., Little, R., MacLeod, A., Parker, S., Pautasso, M., Pietravalle, S., and Maye, D. 2011.

- Integrating natural and social science perspectives on plant disease risk, management and policy formulation. *Philos. Trans. R. Soc. Lond. Ser. B Biol. Sci.* 366:2035-2044.
- Milne, A. E., Gottwald, T., Parnell, S. R., Alonso Chavez, V., and van den Bosch, F. 2020. What makes or breaks a campaign to stop an invading plant pathogen? *PLoS Comput. Biol.* 16:e1007570.
- Mudonyi, B., Vanhaelewyn, L., Tusiime, G., Ssekiwoko, F., Kubiriba, J., Tushemereirwe, W. K., and CM, C. 2019. Banana field resistance to insect-vector transmission of bacterial wilt caused by *Xanthomonas campestris* pv. *musacearum*. *Afr. J. Agric. Res.* 14:24-33.
- Munar-Vivas, O., Morales-Osorio, J. G., and Castañeda-Sánchez, D. A. 2010. Use of field-integrated information in GIS-based maps to evaluate Moko disease (*Ralstonia solanacearum*) in banana growing farms in Colombia. *Crop Prot.* 29:936-941.
- Mustafa, A. S., Tugume, B., Ssenku, J. E., Ssemenda, P., Athman, S. Y., Oryem-Origa, H., Kubiriba, J., Dinesh-Kumar, S. P., and Tugume, A. K. 2022. *Xanthomonas campestris* pv. *musacearum* bacterial infection induces organ-specific callose and hydrogen peroxide production in banana. *PhytoFrontiers* 2:202-217.
- Mwangi, M. 2007. Removing infected banana mats to contain *Xanthomonas* wilt: Experiences in Uganda, Rwanda and the Democratic Republic of Congo. *Crop Crisis Control Project (C3P)*, International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.
- Mwangi, M., and Bandyopadhyay, R. 2006. Managing banana *Xanthomonas* wilt. *Crop Crisis Control Project (C3P)*, International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.
- Mwangi, M., Bandyopadhyay, R., Ragama, P., and Tushemereirwe, W. K. 2007. Assessment of banana planting practices and cultivar tolerance in relation to management of soilborne *Xanthomonas campestris* pv. *musacearum*. *Crop Prot.* 26:203-1208.
- Mwangi, M., and Nakato, V. 2007. Key factors responsible for the *Xanthomonas* wilt epidemic on banana in East and Central Africa. *Acta Hort.* 828: 395-404.
- Mwebaze, J., Tusiime, G., Tushemereirwe, W., and Kubiriba, J. 2006. The survival of *Xanthomonas campestris* pv. *musacearum* in soil and plant debris. *Afr. Crop Sci. J.* 14:121-127.
- Nakato, G. V., Christelová, P., Were, E., Nyine, M., Coutinho, T. A., Doležel, J., Uwimana, B., Swennen, R., and Mahuku, G. 2019. Sources of resistance in *Musa* to *Xanthomonas campestris* pv. *musacearum*, the causal agent of banana *Xanthomonas* wilt. *Plant Pathol.* 68:49-59.
- Nakato, G. V., Wicker, E., Coutinho, T. A., Mahuku, G., and Studholme, D. J. 2018a. A highly specific tool for identification of *Xanthomonas vasicola* pv. *musacearum* based on five Xvm-specific coding sequences. *Heliyon* 4:e01080-e01080.
- Nakato, V., Mahuku, G., and Coutinho, T. 2018b. *Xanthomonas campestris* pv. *musacearum*: A major constraint to banana, plantain and enset production in central and east Africa over the past decade. *Mol. Plant Pathol.* 19: 525-536.
- Nakayinga, R., Makumi, A., Tumuhaise, V., and Tinzaara, W. 2021. *Xanthomonas* bacteriophages: A review of their biology and biocontrol applications in agriculture. *BMC Microbiol.* 21:291.
- Ndah, H. T., Schuler, J., Uthes, S., Zander, P., Triomphe, B., Mkomwa, S., and Corbeels, M. 2015. Adoption potential for conservation agriculture in Africa: A newly developed assessment approach (QAToCA) applied in Kenya and Tanzania. *Land Degrad. Dev.* 26:133-141.
- Ndungo, V., Eden-Green, S., Blomme, G., Crozier, J., and Smith, J. J. 2006. Presence of banana *Xanthomonas* wilt (*Xanthomonas campestris* pv. *musacearum*) in the Democratic Republic of Congo (DRC). *Plant Pathol.* 55:294-294.
- Niko, N., Ndayihanzamaso, P., and Lepoint, P. 2011. First report of Banana *Xanthomonas* Wilt (*Xanthomonas campestris* pv. *musacearum*) in Burundi. *Institut des Sciences Agronomiques du Burundi*, BP 795, Bujumbura, Burundi.
- Nimusiima, J., Köberl, M., Tumuhairwe, J. B., Kubiriba, J., Staver, C., and Berg, G. 2015. Transgenic banana plants expressing *Xanthomonas* wilt resistance genes revealed a stable non-target bacterial colonization structure. *Sci. Rep.* 5:18078.
- Ntui, V. O., Tripathi, J. N., and Tripathi, L. 2020. Robust CRISPR/Cas9 mediated genome editing tool for banana and plantain (*Musa* spp.). *Curr. Plant Biol.* 21:100128.
- Nyombi, K. 2013. Towards sustainable highland banana production in Uganda: Opportunities and challenges. *Afr. J. Food Agric. Nutr. Dev.* 13: 7544-7561.
- Ochola, D., Ocimati, W., Tinzaara, W., Blomme, G., and Karamura, E. B. 2015. Effects of water stress on the development of banana *Xanthomonas* wilt disease. *Plant Pathol.* 64:552-558.
- Ocimati, W., Bouwmeester, H., Groot, J. C. J., Tiftonell, P., Brown, D., and Blomme, G. 2019. The risk posed by *Xanthomonas* wilt disease of banana: Mapping of disease hotspots, fronts and vulnerable landscapes. *PLoS One* 14:e0213691.
- Ocimati, W., Nakato, G. V., Fiaboe, K. M., Beed, F., and Blomme, G. 2015. Incomplete systemic movement of *Xanthomonas campestris* pv. *musacearum* and the occurrence of latent infections in *Xanthomonas* wilt-infected banana mats. *Plant Pathol.* 64:81-90.
- Ocimati, W., Ssekiwoko, F., Karamura, E., Tinzaara, W., Eden-Green, S., and Blomme, G. 2013. Systemicity of *Xanthomonas campestris* pv. *musacearum* and time to disease expression after inflorescence infection in East African highland and Pisang Awak bananas in Uganda. *Plant Pathol.* 62: 777-785.
- Ocimati, W., Tazuba, A. F., and Blomme, G. 2021. Farmer friendly options for sterilizing farm tools for the control of *Xanthomonas* wilt disease of banana. *Front. Agron.* 3:655824.
- Ocimati, W., Tazuba, A. F., and Blomme, G. 2022. Spread of *Xanthomonas vasicola* pv. *musacearum* within banana mats: Implications for *Xanthomonas* wilt management. *J. Plant Pathol.* 104:1111-1122.
- Odiopio, J., Tusiime, G., Tripathi, L., and Aritua, V. 2009. Genetic homogeneity among Ugandan isolates of *Xanthomonas campestris* pv. *musacearum* revealed by randomly amplified polymorphic DNA analysis. *Afr. J. Biotechnol.* 8:5652-5660.
- Padam, B. S., Tin, H. S., Chye, F. Y., and Abdullah, M. I. 2014. Banana by-products: An under-utilized renewable food biomass with great potential. *J. Food Sci. Technol.* 51:3527-3545.
- Pagnani, T., Gotor, E., Kikulwe, E., and Caracciolo, F. 2021. Livelihood assets' influence on Ugandan farmers' control practices for banana *Xanthomonas* wilt (BXW). *Agric. Food Econ.* 9:25.
- PIBID. 2007. Presidential Initiative for Banana Industrial Development (PIBID). <https://www.pibid.org/>
- Premabati, T., and De Mandal, S. 2020. Bacterial diseases of banana: Detection, characterization, and control management. Pages 71-85 in: *Recent Advancements in Microbial Diversity*. S. De Mandal and P. Bhatt, eds. Academic Press, London, U.K.
- Ramírez, M., Neuman, B. W., and Ramírez, C. A. 2020. Bacteriophages as promising agents for the biological control of Moko disease (*Ralstonia solanacearum*) of banana. *Biol. Control* 149:104238.
- Rey, C., and Vanderschuren, H. 2017. Cassava mosaic and brown streak diseases: Current perspectives and beyond. *Annu. Rev. Virol.* 4:429-452.
- Ristaino, J. B., Anderson, P. K., Bebb, D. P., Brauman, K. A., Cunniffe, N. J., Fedoroff, N. V., Finegold, C., Garrett, K. A., Gilligan, C. A., Jones, C. M., Martin, M. D., MacDonald, G. K., Neenan, P., Records, A., Schmale, D. G., Tateosian, L., and Wei, Q. 2021. The persistent threat of emerging plant disease pandemics to global food security. *Proc. Natl. Acad. Sci. U.S.A.* 118:e2022239118.
- Rizzo, D. M., Lichtveld, M., Mazet, J. A. K., Togami, E., and Miller, S. A. 2021. Plant health and its effects on food safety and security in a One Health framework: Four case studies. *One Health Outlook* 3:6.
- Romero-Suarez, S., Jordan, B., and Heinemann, J. A. 2012. Isolation and characterization of bacteriophages infecting *Xanthomonas arboricola* pv. *juglandis*, the causal agent of walnut blight disease. *World J. Microbiol. Biotechnol.* 28:1917-1927.
- Rubaihayo, P., and Gold, C. 1993. Rapid rural appraisal of highland banana production in Uganda. *InfoMusa* 2:15-16.
- Rutikanga, A., Night, G., Tusiime, G., Ocimati, W., and Blomme, G. 2015. Spatial and temporal distribution of insect vectors of *Xanthomonas campestris* pv. *musacearum* and their activity across banana cultivars grown in Rwanda. Pages 139-153 in: *Proc. 7th Congr. Plant Prot.D.* Marčić, M. Glavendekić, and P. Nicot, eds. Plant Protection Society of Serbia, IOBC-EPRS, IOBC-WPRS, Belgrade, Serbia.
- Rutikanga, A., Sivirihauma, C., Murekezi, C., and Anuarite, U. E. A. 2013. Banana *Xanthomonas* wilt management: Effectiveness of selective mat uprooting coupled with control options for preventing disease transmission. Case study in Rwanda and Eastern Democratic Republic of Congo. Pages 116-124 in: *Banana Systems in the humid highlands of sub-Saharan Africa*. CABI, London, U.K.
- Savary, S., Willocquet, L., Pethybridge, S. J., Esker, P., McRoberts, N., and Nelson, A. 2019. The global burden of pathogens and pests on major food crops. *Nat. Ecol. Evol.* 3:430-439.

- Schaart, J. G., van de Wiel, C. C. M., and Smulders, M. J. M. 2021. Genome editing of polyploid crops: Prospects, achievements and bottlenecks. *Transgenic Res.* 30:337-351.
- Selvaraj, M. G., Vergara, A., Montenegro, F., Alonso Ruiz, H., Safari, N., Raymaekers, D., Ocimati, W., Ntamwira, J., Tits, L., Omondi, A. B., and Blomme, G. 2020. Detection of banana plants and their major diseases through aerial images and machine learning methods: A case study in DR Congo and Republic of Benin. *ISPRS J. Photogramm. Remote Sens.* 169: 110-124.
- Selvaraj, M. G., Vergara, A., Ruiz, H., Safari, N., Elayabalan, S., Ocimati, W., and Blomme, G. 2019. AI-powered banana diseases and pest detection. *Plant Methods* 15:1-11.
- Sherman, J., Burke, J. M., and Gent, D. H. 2019. Cooperation and coordination in plant disease management. *Phytopathology* 109:720-1731.
- Shotkoski, F., Tripathi, L., Kiggundu, A., Arinaitwe, G., and Tushemereirwe, W. 2010. Role of biotechnology and transgenics in bananas (*Musa* spp.) in Africa. *Acta Hortic.* 879:275-279.
- Smith, J. J., Jones, D. R., Karamura, E., Blomme, G., and Turyagyenda, F. L. 2008a. An analysis of the risk from *Xanthomonas campestris* pv. *musacearum* to banana cultivation in Eastern, Central and Southern Africa. *Bioversity International*, Montpellier, France.
- Smith, J. J., Waage, J., Woodhall, J. W., Bishop, S. J., and Spence, N. J. 2008b. The challenge of providing plant pest diagnostic services for Africa. Pages 365-375 in: *Sustainable Disease Management in a European Context*. D. B. Collinge, L. Munk, and B. M. Cooke, eds. Springer, Dordrecht, The Netherlands. https://doi.org/10.1007/978-1-4020-8780-6_16
- Ssekiwoko, F., Kiggundu, A., Tushemereirwe, W. K., Karamura, E., and Kunert, K. 2015. *Xanthomonas vasicola* pv. *musacearum* down-regulates selected defense genes during its interaction with both resistant and susceptible banana. *Physiol. Mol. Plant Pathol.* 90:21-26.
- Ssekiwoko, F., Taligoola, H., and Tushemereirwe, W. 2006a. *Xanthomonas campestris* pv. *musacearum* host range in Uganda. *Afr. Crop Sci. J.* 14: 111-120.
- Ssekiwoko, F., Turyagyenda, L., Mukasa, H., Eden-Green, S., and Blomme, G. 2006b. Systemicity of *Xanthomonas campestris* pv. *musacearum* in flower-infected banana plants. In: XVII ACORBAT Int. Meet.: Banana: A Sustainable Business. Joinville, Santa Catarina, Brazil.
- Ssekiwoko, F., Tushemereirwe, W., Batte, M., Ragama, P., and Kumakech, A. 2006c. Reaction of banana germplasm to inoculation with *Xanthomonas campestris* pv. *musacearum*. *Afr. Crop Sci. J.* 14:151-155.
- Stover, R. 1962. Studies on Fusarium wilt of bananas: IX. Competitive saprophytic ability of *F. oxysporum* f. *cubense*. *Can. J. Bot.* 40:1473-1481.
- Strange, R. N., and Scott, P. R. 2005. Plant disease: A threat to global food security. *Annu. Rev. Phytopathol.* 43:83-116.
- Studholme, D. J., Wicker, E., Abrare, S. M., Aspin, A., Bogdanove, A., Broders, K., Dubrow, Z., Grant, M., Jones, J. B., Karamura, G., Lang, J., Leach, J., Mahuku, G., Nakato, G. V., Coutinho, T., Smith, J., and Bull, C. T. 2020. Transfer of *Xanthomonas campestris* pv. *arecae* and *X. campestris* pv. *musacearum* to *X. vasicola* (Vauterin) as *X. vasicola* pv. *arecae* comb. nov. and *X. vasicola* pv. *musacearum* comb. nov. and description of *X. vasicola* pv. *vasculorum* pv. nov. *Phytopathology* 110:1153-1160.
- Thresh, J., Otim-Nape, G., Legg, J., and Fargette, D. 1997. African cassava mosaic virus disease: The magnitude of the problem. *Afr. J. Root Tuber Crops* 2:13-19.
- Thresh, J. M., and Owusu, G. K. 1986. The control of cocoa swollen shoot disease in Ghana: An evaluation of eradication procedures. *Crop Prot.* 5: 41-52.
- Tinzaara, W., Gold, C., Ssekiwoko, F., Bandyopadhyay, R., Abera, A., and Eden-Green, S. 2006. Role of insects in the transmission of banana bacterial wilt. *Afr. Crop Sci. J.* 14:105-110.
- Tinzaara, W., Karamura, E., Blomme, G., Jogo, W., Ocimati, W., Rietveld, A., Kubiriba, J., and Opio, F. 2011. Why sustainable management of *Xanthomonas* wilt of banana in east and central Africa has been elusive. *Acta Hortic.* 986:157-164.
- Tinzaara, W., Kiggundu, A., Gold, C., Tushemereirwe, W., and Karamura, E. 2009. Management options for highland banana pests and diseases in East and Central Africa. *Outlooks Pest Manage.* 20:204-208.
- Tinzaara, W., Mutambuka, M., Oyesigye, E., Blomme, G., Dita, M., Gold, C. S., Rouard, M., and Karamura, E. 2021. Banana wilt diseases: Current status and future research strategies for their management. *Int. J. Pest Manage.* <https://doi.org/10.1080/09670874.2021.1992685>
- Tinzaara, W., Ssekiwoko, F., Kikulwe, E., and Karamura, E. 2019. Effectiveness of learning and experimentation approaches for farmers as a community based strategy for banana *Xanthomonas* wilt management. *J. Agric. Ext. Rural Dev.* 11:128-138.
- Tripathi, J. N., Lorenzen, J., Bahar, O., Ronald, P., and Tripathi, L. 2014. Transgenic expression of the rice Xa21 pattern-recognition receptor in banana (*Musa* sp.) confers resistance to *Xanthomonas campestris* pv. *musacearum*. *Plant Biotechnol. J.* 12:663-673.
- Tripathi, J. N., Ntui, V. O., Shah, T., and Tripathi, L. 2021. CRISPR/Cas9-mediated editing of DMR6 orthologue in banana (*Musa* spp.) confers enhanced resistance to bacterial disease. *Plant Biotechnol. J.* 19:1291-1293.
- Tripathi, L., Atkinson, H., Roderick, H., Kubiriba, J., and Tripathi, J. N. 2017. Genetically engineered bananas resistant to *Xanthomonas* wilt disease and nematodes. *Food Energy Secur.* 6:37-47.
- Tripathi, L., Mwangi, M., Abele, S., Aritua, V., Tushemereirwe, W. K., and Bandyopadhyay, R. 2009. *Xanthomonas* wilt: A threat to banana production in East and Central Africa. *Plant Dis.* 93:440-451.
- Tripathi, L., Ntui, V. O., and Tripathi, J. N. 2022. Control of bacterial diseases of banana using CRISPR/Cas-based gene editing. *Int. J. Mol. Sci.* 23:3619.
- Tripathi, L., Ntui, V. O., Tripathi, J. N., and Kumar, P. L. 2021. Application of CRISPR/Cas for diagnosis and management of viral diseases of banana. *Front. Microbiol.* 11:609784.
- Tripathi, L., Tripathi, J. N., and Kubiriba, J. 2016. Transgenic technologies for bacterial wilt resistance. Pages 197-209 in: *Banana: Genomics and Transgenic Approaches for Genetic Improvement*. S. Mohandas and K. Ravishanker, eds. Springer, Singapore.
- Tripathi, L., Tripathi, J. N., Shah, T., Muiruri, K. S., and Katari, M. 2019. Molecular basis of disease resistance in banana Progenitor *Musa balbisiana* against *Xanthomonas campestris* pv. *musacearum*. *Sci. Rep.* 9:7007.
- Trivedi, P., Batista, B. D., Bazany, K. E., and Singh, B. K. 2022. Plant-microbiome interactions under a changing world: Responses, consequences and perspectives. *New Phytol.* 234:1951-1959.
- Trivedi, P., Leach, J. E., Tringe, S. G., Sa, T., and Singh, B. K. 2020. Plant-microbiome interactions: From community assembly to plant health. *Nat. Rev. Microbiol.* 18:607-621.
- Turner, T. R., James, E. K., and Poole, P. S. 2013. The plant microbiome. *Genome Biol.* 14 209.
- Tushemereirwe, W., Bagamba, F., Katungi, E., Kikulwe, E., Karamura, D., Edmeades, S., and Smale, M. 2006. A Baseline Assessment of Banana Production and Management Practices in Uganda—Uganda Country Report. NARO, Entebbe, Uganda.
- Tushemereirwe, W., Kangire, A., Smith, J., Ssekiwoko, F., Nakyanzi, M., Kataama, D., Musiitwa, C., and Karyajira, R. 2003. Outbreak of bacterial wilt on banana in Uganda. *Infomusa* 12:6-8.
- Tushemereirwe, W., Kangire, A., Ssekiwoko, F., Offord, L. C., Crozier, J., Boa, E., Rutherford, M., and Smith, J. J. 2004. First report of *Xanthomonas campestris* pv. *musacearum* on banana in Uganda. *Plant Pathol.* 53:802-802.
- Tushemereirwe, W., Okaasai, O., Kubiriba, J., Nankinga, C., Muhangi, J., Odoo, N., and Opio, F. 2006. Status of banana bacterial wilt in Uganda. *Afr. Crop Sci. J.* 14:73-82.
- Valverde, R. A., Clark, C. A., and Valkonen, J. P. 2007. Viruses and virus disease complexes of sweetpotato. *Plant Viruses* 1:116-126.
- Varma, V., and Bebb, D. P. 2019. Climate change impacts on banana yields around the world. *Nat. Climate Change* 9:752-757.
- Wasukira, A., Coulter, M., Al-Sowayeh, N., Thwaites, R., Paszkiewicz, K., Kubiriba, J., Smith, J., Grant, M., and Studholme, D. 2014. Genome sequencing of *Xanthomonas vasicola* pathovar *vasculorum* reveals variation in plasmids and genes encoding lipopolysaccharide synthesis, type-IV pilus and type-III secretion effectors. *Pathogens* 3:211-237.
- Wasukira, A., Tayebwa, J., Thwaites, R., Paszkiewicz, K., Aritua, V., Kubiriba, J., Smith, J., Grant, M., and Studholme, D. J. 2012. Genome-wide sequencing reveals two major sub-lineages in the genetically monomorphic pathogen *Xanthomonas campestris* pathovar *musacearum*. *Genes (Basel)* 3: 361-377.
- Were, E. 2016. Endophytic bacteria associated with banana and their potential for controlling *Xanthomonas* Wilt. Master of Science, Makerere University, Kampala, Uganda.
- Xue, C., Ryan Penton, C., Shen, Z., Zhang, R., Huang, Q., Li, R., Ruan, Y., and Shen, Q. 2015. Manipulating the banana rhizosphere microbiome for biological control of Panama disease. *Sci. Rep.* 5:11124.
- Yirgou, D., and Bradbury, J. 1968. Bacterial wilt of onset (*Ensete ventricosum*) incited by *Xanthomonas musacearum* sp. n. *Phytopathology* 58:111-112.
- Yirgou, D., and Bradbury, J. 1974. A note on wilt of banana caused by the onset wilt organism *Xanthomonas musacearum*. *East Afr. Agric. For. J.* 40: 111-114.