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Review Article
Identification and Management Challenges Associated with *Ralstonia solanacearum* (Smith), Causal Agent of Bacterial Wilt Disease of Tomato in Sub-Saharan Africa

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Abstract
Tomato is the world's most consumed vegetable crop after potato and it is source of vitamins, minerals, fiber, lycopene, β-carotene and income. Despite its significant importance tomato can heavily be attacked by different pathogens including *Ralstonia solanacearum* that incites bacteria wilt disease. The disease is very devastating causing a considerable yield loss worldwide. The pathogen can survive in plant debris, infected plants and host weeds and spread from one field to another by irrigation or flood water, soil, farm equipment and workers and weeds which usually grow along waterways and it is difficult to manage due to complication in biology, nature of infestation and wide host range. In areas like the Sub-Saharan Africa where there exists a wide diversity of plant species, the pathogen becomes even more difficult to manage. It is on this basis that this review article, clearly discusses challenges for bacterial wilt disease identification and management in tomato farming systems with respect to the diagnosis methods used, pathogen genetic diversity and host range and pathogen survival mechanisms under different environment. The information will empower the responsible personnel involved in tomato production chain to have clear information about the pathogen and management options available against the disease in Sub-Saharan Africa.

Key words: Bacterial wilt, host range, pathogen diversity, genetic, *Ralstonia solanacearum*

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INTRODUCTION

Tomato (*Lycopersicon esculentum* L.) is the second most important vegetable crop after potato in the world[1]. It is one of the most consumed vegetable as a source of vitamins, minerals and fiber worldwide[2,3]. Tomato contains lycopene and β-carotene that have anti-cancer and antioxidant properties and hence considered as healthy[2]. Tomato has become the world agenda in the international horticultural forums due to its nutritive and economic importance[4]. In Tanzania, tomato is the first most important vegetable crop grown for consumption and income[5,6]. Tomato provides smallholder farmers with much higher income and more jobs per hectare than staple crops[2].

The global tomato production is estimated to be 161 793 834 t/year[7]. Production of tomato in Tanzania is estimated to be 255 000 t/year with average yield of 17.5 t ha^{-1} compared with the global average yield of 33.6 t ha^{-1}[1,7]. Factors for low production of tomato include low soil fertility, drought and poor quality inputs including seeds, unreliable markets and pests[8, 9]. Of these, diseases have been cited to be the most limiting factor of tomato production in Sub Saharan Africa[5,10,11]. Of the diseases, bacterial wilt caused by *Ralstonia solanacearum* is classified as one of the world's most important phytopathogenic bacteria due to its lethality, persistence, wide host range and broad geographic distribution[12,13]. The pathogen is characterized to has a very large group of strains varying in their geographical origin, host range and pathogenic behavior worldwide[14]. It is quarantined organism[15] ranked second after *Pseudomonas syringaepathovars* based on its economic importance worldwide[16]. The *R. solanacearum* is thought to be the most destructive plant pathogenic bacterium causing tomato yield losses ranging from 10-100% worldwide[17]. Yield losses depend on prevailing strain, cropping system, soil, climate and cultivar[18].

Identification of the pathogen is believed to be the strongest foundation towards developing its management strategies[18,19,20]. Techniques for the diagnosis of bacterial wilt disease of tomato include observation of symptoms and bacterial streaming, plating on a semi-selective medium, immunodiagnostic assay by species-specific antibodies and polymerase chain reaction (PCR)[18,21-23]. However, use of such techniques is challenged by factors such as disease symptoms complex[23] which complicate choice of appropriate identification methods[19].

Different management approaches of bacterial wilt disease in tomato consists use of chemicals, biological agents, cultural and physical practices[23]. Efficacy of such methods are challenged by the pathogen genetic diversity of and existence of wide host range for the pathogen[24,25]. Being a complex plant pathogen, *R. solanacearum* is able to infect crops as a soil, water and/or seed borne pathogen[12,26,27]. It is an endophyte pathogen which can form genetically different strains and survive in extremely diverse environment travelling along waterways[13,28]. The bacterium is capable of conquering various host plants which increase its survival and persistence in the environment[13,11,26]. This study discusses identification and management challenges of bacterial wilt disease of tomato in relation to the genetic diversity, host range, plant infection machinery and disease diagnosis methods, thus highlighting the future research study so that sustainable disease management can be developed.

IDENTIFICATION CHALLENGES OF BACTERIAL WILT DISEASE IN TOMATO FARMING SYSTEMS

Identification challenges of bacterial wilt disease of tomato based on symptoms: It is often challenging to differentiate bacterial wilt disease symptoms from those caused by other disease causing factors[29,30]. Plant wilting can be a result of vascular bundles failing to function, high salinity, saturated soil or infection by bacteria, fungi and/or nematodes[31]. Secondary infections by other pathogens may interfere with those of *R. solanacearum*[27]. There are situations that some infected plants by the same bacterial wilt disease-causing pathogens do not show up symptoms[30,32]. This consequently, causes increased spread of bacterial wilt disease in the farming system. Therefore, studies should be conducted to complement symptoms with other plant disease diagnosis methods.

Identification challenges by using bacterial streaming technique: Bacterial streaming is an initial step to detect *R. solanacearum* in a plant tissue showing wilting symptoms under condition of adequate soil moisture in which a cut plant tissue exhibits bacterial slime by suspending vascular vessels in clean water[18]. The technique is simple and convenient to be performed in the field or laboratory[33,34]. However, it gives a generalized indication for the infection caused by bacteria but cannot be informative on the bacterial species or strain[27]. In addition, visibility of bacterial streaming by naked eye depends on bacterial population in the xylem which should not be low[18]. Research is needed to advance this technique in such a way that bacterial species can be detected so long as even at low population.

Identification challenges by using species-specific antibodies: This is a commercially developed diagnosis kit for the detection of *R. solanacearum* in plant tissue and culture in the field or laboratory. Test kit which usually contains immunostrips, sample extraction bags and user guide requires to be stored at lower temperatures of 2-8°C and should be tightly stored in the desiccated container at all times. Prior to use, immonostrips and extraction buffer need to be warmed at temperatures of 18-30°C to make test components ready foruse[35].

In performing the test, a plant tissue of 0.15 g is taken from a wilting plant and put into an extraction buffer of 3 mL in a sample extraction bag. Presence or absence of *R. solanacearum* can then be detected from the strips as a positive or negative result. The test is sensitive with bacterial population from 10^5 CFU mL^{-1}. The whole process usually takes about 5-30 min depending on pathogen titer in the sample. The technique could be one of the quicker and cheaper methods of detecting bacterial wilt disease however its application faces certain challenges in developing countries.

First, immunostrips are not readily available at the community level and hence expensive, this has limited their application and adoption as majority of farmers cannot afford[19]. Secondly, immunostrips is incapable of detecting bacterial population which is below 10^5 CFU mL^{-1} and can only detect *R. solanacearum* to the species level. Since *R. solanacearum* has a quarantine status, presence of bacterium even at low population has to be detected for prevention and management measures[15]. Third, the recommended storage temperature range of 2-8°C may not be achievable in tropical and subtropical countries where average temperature is high. Therefore, the immunostrips technology requires harmonization for the farming community in the Sub-Saharan Africa to use effectively and efficiently.

Identification challenges by using carbon source and semi-selective medium: The carbon source utilization method uses disaccharides and hexose alcohols for the determination of biovars of *R. solanacearum*[35]. Disaccharides used are maltose, cellobiose and lactose while hexose alcohols are sorbitol, dulcitol and Mannitol[18]. Biovars determination is imperative in development of management strategies[18,32]. The procedure is mainly performed by experts in specialized laboratories[18,19]. The semi-selective medium method constitutes isolation of *R. solanacearum* from plant tissues on a specific diagnostic media[18]. A major challenge of this technique is that it takes time (at least 3-6 days) to carry out and obtain diagnosis results. This may look to be long period to implement the required management measure as by then the plant will have wilted resulting into huge yield reduction[14,18]. Developing biosensors could be a way forward for timely implementation of management measures in Sub-Saharan Africa where techniques such as Immunodiagnostic assays still faces some challenges.

Identification challenges by using polymerase chain reaction (PCR): With PCR technique plant, soil or water samples suspected to contain *R. solanacearum* is subjected to DNA testing for identification purposes[18]. Various methods can be used for the DNA extraction using specific primers for *R. solanacearum*[36,37]. The technique is however considered as one of the most complicated and costly pathogen detection method[38] as it depends on bacterium pure culture isolation, DNA extraction and testing. For instance, the procedure of obtaining a pure bacterium culture for DNA extraction, sequencing and sequence alignment is a process which is resources demanding. This limit technological application as well as adaption to benefit from its use in developing countries. Use of isothermal amplification which is more affordable and appropriate than DNA-based methods could be exploited in Sub-Saharan Africa.

MANAGEMENT CHALLENGES OF BACTERIAL WILT DISEASE IN TOMATO FARMING SYSTEMS

Several management methods of bacterial wilt disease have been reported as shown in Table 1. Based on the agent used and mechanism of action in disease management such methods are grouped as chemical, biological, cultural and physical methods[39].

Management challenges due to the pathogen genetic diversity: Despite the availability of the several disease methods to combat bacterial wilt, this disease has not been successfully managed in Sub-Saharan Africa region. Breeding resistant cultivars against *R. solanacearum* for example has been popularly promoted as one of the best strategy to manage bacterial wilt disease[12,26]. However, success of breeding resistant cultivar against bacterial wilt disease is hampered by the genetic diversity of *R. solanacearum*[23,26,113,36].

One of the factors for the failure of management methods could be attributed to the genetic diversity of *R. solanacearum*. There exists a wide genetic diversity of *R. solanacearum* worldwide[13,24] and several authors have

Table 1: Bacterial wilt disease management approaches and mechanisms

Methods	Examples	Mechanisms used	References
Chemicals	Algicide(3-3-Indolyl butanoic acid), fumigants (metamsodium, 1,3-Dichloropropene), chloropicrin, validoxylamine, validamycin, acibenzolar-S-methyl(ASM), thymol, silicon, chitosan and sodium chloride bactericides (triazolothiadiazine, streptomycin sulfate, bleaching powders or weak acidic electrolyzed water and phosphoric acid solution	Induce systemic resistant, increase the amount of soil microorganisms and soil enzyme activity or increase seedling vigor and tolerance to *R. solanacearum* and act as sterilizers, antibacterial and bacteriostatic	Yuliar *et al.*[23], Mbega *et al.*[39], Ndakidemi[40], Boonham *et al.*[41], Vincelli and Tisserat[42], Dannon and Wydra[43], Hacisalihoglu *et al.*[44], Kawabata *et al.*[45], Khanum *et al.*[46], Kurabachew and Wydra[47], Nakaune *et al.*[48], Norman *et al.*[49] and Pradhanang *et al.*[50]
Biological	Bacteria: Avirulent species of *R.solanacearum*, *Streptomyces* spp, *Acinetobacter* sp., *Burkholderia nodosa*, *B. sacchari*, *B. tericola*, *B. pyrrocinia*, *Bacillus thuringiensis*, *B. cereus*, *B. amyloliquefaciens*, *Chryseobacterium daecheongense*, *C. indologenes*, *Chryseomonas luteola*, *Clostridium* sp., *Delftia acidovorans*, *Anterobacter* sp., *Flavobacterium johnsoniae*, *Myroides odoratimimus*, *Paenibacillus marcerans*, *P. polymyxa*, *Pseudomonas brassicacearum*, *R. pickettii*, *Serratia* sp.,*Sphingomonas paucimobilis*, *Staphylococcus auricularis*, *Stenotrophomonas maltophilia*, *Streptomyces rochei*, *S. virginiae* and *Xenorhabdus nematophila*	Competition for nutrients and space, antibiosis, parasitism, induced systemic resistance and root colonization	Kawabata *et al.*[45], Sharma and Kumar[51], Wydra and Dannon[52], Yamasaki *et al.*[53], Alvarez *et al.*[54], Chen *et al.*[55], Ding *et al.*[56], Hoa *et al.*[57], Huang *et al.*[58], Hu *et al.*[59], Hyakumachi *et al.*[60], Ji *et al.*[61], Guo *et al.*[62], Li *et al.*[63,64], Ling *et al.*[65], Lin *et al.*[66], Messiha *et al.*[67], Momma[68], Nion and Toyota[69], Ramesh and Phadke[70], Takahashi *et al.*[71], Tan *et al.*[72], Xue *et al.*[73] and Yamada *et al.*[74]
	Fungi: *Glomus versiforme*, *Pythium oligandrum*, Shiitake mycelia, *Gigaspora margarita*, *Glomus mosseae* and *Scutellospora* sp. and *Parmotrema tinctorum*	Increase in the contents of soluble phenols and cell-wall bound phenols in the root tissue, cell wall proteins which induce resistance and antibiotic ingredient	Yang *et al.*[75], Yuan *et al.*[76], Zhou *et al.*[77], Zhou *et al.*[78], Zhu and Yao[79] and Tahat *et al.*[80]
	Plant residues: chili (*Capsicum annum*), Chinese gall (*Rhuschinensis*), clove (*Szygyum aromaticum*), cole (*Brassica* sp.), eggplant (*Solanum melongena*), eucalyptus (*Eucalyptus globules*), geranium (*Geranium carolinianum*), guava (*Psidium guajava* and *P. quineense*), hinoki (*Chamaecyparis obtusa*), Japanese cedar (*Cryptomeria japonica*), lemon grass (*Cimbopogon citratus*), marigold (*Tagetes patula*), neem (*Azadirachta indica*), palmarosa (*Cimbopogon martini*), pigeon pea (*Cajanus cajan*), sunhemp (*Crotalaria juncea*), tamarillo (*Cyphomandra betacea*), thyme (*Thymus* spp.), woodwax tree (*Toxicodendron xylvestre*) and worm killer (*Aristolochia bracteata*)	Antimicrobial activities and the indirect suppression of the pathogen through improved physical, chemical and biological soil properties	Denny and Hayward[36], Norman *et al.*[49], Pacumbaba *et al.*[81], Hase *et al.*[82], Gomes *et al.*[83], Amorim *et al.*[84], Arthy *et al.*[85], Acharya and Srivastava[86], Almeida *et al.*[87], Cardoso *et al.*[88], Ji *et al.*[89], Matsushita *et al.*[90], Ooshiro *et al.*[91], Ordonez *et al.*[92], Olivier *et al.*[93], Hwang *et al.*[94], Paret *et al.*[95], Pontes *et al.*[96], Posas and Toyota[97], Shimpi *et al.*[98], Texeira *et al.*[99] and Yu[100]
	Animal wastes: pig slurry, poultry and farmyard manure	Shifts in bacterial community profiles and higher microbial activity and numbers of cultural bacteria and fungi	Hase *et al.*[82], Gomes *et al.*[83], Amorim *et al.*[84] and Arthy *et al.*[85]
	Simple organic compounds: Amino acids, sugars and organic acids e.g. lysine, riboflavin, aminobutyric acid and methyl gallate	Shifts in the soil microbial community that led to rapid death of the pathogen, induction of resistance and bactericidal effects	Acharya and Srivastava[86], Almeida *et al.*[87] and Cardoso *et al.*[88]
Cultural	Resistant cultivar, crop rotation, multi-cropping, soil amendment (increasing soil pH and calcium, silicon and NPK levels) and grafting	Limited pathogen movement from the primary xylem to other xylem tissues, reduced disease inoculum, prevention of tomato by root exudates of other plants, induced uptake and distribution of nutrients and resistant of plant	Elphinstone[21], Terblanche and De Villiers[22], Amorim *et al.*[84], Ji *et al*[89], Matsushita *et al.*[90], Ooshiro *et al.*[91], Ordonez *et al.*[92], Olivier *et al.*[93], Hwang *et al.*[94], Paret *et al.*[95], Pontes *et al.*[96], Posas and Toyota[97], Shimpi *et al.*[98], Texeira *et al.*[99], Yu[100], Yuan *et al.*[101], Gorissen *et al.*[102], Islam and Toyota[103], Janvier *et al.*[104], Hassan and Abo-Elyousr[105] and Igawa *et al.*[106]
Physical	Solarization, hot water treatment and biological soil disinfection	Killing *R. solanacearum* with high or low temperatures	Posas *et al.*[107], Boshou[108], Dahal *et al.*[109], Fock *et al.*[110] and Denny *et al.*[111]

described the pathogen using different criteria. For instance[114], grouped species of *R. Solanacearum* in to five races based on geographical location while[24,115] described the pathogen biovars based on their ability to utilize and/or oxidize hexose alcohols and disaccharides. The *R. solanacearum* has extremely wide host range infecting more than 200 species from over 50 plant families[12,116]. More information on distribution and host of the *R. solanacearum* races is as shown in Table 2.

Classifying *R. solanacearum* based on race or host is complex and they often overlap due to a wide range of strains, environments and host range, therefore, isolate biovars have been used to determine pathogen phylotype[18,24]. Phylotyping which is based on DNA sequence analysis divides strains of *R. solanacearum* into four phylotypes according to their geographical origin namely phylotype I, II, III and IV corresponds to strains from Asia, Americas, Africa and Indonesia, respectively[31]. Recent research suggest to group *R. solanacearum* species complex into three species: *R. solanacearum* (phylotype II), *R. pseudosolanacearum* (phylotype I and II), and *R. syzygii* (phylotype IV)[112].

It is thus evidence that the environment in which *R. solanacearum* is found can determine prevailing race and the biovar and its virulence. Based on virulence, race 1 biovar 1 (R1B1) is considered as the most virulent but relatively uncommon as compared to race 1, race 2 biovar 1 and race 3, biovar 2 which are the most common and important strains in Africa[15,117]. Race 2 strains have a more limited host range than race 1 and mostly restricted to tropical environments while Race 3 biovar 2 is common throughout the world[117]. Since *R. solanacearum* has ability to change genetically and form new strains over a time, this may challenge management approach(es). Information on emergence of new strains of *R. solanacearum* in Sub-Saharan Africa is limited and thus calls for a research to generate and quantify the status of the prevailing pathogen stains.

Management challenges due to persistence of wide host range: *R. solanacearum* infect different host plants that are common in tomato farming systems and the host plants overlap as well[24,33]. Managing pathogen which is host of several and commonly cultivated plant species is challenging in the farming system. The use of crop rotation for example is challenged by the long period that *R. solacearum*, is capable to strive in the soil[27,118]. Effective crop rotation for *R. solanacearum* in infected land requires abandoning of land to grow host plants for 2-5 years[119]. This is in practice infeasible in the majority of small holder farmers in Sub-Saharan Africa due to land scarcity issues. Crop rotation can be more challenging to growers who have ventured in protected vegetable cropping where tomato are grown in greenhouse structures and where investment is intense[28]. Once the greenhouse soil is infected by *R. solanacearum*, eradication is difficult and a grower suffers economic losses[23]. The mechanism used by *R. solanacearum* to concur wide range of host plant species is not well known. Study should be conducted to understand factors favoring capability of *R. solanacearum* to infect wide range of host plant species for better disease management.

Management challenges due to endophytic nature of *R. solanacearum*: The *R. solanacearum* enters plants via wounds, root tips or cracks at the sites of lateral root emergence[13,18,120]. Unlike many phytopathogenic bacteria, *R. solanacearum* potentially requires only one entry site to establish a systemic infection that results in bacterial wilt disease[121]. The bacterium subsequently colonizes the root cortex, invades the xylem vessels and reaches the stem and leaves through the vascular system[27]. It can then rapidly multiply in the xylem causing rapid irreversible plant wilting and death[18,122]. Within xylem for example, high densities of the pathogen increase expression of pathogenicity genes such as the hrp genes which control induction of disease development and the hypersensitive reaction[48]. The endophitic nature of *R. solanacearum* makes its management challenging. Chemical control for instance, apart from being potentially harmful to the environment, has been reported to be inefficient[123]. This can be explained by the fact that the bacterium is sheltered in xylem vessels of infected plants. Ways should be explored by targeting management strategies which can be applied via the xylem system.

Management challenges due to pathogen ability to survive without host: After destroying the host, *R. solanacearum* can survive in reservoir plants, soil or water environment[27]. Association of *R. solanacearum* with either reservoir plants or plant debris has been frequently suggested to promote survival of the pathogen in soil and water[119]. The pathogen has ability to persist in deadly environments, for example it can survive for up to one year in agricultural soil even after treatment with an herbicide up to two years after crop removal and withstand a four-year intercropping period[27,124]. Moderate changes in moisture do not negatively affect the pathogen population[121]. The bacterium can multiply in pure water in the absence of nutrients for up to four years[125]. The cells of *R. solanacearum* are capable of forming various forms as survival mechanisms in unfavorable environments such as in soil or water and the most frequently reported forms are as discussed in the following section.

Table 2: Race, biovars, distribution and host plants of *R. solanacearum*

Race	Biovar	Distribution	Common reported host plants		References
			Common name	Scientific name	
1	1,3,4	Asia, Australia and America	Tomato	*Solanum lycopersicum,*	EPPO[15] and Elphinstone[21]
			Groundnut	*Archishy pogaea*,	
			Pepper	*Capsicum* spp.,	
			Coleus	*Plectranthus scutellarioides*	
			Banana	*Musa* spp.,	
			Tobacco	*Nicotiana tabacum,*	
			Roses	*Rosa* spp.,	
			Eggplant	*Solanum melongena,*	
			Potato	*Solanum tuberosum,*	
			Sunflower	*Helianthus annuus*	
			Anthrium	*Anthurium* spp.,	
			Dahlia	*Dahlia* spp.,	
			Heliconia	*Heliconia* spp.,	
			Hibiscus	*Hibiscus* spp.,	
			Lesianthus	*Lesianthus* spp.,	
			Lilium	*Lilium* spp.,	
			Pothos	*Pothos* spp.,	
			Strelitzia	*Strelitzia* spp.,	
			Verbena	*Verbena* spp.,	
			Zinnia	*Zinnia* spp.;	
			Marigold	*Tagetes* spp.	
			Eucalyptus	*Eucalyptus* spp.,	
			Apple	*Maluspumila*	
			Neem	*Azadirachta indica*	
			Cowpea	*Vigna unguiculata*	
			Cucurbits	*Curcurbita* spp.	
			Hyacinth beans	*Lablab purpureus*	
			Jute mallow	*Corchorus olitorius*	
			Moringa	*Moringa oleifera*	
			Mulberry	*Morus* spp.	
			Nutmeg	*Myristica fragrans*	
			Patchoul,	*Pogostemon cablin*	
			Sesame	*Sesamum indicum*	
			Strawberry	*Fragaria ananassa*	
			Water spinach	*Ipomoea aquatic*	
2	1	Caribbean, Brazil and Philippines	Taro	*Colocasia esculenta*,	EPPO[15], Elphinstone[21] and Dasgupta *et al.*[112]
			Pumpkin	*Cucurbita maxima*,	
			Goosegrass	*Eleusine indica*,	
			Cocoa	*Gliricidia sepium*,	
			Banana	*Musa* spp.,	
			Guava	*Psidium guajava*,	
			Heliconia	*Heliconia* spp.	
3	2	Worldwide except US and Canada	Tomato	*Solanum lycopersicum*,	EPPO[15], Elphinstone[21] and Alvarez *et al.*[27]
			Pepper	*Capsicum* spp.,	
			Garden cosmos	*Cosmos bipinnatus,*	
			Tree tomato	*Cyphomandra betacea*,	
			Jimson weed	*Datura stramonium*,	
			Ground cherry, Purslane	*Pysalis* spp.,	
			Bittersweet nightshade	*Portulaca gleracea*,	
			Eggplant	*Solanum dulcamara*,	
			Black nightshade, Potato	*Solanum melongena*,	
			Stinging nettle	*Solanum nigrum*,	
				Solanum tuberosum,	
				Urtica dioica.	
4	3,4	Asia	Ginger	*Zingiber officinales,*	*Elphinstone*[21]
			Mioga	*Zingibe rmioga,*	
			Patumma	*Curcuma alismatifolia.*	
5	5	China	Mulberry	*Morus* spp.	*Elphinstone*[21]

Viable but non culturable (VBNC) form: *R. solanacearum* in soil can change and became VBNC within a month after exposure to low temperature of 4°C[126] with cold-stressed cells progressively losing wilting capacity[27,125]. The VBNC state has also been reported to occur in infected plant where proportion of cells becoming VBNC increase after the plant's extensive necrosis[126].

Starvation-survival response: This is a physiological survival state in energy-deficient condition, in which bacterial cells starve to maintain a non-growing but culturable condition[27,127]. Starved *R. solanacearum* cells remain pathogenic in the water microcosms over four years[119].

Phenotypic conversion (PC) type: This is a form that describes a morphological change of the *R. solanacearum* colonies from fluidal to afluidal form Popoola *et al.*[128]. PC-type which occurs in most *R. solanacearum* strains can be easily observed by prolonged culture on agar plates and when the bacterium is grown in a non-aerated liquid medium with glucose and organic source of nitrogen[129]. PC-type variants have selective advantage over the non PC-type. For example PC-types have higher motility for aerotaxis in oxidative stress environment[27].

Biofilms forms: Some cells of *R. solanacearum* form biofilms on host xylem vessel walls to protect them from host defenses. Biofilms also filter nutrients from the flow of xylem fluid[37]. Different strains of *R. solanacearum* form biofilms on polyvinyl chloride (PVC) wells at the liquid air interface and on the surface of tomato seedlings[130]. Aerotaxis deficient mutants overproduce biofilms on abiotic surfaces which lead cells to avoid toxic oxygen levels at the liquid-air interface by forming protective thicker biofilms to facilitate survival[27,37].

The survival strategies of *R. solanacearum* to live and cope with unsuitable conditions such as starvation response, being viable but non-culturable, physiological and morphological changes and aggregation may raise new concerns about the epidemiology of bacterial wilt disease in tomato farming systems. Although these infecting populations are not as high as those from wilted plants, the continuous flow would contribute to persistence of the pathogen in the environment. Knowledge on the ability of *R. solanacearum* to form different forms in different environmental conditions may have some positive implication towards development of its management strategies in farming system. When environmental condition is unsuitable (soil temperature for example), *R. solanacearum* become avirulent[27], further research is required to investigate the potential of this knowledge in *R. solanacearum* management.

Management challenges due to pathogen ability to travel along waterways: The *R. solanacearum* can enter the surrounding soil, water or plants and be disseminated to uninfected environment through the moving water[131]. Plants which grow along waterways are mostly reported to facilitate *R. solanacearum* movement in waterways. The common examples include bittersweet nightshade, black nightshade and stinging nettle[132]. Roots and stems of bittersweed night shade for example can shelter *R. solanacearum* cells and continuously release them into the water system[21]. The use of contaminated water for field irrigation has been associated to most outbreaks of bacterial wilt disease[119,124,125]. Irrigation water could be treated prior to crop irrigation, but there still some challenges associated with this approach including exposure of the community to the health risks of exposure to chemicals, costly and contamination of water system. Use of management methods which are environmentally friendly like the use of plant extract could be the best approach to combat bacterial wilt disease in the farming system[132]. Because the pathogen stains vary with geographical location, there is a need to investigate effect of various plant species in the management of bacterial wilt disease.

CONCLUSION

This review article has discussed the challenges for the identification and management of bacterial wilt disease in tomato farming systems in Sub-Saharan Africa. It has exposed the reality that the pathogen is indeed challenging. Due to complexities in the identification and management there is urgent need to find ways for simple and quick identification methods. Use of biosensors which can detect low bacterial population densities as well as determining responsible strains and characterizing with molecular methods could a way forward. There is need also to explore sustainable pathogen management options including use of botanical plants.

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