

**Distribution, characterisation and management of
Tomato spotted wilt virus and its vectors in tomato
production systems in Kenya**

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Declaration

I certify that the substance of this thesis has not already been submitted for any degree and is not currently being submitted for any other degree or qualification.

I certify that any help received in preparing this thesis and all sources used have been acknowledged in this thesis.

A solid black rectangular box used to redact the candidate's signature.

Signature of candidate

25th May 2015

Date

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Abstract

Tomato spotted wilt virus (family *Bunyaviridae*, genus *Tospovirus*) is an important virus infecting horticultural crops and is transmitted solely by thrips species. The virus infects a wide range of plant species and presence of *Frankliniella occidentalis*, reported to be the most efficient vector species has complicated its management. TSWV was first reported in Kenya in 1999, causing serious yield losses in tomato production, and has continued to cause sporadic yield losses. This study was undertaken to determine the distribution and genetic diversity of the virus a decade after its incursion into Kenya. The study further evaluated important factors in the epidemiology of the disease and its management. The disease was found to have persisted in the Nakuru area where it was first reported, but had limited distribution. There was low farmer awareness of the virus, its vectors and alternate hosts, despite occurrence of the disease for over a decade. The N partial sequences of 45 isolates collected from production areas were established to be similar with TSWV isolates collected from other countries. The Kenyan isolates clustered together with isolates that were predominantly from Europe, but formed a single subgroup, indicating they had undergone limited diversification.

Cytochrome oxidase 1 (CO1) gene sequences were used in the identification of thrips samples collected from tomato production areas. The analysis of 299 cytochrome oxidase 1 (CO1) gene sequences from thrips species indicated occurrence of a wide range of thrips species in tomato production. *Ceratothripoides brunneus* was the predominant species of thrips in all the areas, whereas *F. occidentalis* and *Thrips tabaci* which have been reported to be important vectors, were abundant in Nakuru, Kirinyaga and Loitokitok. Other vectors of tospoviruses identified in low numbers were *Frankliniella schultzei* and *Scirtothrips dorsalis*. The sequences showed variation within potential vector populations, where the Kenyan isolates of

T. tabaci from tomato production areas belonged to the Arrhenotokous group, and *F. occidentalis* belonged to the western flower thrips G (WFTG). *Frankliniella schultzei* was shown to be a potential species complex. The detection of the TSWV genome sequences in *F. occidentalis* and *T. tabaci* in this survey support their role as important vectors in Kenya.

Research was undertaken to identify weed species in tomato production areas and their role as reservoirs of TSWV and its vectors. Weed species representing 19 families were identified, two thirds of which had been reported as hosts of TSWV. Selected weed species were further evaluated to determine their capacity to act as reservoir host of the virus and as source of inoculum for thrips acquisition and transmission. The weeds were also evaluated for their ability to support reproduction of *F. occidentalis*. The transmission study identified four new hosts of TSWV, namely *Oxalis latifolia*, *Bidens subalternans*, *Solanum chenopodioides* and *Commelina cyanea*. Among the weeds species that were evaluated, *Amaranthus hybridus*, *Solanum nigrum*, *Tagetes minuta* and *Datura stramonium* were shown to be susceptible to the virus and supported high levels of thrips reproduction. These four weeds need to be considered in the management of TSWV. Occurrence of weeds that support thrips reproduction and are susceptible to TSWV is a clear indicator of their role in the epidemiology of TSWV.

Forty-two commercial tomato cultivars were evaluated through mechanical inoculation for their reaction to TSWV and presence of the *Sw-5* gene that confers resistance to TSWV. Twenty-eight were shown to be susceptible, including Rio Grande, which is grown in over 63% of the farms within the major tomato production areas in Kenya. Although cultivars Sandokan, Picus, Veloz, DRD 8465, AB 2 and Shanty were found to contain the resistant *Sw-5* gene, Sandokan and AB 2 exhibited low infection to TSWV. Specific PCR primers for the

SW-5 gene and high resolution melt curve analyses (HRM) consistently distinguished TSWV-resistance in commercial tomato cultivars from TSWV-susceptible cultivars.

This study has provided information on the distribution and genetic diversity of TSWV and its vectors in a tropical environment. The disease had persisted where it was first reported and had limited distribution. The presence of vectors and suitable hosts observed in most of the production areas indicates occurrence of suitable areas where TSWV can establish in Kenya and neighbouring countries. The information on factors related to TSWV epidemiology is important for the development of an effective TSWV management strategies in Kenya.

Table of Contents

Acknowledgements	iii
List of Publications from this Thesis	v
Abstract	vi
Table of Contents	ix
List of Tables	xiii
List of Figures	xiv
Chapter 1. Introduction	1
1.1 Thesis Outline	4
Chapter 2. Literature Review	6
2.1 Introduction.....	6
2.2 Tomato production in Kenya	6
2.3 Constraints to tomato production.....	7
2.4 Tospoviruses	8
2.5 <i>Tomato spotted wilt virus</i> (TSWV).....	16
2.5.1 History and economic importance of TSWV	16
2.5.2 Genomic structure of TSWV	19
2.5.3 Host range of TSWV	21
2.5.4 Symptoms of TSWV	22
2.5.5 Identification of TSWV	23
2.6 Vectors of <i>Tomato spotted wilt virus</i>	27
2.6.1 <i>Frankliniella occidentalis</i> (western flower thrips).....	27
2.6.2 <i>Thrips tabaci</i>	30
2.6.3 <i>Frankliniella schultzei</i>	31
2.6.4 Identification of thrips.....	32

2.6.5 TSWV acquisition and transmission	34
2.7 Weeds as reservoirs of TSWV	37
2.8 Management of TSWV and its vectors	38
2.8.1 Management of TSWV through control of vectors	38
2.8.2 Resistant cultivars	41
2.8.3 Thrips resistance	43
2.9 Molecular Marker Assisted Breeding	44
Chapter 3. Distribution and genetic diversity of <i>Tomato spotted wilt virus</i>	
following an incursion into Kenya	46
3.1 Introduction	46
3.2 Materials and Methods	48
3.3 Results	56
3.4 Discussion	63
Chapter 4. Diversity of thrips species and vectors of <i>Tomato spotted wilt</i>	
<i>virus</i> in tomato production systems in Kenya.....	67
4.1 Introduction	67
4.2 Materials and Methods	69
4.3 Results	73
4.4 Discussion	80
Chapter 5. Weed species in tomato production and their role as alternate	
hosts of <i>Tomato spotted wilt virus</i> and its vector <i>Frankliniella</i>	
<i>occidentalis</i>	86
5.1 Introduction	86
5.2 Materials and Methods	88

5.3 Results.....	94
5.4 Discussion.....	104
Chapter 6. Reaction of tomato cultivars grown in Kenya to <i>Tomato spotted wilt virus</i> (TSWV) infection.....	109
6.1 Introduction.....	109
6.2 Materials and Methods.....	111
6.3 Results.....	121
6.4 Discussion.....	132
Chapter 7. General Discussion, Conclusion and Recommendations	138
References	146
Appendices	172

List of Tables

Table 2.1 Classification of tospoviruses.....	11
Table 2.2 A summary of geographical distribution, host range and vector species of the recognised and tentative tospovirus species	14
Table 2.3 Symptoms produced by <i>Tomato spotted wilt virus</i> on some important indicator plants.....	24
Table 3.1 Number of tomato farms and market collections surveyed in four areas of Kenya for <i>Tomato spotted wilt virus</i> , and number tested with each detection method	50
Table 3.2 A list of primers used for reverse transcription-polymerase chain reaction (PCR) in the detection of <i>Tomato spotted wilt virus</i> and other tospoviruses	55
Table 3.3 Result of testing for <i>Tomato spotted wilt virus</i> in tomato samples collected from four major tomato production areas in Kenya.	58
Table 3.4 Symptoms of selected <i>Tomato spotted wilt virus</i> isolates collected from Nakuru and Loitokitok on indicator plants.....	60
Table 4.1 Numbers of CO1 sequences obtained from thrips species occurring in tomato production systems in four areas in Kenya.....	75
Table 4.2 Thrips species reported on different host plants in tomato production areas in Kenya.....	76
Table 5.1. Weed species used in experiments and their abundance in the field.....	90
Table 5.2 Weeds identified in tomato production areas in Kenya, biological type and their status as hosts of <i>Tomato spotted wilt virus</i>	96
Table 5.3 Frequency (%) of occurrence of weed species in four tomato production areas in Kenya. Species are ranked in order of overall frequency.....	97
Table 5.4 Reaction of selected weed species to <i>Tomato spotted wilt virus</i> infection through mechanically inoculation.....	99
Table 5.5 Transmission of <i>Tomato spotted wilt virus</i> by <i>F. occidentalis</i> from tomatoes to selected weed species	101
Table 6.1. Tomato cultivars used in the evaluation for resistance to <i>Tomato spotted wilt virus</i> and their disease resistance status.....	114
Table 6.2 Tomato cultivars grown in the four major tomato production areas. Data are the number of farms which grew each cultivar.	122
Table 6.3 Source of tomato seeds used in the production areas	122

Table 6.4 Reaction of tomato cultivars to <i>Tomato spotted wilt virus</i> infection under greenhouse conditions in the first trial	125
Table 6.5 Reaction of tomato cultivars to <i>Tomato spotted wilt virus</i> infection under greenhouse conditions in the second trial.....	126
Table 6.6 Means of thrips population from the two field trials in Nakuru and Kirinyaga.....	128

List of Figures

Figure 2.1 Worldwide distribution and status of <i>Tomato spotted wilt virus</i>	17
Figure 2.2 Genome organisation of <i>Tomato spotted wilt virus</i> and the functions of each gene.....	20
Figure 2.3 <i>Frankliniella occidentalis</i> , a) the dark form and b) the common pest form	29
Figure 2.4 <i>Thrips tabaci</i>	31
Figure 2.5 <i>Frankliniella schultzei</i> female of dark form.....	32
Figure 3.1 Map of Kenya indicating the four tomato production areas where sampling for <i>Tomato spotted wilt virus</i> was undertaken.	49
Figure 3.2 Phylogenetic relationships of partial N-gene sequences from <i>Tomato spotted wilt virus</i> isolates collected from tomato production areas in Kenya and databased sequences from other geographic regions	63
Figure 4.1 Phylogenetic tree of CO1 from specimens of <i>Thrips tabaci</i> from tomato production areas in Kenya and databased sequences.	78
Figure 4.2 Phylogenetic tree of CO1 from specimens of <i>Frankliniella</i> species from tomato production areas in Kenya and databased sequences.	79
Figure 5.1. a) Level of damage from <i>F. occidentalis</i> infestation on weed species and tomato cultivars in a detached leaf assay. b) Average number of larvae of <i>F. occidentalis</i> on weeds species and tomato cultivars in a detached leaf assay.	103
Figure 6.1 Alignment of seven tomato sequences (3 susceptible and 4 resistant) indicating three SNPs, A/T, T/C and G/A and position of the three SNPs primer sets used in HRM	120
Figure 6.2 Tomato cultivars infected with <i>Tomato spotted wilt virus</i>	124
Figure 6.3 HRM profiles for 4 tomato cultivars analysed using primers <i>Sw-5-SNP1 AT</i> and <i>Sw-5-HRM1</i>	131