UNIVERSITY OF CAPE COAST

# STUDIES OF TOMATO YELLOW LEAF CURL VIRAL DISEASE IN SOME DISTRICTS IN THE CENTRAL REGION OF GHANA

BY

DORIS MENSAH- WONKYI

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2014

## DECLARATION

### Candidates Declaration

I hereby declare that this thesis is the result of my own original research and that no part of it has ever been presented for another degree in this University or elsewhere.

Candidate's Signature:…… Date:…….

Name: Doris Mensah-Wonkyi

### Supervisors' Declaration

We hereby declare that the preparation and presentation of this thesis were supervised in accordance with the guidelines on supervision of thesis laid down by the University of Cape Coast.

Principal Supervisor

Signature:…….. Date: …….

Name: Dr Elvis Asare-Bediako

Co-Supervisor

Signature:…… Date:……..

Name: Dr. Grace C. van der Puije

## ABSTRACT

*Tomato yellow leaf curl viral* disease (TYLCV) is a destructive disease of tomato in Ghana. The study was conducted during the 2013 minor and 2014 major cropping seasons to determine the knowledge of farmers and their agronomic practices they carry out to manage TYLCV disease in three districts in the Central region, screening of thirty six tomato genotypes against TYLCV disease for a possible tolerant variety and phenotypic and molecular evaluation of selected tolerant genotypes at coastal and forest agro ecological zones. Three tomato producing centres (Effutu municipality, Komenda-Edina-Eguafo-Abirem (KEEA), and Mfantseman district) were selected. Ten farmers were interviewed for awareness. Their farms were assessed for their disease incidence and severity in each of the districts. The highest incidence and severity mean scores of TYLCV disease were recorded at KEEA (52.9±2.7, 26.89±1.2), followed by Effutu (49.5±1.19, 25.29±0.9), and Mfantseman (42.1±2.7, 21.41±0.8) respectively. The awareness of farmers of the presence of the disease was very high (92.6%). About 55.6% of the farmers managed the disease by using synthetic insecticide. Out of the 36 genotypes tested only three (K213, K005 and K100) showed mild symptoms whereas the others showed moderate to severe symptoms. Yield correlated negatively but significantly with incidence and severity of the disease ($-0.07 \geq r \leq -0.47$; $P < 0.05$). Though PCR revealed the presence of TYLCV DNA in K005 and K100, they consistently showed mild symptoms and gave high yields (>8 t $ha^{-1}$) at both agro ecological zones. There was no complete resistance following molecular screening. *Tomato yellow leaf curl viral* disease was prevalent at the study area though less severe, and genotypes K213, K005 and K100 were highly tolerant to TYLCV infection.

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## DEDICATION

This work is dedicated to my dearest mum Sansaba , Semfua, the entire family and to the memory of my late father, Dr Thomas Mensa-Wonkyi.

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| | |
|---|---|
| ANOVA | Analysis of Variance |
| AWARD | African Women in Agricultural Research and Development |
| AVRDC | Asian Vegetable Research and Development Center |
| CABI | Commonwealth Agriculture Bureaux International |
| CIAT | International Center for Tropical Agriculture |
| CSIR | Council for Scientific and Industrial Research |
| CRI | Crop Research Institute |
| DNA | Deoxyribonucleic Acid |
| EPPO | European and Mediterranean Plant Protection Organization |
| ELISA | Enzyme-Linked Immunosorbent Assay |
| FAO | Food and Agriculture Organization |
| FAOSTAT | Food and Agriculture Organization Statistics |
| MoFA | Ministry of Food and Agriculture |
| PCR | Polymerase Chain Reaction |
| RCBD | Randomized Complete Block Design |
| RNA | Ribonucleic Acid |
| SARI | Savannah Agriculture Research Institute |
| SPSS | Statistical Package for Social Science |
| ToMoV | Tomato mottle virus |
| TYLCV | Tomato Yellow Leaf Curl Virus |
| TYLCSV | Tomato Yellow Leaf Curl Sardinia Virus |
| TYLCV-Is | Tomato Yellow Leaf Curl Virus-Israel |
| UV | Ultraviolet |
| WTGV | Whitefly Transmitted Geminivirus |

# CHAPTER ONE

# INTRODUCTION

Tomato (*Solanum lycopersicon* Lsyn *Lycopersicon esculentum* Mill), is the most popular and widely grown vegetable in the World. It ranks first in the world vegetables and accounts for 14% of the world vegetable production (Bauchet, & Causse, 2012). Tomato originated in the New World in the Andean region extending from Columbia to Chile. The crop was introduced into West Africa in the $16^{th}$ century by the Portuguese traders (Jenkins, 1948). According to Glick, Levy, and Gafni, **(**2009), tomato is now the most important vegetable in the tropics (Foolad, 2007). World production is around 100 million tons on 3.7 million $ha^{-1}$ with its production reported in 144 countries (FAO, 2004). The leading producer of tomato in the world is China producing 25.3% of the total production, followed by U.S.A, Mexico and Egypt (Asgedom, Struik, Heuvelink, & Araia, 2011).

Production of tomatoes is a source of livelihood for young men and women in both the rural and urban centres in Ghana and the world (Tshiala, & Olwoch, 2010). In terms of health, it contains large quantity of water, calcium, niacin and a good source of vitamins A, C and E which are of great importance in the metabolic activities of man (Olaniyi, Akanbi, Adejumo, & Akande, 2010). Tomatoes are fast becoming one of the much-loved foods, as they are a good source of antioxidants (Anese, Manzano, & Nicoli, 1997). They reduce lipid oxidation in oil and fatty foods and also ward off certain

kinds of cancer, prevent brain degeneration, cataracts, and help maintain mental function as humans age (Adeyemi & Olorunsanya, 2012). Tomatoes contain lycopene, a comparatively exceptional member of the carotenoid family, which is twice as powerful as beta-carotene (Yvon, 2013). Studies have shown that men who eat more tomatoes or tomato sauce have significantly lower rates of prostate cancer (Adeyemi & Olorunsanya, 2012). Other studies suggest that lycopene can help prevent lung, colon and breast cancer (Kahl & Kappus, 1993). Tomato helps boost immunity since it contains glutathione which is an antioxidant (Adeyemi & Olorunsanya, 2012).

In the area of food preparation, tomato is used in Ghana and worldwide as a fresh vegetable or as a spice in food preparation (Horna, Smale, & Falck-Zepeda, 2006; Olaniyi, 2010). Among all vegetables in Ghana, tomato is normally used in large quantities and grown for fresh market and for processing (Norman, 1974**).** It is a very popular and important vegetable crop which is consumed nearly on a daily basis by every household in Ghana and an important condiment. It is used in soup, salad, gravy and stew (Horna *et al*., 2006; Osei, Akromah, Lamptey, & Quain, 2012).). In Ghana, tomato production covers about 3700 hectares of land **(**Eshun, Apori, & Oppong-Anane, 2011). Major producing centres are Tono, Vea (Upper-East Region), Derma, Amate (Brong-Ahafo Region), Akumadan, Agogo, Kumawu, and Adjamesu (Ashanti Region) (Osei, Akromah, Shih**,** Lee**,** & Green, 2008).).

In spite of the economic importance and health benefits of tomatoes, farmers have been recording low yields. The current yield of 7.5 t $ha^{-1}$ is far below the achievable yield of 15 t $ha^{-1}$ (MoFA, 2011). Consequently, local production does not meet the domestic demand, and so tomatoes are imported

from Burkina Faso which affects the economy (MoFA, 2011; Osei*et al*., 2012). This wide yield gap of tomato in Ghana is due to a number of constraints which include biotic and abiotic factors. The abiotic factors include erratic rainfall, high temperature, and poor soils, among others whilst the biotic factors include diseases such as *Tomato yellow leaf curl virus*, bacterial wilt, bacterial spot, early blight, and *Tomato mosaic viruses* (Asante *et al*., 2013).

Among the diseases of tomato in Ghana, one which is of most economic importance is the *Tomato yellow leaf curl virus* (TYLCV) (Osei *et al*., 2012). TYLCV can cause yield losses of up to 80% especially when plants are infected in the early stages of growth. The virus infection results in a decrease in leaf size, leaf curling upward, severe stunting and distortion linked with interveinal chlorosis. The plant becomes severely stunted, drops its flowers and stops producing marketable fruits when infection occurs at the early stages of growth (Al-ani, Mustafa, Samir, & Saber, 2011).

The TYLCV is transmitted efficiently by the whitefly *Bemisia tabaci* (Gennadius) in a persistent circulating manner. Severe population outbreaks of the whitefly are usually associated with high incidence of the disease (Al-ani *et al.* 2011).

Effective management of the TYLCV is therefore quite important in order to improve yields. Limiting the population of the vector by the use of insecticide has been one of the main ways to control the spread of the disease (Hilje, Costa, & Stansly, 2001; Palumbo, Horowitz, & Prabhaker, 2001). Other management practices include the use of plastic mulch and physical obstructions like whitefly-proof screen and UV absorbing plastic and screen

(Polston & Lapidot, 2007).So far all the above control measures have not been successful in decreasing the incidence of TYLCV disease on tomato crop (Bhyan, Chowdhury, Alam, & Ali, 2007; Reynaud *et al.,* 2003). Therefore, breeding for resistance to TYLCV disease appears to be a promising and environmentally friendly approach to controlling the disease (Chague, Mercier, Guenard, Courcel de, & Vedel 1997). Host plant resistance is therefore an important component of an overall whitefly-transmitted geminivirus control strategy.

The polymerase chain reaction (PCR) technique provides a sensitive and specific means for the detection and identification of whitefly transmitted geminiviruses (WTGV) in infected plants (Cohen *et al.*, 1989; Mehta, Wyman, Nakhla, & Maxwell, 1994; Fargette, Leslie, & Harrison, 1996; El-Din, El-Abbas, Aref, & Abdallah, 2005; Tsai, Kuo-Kuan, Green, Rauf, & Hidayat, 2006; Bhyan *et al.,* 2007).

Information on the TYLCV disease in the southern Ghana including Central region, is however quite limiting since most research works (Personal communication, Mr Michael Osei, Research Scientist CSIR-CRI, Kumasi, 17th May 2014) are concentrated in the northern sector which are the major producing centres in Ghana. Central Region is an important tomato growing centre in the southern sector. It is therefore important to know the status of this disease in Central Region and other regions for a holistic approach to its control.

The foregoing reasons for the problem stated are key drivers to investigate the incidence and severity of TYLCV disease in the Central Region of Ghana. This will make available information on the disease and its

status in three districts of the Central region and help identify stable sources for breeding against TYLCV infection to increase the yield of tomato and increase income of farmers.

**General Objective**

The general objective of this study was to assess the prevalence of the TYLCV disease in the Central Region, identify the agronomic practices of farmers used in managing the disease and identify tomato genotypes resistant to TYLCV infection.

**Specific Objectives**

The specific objectives are:

1. To determine awareness of farmers on TYLCV disease and the agronomic practices used in managing the disease.
2. To determine the incidence and severity of the TYLCV disease in the selected districts in the Central Region through a field survey.
3. To screen tomato genotypes against TYLCV infection in order to identify source of resistance and/or tolerance.
4. To evaluate the agronomicperformanceof the identified TYLCV resistant or tolerant genotypes of tomato at both forest and coastal savannah ecological zones.

# CHAPTER TWO

# LITERATURE REVIEW

## Botany

Tomato plant has two growth patterns: Indeterminate and determinate. The indeterminate plant produces seven to ten leaves and an inflorescence, then three leaves and a second inflorescence and continues this pattern indefinitely whilst the determinant plant stops its development after two to five inflorescences; lateral shoots stop growing after one to three inflorescences (Blancard, 2002).

Tomato leaves are imparipinnate with indented leaflets though there are some varieties with very seldom indented leaves and nonserrated edges (Blancard, 2002). All the species of tomato are bisexual. Flowers of the cultivated varieties are grouped into simple or branched inflorescences. The number of flowers is variable, ranging from five to twelve and made up of five to eight sepals, five to eight petals, five to eight stamens, and an ovary containing two to ten carpels. The stamens are fused into a cone surrounding the pistil that is the ovary, style, and stigma. Each stamen releases the pollen it contains through a longitudinal slot located inside the staminal cone which is received by the stigma. The pollen grains germinate on the stigma, and their pollen tubes penetrate the style to reach the ovary and the widely varying number of ovules depending on variety (Blancard, 2002).

Tomato fruits, fleshy and tender, are actually berries, and vary in size, colour, and texture depending on the variety. The shape also varies**,** and their weight can vary from 10g to more than 1 kg. The colour is more or less dark green when immature and evolves during maturity to reach various shades according to the cultivars: cream, yellow, orange and pink, red, or brown (Blancard, 2002).

**Ecology**

Crop production is largely influenced by variations in climatic factors such as temperature, solar radiation and precipitation (Tshiala & Olwoch, 2010). Apart from these, other factors such as carbon dioxide, oxygen, soil nutrient, soil pH among others also have some effect or influence on tomato production and storage (Abubakari & Rees, 2011).

**Effect of Temperature**

Tomato is an important vegetable that is prone to heat stress. Generally, crop growth and development is influenced by temperature as a result of its impact on enzyme and membrane controlled processes (Yáñez-López, 2012). The optimal temperature of tomato is around 22-25°C. This temperature range promotes and enhances development and growth in tomato production. Temperatures exceeding 25°C are likely to decrease tomato production (Tshiala & Olwoch, 2010). In storage, it has been stated by Hardenburg, Warada, and Wang (1986) that, storage under quite low temperature is the generally efficient method to maintain quality of most fruits and vegetables as a result of their effect of reducing respiration rate, transpiration, ethylene production, ripening, senescence, and rot development. It is established that mature green tomato can be stored at a temperature of

10°to 15°C for relatively longer period (Castro, Vigneault, Charles, & Cortez, 2005).

Temperature goes a long way to affect the physiology of the plant. For example high air temperature cause physiological defect such as blossom end rot (Dorais & Papadopoulos, 2001), catface (Brunell, 2000; Lund, 2012) and cracking (Valley, 2002).

**Effect of Moisture**

Generally, water availability, is one of the most controlling environmental factors affecting crop productivity and tomato plant as a whole. Water stress on the other hand drastically affects crop growth, ultimately leading to a massive loss in yield and quality (Pirzad, Shakiba, Zehtab-Salmasi, Mohammadi, Darvishzadeh, & Samadi, 2011). Tomato plants show high correlation between evapotranspiration and crop yield. It has been found out by Yoon, Green, Tschanz, Tsou. & Chang, 1989) that the level of water stress for tomato plants affects the periods of flower formation and fruit enlargement by slowing down the rate of flower initiation, inhibiting fruit formation, and hence reducing the number of flowers and fruits. Over watering on the other hand causes damping off and at the same time leads to less stress and salinity extremes. Soils with excessive moisture cause plants to experience weak root systems and cracked fruit. Conversely, under-watering and fluctuations in watering expose tomato plants to diseases and pests (Smith, 2009). Bacterial wilt disease causes the leaves and shoots lose turgor, wilt and finally turn brown and die as a result of deficient moisture (Smith, 2009).

During the phase of fruit enlargement water stress causes blossom end rot disease (Male, 2001; Koesriharti & Syamira, 2012). Water stress during

vegetative phase tends to decrease the dry weight of the larger canopy, but increases the number of bunches of flowers, the number of bunches of fruit and fruit number. Stress that occurs at the beginning of growth does not have effect on reducing the weight of the fruit harvest since plants recover more quickly. Ideally moderate water stress before flowering can accelerate flowering and fruit formation (Koning & Hurt, 1983)

**Soil Fertility**

Fertility status of soil is important in the cultivation of tomato. Studies conducted in the tropics showed significant increase in nutrient status and yield of tomato as a result of application of inorganic fertilizers, as well as organic source (Ewulo, Ojeniyi, & Akami, 2008). It has been reported that tomato can grow on a variety of soils except worst soils such as gravelly soils and water-logged soils (Oyinlola & Jinadu, 2012).

For fruit quality to be maximized there should be good volumes of nitrogen, phosphorus, and high amounts of calcium and often very high levels of potassium. Phosphorus is an indispensable nutrient in the soil. Large volumes of phosphorus are necessary for seed formation since plant absorbs more phosphorus when fruiting and during the vegetative stage (Chu & Toop, 1975). It functions mainly in pH stabilization, osmoregulation, enzyme activation and membrane transport processes (Okturen& Sonmez, 2012). Deficiencies in phosphorus include stunting, dark green young leaves and yellowing of older leaves, curled leaflets, thin stems with purple colouring, and poor fruit production (Bergmann, 1992).

Calcium is a major component in the growth of tomato and acts by holding cells together and helping in nutrient uptake. Deficiency of it causes

blossom end rot. Relatively large concentrations of calcium are needed for normal cell growth. The tissue of rapidly growing fruit deficient in necessary calcium breaks down into a characteristic dry, sunken lesion on the blossom end (Draper, Burrows, & Munk,2002.; Masarirambi, Norman, Oseni, & Shonguwe, 2009).

Nitrogen has a distinct effect on growth and development of tomato since it stimulates both vegetative and reproductive growth and impacts the characteristic deep green colour of leaves. Optimum application of N-fertilizer to the soil produces high tomato fruit yield and improves fruit quality (Adams, Graves, & Winsor, 1978). However, excessive application leads to dense increase of vegetative parts of the plant at the cost of reproductive growth. Deficiency in nitrogen has the tendency to slow down vegetative growth and accelerate flowering, though yields of fruit are reduced when nitrogen is adequate. Nitrogen deficiency also has hormonal effects on the plant, impeding cytokinin synthesis and accelerating synthesis of abscisic acid. This causes yellowing rapidly reducingthe lifespan of the plant. Tomatoes suffering from nitrogen deficiency tend to be rigidly upright, with hard, thin stems and small yellowish leaves and high rates of flower abortions (Bergmann, 1992).

The requirement of potassium in the early crop stages (from seedling through to fruit development) is about the same as for nitrogen. After this, the requirement for potassium keeps increasing with fruit load while nitrogen levels off. Potassium is the predominant cation in tomato fruit and has major effects on fruit quality (Bergmann, 1992).

**Diseases of Tomato**

Tomato is usually affected by several disease-causing organisms. These include fungi, bacteria, viruses among others (Agrios, 2005).

**Bacteria Diseases of Tomato**

Bacteria canker and wilt of tomato disease is caused by *Clavibacter michiganense* subsp. *Michiganense* and results in dark necrotic lesions at the margins of older leaves. As the disease progresses, small raised white blisters are seen on young green fruits. The blisters become yellowish as the fruit matures making them unmarketable.This results in significant yield loss. In early infection, entire branches or even whole plant dies. The disease is controlled through the use of seeds that are free from bacteria (since the bacteria overwinter in or on the seed), protective application of copper or streptomycin in the seed bed, and soil sterilization of the seedbeds (Agrios, 2005).

Bacteria soft rot of vegetablesis caused by *Erwinia carotovora* and *E. chrysanthemi.* The disease starts as water soaked translucent spots on the fruit, leaves, stems and underground part which later enlarges. As the disease progresses slimy masses of bacterium and cellular debris ooze out from cracks in the tissue and plant; corms, bulbs and any other growth may rot and collapse within 20 to 72 hours giving off a rotten odour. Good sanitary and cultural practices can help in the control. Chemical sprays are generally not recommended for the control of soft rots (Agrios, 2005; Schumann & D'Arcy, 2000).

Bacterial spot of tomato is caused by a bacterium called *Xanthomonas campestris* pv *vesicatoria.* It can be recognized by numerous angular spots

with small blister-like and irregular spots which latter turn brown and develop into a warty appearance. The spots are normally water soaked on the leaves which deform the leaves when infected at the early stage. Attack on the flower and fruits result in flower drop and greenish-white halos which become black and slightly sunken with a scabby surface. Control is by the use of seeds that are free from bacteria as well as seedlings, resistant varieties, crop rotation and spraying with copper fungicide (Agrios, 2005).

**FungalDiseases of Tomato**

Late blightis caused by *Phytopthora infestans* and affects leaves, stems and fruits of the plant. On leaves, black lesions appear within 3-4 days after infection which later become brown, greasy looking. These lesions latter turn brown when dry surrounded by gray-green tissue bringing white spores into view. On the fruit, the disease causes firm, dark, greasy looking lesions from which the pathogen spores are produced. (Schumann & D'Arcy, 2000). The disease can be controlled by combination of sanitary measures, use of resistance varieties, and a well-planned or well-timed chemical spray regime (Schumann & D'Arcy, 2000; Agrios, 2005).

Early blight disease of tomato is caused by *Alternaria solani*. The disease affects fruit, stem and foliage. Leaves appear to have black or brown lesions which are about 1-2mm large. There is dark pigmentation on the leaves when the diameter is greater than10mm. The lesion expands turning into a chlorotic appearance followed by defoliation. On the stem, there are sunken concentric rings on the centre. Infection on the fruit causes the fruit to become leathery and may have concentric ring with the fruit dropping continuously (Agrios, 2005). The disease is managed by fungicides, crop rotation, removal

and burning of plant debris, eradication of weed hosts which helps to reduce the amount of inoculums. The use of resistant varieties has also proven to be effective (Calis & Topkaya, 2011).

Fusarium wilt is caused by *Fusarium oxysporum* and causes the plant to yellow and wilt. Growth of plant normally becomes stunted with little or no fruit. One characteristic feature of this disease is the brown colour found in the vascular tissue of infected stem. Symptoms are first seen on older leaves which progress with time to affect the younger ones resulting in the death of plant. This disease becomes prevalent in dry weather and low soil moisture (Agrios, 2005; Javis, 2010). The disease is managed by the use of resistant variety. However due to breakdown of resistance, resistant variety should be used in conjunction with crop rotation (Agrios, 2005).

**Viral Diseases**

Viral diseases of tomatoes cause severe harm and huge economic losses. Depending on the viral disease involved, the strain of the virus, the variety of tomato, the age of the plant atthe time of infection, the extent that the viruses have spread during the planting of the cropand the presence of other diseases, the loss may be great or small (Sawalha, 2012).

*Tobacco mosaic virus* is one of the worldwide viruses causing serious losses of 20% in their hosts (Scholthof, 2004). It affects not only tobacco but other plants including tomato. Mode of transmission is mechanical usually through a wound. The virus can also be transmitted through seeds but this can be treated by acid extraction when the virus is on the surface of the seed but not in the inside. The virus infects by assembling all viral RNA and protein produced by the host plant into new viruses (World Microbiology and

Immunology, 2003). Infected plants are usually mottled, stunted, and sometimes distorted. There is normally a light and dark green mottled area which tends to be thicker than the lighter portions of the leaf (Agrios, 2005).

*Tomato mottle virus* (ToMoV) is spread by whitefly and can cause a yield loss as high as 95%. Plants that are attacked show chlorotic yellowing, leaf distortion, curling and stunting reducing yield drastically. The virus can effectively be managed by planting virus free transplant at the time when there are no older tomato plants on the field (Agrios, 2005; Averre & Gooding, 2000).

***Tomato yellow leaf curl virus***

This virus causes one of the most destructive diseases of tomato worldwide (Pan *et al.*, 2012). It is a single stranded DNA (ssDNA) belonging to the genus *Begomovirus* and family *Geminiviridae* (Matthew, 1979; Hull, 2002; Agrios, 2005) with a characteristic of their genetic material packaged into geminate or twinned particles (Harrison, 1985). Based on the type of insect vector, host range, and genome organization, geminiviruses are classified into four genera *Curtovirus, Mastrevirus, Topocuvirus* and *Begomovirus* (Rybicki *et al*., 1967; Agrios, 2005; El-Din *et al*., 2005). The earlier two containing viruses causing *Maize streak virus* and beet curly top virus respectively (Ssekyewa, 2006) with the last two infecting dicotyledons (Prajapat *et al.*, 2012).

**Genus Begomoviruses**

Begomoviruses are the only viruses infecting both the new and the old generation of crops (Ssekyewa, 2006). They are transmitted by *B. tabaci* which is a problem in both solanaceous (pepper and tomato) and other crop families (cassava, beans, cotton and cucubits) (Prajapat, Marwal,Shaikh, &

Gaur, 2012). A good number of the begomoviruses are bipartite (DNA A and DNA B). DNA A is responsible for viral protein essential in replication and encapsidation of both components while the B is responsible for proteins (Hanley-Bowdoin, Settlage, Orozco, Nagar, & Robertson 1999).

The monopartites are linked with betastatellites with sequences approximately 1.4kb. The betastatellites depend on the monopartite genome for replication, transmission and spread (Briddon, Mansoor, Bedford, Pinner, Markham, 2000). The betastatellites decide the host range of the begomovirus and also encode a gene silencing suppressor protein (Jose & Usha, 2003; Cui, Tao, Xie, Fauquet, & Zhou, 2004).

**Origin and Diversity of TYLCV**

The disease probably arose somewhere in the Middle East between the 1930s and 1950s (Czosnek & Laterrot, 1997; Lefeure *et al.*, 2010; Pan *et al.*, 2012). The disease after its discovery stayed unimportant due to its limited geographical distribution. However it became important only in 1980 after the emergence of two strains (TYLCV-Mld and TYLCV-IL) and this spread dramatically through the European and Mediterranean Plant Protection Organization (EPPO) region (Czosnek & Laterrot, 1997; Lefeure *et al.*, 2010; Pan *et al.*, 2012). These two species: *Tomato yellow leaf curl virus*-Israel (TYLCV-Isr) and *Tomato yellow leaf curl Sardinia virus* (TYLCSV) of TYLCV, have been formally acknowledged by the International Committee on Taxonomy of Viruses with TYLCV-Isr as being the most prevalent species in Europe affecting pepper (*Capsicum annum*) and probably the common bean (*Phaseolus vulgaris*) (Glick, Levy, & Gafni, 2009). In Ghana, three new distinctive viral strains have been found. They are *Tomato yellow leaf curl*

*Mali virusTomato yellow leaf curl Kumasi virus* and *Tomato yellow leaf curl Ghana virus* (Osei *et al*., 2008).

According to Glick *et al.* (2009) the disease started spreading to Africa specifically to Eastern Africa around 1965 with Sudan being the first to observe the infection. Zhou *et al*. (2008) reported that, TYLCV was severe in Mali and other West Africa countries. TYLCV has been reported to be widespread in Ghana with severe losses in yield (Horna *et al.*, 2006; Osei *et al*., 2008). In Ghana, the disease has caused devastating losses in the Upper East region since 2002(Osei *et al.*, 2012).

**Host Range**

The virus has an extensive host range with more than 30 species in over 12 plant families including weeds such as blackberry, nightshade *(Solanum nigrum),* bindweed *(Convolvulus arvensis)* and thorn apple (*Datura stramonium*) (Singh & Reddy, 1993). Crop families such as Acanthaceae, Asteraceae, Canicaceae, Euphorbiaceae, Leguminosae, Malvaceae, Oxalidaceae, Pedaliacea, Plantaginaceae and Solanaceae are also hosts (Singh & Reddy, 1993). Other hosts include cultivated plants such as capsicum (*Capsicum annuum*) and green beans (*Phaseolus vulgaris*).However the tomato plant (*Lycopersicon esclentum*) is the preferred host (Persley, 2012).

Wild tomato species, such as *Lycopersicon chilense*, L. *hirsutum,* L. *peruvianum* and L. *pimpinellifolium* show no symptoms. Weeds like *Datura stramonium* and *Cynanchum acutum* present distinct symptoms, while others, such as *Malva parviflora*, are symptomless carriers (Zakay *et al.*, 1991).

**Economic Impact**

TYLCV disease has been a problem all over the world and can cause heavy economic losses wherever it occurs. It reduces yield by reducing the number of fruits produced. Before infection, fruit set would be high but very few fruits will set after infection (CABI, 2013). The virus is so destructive that it can cause a yield loss as high as 100% (Glick *et al.*, 2009). The loss is not different in West Africa were it has caused a shift of Mali being a net exporter to a net importer. Also in Ghana, the infection has caused the importation of tomato from neighbouring Burkina Faso (Horna *et al*., 2006).

**Symptoms of TYLCVDisease**

When plants are infected at an early stage, they have reduced internodes, giving the plant a stunted form. New leaves formed are also significantly reduced in size and wrinkled with strong yellowing at the edges and in between the veins having margins that curl upward, giving them a cup-like appearance (Melzer *et al*., 2011; Persley, 2012).Flowers may appear but frequently will drop prior to fruit set. Later growth stage infections may result in stunting of the growth of laterals; abnormal erect or upright growth, and a bushy appearance (Melzer *et al*., 2011; Persley, 2012).

**Transmission, Acquisition and Spread of the Virus**

Plants acquire the virus through insect vector called whitefly (*Bemisia tabaci*) of the family *Aleyrodidae* (Hull, 2002; Agrios, 2005). *B. tabaci* is an insect pest capable of reducing plant efficiency and longevity, as well as being a virus vector (Bourland, Hornback, Calhun, 2003). It is a devastating pest in tropical countries having both nymphs and adults feeding by piercing the leaf

surface and removing phloem sap from sieve tubes using their sucking mouthparts (Khan, Ghani, Ghaffar, & Tamkeen, 2011).

The insects have six life stages: the egg, four nymphal stages, and the adult (Mau & Kseeing, 2007). According to Schmutterer (1969) whiteflies are known to reproduce bisexually or parthenogenetically, and can therefore produce several generations within a year. Eggs are whitish when first laid but progressively turn brown. The eggs are laid typically in circular cluster, on the base of the leaves which hatches after 5-9 days at 30 °C. Hatching, as a developmental activity depends on host species, temperature and humidity taking 15-70 days for the insect to develop from egg to adult at a temperature of 10 to 32 °C (EPPO/CABI, 1996).

A female adult lays 200 eggs in a generation and it has 11-12 generations in a year (EPPO/CABI, 1996). The first instar on hatching is flat, oval and scale-like which is the only larval stage of this insect that is mobile. The insect moves from the egg site to an appropriate feeding site on the lower surface of the leaf where its legs are lost in the resulting moult making the larva sessile (EPPO/CABI, 1996). The major flight activity of the adult insect takes place in the early morning hours and a short peak in the late afternoon, travelling between distanceof 7 km and 10 km (CABI, 2013).

The insect acquires TYLCV while feeding on virus-infected plants. An adult insect needs to feed on an infected plant for at least 15-30 minutes to acquire the virus and a latent period of 6 to 24 hours for the virus to spread to the host after which adults are normally able to transmit TYLCV for life (Persley, 2012).

The whitefly larvae are normally found more in the lower leaf stratum than in the middle and upper strata. Incidence is high when the plant is flowering as reported by Rasdi, Fauziah, Fairuz, Mohd, and Jamaludin, (2009). In their study, they observed that whitefly population increased and reached the highest peak during flowering and fruiting stages with the population decreasing when the plants attained the end of economic life. According to Rasdi., *et al.*, (2009) the fluctuations were related to the availability of food, good shelter decline and the older leaves which are not appropriate for immature whiteflies. The whitefly lifecycle takes 18 to 28 days in warm weather and 30 to 48 days in winter (Persley, 2012).

So far movement of agricultural materials such as cut flower, infected seedlings, translocation of viruliferous whiteflies by wind or by plane transportation (on ornamentals) have been the main means of spreading TYLCV disease since the disease is not transmitted by seed (CABI, 2014).

**Impact of *Bemisia tabaci***

The whitefly like any other insect has some negative impact on agriculture both economic, social and health. Economic impact arises from farmers trying to control whitefly population. They do this by using pesticides in whitefly-stricken areas which increases production cost (Anderson, 2005). Household surveys conducted in two regions of Colombia and the northern part of Ecuador involving 893 farmers revealed that in an effort to control whitefly in green houses, 100% of the farmers sprayed their crops up to 24 times in a crop cycle of 90-100 days (CIAT, 1994) thereby increasing the production cost.

Apart from this many small scale farmers who made effort to vary their cropping system have failed because of whitefly associated problems. In developing countries, many small scale farmers are rendered jobless as major or prime agricultural lands remain idle in the dry season notwithstanding the availability of water (irrigation districts), all because there is a high population of whitefly in the dry season (Anderson, 2005).

Generally, farmers depend on insecticides to protect their cash crops from whitefly and whitefly-borne viruses (Schuster, Stansly, Polston, Gilreath, & McAvoy, 2007). The extensive use of pesticides by farmers has brought about resistance of the whitefly vector and also systemic destruction of natural enemies since most of the pesticides are not selective (Schuster *et al.,* 2007).

Uninterrupted heavy usage of these insecticides also causes contamination of agricultural products (residual effect). These products are rejected on the international markets, but sold in developing countries with its detrimental health effect to the citizenry (Anderson, 2005; CABI, 2014).

Tomato farms all over the world are threatened by TYLCV due to the high population of whitefly. Infected fields do not produce fruits and sometimes loses its entire crops when the disease is not swiftly brought under control. However, it accompanying high cost of control and the negative environmental impact has led to many abandoning tomato businesses and or selling the fields out (CABI, 2013).

**Effect of Climatic Conditionson *Bemisia tabaci***

In the tropics, climatic conditions such as temperature, rainfall and relative humidity are the essential factors that regulate seasonal fluctuations in sucking insects with the most important factor being the combined effect of

evaporation and transpiration (evapo-transpiration) (Banjo, 2010). The population of whitefly varies throughout the year with the peak from October to April (Anitha, & Nandihalli, 2008). According to Shivanna, Gangadhara, Basavaraja, Nagaraja, Kalleswara, and Karegowda (2011), maximum temperature is known to have a positive relationship on the population of sucking insects for which whitefly is part but moderate rainfall combined with high temperature is known to increase the population of the whitefly (Banjo, 2010). On the other hand, rainfall and minimum temperature are negatively correlated with relative humidity showing insignificant effect (Shivanna *et al*., 2011). Shivanna *et al*. (2011) stressed that high temperature with very little rainfall enhances the activities of whitefly. According to Harry *et al*. (1993), whiteflies prefer to grow on crops with low soil moisture. They observed that the flies had affinity for potted squash with low soil moisture (45% moisture) and less affinity for high soil moisture content (75%). They further noted that the pot with low soil moisture had the highest incidence of the disease (leaf silvering) and vice versa.

**Diagnosis of TYLCV**

In agriculture, viruses are a major problem and cause a lot of losses. It is therefore important to diagnose a particular virus, whether known or unknown. This can be done by knowing where the virus originates, its spread through epidemiology and quarantine situation and assay for a known virus. These are the basic conditions or situations in which techniques for recognizing and identifying a virus is based on. The differences between the various technique used depend on these factors: virus strain and its reproduction, sensitivity and accuracy of the technique, number of samples

that can be processed in a given time, operator, cost of apparatus, the degree of operator training and adaptation to field conditions (Hull, 2002). The methods used in diagnosis are as follows:

**Molecular DNA-DNA Hybridization**

Under this method, there are two approaches: Southern blot hybridization and tissue print hybridization

**Southern Blot Hybridization**

This method is the most commonly used procedure for testing large number of samples. The method involves extracting small amount of sap from the plant (Hull, 2002) using CTAB-base method or SDS-Proteinase K whitefly (Zeidan & Czosnek, 1997; CABI, 2013). From this, the nucleic acid of the virus is denatured by alkali treatment (Hull, 2002). DNA is subjected to agarose gel electrophoresis, blotted, pre-hybridized and hybridized with a virus-specific DNA probe (Ber *et al*., 1990). The probe may consist of the full-length viral genome or virus species-specific sequences such as the intergenic region. The probe is labelled either with a radioactive nucleotide (e.g. 32P-adCTP) or with a non-radioactive nucleotide (e.g. digoxygenin-11-dUTP). The blots are then washed at 65°C for 30 min (twice) in 150 mM NaCl and 15 mM trisodium citrate (1 x SSC). Washing the blot at 70°C in 0.1 x SSC allows distinction between closely related TYLCV isolates, such as viruses from Israel and from Italy (Czosnek, Ghanim, Rubinstein, Morin, Fridman, &Zeidan, 2001). The probe is then exposed to an X-ray film by radio labelling the blot. For non-radioactive probing, the blot is subjected to immunological detection. After blocking, the filter is incubated with an anti digoxygenin alkaline phosphatase conjugate (diluted 1:5000). After washing, the filter may

be incubated with alkaline phosphatase substrates, Nitro Blue Tetrazolium (NBT) and 5-Bromo-4-chloro-3-indolyl phosphate (BCIP), until a dark blue colour is obtained. Alternatively the virus-probe complex can be detected by chemiluminescence (Caciagli & Bosco, 1996). Non-radioactive digoxygenin-labelled DNA probes can be almost as sensitive as radioactive probes (CABI, 2013). To reiterate, the technique is now widely used and has successfully been applied in screening large number of potatoes for resistance to several viruses. Again it has been employed in assessing differences between tombus viruses (Hull, 2002).

**Tissue Print Hybridization**

This involves detecting TYLCV DNA by sequencing; this can be done specifically and sensitively by hybridization of infected plant tissues (tomato leaves, roots, stems, flowers and fruits) squashed onto a nylon membrane (squash-blot) with a radiolabelled specific DNA probe (Hull, 2002). Viral sequences can also be detected in whiteflies that have fed on infected tomato plants with an assay (Zilberstein, Navot, Ovadia, Reinhartz, Herzberg, & Czosnek, 1989) or Specific probes which can detect (+) and (-) strands or even specific parts of the genome (Hull, 2002). Plant and insect tissue squashes are hybridized with sulfonated virus complementary (-) strand DNA produced from a full-length DNA clone using the M13K07 helper phage. A mouse monoclonal antibody binds to the sulfone groups of the DNA hybrid.This is recognized by a goat anti-mouse immunoglobulin antibody conjugated to alkaline phosphatase which enzyme transforms a colourless substrate into a coloured product. The coloured product indicates the presence of viral nucleic

acids. Virus can also be detected in the whitefly vector at the individual level (CABI, 2013).

**Polymerase Chain Reaction (PCR)**

This technique allows the detection of very small amounts of the disease agent in the infected plant and vectors, and also the cloning of genomic fragments of the pathogen (CABI, 2013). It engages two principles: hybridization of synthetic complementary oligonucleotide primers to the target sequence and using heat stable DNA polymerase to synthesize multiple copies of complementary DNA of the sequence between the primers (Hull, 2002). PCR cannot be used for most plant viruses with RNA genome, it is applicable to viruses with DNA genome. However, there is a system called Real time-PCR where cDNA is made to the desired region of RNA genome using a primer or reverse transcriptase. In refining PCR, virus particles are captured by immobilised antibodies. This is called immune capture PCR(IC-PCR or IC-RT-PCR) (Hull, 2002). The method has been reported to be the most simple, rapid and reliable in diagnosis for the detection of the TYLC virus and genetic differences among the virus (Ieamkhang, Riangwong, & Chatchawankanphanich 2005 & Ueda, Takeuch, Olcabayash, Hanad, Tomimura, & Iwanam, 2005). According to Hull (2002) this PCR method has been used to get rid of host chromosomal DNA in the diagnosis of *Banana streak virus* (BSV) in which sequencing are found in the host genome before PCR. Once more, degenerate primers have been used to detect whitefly transmitted geminivirus. For example biotypes of leaf hoppers that transmit *Wheat dwarf virus* has been distinguished by using universal and strain specific promoters. PCR helps in the early detection of virus as observed in the

detection of *Beet necrotic yellow vain virus* (BNYVV) in plant soil and vector (Hull, 2002).

**Rolling-Circle Amplification**

TYLC virus can be detected or diagnosed by using this method. This involves amplification of total DNA of infected plant by the use of bacteriophage phi29 DNA polymerase (Jeske, 2007; CABI, 2013). The viral DNA that has been amplified induces symptoms after biolistic inoculation of the test plant. According to Guenoune-Gelbart *et al*. (2010), plant material that has been collected and dried for 25 years yielded infectious DNA by this method.

**Microarray**

This method has the prospect of detecting a number of viruses in a single reaction. The theory behind this method is the hybridization of fluorescent labelled target sequences to probe sequence spotted into a microscopic glass slide. RNA of infected plant is converted to DNA by RT-PCR and labelled with a fluorescent dye which localizes the pathogen. It has been effective in detecting TYLC virus and others such as *Cocumber mosaic virus* and *Tobacco mosaic virus* (Boonham, Tomlinson, & Mumford 2007; Hull, 2009; Tiberini, Tomassoli, Barba, & Hadidi2010).

**Immunological Methods**

In revealing and estimating the combination between antibodies and antigens, the most widely used methods are the enzyme-linked immunoabsorbent assay(ELISA), immunosorbent electron microscopy (ISEM) and dot blot that uses either polyclonal or monoclonal antibodies. One disadvantage of all immunological methods is that, the antibodies available are

usually unable to distinguish TYLCV from other begomoviruses, strains and species that are closely related (Hull, 2002; CABI, 2013).

**Dot Immuno-Binding Assay (DIBA)**

This technique uses nitrocellulose or nylon membranes as the solid substrate for ELISA but for the development of the final colour, a substrate that will link up to the IgG is added which will convert it to an insoluble coloured material. This method has advantages of being fast, low cost and requires small amount of reagents. In routine detection of viruses in seeds or seed samples and for inexpensive simple test, this method is useful (Hull, 2002).

**Management of Tomato yellow leaf curl virus Diseases**

A number of strategies are employed in the management of TYLCV disease, thus:

**Control of Whitefly Vector**

Generally limiting or reducing whitefly population will often have a significant impact on incidences of TYLCV-infected plants (Polton & Lapidot, 2007). Many techniques have been employed in the management of whitefly in the bid to control TYLCV disease. These include mechanical methods (Whitefly-proof screens; UV absorbing plastics and screens, and plastic mulches), cultural methods (farm sanitation and roguing), chemical control of whitefly vector and planting of resistant varieties.

**Mechanical Methods**

Fine-mesh screens serving as physical barriers have been used in the Mediterranean Basin since 1990 to protect crops from TYLCV disease (Polston & Lapidot, 2007). According to Polston and Lapidot (2007) net

houses sheltered by mesh screens combined with a few insecticide sprays for 18 weeks after planting diminishes dramatically the number of whitefly infestation to only 1% which is far below the level required for significant economic damage. According to them, this was not so at the control unscreened greenhouse where TYLCV incidence reached 100%. They further observed that the disadvantage, however, is that these screens can create problems of shading, overheating, and poor ventilation (Polston & Lapidot, 2007).

UV-absorbing plastics andscreens are able to blind those whiteflies which use the light UV wavelengths to navigate by decreasing the levels of UV light (Polston & Lapidot, 2007). These UV-absorbing films have been shown to inhibit penetration of whiteflies into greenhouses and to reduce movement of whiteflies within greenhouses. This has been confirmed by Antignus, Nestel, Cohen, and Lapidot, (1996, 1998, 2001) in Israel where ultraviolet absorbing plastic films were used as greenhouse covers or insect-proof nets. According to them, TYLCV disease incidence in tomato grown under the UV-absorbing sheets was only 1% compared with approximately 80% in control conditions.

Plastic mulches have successfully been used to decrease incidences of TYLCV disease in tomato fields. These reflective mulches are completely or partly aluminized and reflect a lot of daylight disorienting whiteflies and decreasing their landing on plants in the field. However, like other mulches, their effectiveness decreases as the tomato canopy enlarges and cover up the mulch. Nonetheless this approach has the added advantage of interfering with

other virus vectors such as aphids and thrips and it is connected with lower incidences of several other tomato viruses (Polston & Lapidot, 2007).

The use of yellow plastic mulch to protect open-field tomato plants from the whitefly-borne TYLCV is a common practice in Israeli agriculture (Zaks, 1997). Cohen and Melamed-Madjar (1978) demonstrated that the colour yellow attracts whiteflies. He suggested that yellow radiation may be a component of the whitefly's host-selection mechanisms. In his study it was found out that the protective effect of the yellow mulch lasted about 20-30 days after transplanting. This could be as a result of change in time in the ratio of canopy to mulch. This technique according to Polston & Lapidot (2007) can reduce the incidence of TYLCV disease by 10%. The managing effect of yellow mulch is due to a blend of the attraction of the whitefly to the yellow colour of the mulch and its consequential death due to dehydration induced by the high temperature of the mulch (Cohen, 1982).In addition to reducing incidences of whitefly-transmitted viruses such as TYLCV, reflective mulches can also reduce incidences of virus vectors such as aphid and thrips (Polston & Lapidot, 2007).

**Farm Sanitation**

The main important source of TYLCV and whiteflies could even be an old tomato plant. The virus can spread speedily in older or deserted farms where whitefly control has stopped. Farm sanitation such as removal of tomato plants instantly after harvest reduces whitefly populations in an area and helps reduce the progress of TYLCV into nearby farms (Polston & Lapidot, 2007; Persley, 2012).

Proper weed management can also reduce the population of whitefly. Since weeds can harbour whitefly, it is imperative that the farm be kept clean from weeds (Polston & Lapidot, 2007; Persley, 2012). However, it has been found in Florida that wild plants outside the field that are not sprayed with insecticides can act as reservoirs of natural predators and entomophagous fungi that can be very effective in reducing whitefly populations. It is recommended that these areas should not be treated with herbicides to allow natural whitefly predators and pathogens to function (Polston & Lapidot, 2007).

Roguing has been known to reduce infection within a field. It has been observed that roguing young infected plants tends to reduce the rate of secondary spread within a field when incidences are low. It been noted that, this method becomes unrealistic when the plants have been in the field for more than six weeks (Polston & Lapidot, 2007).

**Chemical Control of Whitefly Vector**

Another approach in minimizing the population of whitefly in an attempt to reduce economic losses in tomato to TYLCV infection is the use of pesticides which is the most common in areas where tomatoes are grown (Cahill, Gorman, Kay, & Denholm, 1996; Polston & Anderson, 1997; Ahmed, Kanan, Sugimoto, Ma, & Inanaga, 2001). Pesticides used to reduce whitefly populations include chlorinated hydrocarbons, organophosphates, neonicotinoids, pyridine-azomethines, and pyrethroids (Cahill *et al.*, 1996; Polston & Anderson, 1997; Ahmed *et al.*, 2001). Apart from these insecticides, oils, insecticidal soaps, and insect growth regulators have been used. The most effective and widely used class of insecticides in reducing

whitefly populations is the neonicotinoids of which at least three (thiomethoxam, imidacloprid, and dinotefuron) have been used to reduce incidence of TYLCV (Cahill *et al.*, 1996; Polston & Anderson, 1997; Ahmed *et al*., 2001). However the major problem associated with the use of insecticides is the development of resistance of whitefly to many of these chemicals. This results in decreased efficacies over time due to persistent and frequent use. The use of these insecticides also brings about secondary pests such as leafminers (Polston & Lapidot, 2007).

**Use of Resistant Cultivars**

The best approach to reduce losses due to TYLCV infestation is by the use of resistant variety. This appears to be the only promising and environmentally friendly means for managing the disease (Chague *et al.*, 1997). Sources of resistance using genes are usually from wild tomato species (Lapidot & Friedmann, 2002). These wild relatives are: *S. cheesmaniae,* S. *chilense, S. habrochaites, S. peruvianum* and *S. pimpinellifolium*. The resistantgene has been reported to be either recessive or dominant depending on the wild relative used. The resistance genes are located between the 1$^{st}$ and 5$^{th}$ loci (Zakay *et al*., 1991; Pico, Dfez, & Nuez, 1996; Nakhla& Maxwell, 1998). Due to the presence of interspecific barriers between the wild and domesticated tomato species, there is the complexity of transferring the resistance to commercial cultivars.This makes progress in introgression of TYLCV resistance slow. The challenge today is obtaining a cultivar that merges high levels of resistance with high fruit quality (Polston & Lapidot, 2007).

Genetically, tolerance to TYLCV is controlled by five recessive genetic factors. Of these Zamir *et al*. (1994*)* has mapped one which is a major TYLCV tolerance locus (*TY-1*) in the tomato wild relative *S. chilense* on chromosome 6 while Chague *et al*. (1997) has described four random amplified polymorphic DNA (RAPD) markers linked to a quantitative trait locus involved in the resistance to TYLCV. According to CABI (2013) tolerant varieties need to be protected with insecticide during the first week after transplanting. Again some of the breeding lines available could be symptomless whiles others are tolerant. A breeding line with its tolerant gene from *S.peruvianum* is symptomless whether in the greenhouse or field. However, breeding lines with its resistance gene from *S. habrochaites* supports little virus accumulation. In Ghana complete resistance to the TYLCV disease following whitefly screening, field screening and molecular screening has not been identified in any of the tomato genotypes studied (Osei *et al.,* 2012). Genotypes showed high tolerant levels but not complete resistance.

**Farmers' Knowledge**

The knowledge of farmers is an effective tool in improving and managing plant health. According to Bentley and Thiele (1999), scientists have to sometimes contact farmers to find out their knowledge on certain diseases to stimulate further farmer-scientist collaboration in the appropriate management of diseases. On their research on late blight, caused by *Phytopthora infestans*, Bentley and Thiele (1999) had to seek information from farmers on symptoms of the disease, best indigenous practices and improved technology to help alleviate and manage the disease. Another

disease that farmer's knowledge helped in getting detailed literature is maize ear rot, as reiterated by Bentley and Thiele (1999). The knowledge of farmers on this disease was more detailed than that of plant pathologists.

On language usage, farmers usually use medium-sized vocabulary to describe and explain diseases and symptoms of plants which end up connoting the same as that of plant pathologists. With reference to Bentley and Melare (1990), farmers used medium-sized vocabulary to describe bean diseases and all their description meant the same as that of the plant pathologists, however most of them often confuse fungi diseases with viral disease and insect damage.

Notwithstanding the immense contribution of farmer's knowledge to the development of plant pathology, there have been instances where most of this knowledge has been disproved by scientists. Heong and Escalada (1997) showed that the perception of farmers on insecticides usage and spraying were wrong. In that study farmers in Malaysia did not believe that it was leafhopper that causes Tungro virus disease so they sprayed insecticide as they probably thought other insects were the causes.

Farmers' knowledge of their local ecosystem could be extensive but their perception of plant disease may differ from that of scientists (Bently, 1992). In order to improve management options for plant disease, farmers' knowledge and perception need to be known. So far work done on perception of farmers in India and Philippine concerning plant viruses reveals that, farmers have heard of some viral diseases and majority have experienced them in their fields, they are able to describe the symptoms but do not know the

causes and epidemiology (Nagaraju, Venkatesh, Warburton, Muniyappa, Chancellor, & Colvin, 2002).

Nagaraju*et al*. (2002) in their study on tomato revealed that farmers ranked *Tomato leaf curl virus* (TYLCV*)* as the most important disease in the summer season. In the study, majority of farmers were not aware of the vector of the disease, *Bemisia tabaci,* but associated the disease with climatic factors. According to them, farmers were not able to see the fly because of its small size. The most common control method used by farmers during their study was insecticides though farmers knew the insecticides were not effective. Some of the farmers, about one third of them did not take measures when the disease occurred since they thought the control would not work (Nagaraju*et al*., 2002). Interestingly, farmers in the middle and northern part of Ghana wrongly attribute TYLCV disease to high temperature, nutrient deficiency, drought and pest (flies) (Osei, *et al.*, 2012).

# CHAPTER THREE

# MATERIALS AND METHODS

## Introduction

The study involved a household survey to identify farmers' knowledge and their management practices, and a field survey to determine the incidence and severity of TYLCV infection in the study area. It also involved screening of some tomato genotypes to identify a resistant or tolerant genotype(s), and the evaluation of resistant or tolerant genotype(s) in the coastal and forest agro ecological zones.

## Survey to Identify the Farmers Perception of TYLCVDisease and Their Agronomic Practices

### Population and Sampling

The population for this study was tomato farmers in the Central Region of Ghana.

### Reconnaissance Survey

Visits were made to both regional and district directorates of the Ministry of Food and Agriculture (MoFA) for the purpose of familiarizing with the study area**.** Through interactions with the officials from the regional directorates of Ministry of Food and Agriculture (MoFA), secondary data as the most important vegetable growing districts in the region was collected. Further interactions with tomato growers and retailers were made. Other information like the most important vegetable growing areas/communities in

each district was collected from the officials of district directorate of MoFA, to guide the sampling plan.

**Choice of Study Area**

Mfantseman district, Effutu Municipality and Komenda-Edina-Eguafo-Abrim district which are leading tomato producing areas in the Central region were purposively selected for the study.

**Description of the Study Areas**

**Effutu Municipal**

Effutu municipal covers a land area of 95 square kilometres on latitudes 5ºC N and longitude 0º 32 E. The municipality is a low lying area with protruding granites and lies within the dry equatorial climate zone characterized by low annual rainfall of 400 mm – 500 mm and a mean temperature ranging from 22 ºC-28 º C (MoFA, 2011). The vegetation type is that of coastal savannah grassland suitable for vegetable cultivation or dry season irrigation farming since it has a long dry season of five months. The soil type is largely clay with high salinity (MoFA, 2011).

Crop production is the major economic activity in the municipality especially in the small settlements such as New Winneba, Gyangyanaze, Ateitu, Okyereko, Osubumpeyin and Nsuekyir. The vegetables grown in these communities are pepper, tomato, okra, garden eggs, onions, exotic vegetables and groundnut (MoFA, 2011).

In 2010, land area for tomato production was 350 ha producing 4.10 mt/ha and being the third highest major crop produced in the municipality (MoFA, 2011).

**Komenda-Edina-Eguafo-Abrim District**

The municipality covers an area of 95 square kilometres of which 80% is available for the cultivation of crops. The rainfall pattern differs depending on the location. The area's closeness to the sea experiences lower rainfall compared to the interior. The temperatures are generally high making the variability in climate and vegetation being influenced more by rainfall. The annual rainfall ranges between 750 mm-1000 mm for the coastal and 1200 mm-1500 mm for the interior areas (MoFA, 2011).

The area is noted for the cultivation of cereals, vegetables and cash crops such as tomato, pepper, garden eggs, okro etc. In 2010, the land area for the cultivation of vegetables was 16.8 ha which yielded 2.1 mt (MoFA, 2011).

**Mfanstseman District**

This covers an area of 612 square meter within latitude 5º 07′ to 5º.20′ North of equator and between longitude 0′.44′ to 1º.11′ west of Greenwich meridian. Out of the available land, an area of 280,000 ha is being used for arable crop production. It has two types of vegetation: Coastal shrub for the upland and grasses for the flood plains. The district is characterized by temperature range of 24-28 ºC and a bimodal type of rainfall ranging from 100-120 mm. Agriculture is the major economic activity and noted for the production of vegetables like okra, tomato, garden eggs pepper etc (MoFA, 2011).

**Selection of Villages /Communities**

In each of the three districts, five communities were selected randomly **(**Table 1**),** and in each community, ten households selected using purposive and snowball sampling methods (Oliver, 2006). A total of 150 respondents

were interviewed of which 71 were males and 79 were females. The farmers interviewed consisted of those who had tomato farms at the time of the study and those who had tomato farms in the previous year.

**Instrumentation and Data Collection**

The research utilized primary data collected using interview schedule by self-administration and observation during the field survey. Structured interview schedule with both open ended and closed ended questions was prepared. The questions were written in English and administered in both English and local languages (Akan). The survey questionnaire was made up of three categories of questions which were based on (1) socio-economic characteristics of the farmers (age, sex, educational background); (2) farmers' knowledge of TYLCV disease (incidences, causes, and effect of the disease on tomato crop), and (3) crop history and agronomic practices (time of planting, nursery practices, disease management methods, etc) (see appendix 1).

**Pre-Testing of Instrument**

The survey questionnaire was pre-tested to determine the ability of the researcher to administer it. This was done to validate the content of the questionnaire before it was administered to the respondent farmers (Whitehead, 2000). The pre-test was done at Ateitu in the Effutu municipality. The location was selected because it has the same characteristic as the areas of research interest.

**Table 1: Tomato Growers Sampled From Each of the Selected Communities in Three Districts of the Central Region**

| District/ Municipality | Selected communities | No of households |
|---|---|---|
| Mfantseman | Nsanfo | 10 |
| | Baafikrom | 10 |
| | Kwesiransah | 10 |
| | Obidan | 10 |
| | Ehyerew | 10 |
| Effutu | Essuekyir | 10 |
| | Gyangyanadze | 10 |
| | Gyahadzi | 10 |
| | Okyireko | 10 |
| | Osubumpeyin | 10 |
| KEEA | Dwabor, | 10 |
| | Abeyee | 10 |
| | Aanser | 10 |
| | Dabir | 10 |
| | Ankwanda | 10 |

**Data Analysis**

The data was cleaned and coded into Statistical Package for Social Science (SPSS version 16) and then analyzed into frequencies and percentages.

**Determination of Incidence and Severity of TYLCV Disease in the Selected Districts**

A field survey for incidence and severity of TYLCV disease was done in the three districts of the Central region: Mfantseman district, Effutu Municipality and the Komenda-Edina-Eguafo-Abirem district, between August and December of the 2013 cropping season. The disease assessment was carried out in the same communities covered during the household survey.

Ten farms were selected per community, and in each farm, fifty tomato plants were randomly assessed for incidence and severity of TYLCV disease. These farms belonged to farmers who were earlier interviewed during the household survey (Table. 1). Averagely, each farm surveyed measured between half an acre to two acres.

Incidence of TYLCV disease for the various fields were calculated using the formula by Imran *etal.*(2012)

Disease incidence=$\frac{Numberofinfectedplants}{Totalnumberofplants} \times 100$

The severity of TYLCV disease in each field was assessed based on the 0-4 symptom severity scale developed by AVRDC (Lapidot and Friedman, 2002) (Table 2).

**Table 2: Scale for Assessing the Severity of *Tomato Yellow Leaf Curl Virus* (TYLCV) Disease**

| Disease score | Description |
|---|---|
| **0** | No Symptoms (healthy) |
| **1** | Slight yellowing (mild symptom) |
| **2** | Leaf curling and yellowing (moderate symptom) |
| **3** | Yellowing, curling and cupping (severe symptom) |
| **4** | Severe stunting, curling and cupping (very severe symptom) |

The disease severity index was also calculated using the formulaby Chomdej, Chatchawankanpanich, Kositratana, and Chunwongse, (2007)

Disease severity index=

$$\frac{\sum(Ratingscale \times Numberofplants)}{TotalNumberofPlants \times HeighestRating} \times 100$$

**Data analysis**

Data on percentage incidence, and severity index of TYLCV from the various fields were transformed using angular transformation and subjected to the analysis of variance (ANOVA) using GenStat Statistical Software version 12 (VSN International). The means were separated using least significant difference (LSD) method at 5% probability level.

**Screening of Tomato Genotypes for Resistance /Tolerance to TYLCV Disease**

**Experimental Site**

The study was conducted at the School of Agriculture Teaching and Research farm of the University of Cape Coast during the 2013 major crop season. This location (5°10'N, 1.2°50'W) falls within the coastal savannah vegetation zone, with Acrisol soil type (Parker, Osei, Armah, & Yawson, 2010) and is a highly endemic site for TYLCV disease (Personal Communication, E. Asare-Bediako 4$^{th}$ March 2013). The area has a bi-modal rainy season from May to June and August to October with annual rainfall ranging between 750 mm and 1000 mm (Parker *et al.,* 2010) and temperatures ranging between 23.2 ºC and 33.2 ºC, with an annual mean of 27.6 $^{o}$C (Owusu- Sekyere, Alhassan, & Nyarko, 2011).

**Plant Materials**

Thirty five tomato genotypes obtained from the Crop Research Institution, Kumasi, and a farmer's local variety obtained from a local market in Cape Coast was added as a check. In all 36 genotypes were used for the study. Table 3 shows the source, local names and codes of the 36 tomato genotypes.

**Raising of Tomato Seedlings**

The seeds of the 36 tomato genotypes described in Table 3 were first sown on the 16$^{th}$ August 2013. The nursery site was prepared by clearing the weeds and the stubbles burnt on the site to sterilize the soil against any soil-borne organisms/pathogens. Thirty-six beds were prepared with each measuring 0.54 m x 0.9 m. The seeds were then thinly sown in drills at a depth of about 0.5 cm and watered. Watering was done with a watering can every day and reduced to three days a week after germination and establishment.

**Experimental Design and Field Layout**

**Land Preparation**

The land was initially slashed and then ploughed and harrowed to make the soil loose and also expose some soil borne pests to higher temperature for desiccation. The experimental design used was Randomized Complete Block Design (RCDB), with three replications. Each replication was divided into 36 plots with each plot measuring 1 m × 0.5 m and a spacing of 0.5 m between plots. Each plot represented a tomato genotype.

**Table 3: Code, Name and Sources of 36 Tomato Genotype Used for the Study**

| Codes | Genotype names | Source |
|---|---|---|
| K 116 | Ashanti 2 | Ghana(Ashanti Region) |
| K 045 | Tomatose | Ghana(Volta Region) |
| K 042 | Tomatose | Ghana(Volta Region) |
| K 100 | Local 3 | Ghana(Upper East) |
| K 074 | Local 6 | Ghana(Northern Region) |
| K 144 | BK-Dotvert Yako | Burkina Faso(Burkina Faso) |
| K 124 | Local 1 | Ghana(Ashanti Region) |
| K 005 | Petomec | Ghana(Eastern Region) |
| K 214 | AVTO 9001 | Taiwan(AVRDC) |
| K 138 | BK-Koly zy | Burkina Faso |
| K 146 | BK-Kong-L6 | Burkina Faso |
| K 194 | Magmet | Korea |
| K 087 | 5(K) | Ghana(SARI) |
| K 084 | 1R | Ghana(SARI) |
| K 188 | Madiso | Korea |
| K 027 | Local | Ghana(Volta Region) |
| K 098 | Local 1 | Ghana |
| K 088 | Local1 | Ghana(Upper East) |
| K205A | AVTO 1006 | Taiwan(AVRDC) |
| K 197 | REX | Ghana(Eastern Region) |
| P 077 | Local 9 | Ghana(Northern Region) |
| K 213 | AVTO 9804 | Taiwan(AVRDC |
| K 083 | 6(A) | Ghana(SARI) |
| K 050 | Asante tomato | Ghana(Western Region) |
| K 011 | Ntose | Ghana(Eastern Region) |
| K 106 | Local 2 | Ghana(Upper East) |
| P 085 | 21(B) | Ghana(SARI) |
| K200 | 2001 heat tolerant | Ghana(Eastern Region) |
| K 191 | Dyune | Korea |
| K 186 | Superdotaerang | Korea |
| K 190 | Orange carl | Korea |
| K 006 | Power Rano | Ghana(Eastern Region) |
| K 202 | AVTO 0102 | Taiwan(AVRDC) |
| P 009 | Mmoboboye | Ghana(Eastern Region) |
| K 206 | AVTO 1008 | Taiwan(AVRDC) |
| L.V | Fadzebegye | Ghana(Central Region) |

**Transplanting**

Transplanting of three-week-old seedlings onto the main field was done in a triangular pattern and at a spacing of 1m between plants and between rows. There were two rows per plot, withfive plants in a row, giving ten plants per plot. Five plants were selected and tagged for data collection.

**Agronomic Practices**

Watering and weeding was done as and when necessary. N.P.K (15-15-15) fertilizer was applied at the rate of 250 kg $ha^{-1}$ three weeks after planting.

**Data Collection**

Data were taken on the following parameters: incidence, severity of the disease, whitefly population, fruit per plant and yield.

The number of whiteflies was visually counted and the incidence and severity of TYLCV disease were determined by observing visual symptoms at 30, 45 and 60 days after transplanting (DAT). Fruit yield was based on when the fruit reached physiological maturity. In each case, the data were taken on five plants per plot and the mean determined.

**Number of Adult Whitefly**

Whitefly counting was done between 0600 and 0800 hours when the environment was cooler and whiteflies were relatively immobile than later in the day as reported by Fauquet, Fargette, and Thouvenel, (1987) and Asare, Galyuon, Asare-Bediako, Sarfo,and Tetteh, (2014). Total adult whitefly populations on the five topmost expanded leaves of five plants were determined and the mean number of whitefly per plant calculated. On each plant, leaves were carefully turned over and the number of adult whiteflies on

the abaxial leaf surfaces were counted and recorded, as described by Asare *et al.* (2014).

**Incidence and Severity**

Incidence of TYLCV disease (DI), based on visual symptoms, was determined as the proportion of infected plants per plot, expressed as a percentage of total number of plants observed, according to Imran *et al.* (2012).

Disease severity was rated on individual plants using a visual scale of 0-4 developed by AVRDC (Lapidot & Friedman, 2002) as already described.

**Number of Fruit**

The number of fruits was taken on the five tagged plants. This was done by counting the number of fruits available on the plant. The mean per genotype was calculated.

**Yield**

The fruit yield of tomato per plot was obtained by harvesting the mature fruits on each plant per plot to get the number of fruits per plot. The harvested fruits were weighed using the electronic balance (WPT 12CI model, RADWAG WAGI, Witold Lewandowsk Poland), to obtain the fruit weight (kg $ha^{-1}$) and yield (t $ha^{-1}$). The total fruit yield per plot was determined as a sum of the fruit yield taken as and when the fruits reached physiological maturity until senescence.

**Data Analysis**

Data on percentage incidenceand severity index were transformed using angular transformation, and those on whitefly population, and number of fruits per plant were transformed using square root transformation in order to

homogenize the variance. Data was then subjected to ANOVA using GenStat Statistical package version 9 (VSN International), and the means separated using least significant difference (LSD) method at probability level of 5%.

**Evaluation of Performance of Selected TYLCV Disease-Tolerant Tomato Genotypes against TYLCV at Forest and Coastal Savannah Ecological Zones**

**Study Area**

The reaction of some selected tomato genotypes against TYLCV infection were evaluated at the coastal savannah zone (Teaching and Research Farm of School of Agriculture, UCC) and forest ecology (Asuansi Agricultural Station) during the major rains of the 2014 cropping season.

Asuansi Agricultural station is located in the forest zone of Abura-Asebu-Kwamankese district in the Central Region of Ghana. It is about 30 km north of Cape Coast and covers a land area of 256 ha (640 acres). The station has a mean rainfall of 980 mm and follows the traditional double maxima (bimodal) distribution. The average monthly temperature is 26.9 ºC. The soil is known to be rich in minerals especially potassium (MoFA, 2011).

The ecology of the teaching and research farm of the School of Agriculture, University of Cape Coast, has already been described.

**Selection of Plant Materials**

Seven tomato genotypes were selected from the previous experiment, based on their reaction to TYLCV and yields, together with one current commercial cultivar. The tomato genotypes were K100, K042, K116, K005, K213, K027, K202, and CV. Genotypes K100, K042, K116 and K005 showed mild symptoms with high yields. Genotypes K213 with mild symptoms and

low yield, genotype K027 with very severe symptoms but high yield and genotype K202 with very severe symptom but low yield were added as controls. The commercial variety CV was also added to compare it yield with the selected genotypes.

**Raising of Tomato Seedlings**

The seeds of the selected tomato genotypes mentioned were first sown at the nursery at the various agro ecological zones. The nursery site was prepared by clearing of the weeds and the stubbles burnt on the site to sterilize the soil against any soil borne pathogen. There were eight beds in the nursery with each measuring 0.54 m x 0.9 m. The seeds were nursed on the 11$^{th}$ February 2014 with the seeds thinly sown in drills at a depth of about 0.5 cm deep and watered. Watering was done with watering can every day and reduced to three days a week after germination and establishment.

**Experimental Design and Field Layout**

The land was initially slashed and then ploughed and harrowed to make the soil loose and also expose some soil borne pests to higher temperature for desiccation.RCBD, with three replications was used. The total land area was 20 m x 11 m, each bed representing a genotype and measuring 1 m x 5 m and 0.5 m from one bed to another. The transplanting of three weeks old seedlings was done on the 4$^{th}$ and 5$^{th}$ March 2014 in a triangular pattern and at a spacing of 1 m between plants and between rows. There were 2 rows per plot, with 5 plants in a row, giving 10 plants per plot. Five healthy plants were selected and tagged for data collection.

**Agronomic Practices**

Watering and weeding was done as and when necessary. N.P.K fertilizer (15-15-15) was applied at a rate of 250 kg $ha^{-1}$ three weeks after transplanting.

**Morphological Evaluation of Tomato Genotypes against TYLCV Infection**

The eight tomato genotypes were evaluated at 30, 45 and 60 DAT at both the Cape Coast and Asuansi experimental sites. Data were taken on incidence and severity of TYLCV disease, whitefly population, percentage number of fruits per genotype and yield per plot, as previously described.

**Molecular Evaluation of Tomato Genotypes against TYLCV Infection**

The molecular assay to confirm the infection or otherwise of the selected genotypes by TYLCV was done at the Biotechnology Laboratory of the College of Agriculture and Consumer Sciences, University of Ghana, Legon.

**Collection of Tomato Leaf Samples**

Fresh leaf samples from all the eight tomato genotypes were taken at 30 days after transplanting. Before the samples were taken, they were clean with 70% ethanol and then placed on ice.

**DNA Extraction**

The DNA of the leaf samples were extracted by the use of E.Z.N.A Plant DNA Mini Kit (Omega Biotek store) according to the instructions of the manufacturer. Fresh tomato leaves (0.2 g) were weighed, frozen in liquid nitrogen and ground in microfuge tubes. Buffer SP1 (400 µL) was instantly added after which RNase A solution of 5 µL was also added. The samples

were then incubated at 65 ºC for 10 minutes. Buffer SP2 (140 µL ) was then added to the sample and mixed on vortex, strongly after which samples were incubated again for 5minutes on ice and centrifuged at 10,000 × g for 10 minutes.

The resultant supernatant was then aspirated into an Omega® Homogenizer Column placed in 2 mL collection tube and centrifuged at 10,000 × for 2 minutes resulting in the formation of a clear lysate. The clear lysate was then transferred into a 1.5 mL microtube taking note of it volume. In order to adjust binding conditions of the samples, 1.5 volumes of buffer SP3/ethanol mixture were added to the clear lysate and vortexed.

Two hundred microliters (200 µL) of equilibration buffer was placed in a 2 mL collection tube and centrifuged at 10,000 rpm for 1 minute and the flow through disposed off. The supernatant obtained (650 µL) was transferred into a Hiband® DNA Mini Column placed in a 2 mL collection tube and centrifuged for 1 minute at 10,000 × g subsequent to this, the flow through was disposed off and the tubesreused in the succeeding steps.

The Hiband® DNA Mini Column was then placed into a new 2 mL collection tube and 650 µL of SPW wash buffer added centrifuging at14000 rpm for 1 minute and discarding the flow through. With equal volume of buffer SPW wash buffer the previous step was repeated and columns were used again after flow through was discarded. The empty column was centrifuged at 14000 rmp for 1 minute.

Hiband DNA column was then placed into a new 2 mL collection tube with 100 µL pre-warmed (65 $^{o}$C) elution buffer added. This was centrifuged at

14000 rpm for 1 minute to elute DNA. Elution buffer was then used afterward to repeat this step.

**Polymerase Chain Reaction (PCR)**

The Polymerase chain reaction (PCR) was done with three pairs of degenerate primers. These were PTYv787/PTYc1121, AC1048/AV494 and PAR1c496/PAL1v1978 (Table 4). The reaction mixture contained 4 µL of premix, 1 µL of primer pairs, 12 µL of water and 10 µL of the DNA. The reaction was performed in Applied Biosystems 2720 thermal cycler PCR machine with the following reaction conditions: 94 ºC for 4minutes, 35 cycles of 94 ºC for 30 seconds with annealing temperature of 53 ºC for 1 minute, 72 ºC for 1 minute and final extension at 72 ºC for 10 minutes.

**Gel Electrophorosis**

Agarose gel at 1% was prepared and the quality of the DNA tested. The gel was prepared by weighing 1.14 of agarose powder. The solution was reweighed after heating and water added to make up to the original volume of 0.5 µL. About one to two drops of ethidium bromide was added to the solution. The final gel was allowed to cool and then poured into a casting electrophoresis with walls set in place and allowed to solidify.

After 35 minutes, the gel was transferred into 114 $cm^3$ electrophoresis tank with the walls oriented at the anode and filled with 1X TAE. This was done after the combs had been removed. Loading dye was mixed with 5 µL of each DNA and loaded into the walls using sterilized pipette. The DNA samples in electrophoresis tank were then allowed to run for 45 minutes at 100 V after the tank had been closed and connected to the electrical leads.

Afterwards, the gel was then taken out and visualized by using the gel documentary system.

**Table 4: Primers Used For PCR Detection of TYLCV**

| Primer Name | Primer sequence (5' – 3') | Expected band size (bp) | Reference |
|---|---|---|---|
| PARc1496<br>PAL1v1978 | F:GCATCTGCAGGCCCACATYGTCTTRGG<br>R:AATACTGCAGGGCTTYCTRTACATRGG | 1100-1400 | 1* |
| AV494<br>AC1048 | F-GCCCATGTATAGAAAGCCAAG<br>R:GGATTAGAGGCATGTGTACATG | 550-600 | 2* |
| PTYv787<br>PTYc1121 | F-GTTCGATAATGAGCCCAG<br>R-ATGTAACAGAAACTCATG | ~300 | 3* |

1* Rojas, Gilbertson, Russell, & Maxwell, (1993),
2* Wyatt & Brown. (1996),
3* Zhou *et al.* (2008)

**Climatic Data**

The mean temperature, rainfall, and mean humidity at both the coastal savannah and forest ecological zones, during the study were obtained from the Central Regional Meteorological Station for comparison (Appendix D).

**Data Analysis**

Data on percentage incidence and severity index; the whitefly population; and number of fruit were analyzed as described during the screening of tomato genotypes for resistance/tolerance to TYLCV disease

# CHAPTER FOUR

# RESULTS

## Farmers Awareness and Knowledge of TYLCV Disease

### Demographic Characteristics of Farmers

The background information of the respondent farmers is shown in Table 5. Out of the 150 tomato farmers interviewed, 79 farmers representing 52.7% were females, whereas 71 representing 47.3% were males.

Most of the farmers interviewed (39.3 %.) were between the ages of 51 and 60 years. This was followed by farmers (27.3%) in the age range of 61 and 70 years, and those between 41-50 years (13.3 %,). Farmers within the age range of 31 and 40 years constituted 12%, those in the age range of 21 and 30 years were 4.7%, whereas 3.3% fell between 10 and 20 years

Over 46.7% farmers of the had primary education, 7.3% (11 farmers) had Junior High School Education/Middle School, 2% (3 farmers) had Senior High School Education whereas most farmers (44%) had no formal education.

Generally, majority of the farmers (48.7%) had been in tomato production for more than 5 years. About 44% of the farmers had been in the production between 1 and 5 years whereas 7.3% had less than a year experience in tomato production.

Majority of the farmers (52.6%) had small farm holdings that were less than one acre (Table 5). About 33.6% had farm holdings between 1 and 2 acres, whereas the other 14% have farm holdings greater than 2.5 acres.

**Table 5: Household Characteristics of the Respondent Farmers**

| Variable | Frequency | Percentage |
|---|---|---|
| **a) Sex of the head of household** | | |
| Female | 79 | 52.7 |
| Male | 71 | 47.3 |
| Total | 150 | 100 |
| **b) Age of the head of household (years)** | | |
| 10-20 | 5 | 3.3 |
| 21-30 | 7 | 4.7 |
| 31- 40 | 18 | 12.0 |
| 41-50 | 59 | 39.3 |
| 51-60 | 20 | 13.3 |
| 61-71 | 41 | 27.3 |
| Total | 150 | 100 |
| **c) Education of head of household** | | |
| No formal education | 66 | 44 |
| Primary | 70 | 46.7 |
| J.H.S | 11 | 7.3 |
| S.H.S | 3 | 2 |
| Total | 150 | 100 |
| **d) Years in tomato production** | | |
| > 1 year | 11 | 7.3 |
| 1-5 years | 73 | 48.7 |
| < 5 years | 66 | 44.0 |
| Total | 150 | 100 |
| **e) Average land size** | | |
| > 1 acre | 79 | 52.6 |
| 1 -2 acres | 50 | 33.6 |
| < 2.5 acres | 21 | 14 |
| Total | 150 | 100 |

**Farm Characteristic and Agronomic Practices of Respondents**

Majority of the farmers (60.7%) practiced mixed cropping while 39.3% practiced monocropping (Table 6). Out of the 91 farmers that practiced mixed cropping, 42.8% intercropped with pepper, 26.4 intercropped with garden eggs, 18.7% intercropped with cassava and 12.1% intercropped with

beans and sweet potatoes. Only 59 farmers representing 39.3% practiced monocropping (Table 6).

Majority of farmers (48%) cultivated tomato in both major and minor seasons, 42.7% practiced major season farming only whereas 9.3% cultivated theirs in the minor season only (Table 6).

With regards to nursery practices, about 46.0% (69 farmers) only watered without any other cultural practices, 24.7% (37 farmers) applied a starter solution, 7.3% (11 farmers) covered the beds with a net to exclude whiteflies, 19.3% (29 farmers) applied insecticide, whereas 2.7% (4 farmers) burnt stubbles to sterilise the soil with heat before nursing their seeds (Table 6).

A large percentage of the farmers (44.7%) used improved variety in the cultivation of tomato, 29.3% (44 farmers) used the local variety while 26% (39 farmers) used exotic varieties (Table 6).

**Table 6: Farm Characteristic/Agronomic Practices of Respondents**

| Variable | Frequency | Percentages |
|---|---|---|
| Cropping systems | | |
| Mixed cropping | 91 | 60.7 |
| Mono cropping | 59 | 39.3 |
| Total | 150 | 100 |
| Intercrops | | |
| Pepper | 39 | 42.8 |
| Garden eggs | 24 | 26.4 |
| Cassava | 17 | 18.7 |
| Others (beans, sweet potatos) | 11 | 12.1 |
| Total | 91 | 100 |
| Time of planting | | |
| Minor | 14 | 9.3 |
| Major | 64 | 42.7 |
| Both | 72 | 48 |
| Total | 150 | 100 |
| Nursery practices | | |
| Covering | 11 | 7.3 |
| Fertilizer (Starter solution) | 30 | 24.7 |
| Watering | 69 | 46.0 |
| Insecticide | 29 | 19.3 |
| Heat treatment | 4 | 2.7 |
| | 150 | 100 |
| Varieties grown | | |
| Local | 44 | 29.3 |
| Improved | 67 | 44.3 |
| Exotic | 39 | 26 |
| Total | 150 | 100 |

**Farmers Awareness of TYLCV Disease**

The awareness and knowledge levels of farmers in terms of the existence, cause, growth stage at which TYLCV disease occurs and the management strategies adopted are presented in Table 7. From Table 7, it can be seen that 139 farmers representing 92.6 % had knowledge about the

existence of the disease while 28 farmers representing 18.7% were unaware of the existence of the disease.

Out of the 139 farmers who were aware of the disease, 80 (57.5%) did not know the cause of the disease whilst 59(42.5%) claimed they knew the cause of the disease (Table **7**). Among the 52 farmers who said they knew the cause of the disease, majority of them (61.0%) attributed it to unfavourable climatic conditions and, 23.7% to soil deficiency, whereas the rest (15.3%) indicated the disease was transmitted by whitefly.

In terms of the growth stage at which farmers observed the symptoms of the disease, 19 farmers representing 13.7% responded, they saw the symptoms of the disease during the seedling stage, 105 farmers accounting for 75.5% said they saw the disease at the flowering stage whereas 15 farmers representing 10.7% said it was at the fruiting stage.

Out of the 139 farmers, 23 representing 16.5% reported the disease causes total death of plants, 80 farmers representing 57.6% indicted the disease brings about yield losses and 36 farmers representing 25.9% said the disease results in flower loss (Table **7**).

With regards to yield losses attributed to TYLCV, 48.9% of the farmers said TYLCV causes more than 41% yield losses, 17.3% said the disease causes yield losses ranging between 31-40% while 14.4% and 12.9% said TYLCV caused yield losses between 21-30% and 10-20% respectively. Only 6.5% reported yield losses of less than 10% (Table 7).

Apart from TYLCV, *Fusarium wilt* was reported by 20% of the farmers to be a problem. Less than 10% of the farmers saw either fruit rot, root-knot or damping off as a problem (Table 7).

**Table 7: Farmers' Awareness of TYLCV Disease**

| Variable | Frequency | Percentages |
|---|---|---|
| Are you aware of TYLCV disease? | | |
| Yes | 139 | 92.6 |
| No | 11 | 7.3 |
| Total | 150 | 100 |
| Are you aware of the causes of TYLCV disease? | | |
| Yes | 59 | 42.5 |
| No | 80 | 57.5 |
| Total | 139 | 100 |
| If yes, state the causes | | |
| Unfavourable climatic conditions | 36 | 61.0 |
| Soil deficiency | 14 | 23.7 |
| Whitefly | 9 | 15.3 |
| Total | 59 | 100 |
| At what growth stage do you see the symptoms of TYLC disease in your tomato farm? | | |
| Seedling | 19 | 13.7 |
| Flowering | 105 | 75.5 |
| Fruiting | 15 | 10.7 |
| Total | 139 | 100 |
| How does the TYLCV disease affect your tomato crop? | | |
| Total plant death | 23 | 16.5 |
| Yield loss | 80 | 57.6 |
| Flower drop | 36 | 25.9 |
| Total | 139 | 100.0 |
| State the yield effect of the TYLCV disease on the tomato | | |
| Less than 10% | 9 | 6.5 |
| Between 10-20% | 18 | 12.9 |
| Between 21-30% | 20 | 14.4 |
| Between 31-40% | 24 | 17.3 |
| Greater than 41% | 68 | 48.9 |
| Total | 139 | 100.0 |
| Apart from TYLCV disease, what other diseases have you experienced in your farm? | | |
| Fusarium wilt | 30 | 20 |
| Fruit rot | 9 | 6.0 |
| Root knot | 9 | 6.0 |
| Damping off | 14 | 9.3 |
| Total | 62 | 100 |

**Management of TYLCV Disease by the Respondent Tomato Farmers**

Majority of the farmers (60.4%) said they control the TYLCV disease and the rest, 39.6% saying they do not control the disease (Table 8).

With respect to the management strategies adopted by farmers, 55.6 % (40 farmers) reported they use of pesticides, 43.1% (31 farmers) practiced roguing of diseased plants, whereas 15.3% (11 farmers) covered seedlings with mosquito nets at the nursery (Table 8).

**Table 8: Management of TYLCV Disease by the Respondent Tomato Farmers**

| Variable | Frequency | Percentage |
|---|---|---|
| Do you manage the TYLCV disease when it occurs in your field? | | |
| Yes | 84 | 60.4 |
| No | 55 | 39.6 |
| Total | 139 | 100 |
| | | |
| If no give reasons | | |
| High cost of insecticide | 18 | 32.7 |
| No effect after insecticide application | 29 | 52.7 |
| No reason | 8 | 14.6 |
| Total | 55 | 100.0 |
| | | |
| If yes, state your management method * | | |
| Application of insecticides | 40 | 55.6 |
| Covering of seedlings at the nursery with nets | 11 | 15.3 |
| Removal of infected plant (Roguing) | 31 | 43.1 |

*Respondents gave multiple answers

**Incidence of TYLCV Disease in the Selected Districts**

Table 9 shows the mean incidence of TYLCV disease recorded at the three districts surveyed. It can be seen that the disease was prevalent in all the districts. Analysis of variance showed significant difference in the incidences

of TYLCV disease recorded at the various districts ($F_{2,138}$ = 6.65; $P$< 0.01). The highest mean incidence was recorded at KEEA (52.9± 2.7%), but it was not significantly different from that of Effutu municipal (49.5 ±1.2%). It was however significantly higher than that of Mfantsiman district (42.1± 2.7%) ($P$< 0.01).

The ANOVA also revealed significant differences among the communities across the districts in respect of the mean incidences of TYLCV diseases recorded ($F_{14,126}$= 10.12; $P$< 0.01). At KEEA, the highest mean incidence of TYLCV disease was recorded at Dwabor (66.4± 5.1 %) which was significantly higher than all the other communities. However, incidences at Abeyee (48.4 ± 5.5%), Asanser (48.5 ± 6.5%), Dabir (50.8 ± 2.7%) and Ankwanda (50.3 ± 5.2%), were not significantly different from each other ($P$> 0.05).

At Effutu municipal, incidence of the TYLCV disease at Gyangyanadzi (64.7 ± 2.2%) was not significantly different from Gyahadzi (56.9 ± 4.0%) but significantly higher than the other communities in the municipality. Incidence of the disease recorded at Gyahadzi was not significantly different from that of Osubumpeyin (53.9 ± 2.7%) but significantly higher than Okyireko (47.8±2.2 %) and Nssuekyir (24.4±3.5%).

In the Mfantseman district, Nsanfo (55.5±3.9%) had the highest incidence which was significantly higher than other communities. However, incidences at Kwesiransah (32.3± 2.3%), Baafikrom (37.8 ± 3.4 %), Ehyerew (42.2 ± 4.5%) and Obidan (42.9 ±3.1%) were the same.

**Table 9: Mean Incidence of TYLC Disease Recorded for Effutu Municipal, KEEA and Mfantseman Districts in the Central Region**

| Districts | Towns | Mean incidence* (%) | Mean incidence* (%) |
|---|---|---|---|
| Effutu | Nssuekyir | 24.4 ±3.5f | 49.5 ±1.19 ab |
| | Okyireko | 47.8 ±2.2 de | |
| | Osubumpeyin | 53.9 ± 2.7 cd | |
| | Gyahadzi | 56.9 ± 4.0 bc | |
| | Gyangyanadze | 64.7 ± 2.2 ab | |
| Mfantseman | Kwesiransah | 32.3± 2.3fg | 42.1 ± 2.7 b |
| | Baafikrom | 37.8 ± 3.4ef | |
| | Ehyerew | 42.2 ± 4.5def | |
| | Obidan | 42.9 ±3.1de | |
| | Nsanfo | 55.5 ± 3.9abc | |
| KEEA | Abeyee | 48.4 ± 5.5 bcd | 52.9 ± 2.7 a |
| | Asanser | 48.5 ± 6.5bcd | |
| | Ankwanda | 50.3 ± 5.2bcd | |
| | Dabire | 50.8 ± 2.7bcd | |
| | Dwabor | 66.35 ± 5.1 a | |
| Mean | | 48.13±1.3 | 48.7 ± 1.4 |
| $Lsd_{(0.05)}$ | | 9.9 | 8.8 |

Means in the same column bearing the same letters are not significantly different from each other ($P < 0.05$)
*Mean ± Standard error

**Mean Severity Indices of TYLCV Disease Recorded for Five Communities Each at Three Districts in the Central Region**

Table 10 shows the mean severity indices of TYLCV disease recorded at the three districts surveyed. Varying levels of severity of TYLCV disease occurred among tomato farms in the three districts.ANOVA showed significant difference in the severity of TYLCV disease recorded at the various districts ($F_{2,138}$ = 6.83; $P$< 0.01). The highest mean severity was recorded at KEEA (26. 9±1.2) which was not significantly different from that of Effutu municipal (25.3±0.9%) but significantly higher than that of Mfantseman district (21.4±0.8%) ($P$< 0.05).

The ANOVA also revealed a significant difference among the communities across the districts in respect of the mean severity indices of TYLCV diseases recorded ($F_{14,126}$ = 11.07; $P$< 0.05). At KEEA, the highest mean severity index of TYLCV disease was recorded at Dwabor (34.57±5.1%) which was significantly higher than all the other communities. However mean severity recorded at Abeyee (24.7±2.4%), Asanser (23.0 ± 5.5%), Dabir (25.4±2.7%) and Ankwanda (26.7±1.6%) were not significantly different from each other.

At Effutu municipal, severity index of TYLCV disease recorded for Gyangyanadzi (32.2± 2.2 %) was not significantly different from Gyahadzi (28.1± 4.0 %) but significantly higher than that of the other communities in the district. The mean severity index recorded for Gyahadzi was however not significantly different from Osubumpayin (27.0 ± 2.7 %) and Okyireko (25.1 ± 2.1 %) but significantly higher than Nssuekyir which had the least severity index of 14.2 ± 3.2 %.

Nsanfo in the Mfantseman district had the highest severity index of 31.2 ± 3.9 % which was significantly higher than all the other communities. The mean severity index recorded for Obidan (21.7 ± 3.1 %) was not significantly different from that of Ehyerew (21.0 ± 4.5 %) but significantly higher than Kwesiransah (15.5 ± 2.3 %) and Baafikrom (17.6 ± 3.4 %) ($P < 0.05$) which did not differ significantly from each other (Table 10).

**Table 10: Mean Severity Indices of TYLCVDisease Recorded for Five Communities Each of the Three Districts in the Central Region**

| Districts | Towns | Mean severity* (%) | Mean severity* (%) |
|---|---|---|---|
| Effutu | Nssuekyir | 14.16 ± 3.2 f | 25.3 ± 0.9 a |
| | Okyireko | 25.07 ± 2.1 cde | |
| | Osubumpeyin | 26.96 ± 2.7 cd | |
| | Gyahadzi | 28.08 ± 4.0 bc | |
| | Gyangyanadze | 32.19 ± 2.2 ab | |
| Mfantseman | Kwesiransah | 15.54 ± 2.3 f | 21.4± 0.8 b |
| | Baafikrom | 17.61 ± 3.4 ef | |
| | Ehyerew | 21.04 ± 4.5 de | |
| | Obidan | 21.69 ± 3.1 de | |
| | Nsanfo | 31.16 ± 3.9 abc | |
| KEEA | Asanser | 23.01 ± 5. 5 cd | 26.9 ± 1.2 a |
| | Abeyee | 24.74 ± 2.4 bcd | |
| | Ankwanda | 26.72 ± 1.6 bcd | |
| | Dabire | 25.39 ± 2.7 bcd | |
| | Dwabor | 34.57 ± 5.1 a | |
| Total | | 24.53 ± 1.4 | 24.53 ± 0.6 |
| $Lsd_{(0.005)}$ | | 5.0 | 3.0 |

Means in the same column bearing same letters are not significantly different from each other ($P < 0.05$)
*Mean ± Standard

**Field Screening of Thirty Six Tomato Genotypes for Resistance to TYLCV Disease**

## Incidence of TYLCV disease

Substantial variability in disease incidence was found among the 36 tomato genotypes tested (Table 11). Disease incidence varied from 0 to 91.6% for the 30 DAT, from 19.5 to 100% for the 45 DAT and from 20.1 to 100% for the 60 DAT. The ANOVA on the mean incidence of TYLCV disease at 30DAT showed significant difference among the genotypes ($F_{35,\ 70}$ = 4.00; $P$<0.05). There was no incidence of TYLCV disease in genotypes K005, K100, K042 and K116 at 30 DAT, whereas significantly different levels of incidences were recorded for the other genotypes (Table 11).

At 45 DAT, all the thirty six tomato genotypes showed symptoms of TYLCV disease. ANOVA however, showed significant differences among the genotypes in terms of the levels of incidence ($F_{35,\ 70}$ = 2.79; $P$< 0.05). Similarly, at 60 DAT, all the genotypes showed symptoms of TYLCV disease but at significantly different levels of incidences ($F_{35,\ 70}$=3.00; $P$<0.05).

## Severity of TYLCV Disease

Table 12 shows the severity of TYLCV disease in the thirty six tomato genotypes tested. All the genotypes showed varying levels of susceptibility to TYLCV at the various sampling dates of 30, 45 and 60 DAT (Table 12). Mean disease severity scores varied from 0.0 to 2.3 for the 30 DAT and from 1.0 to 3.7 for both the 45 DAT and 60 DAT.

ANOVA on the mean severity of TYLCV disease in the genotypes at 30 DAT showed significant differences among them ($F_{35,70}$ = 57.27; $P$< 0.05).

**Table 11: Mean Incidences of TYLCV Disease on 36 Tomato Genotypes**

**30, 45 and 60 Days after Transplanting (DAT)**

| | Mean disease incidence (%) at various sampling date | | |
|---|---|---|---|
| Genotypes | 30DAT | 45DAT | 60DAT |
| K005 | 0 (0.0)m | 46.9 (53.3) dfhi | 46.9 (53.3) dfg |
| K006 | 30 (25.0) defghijkl | 81.1 (97.6) bc | 81.1 (97.6) bc |
| K011 | 30 (25.0) defghijklm | 68.1(86.1)bdfhi | 68.1 (86.1) bdfg |
| K027 | 55.4 (67.8)abcd | 72.3(90.7) bdfg | 72.3 (90.8) bdfg |
| K042 | 0 (0.0)m | 26.2 (19.5) i | 39.2 (40.0) g |
| K045 | 8.9 (2.4)lm | 33.8(31.0) hi | 42.7 (46.0) fg |
| K050 | 13.1 (5.1)jklm | 68.9 (87.0) bdfhi | 68.9 (87.0) bdfg |
| K083 | 73.1 (91.6)a | 90 (100.0) a | 90 (100.0) a |
| K084 | 46.9 (53.3)abcdefg | 55.4(67.7) bdfhi | 55.4 (67.8) bdfg |
| K087 | 59.2 (73.9)abc | 90 (100.0) bdfhi | 90 (100.0) a |
| K088 | 38.9 (39.4)bcdefghijk | 72.3 (90.8) bdfg | 72.3 (90.7) bdfg |
| K098 | 60 (75.0)ab | 90 (100.0) a | 90 (100.0) a |
| K100 | 0 (0.0)m | 26.6 (20.1) i | 26.6 (20.1) g |
| K106 | 21.9 (13.9)fghijklm | 72.3 (90.8) bdfg | 72.3 (90.8) bdfg |
| K116 | 0(0.0)m | 38.9(39.4) fhi | 46.9 (53.3) dfg |
| K124 | 38.1 (38.1)bcdefghijk | 76.9(94.9) bde | 76.9 (94.9) bde |
| K138 | 38.1 (38.1)bcdefghijk | 81.1(97.61) bc | 81.1 (97.6) bc |
| K144 | 25.8 (18.9)defghijklm | 76.9(94.86) bde | 76.9 (94.9) bde |
| K146 | 59.2 (73.8)abc | 90(100.00) a | 90 (100.0) a |
| K186 | 42.7 (50.0)bcdefghi | 81.1(97.61) bc | 81.1 (97.6) bc |
| K188 | 38.9 (39.4)bcdefghijk | 47.3(54.01) dfhi | 47.3 (54.0) dfg |
| K190 | 8.9 (2.4)lm | 43.1(46.69) dfhi | 43.1 (46.7) fg |
| K191 | 17.7 (9.4)fghijklm | 60(75.00) bdfhi | 55.8 (68.4) bdfg |
| K194 | 21.9 (13.9)efghijklm | 72.3 (90.8) bdfg | 72.3 (90.8) bdfg |
| K197 | 47.3 (54.0)abcdef | 60 (75.0) bdfhi | 60 (75.0) bdfg |
| K200 | 38.9 (39.4)bcdefghijk | 60 (75.0) bdfhi | 60 (75.0) bdfg |
| K202 | 51.1 (60.6)abcde | 90 (100.0) a | 90 (100.0) a |
| K205A | 16.9 (8. 5)hijklm | 51.9 (61.9) bdfhi | 51.9 (61.9) dfg |
| K205B | 39.2 (40.0)bcdefghij | 68.1 (86.1) bdfhi | 68.1 (86.1) bdfg |
| K213 | 0.0 (0.0)m | 30 (25.0) hi | 30 (25.0) g |
| K214 | 43.1 (46.7)bcdefgh | 90 (100.0) a | 90 (100.0) a |
| LV | 42.7 (46.0)bcdefgh | 60 (75.0) bdfhi | 68.9 (87.0) bdfg |
| P000 | 60 (75.0)ab | 73.1(91.6) bdfg | 73.1 (91.6) bdfg |
| P074 | 35 (32.9)bcdefghijkl | 64.2 (81.1) bdfhi | 64.2 (81.1) bdfg |
| P077 | 51.1 (60.6)abcde | 55.4 (67.8) bdfhi | 55.4 (67.8) bdfg |
| P085 | 38.9 (39.4)bcdefghijk | 68.1 (86.1) bdfhi | 68.1 (86.1) bdfg |
| $Lsd_{(0.05)}$ | 27.5 | 32.0 | 32.0 |

Values in parentheses are the back transformed or actual values. Values with same alphabet are significantly the same. Means in the same column bearing same letters are not significantly different from each other ($P < 0.05$)

From Table 12, genotypes K213, K005, K042, K100, K116 at 30 DAT, had mean severity score of 0, indicating they were not infected by TYLCV. The other 31 genotypes were however infected by the virus to significantly varying degrees. Genotypes K083 had the highest severity of 2.3 which was significantly.different ($P < 0.05$) from all the other genotypes.

At 45DAT, ANOVA on the severity of TYLCV disease showed significant difference between genotypes ($F_{35, 70} = 32.16$; $P< 0.05$). Genotypes K213, K005, K042, K100, and K116, showed mild infection with severity scores of 1.0, 1.2, 1.2, 1.2 and 1.3 respectively, which were significantly lower ($P< 0.05$) than the other genotypes. K146 had the highest severity score of 3.7 which was not significantly different from K098, K083, K144, K027, K186, K202, K087 and K124 ($P <0.05$).

At 60 DAT, ANOVA showed significant differences between the genotypes with respect to their mean severity of TYLCV disease ($F_{35, 70} = 28.36$; $P<0.05$). Genotypes K213, K005, K042, K100, and K116 still showed mild symptoms with severity scores ranging between 1.1 and 1.2 whereas the others showed moderate to severe symptoms. Genotype K202 had the highest severity score of 3.6 which was not significantly different from K098, K146, K214, K027 and K186 ($P <0.05$).

In all, 22.2% of the genotypes (K027, K083, K186, K087, K098, K146, K202, and K214) after the screening (60 DAT) had severity scores of greater than 3 (between 3.3 and 3.6), indicating that they were highly susceptible to TYLCV infection. Genotypes K005, K116, K100, K042 and K213 representing 13.9% at the end of the screening had severity scores of less than 2 (between 1 and 1.2) showing mild symptom (MS) and were

considered to have field tolerance. The other twenty three genotypes representing 66.7% had severity scores of ranging between 2.0 and 2.7, showing moderate symptom after 60 DAT.

**Whitefly Population**

The tomato genotypes showed varying degrees of infestations with the whitefly vector at various sampling dates of 30, 45 and 60 DAT (Table 13). The mean whitefly population per plant varied between 2.5 to 9.5 for the 30 DAT, between 0.6 and 4.8 for the 45 DAT, and between 0.5 and 4.3 for the 60 DAT. This indicates that the whitefly population on the tomato genotypes declined with age.

The ANOVA showed that significant differences exist between the genotypes at 30 DAT ($F_{35,\ 70}$ = 1.98; $P$< 0.05). The highest population was recorded on K205A (9.5) which was not significantly different from that of K146, K098, K144, K042, K200, P077, K191, P000, K100, K197, P085, K138 and K116 but was significantly different from the rest of the genotypes ($P$< 0.05).

At 45 DAT, ANOVA revealed significant difference among the genotypes ($F_{35,\ 70\ =}$ 1.45; $P$< 0.05). Genotype K186 had the lowest mean population of 0.9 which was not significantly different($P < 0.05$) from genotypes K186, K213, K084, K100, P074, K087, K190, K200, K106, K011, LV, K202, P077, K027, K088, K144, K194, K098, K006, K042, K045, K124, K146 and K205B but differed significantly ($P < 0.05$) from the rest of the genotypes.

No significant differences in whitefly population existed among the genotypes at 60 DAT ($F_{35, 70} = 0.82$; $P > 0.05$). Genotype LV had the highest mean population of 2.9 per plant whereas K006 had the lowest (1.0 per plant).

**Mean Number of Fruit and Mean Fruit Weight (t ha$^{-1}$)**

Table 14 shows the mean number of fruits per plant produced by each of the 36 tomato genotypes screened. The ANOVA revealed significance differences between the genotypes ($F_{35, 70} = 10.2$; $P < 0.05$). The highest number of fruits per plant was recorded for genotype K100 which was significantly different from all the other genotypes. Genotype K202 had the lowest number of fruits per plant (3.8) which was not significantly different from that of genotype K200, K087, K146, K190, P000, K214, K006, P085, K213, K083, K011, K205B, K084, K074, K191 and K186 but significantly different from the other genotypes.

ANOVA also showed significant difference among the genotypes with respect to fruit yield (t ha$^{-1}$) recorded ($F_{35,70} = 17.8$; $P < 0.05$) (Table 14). Genotype K100 had the highest mean yield of 12.6 t ha$^{-1}$ which was not significantly different from genotypes K116, K005, and K042 but significantly higher than all the other genotypes ($P < 0.05$). Genotype K202 had the lowest yield of 2.2 t ha$^{-1}$which was not significantly different from genotypes K083, K213, K085, K087, K188, K191, P077, K205B, K190, K146, K138, P074, K200, K106, K186, K098, P000, K214, K006, K197, K214, K045, K084 and K124.

**Table 12: Mean Severity of TYLCV Disease on 36 Tomato Genotypes**

| | Mean disease severity at various sampling dates | | | |
|---|---|---|---|---|
| Genotypes | 30DAT | 45DAT | 60DAT | Disease reaction |
| K005 | 0.0 (0.0) i | 6.3 (1.2) lm | 6.1(1.1) i | MS |
| K006 | 5.9 (1.1) h | 8.9 (2.4) cef | 9.0 (2.5) cef | MoS |
| K011 | 6.6 (1.3) cegh | 8.7 (2.3) cef | 9.5 (2.7) b | MoS |
| K027 | 7.4 (1.7) cd | 10.6 (3.4) a | 10.6 (3.4) a | SS |
| K042 | 0.0 (0.0) i | 6.3 (1.2) lm | 5.9 (1.1) i | MS |
| K045 | 6.7 (1.4) cegh | 7.6 (2.0) j | 7.9 (2.0) h | MoS |
| K050 | 6.9 (1.5) cegh | 8.3 (2.1) gij | 9.0 (2.5) cef | MoS |
| K083 | 8.7 (2.3) a | 10.5 (3.3) a | 10.7 (3.5) a | SS |
| K084 | 7.1 (1.5) cef | 8.8 (2.4) cef | 8.7 (2.3) cegh | MoS |
| K087 | 7.6 (1.7) b | 10.7 (3.5) a | 10.5 (3.3) a | SS |
| K088 | 7.1 (1.5) cef | 9.3 (2.6) cd | 8.5 (2.2) gh | MoS |
| K098 | 6.6 (1.3) cegh | 10.5 (3.3) a | 10.4 (3.2) a | SS |
| K100 | 0.0 (0.0) i | 6.3 (1.2) lm | 6.3 (1.2) i | MS |
| K106 | 6.4 (1.3) cegh | 8.7 (2.3) cef | 9.0 (2.4) cef | MoS |
| K116 | 0.0 (0.0) i | 6.5 (1.3) lk | 6.3 (1.2) i | MS |
| K124 | 6.7 (1.4) cegh | 10.8 (3.5) a | 8.9 (2.4) cef | MoS |
| K138 | 7.1 (1.5) cef | 8.4 (2.1) gh | 9.0 (2.5) cef | MoS |
| K144 | 7.3 (1.6) cd | 10.6 (3.4) a | 9.0 (2.5) cef | MoS |
| K146 | 6.8 (1.4) cegh | 11.1 (3.7) a | 10.5 (3.3)cef | SS |
| K186 | 6.9 (1.5) cegh | 10.7 (3.5) a | 10.7 (3.5) a | SS |
| K188 | 7.2 (1.6) cef | 8.3 (2.1) gij | 8.5 (2.2) egh | MoS |
| K190 | 5.9 (1.1) h | 7.7 (1.8) ij | 8.7 (2.3) cegh | MoS |
| K191 | 6.1 (1.1) gh | 8.9 (2.4) cef | 8.5 (2.2) egh | MoS |
| K194 | 6.3 (1.2) egh | 9.3 (2.6) cd | 8.8 (2.3) cef | MoS |
| K197 | 7.1 (1.5) cef | 8.7 (2.3) cef | 9.4 (2.7) cd | MoS |
| K200 | 6.8 (1.4) cegh | 9.3 (2.6) cd | 9.0 (2.5) cef | MoS |
| K202 | 7.6 (1.7) b | 10.7 (3.5) a | 10.7 (3.5) a | SS |
| K205a | 6.4 (1.3) cegh | 8.9 (2.4) cef | 8.9 (2.4) cef | MoS |
| K205B | 6.8 (1.4) cegh | 9.4 (2.7) b | 9.1 (2.5) ef | MoS |
| K213 | 0.0 (0.0) i | 5.7 (1.0) m | 5.7 (1.0) i | MS |
| K214 | 6.9 (1.5) cegh | 8.8 (2.3) cef | 10.6 (3.4) a | SS |
| LV | 7.1 (1.5) cef | 8.6(2.2) cef | 8.6 (2.2) egh | MoS |
| P000 | 6.8 (1.4) cegh | 8.7 (2.3) cef | 9.4 (2.7) cd | MoS |
| P074 | 6.9 (1.5) cegh | 8.5 (2.2) ef | 8.4 (2.1)gh | MoS |
| P077 | 6.4 (1.2) egh | 8.6 (2.2) cef | 8.5 (2.2) gh | MoS |
| P085 | 6.8 (1.4) cegh | 8.9 (2.4) cef | 8.9 (2.4) cef | Mos |
| $Lsd_{(0.05)}$ | 0.9 | 0.7 | 0.7 | |

0=No Symptom (NS) 1=Mild Symptom (MS) 2=Moderate Symptom (MoS) 3=Severe Symptom (SS) 4= Very Severe Symptom (VSS).Values in parentheses are the back transformed or actual valuesusing angular transformation.Values with same alphabet are significantly the same.Means in the same column bearing same letters are not significantly different from each other ($P < 0.05$). Severity scores are based on the back-transformed values

**Table 13: Mean Population of Whitefly on 36 Tomato Genotypes Recorded From 30-60 DAT**

| | Mean whitefly population at various sampling dates | | |
|---|---|---|---|
| Genotype | 30 DAT | 45 DAT | 60 DAT |
| K005 | 1.9 (3.3) hjk | 2.0 (3.6) bde | 1.6 (2.0) bc |
| K006 | 1.7 (2.5) k | 1.9 (3.00) bdfg | 1.0 (0.5) c |
| K011 | 1.9 (3.3) hjk | 1.5 (1.6) bdfg | 1.5 (1.6) bc |
| K027 | 2.1 (4.0) fhjk | 1.8 (2.6) bdfg | 1.2 (1.0) bc |
| K042 | 2.4 (5.2) bdhjk | 1.9 (3.2) bdfg | 1.8 (2.8) bc |
| K045 | 2.0 (3.7) hjk | 1.9 (3.3) bdfg | 1.9 (3.0) bc |
| K050 | 1.8 (2.6) jk | 2.9 (3.8) bde | 1.9 (3.0) bc |
| K083 | 1.9 (3.2) hjk | 2.0 (3.4) bde | 2.1 (4.0) a |
| K084 | 2.0 (3.3) hjk | 1.2 (0.9) dfg | 1.4 (1.4) bc |
| K087 | 2.0 (3.4) hjk | 1.4 (1.3) bdfg | 1.4 (1.3) bc |
| K088 | 2.1 (4.0) fhjk | 1.8 (2.6) bdfg | 1.5 (1.9) bc |
| K098 | 2.3 (5.0) bdfhjk | 1.9 (3.0) bdfg | 1.3 (1.3) bc |
| K100 | 2.6 (6.4) bdfhjk | 1.2 (0.9) dfg | 1.3 (1.3) bc |
| K106 | 2.0 (3.7) hjk | 1.4 (1.4) bdfg | 1.0 (0.5) c |
| K116 | 3.1 (8.8) bc | 2.2 (4.5) bc | 1.7 (2. 5) bc |
| K124 | 1.9 (3.0) jk | 1.9 (3.3) bdfg | 1.8 (2.7) bc |
| K138 | 3.0 (8. 6) bde | 2.1 (3.9) bde | 1.3 (1.1) bc |
| K144 | 2.3 (5.0) bdfhjk | 1.8 (2.8) bdfg | 1.4 (1.4) bc |
| K146 | 2.3 (4.9) bdfhjk | 1.9 (3.3) bdfg | 1.3 (1. 1) bc |
| K186 | 1.9 (3.2) hjk | 0.9 (0.3) g | 1.5 (1.7) bc |
| K188 | 2.1 (4.0) fhjk | 2.0 (3.6) bde | 1.7 (2.3) bc |
| K190 | 2.0 (3.3) hjk | 1.4 (1. 3) bdfg | 1.5 (1.7) bc |
| K191 | 2.5 (5.9) bdfhjk | 2.2 (4.3) bc | 1.3 (1.2) bc |
| K194 | 2.2 (4.26) dfhjk | 1.8 (2.8) bdfg | 1.4 (1.4) bc |
| K197 | 2.7 (6.7) bdfhi | 2.1 (3.8)bde | 1.7 (2.5) bc |
| K200 | 2.5 (5. 6) bdfhjk | 1.4 (1.3) bdfg | 1.3 (1.2) bc |
| K202 | 2.2 (4.3) dfhjk | 1.6 (2.2) bdfg | 1.5 (1.7) bc |
| K205A | 3.2 (9. 5) a | 2.0 (3.6) bde | 1.5 (1.7) bc |
| K205B | 2.2 (4.3) dfhjk | 1.9 (3.3) bdfg | 1.5 (1.9) bc |
| K213 | 2.0 (3.6) hjk | 1.1 (0.6) fg | 1.2 (0.9) bc |
| K214 | 2.2 (4.3) dfhjk | 2.1 (4.0) bde | 1.6 (1.9) bc |
| LV | 1.8 (2.7) jk | 1.6 (2.0) bdfg | 2.2 (4.3) a |
| P000 | 2.6 (6.3) bdfhjk | 2.3 (4.8) a | 1.9 (3.3) bc |
| P074 | 2.2 (4.2) dfhjk | 1.3 (1.2) bdfg | 1.2 (0.9) bc |
| P077 | 2.5 (5.8) bdfhjk | 1.7 (2.2) bdfg | 1.7 (2.42) bc |
| P085 | 2.8 (7.4) bdfg | 2.2 (4.4) bc | 1.7 (2.32) bc |
| $Lsd_{(0.05)}$ | 0.7 | 0.9 | 0.9 |

Values in parentheses are the back transformed or actual values using square root transformation.Values with same alphabet are significantly the same. Means in the same column bearing same letters are not significantly different from each other ($P < 0.05$)

**Relationships between Variables**

In order to ascertain the relationships between different variables that measure the TYLCV disease, the Pearson coefficient of correlation were estimated. Correlation among the variables measuring the disease was positive and significant (Table 15). Disease incidences recorded at 30, 45 and 60 DAT were significantly and positively correlated with the disease severities scores at 30, 45 and 60 DAT ($0.51 \geq r \leq 0.98$; $P < 0.01$).

Fruit yield negatively and significantly correlated with disease severity at 30 DAT ($r = -0.18$; $P < 0.01$), 45 DAT ($r = -0.17$; $P < 0.01$) and 60 DAT ($r = -0.24$; $P < 0.01$). Whitefly population positively and significantly correlated with severity at 30 DAT ($r = 0.86$; $P < 0.01$), 45DAT ($r = 0.91$; $P < 0.01$) and 60 DAT ($r = 0.67$; $P < 0.01$) (Table 15).

**Table 14 Mean Numbers of Fruits per Plant and Mean Fruits Weight (t/ha)**

| Genotypes | Mean number of fruits | Yield (t/ha) |
|---|---|---|
| K005 | 8.9 (79.0) ab | 11.8 a |
| K006 | 4.6 (20.6) hij | 4.8 cdef |
| K011 | 5.2 (26.2) fghij | 5.6 cd |
| K027 | 6.4 (39.9) cdefg | 9.0 b |
| K042 | 10.2 (103.0) a | 10.8 a |
| K045 | 6.6 (43.1) cdef | 5.0 cde |
| K050 | 5.7 (31.9) defghi | 5.6 cd |
| K083 | 5.1(25.1) fghij$_1$ | 2.4 f |
| K084 | 5.4 (28.7) efghij | 5.0 cde |
| K087 | 4.2 (17.5) ij | 2.8 ef |
| K088 | 5.9 (33.8) defghi | 5.8 c |
| K098 | 7.0 (47.8) cde | 4.4 cdef |
| K100 | 10.6 (111.6) a | 12.6 a |
| K106 | 7.4 (53.9) bcd | 4.0 cdef |
| K116 | 9.4 (88.3) ab | 11.8 a |
| K124 | 6.3 (39.0) cdefg | 5.0 cde |
| K138 | 6.0 (35.5) defgh | 3.6 cdef |
| K144 | 8.0 (63.3) bc | 5.8 c |
| K146 | 4.4 (18.7) hij | 3.4 cdef |
| K186 | 5.5 (30.1) efghij | 4.0 cdef |
| K188 | 6.4 (40.8) cdefg | 3.0 def |
| K190 | 4.4(18.9) hij | 3.4 cdef |
| K191 | 5.5 (29.3) efghij | 3.2 cdef |
| K194 | 6.8 (46.3) cdef | 4.6 cdef |
| K197 | 6.2 (37.4) defg | 4.8 cdef |
| K200 | 4.1 (16.5) ij | 4.0 cdef |
| K202 | 3.8 (14.1) j | 2.2 f |
| K205a | 6.1 (36.6) defgh | 5.8 c |
| K205B | 5.2 (27.0) fghij | 3.4 cdef |
| K213 | 4.8 (22.5) ghij | 2.6 ef |
| K214 | 4.5 (19.9) hij | 4.8 cdef |
| LV | 5.8 (33.6) defghij | 5.2 cde |
| P000 | 4.5 (19.6) hij | 4.4 cdef |
| P074 | 5.4 (29.1) efghij | 3.6 cdef |
| P077 | 5.7 (32.2) defghi | 3.2 cdef |
| P085 | 4.7 (21.8) ghij | 2.6 ef |
| $Lsd_{(0.05)}$ | 1.7 | 2.6 |

Values in parentheses are the back transformed or actual values and are square root transformed means. Values with same alphabet are significantly the same. Means in the same column bearing same letters are not significantly different from each other ($P < 0.05$)

**Table 15: Correlation between Different Variables**

| | Severity 30 | Severity 45 | Severity 60 | Incidence 30 | Incidence 45 | Incidence 60 | Whitefly 30 | Whitefly 45 | Whitefly 60 | Yield |
|---|---|---|---|---|---|---|---|---|---|---|
| Severity 30 | 1 | | | | | | | | | |
| Severity 45 | 0.61** | 1 | | | | | | | | |
| Severity 60 | 0.53** | 0.76** | 1 | | | | | | | |
| Incidence 30 | 0.84** | 0.66** | 0.53** | 1 | | | | | | |
| Incidence 45 | 0.51** | 0.79** | 0.60** | 0.59** | 1 | | | | | |
| Incidence 60 | 0.51** | 0.81** | 0.59** | 0.60** | 0.98** | 1 | | | | |
| Whitefly 30 | 0.86** | 0.61** | 0.45** | 0.93** | 0.49** | 0.52** | 1 | | | |
| Whitefly 45 | 0.63** | 0.91** | 0.69** | 0.67** | 0.80** | 0.81** | 0.61** | 1 | | |
| Whitefly 60 | 0.59** | 0.90** | 0.67** | 0.66** | 0.80** | 0.81** | 0.60** | 0.97** | 1 | |
| Yield | -0.18 | -0.17 | -0.24* | -0.12 | -0.26** | -0.21* | -0.04 | -0.09 | -0.07 | 1 |

** significant at $P < 0.01$
* significant at $P < 0.05$

**Resistance/Reaction of Selected Tomato Genotypes to TYLCV Infection at Forest and Coastal Savannah Agro Ecological Zones**

**Incidenceof TYLCV Disease**

The incidence of TYLCV disease on tomato genotypes at both UCC (coastal savannah zone) and Asuansi (forest zone) recorded at different sampling dates is shown in Table 16. Generally, disease incidence was higher at Asuansi than at UCC at each sampling dates of 30, 45 and 60 DAT, indicating that the disease pressure was higher in Asuansi than at UCC. Also, the average incidence at both locations increased from 30 DAT to 60 DAT, indicating that on the average, more plants got infected with time at both locations.

ANOVA revealed that Asuansi had on average significantly higher incidence than UCC at both 30 and 45 DAT ($P< 0.05$) but did not differ significantly from each other at 60 DAT ($P> 0.05$).

The ANOVA also showed a significant interaction between location and tomato genotypes at all the sampling dates of 30, 45 and 60 DAT ($P< 0.05$), indicating that the incidence of TYLCV disease at both locations differed among the tomato genotypes (Table 16). At 30 DAT incidence of TYLCV disease on genotypes CV, K005 and K100 were significantly higher at Asuansi than at UCC ($P< 0.05$). However, disease incidence on genotypes K027, K042, K116 and K213 did not differ at the two locations ($P> 0.05$). At 45 DAT, incidence of TYLCV disease on K005, K042, K100 and K213 were significantly different between the two locations ($P< 0.05$). However the disease incidence on genotypes CV, K116 and K027 were not significantly different between the two locations ($P> 0.05$). The incidence of TYLCV

disease on K213 differed between Asuansi and UCC whereas the disease incidence on the other genotypes did not differ between the two locations.

**Table 16: Mean Incidence of TYLCV Disease in U.C.C and Asuansi**

| | Incidence of TYLCV (%) at indicated DAT and locations | | | | | |
|---|---|---|---|---|---|---|
| | 30 DAT | | 45DAT | | 60DAT | |
| Genotypes | UCC | Asuansi | UCC | Asuansi | UCC | Asuansi |
| CV | 35.0 (32.9) efh | 55.4 (67.8) cd | 51.1 (60.6) cdfh | 59 (73.5) cd | 46.9 (53.3) bc | 55.0 (67.1) b |
| K005 | 17.7 (9.2) i | 39.2 (39.9) efh | 26.6 (20.0) k | 55 (67.1) cdf | 35.0 (32.9) bceg | 38.9 (39.4) bce |
| K027 | 68.1 (86.1) ab | 81.1 (97.6) a | 90 (100.0) ab | 90 (100.0) a | 90.0 (100.0) a | 81.1 (97.6) a |
| K042 | 35.0 (32.9) efh | 47.3 (54.0) cdf | 35 (32.9) gh | 59.2 (73.8) cd | 39.2 (39.9) bce | 30.0 (25.0) deg |
| K100 | 17.7 (9.2) i | 43.1 (46.7) efh | 30.8 (26.2) ij | 55.8 (68.4) cdf | 30.8 (26.2) deg | 21.9 (13.9) fg |
| K116 | 30.8 (26.2) efh | 38.9 (39.4) efh | 35 (32.9) ghj | 38.9 (39.4) efh | 43.1 (46.7) bc | 38.9 (39.4) bce |
| K202 | 81.1 (97.6) a | 90.0 (100.0) a | 73.1 (91.5) a | 90 (100.0) a | 90.0 (100.0) a | 90.0 (100.0) a |
| K213 | 21.9 (13.9) gh | 26.6 (20.0) gh | 30.8 (26.2) ij | 26.6 (20.0) k | 30.8 (26.2) deg | 17.7 (9.2) h |
| Mean | 38.4 (38.6) b | 52.7 (63.3) a | 46.5 (52.6) b | 59.3 (73.9) a | 50.7 (59.9) a | 46.7 (53.0) a |

$Lsd_{(0.05)}$ (30 DAT): 22.3; $Lsd_{(0.05}$ (45 DAT); 20.3; $Lsd_{(0.05}$ (60 DAT): 17.9

Values in parentheses are the back transformed or actual values using angular transformation
Values with same alphabet are significantly the same
Means in the same column bearing same letters are not significantly different from each other ($P < 0.05$)

**Mean Severity of TYLCVDisease**

Table 17 shows the mean scores of TYLCV disease severity on eight tomato genotypes at both Asuansi and UCC experimental sites at different sampling dates of 30, 45 and 60 DAT. Generally, disease severity was higher at Asuansi than at UCC at all three sampling dates. However, ANOVA did not indicate significant difference between the two locations ($P > 0.05$).

The ANOVA on the mean disease severity scores showed significant interaction effects between location and tomato genotypes at all the sampling dates ($P < 0.05$). Genotypes K005, K100 and K213 showed mild symptoms at the two locations at 30, 45 and 60 DAT with the mean severity scores ranging between 1.1 and 1.6. However, genotype K042 showed mild symptoms at UCC with mean severity scores of 1.3, 1.5 and 1.6 but moderate symptoms at Asuansi with mean scores of 2.1, 2.3 and 2.3 at 30, 45 and 60 DAT respectively. It can also be seen from Table 17 that genotype CV with severity scores ranging between 2.1 and 2.7 showed moderate symptoms at both locations at 30, 45 and 60 DAT. On the contrary, genotype K116 showed moderate symptoms at UCC but severe symptoms at Asuansi at 30, 45 and 60 DAT. Further, genotypes K027 and K202 showed severe symptoms at UCC but very severe symptoms at Asuansi at 30, 45 and 60 DAT (Table 17).

**Table 17: Mean Severity of TYLCV Disease on Eight Tomato Genotypes at UCC Farm and Asuansi Experimental Sites between 30 DAT and 60 DAT**

| | Severity of TYLCV disease at indicated DAT and locations | | | | | |
|---|---|---|---|---|---|---|
| 30 DAT | | | 45 DAT | | 60 DAT | |
| Genotype | U.C.C | Asuansi | U.C.C | Asuansi | U.C.C | Asuansi |
| CV | 8.8 (2.3) c | 8.5 (2.2) c | 9.4 (2.7) b | 8.7 (2.3) b | 8.7 (2.3) d | 8.4 (2.1) de |
| K005 | 6.8 (1.4) d | 6.3 (1.2) d | 7.3 (1.6) c | 6.8 (1.4) c | 6.8 (1.4) h | 6.8 (1.4) h |
| K027 | 10.6 (3.4) a | 11.3 (3.9) a | 10.9 (3.6) a | 11.3 (3.9) a | 10.1 (3.1) b | 11.5 (4.0) a |
| K042 | 6.5 (1.3) d | 8.7 (2.3) c | 7.1 (1.5) c | 8.7 (2.3) b | 7.2 (1.6) fg | 8.4 (2.1) de |
| K100 | 5.9 (1.1) d | 6.9 (1.4) d | 6.3 (1.2) c | 6.6 (1.3) c | 6.6 (1.3) h | 6.8 (1.4) h |
| K116 | 8.7 (2.3) c | 10.1 (3.1) ab | 9.0 (2.5) b | 10.5 (3.3) a | 8.9 (2.4) bc | 10.0 (3.0) b |
| K202 | 10.5 (3.3) a | 11.2 (3.8) a | 10.8 (3.5) a | 11.2 (3.8) a | 10.1 (3.1) b | 11.6 (4.0) a |
| K213 | 6.1 (1.1) d | 6.2 (1.2) d | 6.5 (1.3) c | 6.4 (1.2) c | 6.3 (1.2) h | 6.7 (1.4) h |
| Mean | 8.0 (1.9) | 8.6 (2.3) | 8.4 (2.1) | 8.8 (2,1) | 8.1 (2.0) | 8.8 (2.3) |

$Lsd_{(0.05)}$ (30DAT): 1.4; $Lsd_{(0.05)}$ (45DAT): 0.9; $Lsd_{(0.05)}$ (60DAT): 1.2

Values in parentheses are the back transformed or actual values; those outside are angular transformed means
Values with same alphabet are significantly the same.
Means in the same column bearing same letters are not significantly different from each other ($P < 0.05$)

**Whitefly Population**

Varying levels of mean whitefly populations were recorded for both Asuansi and UCC locations and for the tomato genotypes at different sampling dates of 30, 45 and 60 DAT (Table 18). The mean whitefly population recorded at UCC was significantly higher than Asuansi at 30 DAT ($P< 0.05$). However, at 45 and 60 DAT, Asuansi had on the average higher whitefly populations than UCC ($P< 0.05$).

ANOVA on the mean whitefly populations recorded on the tomato genotypes at both Asuansi and UCC, showed significant genotype x location interaction effect ($P< 0.05$) at 30, 45 and 60 DAT. At 30 DAT, the mean whitefly population on genotypes CV, K100 and K116 recorded at UCC were significantly higher than Asuansi. However, the mean insect population on K005, K027, K042, K202 and K 213 at both UCC and Asuansi were not significantly different ($P> 0.05$). At 45 DAT, the mean whitefly population on K027 at UCC was not significantly different from Asuansi, but that of the other seven genotypes at Asuansi were significantly higher than UCC ($P< 0.05$). At 60 DAT, the mean whitefly population on all the tomato genotypes at Asuansi were significantly higher than UCC ($P> 0.05$).

**Table 18: Mean Population of Whitefly Recorded For Eight Genotype in U.C.C and Asuansi at 30, 45, 60 DAT**

| | Whitefly population of TYLCV | | | | | |
|---|---|---|---|---|---|---|
| | 30 DAT | | 45 DAT | | 60 DAT | |
| Genotype | U.C.C | Asuansi | U.C.C | Asuansi | U.C.C | Asuansi |
| CV | 1.7 (2.3) cdf | 1.1 (0.8) g | 0.91 (0.3) k | 2.5 (5.6) cfdh | 0.7 (0.0) h | 2.8 (7.4) e |
| K005 | 1.8 (2.7) cdf | 1.5 (1.7) cdf | 1.72 (2.5) ij | 3.3 (9.3) abd | 0.7 (0.0) h | 3.0 (8.4) cd |
| K027 | 2.0 (3.7) abd | 1.6 (2.1) cdf | 3.86 (14.4) a | 3.0 (8.2) abdf | 0.9 (0.3) fg | 3.0 (8.0) cd |
| K042 | 2.1 (3.7) abd | 1.6 (2.1) cdf | 1.94 (3.3) efhj | 3.7 (12.8) ab | 1.0 (0.5) fg | 3.3 (9.8) cd |
| K100 | 2.7 (6.9) a | 1.2 (1.0) e | 1.84 (2.9) ghj | 4.2 (16.5) a | 1.1 (0.7) fg | 3.5 (11.8) ab |
| K116 | 2.2 (4.5) ab | 1.3 (1.1) e | 1.48 (1.7) ij | 4.1 (16.1) a | 1.4 (1.4) f | 3.9 (14.6) a |
| K202 | 1.6 (2.1) cdf | 1.6 (2.2) cdf | 0.84 (0.2) k | 3.4 (11.0) ab | 0.9 (0.2) fg | 3.3 (10.3) cd |
| K213 | 1.8 (2.0) cdf | 1.7 (2.4) cdf | 1.4 (1.5) ij | 3.1 (8.8) abdf | 1.0 (0.5) fg | 3.2 (9.4) ad |
| Mean | 2.0 (3.3) | 1.5 (1.6) | 1.7 ( 2.6) | 3.4 (10.8) | 0.9 (0.4) | 3.2 (9.9) |

$Lsd_{(0.05)}$ (30DAT): 0.7; $Lsd_{(0.05)}$ (45DAT):1.1; $Lsd_{(0.05)}$ (60DAT): 0.6

Values in parentheses are the back transformed or actual values using square root transformation
Values with same alphabet are significantly the same.
Means in the same column bearing same letters are not significantly different from each other ($P < 0.05$)

**Number of Fruits/Plant**

Table 19 shows the effect of different locations on the mean number of fruits per plant for eight tomato genotypes. An ANOVA showed significant differences within both main factors (genotypes: $F_{7, 21}$ = 31.9; $P$< 0.05 and location: $F_{1, 27}$= 6.5; d.f. = 1; $P$< 0.05) as well as a significant interaction effect ($F_{7, 21}$= 1.6; $P$< 0.05). The mean number of fruits recorded at UCC (35.5) was significantly higher than Asuansi (28.7)/plant ($P$< 0.05).

The mean number of fruits recorded for K005 and K100 were not significantly different but were significantly higher ($P$< 0.05) than that of CV, K027, K042, K116, K202, and K213.With respect to genotype x location interaction effect, the mean number of fruits recorded for CV, K005, K027, K100, K116, K202 and K213 at both UCC and Asuansi were not significantly different ($P$> 0.05). On the contrary, significantly higher mean number of fruits/plant was recorded for K042 at UCC than at Asuansi ($P$< 0.05).

**Table 19: Means Number of Fruits/Plant for Eight Tomato Genotype at U.C.C and Asuansi Ecological Zones**

| Genotype | Number of fruits UCC | Asuansi | Mean (genotype) No of fruit |
|---|---|---|---|
| CV | 5.9 (34.1) b | 5.8 (33.4) bc | 5.9 (33.7) c |
| K005 | 9.1 (82.9) a | 8.0 (63.7) a | 8.6 (72.9) a |
| K027 | 4.3 (17.8) bcd | 4.7 (21.8) cd | 4.5 (19.8) d |
| K042 | 8.3(67.7) a | 5.8 (33.0) bc | 7.0 (48.8) b |
| K100 | 7.9 (62.4)a | 8.0 (63.0) a | 8.0 (62.7) a |
| K116 | 5.0 (24.0) bcd | 4.1 (16.6) d | 4.5 (19.8) d |
| K202 | 3.7 (13.2) d | 3.4 (11.1) d | 3.6 (12.1) e |
| K213 | 3.6 (12.1) d | 3.8 (13.6) d | 3.7 (12.8) e |
| Mean | 6.0 (35.5) a | 5.4 (28.7) b | 5.7 (32.0) |

Lsd $_{(0.05)}$ Genotype: 1.0
Lsd $_{(0.05)}$ Location: 0.5
Lsd $_{(0.05)}$ Genotype*location interaction: 1.4
Values in parentheses are the back transformed or actual values using square root transformation
Values with same alphabet are significantly the same.
Means in the same column bearing same letters are not significantly different from each other ($P< 0.05$)

**Mean Fruit Yield per Plot in t ha$^{-1}$**

Effects of location on the mean fruit yields of the eight tomato genotypes are presented in Table 20. Significantly higher fruit yield was recorded at UCC location than Asuansi ($F_{7,\ 21} = 19.2$; $P \leq 0.05$). The ANOVA also showed a significant effect of the genotypes on the mean fruit yields recorded ($F_{7,\ 21} = 59.5$; $P \leq 0.05$). The mean fruit yield recorded for K100 (8.6 t ha$^{-1}$) per plant was not significantly different from that of K005 (8.2 t ha$^{-1}$) per plant but significantly higher than that of the other genotypes. The mean fruit yield recorded for K202 (1 t/ha) per plant was also not significantly different from that of K213 (1.4 t ha$^{-1}$) per plant but significantly lower than the other genotypes.

The ANOVA further revealed a significant interaction between genotypes and location ($F_{26,\ 163} = 2.11$; $P \leq 0.01$). The mean fruit yield per plant recorded for K027, CV, K042 and K116 at UCC were significantly higher than Asuansi ($P \leq 0.01$). There was however, no significant difference in the mean yields recorded for K005, K100, K202 and K213 at both UCC and Asuansi.

**Table 20: Mean Fruit Yield (t ha$^{-1}$) On Eight Genotypes at U.C.C and Asuansi Ecological Zones.**

| Genotype | Fruit weight t ha$^{-1}$/location | | |
|---|---|---|---|
| | UCC | Asuansi | Mean (genotype) |
| CV | 6.2 b | 4.8 c | 5.5 |
| K005 | 8.0 a | 8.2 a | 8.2 |
| K027 | 5.8 bc | 2.8 d | 4.2 |
| K042 | 6.2 b | 3.4 d | 4.8 |
| K100 | 8.8 a | 8.4 a | 8.6 |
| K116 | 6.2 b | 2.6 d | 4.4 |
| K202 | 1.0 e | 1.0 e | 1.0 |
| K213 | 1.2 e | 1.4 e | 1.4 |
| Mean | 5.4 a | 4.0 b | 4.8 |

Lsd for genotype: 0.8
Lsd for location: 0.4
Lsd for genotype*location interaction: 1.0
Values in parentheses are the back transformed or actual values using square root transformation
Values with same alphabet are significantly the same.
Means in the same column bearing same letters are not significantly different from each other ($P< 0.05$)

**Molecular Detection of *Tomato yellow leaf curl virus* in Eight Genotypes in the Forest and Coastal Agro Ecological Zones**

Molecular results from the three degenerate primers are presented in figure 1-3. In all the three figures, lanes 1-8 (**1**- K100, **2**- K027, **3**- K116, **4**- K005, **5**- K202, **6**- CV, **7**- K213 and **8**- K042 ) denotes samples from UCC and 9-16 denote the corresponding samples from Asuansi, C denote the negative control while M is 1 kb DNA Ladder.

Figure 1 is the amplicon of TYLCV obtained from tomato samples using primer pairs PAR1c496/PAL1v1978 of band size 1100-1400bp. The primer detected the virus from 5 out of the eight samples from Asuansi farm (K027, K005, K202, CV and K042). It did not however, detect the virus from any of the samples from UCC farm (Figure 1).

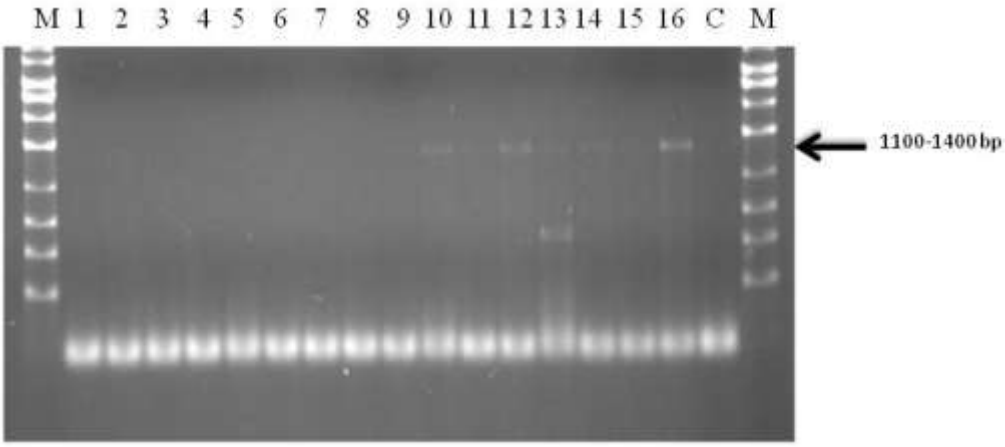


Figure 1. Amplicon of TYLCV obtained from tomato leaves using PAR1c496/PAL1v1978 primer pairs of size 1100-1400bp, lanes 1-8 (1- K100, 2- K027, 3- K116, 4- K005, 5- K202, 6- CV, 7- K213 and 8- K042 ) denote samples from UCC and 9-16 denote the corresponding samples from Asuansi, C denote the negative control while M is 1 kb DNA Ladder. C = Negative control; M = 1 kb DNA Ladder.

Figure 2 indicates that primer AV494/AC0148 detected the viral DNA in the 8 genotypes with band characteristics of approximately 550-600bp. However band from tomato samples from UCC were stronger than those from Asuansi farm. The primers could not however amplify the viral DNA in genotypes CV and K213.

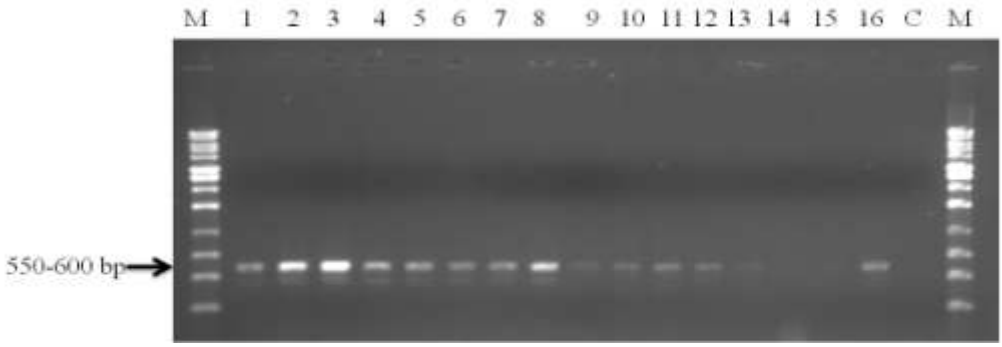


Figure 2 Amplicon of TYLCV obtained from tomato leaves using AV494/AC0148 primer pairs of size 550-600bp, lanes 1-8 (1- K100, 2- K027, 3- K116, 4- K005, 5- K202, 6- CV, 7- K213 and 8- K042 ) denote samples from UCC and 9-16 denote the corresponding samples from Asuansi, C denote the negative control while M is 1 kb DNA Ladder.

Primers PTYv787/PTYc1121were able to amplify the viral DNA in all the tomato samples from both UCC and Asuansi with band characteristics of 300 bp.However, the DNA resulted in stronger bands in the UCC samples, except genotypes K213, compared with the Asuansi samples which yielded weaker bands except genotypes K213 and K042 which produced stronger bands (Figure 3).

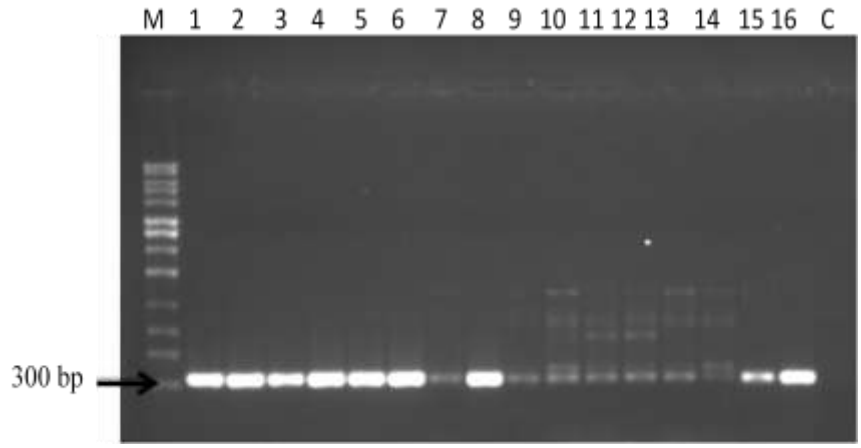


Figure 3 Amplicon of TYLCV obtained from tomato leaves using PTYv787/PTYc1121 primer pairs of size 300 bp, lanes 1-8 (1- K100, 2- K027, 3- K116, 4- K005, 5- K202, 6- CV, 7- K213 and 8- K042) denote samples from UCC and 9-16 denote the corresponding samples from Asuansi, C denote the negative control while M is 1 kb DNA Ladder.

# CHAPTER FIVE

# DISCUSSION

## Farmers' Awareness and Knowledge of TYLCV Disease and Their Agronomic Practices

The study has revealed that majority of the respondent farmers had experienced the TYLCV disease in their farms. The disease was well known to farmers in all the three major tomato producing areas in the region as most of them were able to give vivid description of the disease. However, they did not know the exact cause of the disease. Farmers in the study area rather attributed it to climatic factors such as high sunlight, soil factor and low rainfall. This is similar to findings of the work done by Nagaraju*et al*. (2002) where majority of tomato farmers at Karnataka, India were aware of TYLCV. In the said study, majority of the farmers were not aware of *B. tabaci* as the vector of the TYLCV disease, but rather associated the disease with climatic factors. Nagaraju*et al*. (2002) further reported that the farmers were able to describe the symptoms but did not know the causes and epidemiology of the viral disease.

The high awareness of the TYLCV disease among the respondent farmers could also be due to their experience in tomato production. It was observed that majority of the farmers have been in tomato production for over5 years. Meanwhile, according to Owusu, (1994) the incidence of TYLCV disease in tomato crops in Ghana has been reported since 1994. Moreover, the proportion

of the farmers who were not aware of the disease (Table 7) could at least in part be, attributable to the fact that they were new in tomato production. The study revealed that about 7.3% had been in tomato production for less than a year (Table 5). This therefore agrees with the report of Nagaraju*et al*. (2002) that apart from formal education being a source of information to farmers, experience in farming or number of years in farming can also serve as a means through which farmers get informed.

Most farmers indicated that they observed the symptoms during the flowering stage. This suggests that the plants might have been infected by the virus earlier at the vegetative stage with the disease expressing itself later at the reproductive (flowering) stage. There could also be the possibility that the whiteflies were attracted to the yellow colour of tomato flowers leading to high infestation of the crops and consequent transmission of the disease as was observed by Osei *et al*. (2012).

Although majority of the farmers werein the active age, there is an equally high number of older range (51-60 & 61.71) hence they could not adopt intensive good agronomic practices (such as early weeding, covering of seedlings at nursery among others) as those in the active range hence the high incidence in the Central region (van der Berge, 2013). This therefore might have contributedto the high prevalence of the virus disease in the region.

The majority of the respondent farmers adopted various methods in the management of the disease on their farms suggestive, of their high awareness of the presence of the disease on their farms and it effect on tomato crops in terms of yield loss, flower abortion and even death of plants. Stefferud (1953) and Lewis& Miller (2004) reported that basic knowledge about prevalence of

a disease is one of the main tools in its management. Over 30.7% of the respondents did not adopt any management practice as this could be attributed to their high illiteracy level as over 44% of the respondent farmers were observed being illiterates. According to Mr R. Oduro, MoFA Director of Effutu Municipality, farmers especially those from the Effutu municipality had been taught the need to cover their tomato seedlings with a net in order to exclude the whitefly vector, yet majority of them did not adopt this technology (Personal Communication, 15th January, 2014) as it was discovered in the present study that only 7.3% of the farmers cover their seedlings with net at the nursery.

The cultivation of tomato mainly in the major season by majority of the respondent farmers could be due to the availability of water during this period of the year. Huho, Ngaira, Harun, Ogindo, and Masayi, (2012) made similar observation that smallholder farming families in subsistence agriculture depend mainly on rainfall. The higher incidence of TYLCV disease in the major season than in the minor season could probably be due to higher whitefly vector population in the major season than in the minor season. This confirms the findings of Asare *et al.*, (2014). This suggests that thefarmers will probably go into dry season production when there is a source of irrigation water as reported by Kaguongo *et al.* (2008). The high awareness of the TYLCV disease among the respondent farmers in the study areas could partly be attributed to their familiarity with the disease as a result of farmers cultivating tomato in the major season.

The management practices employed by the farmers were covering of seedlings at nursery, application of insecticides and removal of infected plant

(rouging). Even though the majority of the farmers use insecticides to manage the TYLCV disease, some farmers considered the use of insecticide expensive and ineffective. It is likely that the low returns discouraged their use of insecticides. Their observation of the ineffectiveness of the insecticide could be due to the development of resistance of the whitefly vector. This is also suggestive that the right insecticide were not used or misapplied by the farmers (Ahmed, 1995 & Ntow, 2001).However, farmers who were rouging explained that they had no other alternative than the application of insecticide which had not been effective. The few farmers who were covering their crops explained that the practice protects tomato plants from some insects that destroy the seedlings but had not checked if it was effective against TYLCV infection. Thus, the benefit of protecting their crops against pest attack was the main reason why they adopted this technology. Never, Nyeverwai, Dadirayi, Maponga, and Edga, (2014) has also reported that farmers' adoption level depends on the claims and benefit of the innovation being introduced.

The yield losses up to 50% due to TYLCV reported by farmers confirms the observations of Pico *et al.,* 1996; Vidavsky & Czosnek, 1998; Morienes & Navas-Castillo, 2000 who reported that yield lose can reach 100% as a result of transmission occurring either at the nursery or at flowering.

**Incidence and Severity of the TYLCV Disease in the Selected Districts**

TYLCV disease were observed in all the farms surveyed with mean disease incidence ranging between 24.4 ±3.5% and66.35 ± 5.1% suggesting that the virus was quite prevalent in the area of study. High prevalence of the TYLCV disease has also been reported in the major tomato growing areas in Northern,

Upper East, Brong Ahafoand the Ashanti regions of Ghana (Horna *et al.*, 2006; Osei *et al*., 2012).

Significant differences in the mean incidences and severities of the TYLCV diseases recorded in the study could be attributed to the types of cropping system and other cultural practices adopted by the tomato farmers. Cropping systems are known to affect disease pressure either positively or negatively (Agrios, 2005). It was realized from the household survey that some tomato farmers practiced mixed cropping, and intercropped tomato with pepper and garden eggs which are known alternate hosts of TYLCV (Persley, 2012; Ahmad, Rizvi, & Nisar, 2014). TYLCV has been reported to have a wide host range and its vector *B. tabaci* is polyphagous (Persley, 2012). Continuous cropping could also bring about the build-up of TYLCV and its vector (Glick, *et al.,* 2009). Differences in the cultural practices taking into account the type of insecticide, the time of application and covering of seedlings at the nursery could potentially affect the disease incidence and severity (Neya & Normand, 1998; Marley, 2004). Differences in the incidence and severity of the disease recorded in the study could also be attributable to possible variation in the strains of TYLCV virus present, with different levels of virulence. Three strains of TYLCV (*Tomato yellow leaf curl Mali virus, Tomato yellow leaf curlKumasi virus* and *Tomato yellow leaf curl Ghana virus* have been identified in tomato crops in Ghana by Osei *et al*. (2012).

Even though TYLCV disease was prevalent in all the farms surveyed from the three districts in the Central Region, the mean disease incidence in each farm or community was low. This could at least partly be attributed to the fact that most of the farmers surveyed cultivate the land racelocal and

improved varieties of *S pimpilifolium* locally called Fadzebegye and Fadzebegye tires respectively which are known to carry a resistance gene against TYLCV (Lapidot & Friedmann, 2002).

Personal observation in the local market showed that the improved varietieshave bigger fruits and hence higher consumer demand and higher profit to the growers, compared to their ancestors or parent breeds. This could perhaps be the reason why most of the farmers cultivated the improved variety as observed by Estrada-Castellanos, Carrillo-Rodriguez, Jerez-Salas, Chavez-Servia, and Perales-Segovia (2011) who found out that farmers preferred a landrace tomato due to its high demand by customers and high market price thereby resulting in high profits to farmers.

**Agronomic Performance of Thirty-Six Tomato Genotypes**

All the 36 tomato genotypes showed symptoms of the TYLCV disease but at varying levels. The rate of infection by TYLCV and disease development varied from one genotype to the other at various sampling dates after transplanting (DAT). The variations observed within the 36 genotypes studied could be due to the differences in the genetic makeup of the different genotypes, viral strains and the biotype of whitefly as observed by Navas-Castillo, Sanchez-Campos, Diaz, (1999); Delatte, Holota, Reynaud, & Dintinger, (2006); Azizi, Mozafari, & Shams-bakhsh, (2008) and Abu, Uguru, & Obi, (2011).

The variation in the incidence could also be attributed to the whitefly vector preference for to some genotypes thereby stayed longer on these plants and produced higher population on those genotypes, facilitating the transmission of the TYLCV (Osei *et al.*, 2012).This probably explains the

positive and significant correlation between whitefly populationand disease incidence and severity at all the sampling dates.

The diverse genetic background of the tomato genotypes could also have affected their response to stress factors (Abu *et al*., 2011), and hence the variation in incidence and severity of the TYLCV disease among the tomato genotypes.

It is likely that the variation in the incidence and severity of TYLCV disease could again be due to the age of plants at the time of infection because according to Pico *et al.* (1996), plants infected or inoculated at older age produce milder symptoms which may be wrongly considered as manifestation of genetic resistance. This probably partly explains why genotypesK005, K100, K042, K116 and K213 were symptomless at 30 DAT, but showed mild symptoms of infection at 45 and 60 DAT. The late occurrence of the late disease symptoms could be as a result of less attraction of the whitefly vector to the tomato plants (Osei *et al.*, 2012) due probably to the physical characteristic such as glandular secreting trichomes and production of strong chemical compound such as acyle sugars that acted as antibiosis or antixenosis that prevented the whitefly from infecting the plant at early stage. This secretion is known to contribute to plant resistance to insect (Schilmiller, Charbonneau, & Last, 2012).

The symptomless condition of some of the genotypes could also be as a result of the plant being tolerant to the virus making the plant able to withstand or recover from the damage by the whitefly or activities of the whitefly and virus as noted by Teetes (2013). The plant probably does that by

increasing its photosynthetic capacity, nutrient uptake or oxidative enzyme activity (Kessler & Baldwin, 2002).

The variation in the yield of the genotypes studied is an indication of the time of infection having effect on the incidence of TYLCV.Ghimire, Subedi, and Green, (2001) in a similar study in Nepal made a similar observation that increased incidence and severity resulted in yield losses of up to 95% when infection occurred early before flowering.

This may also explain why genotype K202 which experienced early and 100% infection,had the highest severity score (3.6) and had the lowest mean fruit yield of 2.2 t $ha^{-1}$. It can then be deduced that, the higher the incidence and severity of TYLCV disease the higher the yield losses.The observed variation is suggestive of the wide diversity in the genetic makeup of the genotypes as observed by Navas-Castillo *et al.*,(1999), Delatte *et al*., (2006), Azizi *et al*., (2008) and Abu *et al*., (2011). The negative and significant correlation between disease severity and fruit yield is a further indication of the negative effect of TYLCV in the yield of tomato.Other authors like Zakey *et al.* (1991), Fargette *et al.* (1996) and Lapidot *et al.* (1997) had also confirm similar relationships.

The high yield of genotype K027 that had early infection (severe infection) had a yield of 9.0 t $ha^{-1}$ which was higher than the average yield could be due to the plant being able totolerate viral infection or recover from the damage by the disease (Kessler & Baldwin, 2002; Teetes, 2013).

Genotypes K100, K005, K042 and K116 should therefore be evaluated further to check how stable their resistance/tolerant gene(s) are. However, genotype K213, with mild infection but low yield could be incorporated in a

breeding programme to breed for TYLCV resistance or tolerant cultivars. According to Reddey (2009) and Kasettranan, Somta, & Srinives (2009), genetic studies using different resistance sources reveals different modes of inheritance suggesting that there are different mechanisms or genes conferring resistance to plant disease. Plant breeders therefore need to investigate the nature of disease resistance in these tolerant genotypes and to identify the resistance genes present in them in order to add up to the existing ones.

Surprisingly, genotype LV which is an improved variety of the *S. pimpinellifolium* locally called the "Fadzebegye"supposedly known to carry a resistance gene (Lapidot & Friedmann, 2002) had moderate infection and low yield (5.2t/ha) compared to the genotypes with mild infection and high yields (K100, K005, K042 and K116).This poor performance could possibly be due to the breakdown of the resistant gene under high disease pressure or virulence variability (Chiba, Kondo, Miyanishi, Andika, Han, & Tamada 2011).

**Performance of Selected Tomato Genotypes at Two Different Ecological Zones**

Genotypes or varieties behaved differently when placed under different ecological zones. Genotype that performed better in the coastal zone may perform poorly in the forest zone and vice versa (Gibson *et al*., 1998). It is therefore better to evaluate different genotypes or germplasms in different ecological zones in order to know their genetic diversity and how they respond to disease pressure, incidence, severity and physiological stress (Obeng-Antwi, Craufurd, Menkir, Ellis, & Sallah, 2012).All the eight genotypes showed symptoms of TYLCV disease but at varying degrees. The varying degree of the symptoms expressed by the eight genotypes probably suggests

the level of their susceptibility to TYLCV because the PCR test showed amplifications of the TYLCV DNA in all the eight genotypes. This confirms the observations of Agrios (2005) and Jacquemond, Verdin, Dalmon, Guilbaud, & Gognalons (2009) that symptoms alone are not effective in the detection of the plant virus and that be confirmed by molecular or serological means and DNA based laboratory assumption.

Whereas K100, K005, K042, K116 and K213 were symptomless at 30 DAT, during the previous screening at UCC (Table 12), they showed early symptoms at 30 DAT at both UCC and Asuansi during the evaluation studies (Table 17). This could be as a result of higher disease pressure in UCC during the evaluation period which was a major or raining season as also confirmed by Asgedom *et al.*, (2011). This was again verified by a personal communication with a farm supervisor in UCC confirms that, diseases of tomato including TYLCV are higher during the raining seasons than the minor seasons (Mr Arkoh, Farm supervisor, UCC). Again this could be as a result of disease escape during the screening making them symptomless at 30DAT as observed by (Malay 2005). Notwithstanding, disease incidence and severity during the evaluation were higher at Asuansi than UCC. This could be as a result of the dynamics of the whitefly population which was generally higher in Asuansi than UCC (Table 18) and possibly new strains.

The effect of the climate can also bring about the differences since genotypes behave differently at different ecologies (Appendix D) (Ashfaq, Noor ul Ane, Zia, & Nasreen, 2010; Al-ani *et al.*, 2011).

Disease pressure prevailing at different planting dates and at different locations could also be due to different seasons in which the crops were grown

and differential reaction of genotypes to the different location (Egesi, Onyeka, Asiedu, 2007) suggesting that host plant resistance is the most effective means of controlling virus disease (Thottapilly, 1992). This is consistent with the finding of Nakitandwe, Adipala, El-Bedewy, Wagoire, and Lemaga, (2005) where sweetpotato genotypes behaved differently when grown at different locations. Accordingly to them genotypes behaved differently to yield and disease resistance with regard to time of planting, climatic differences, biotype of whiteflies and strains of virus. This is evident in the present study where genotypes K116, K027, K042 and K202 reacted differently to the TYLCV infection at the two agro- ecological zones. Genotype K042 showed mild symptom during the screening and evaluation at UCC but showed moderate symptoms at Asuansi. Genotype K116 which showed mild symptoms during evaluation at UCC showed moderate and severe symptoms when evaluated at UCC farm and Asuansi farm, respectively. Similarly, symptom severity of genotypes K202 and K027 changed from severe s to very severe symptoms when evaluated at UCC and Asuansi farm (Table 17). These differences could probably be attributed toreports by Nakitandwe *et al.* (2005) and the Saskatchewan Ministry of Agriculture (2014) which state that a resistant or tolerant variety could display poor resistance to the disease and a susceptible variety having more and worse disease severity at different environment.

The possible existence of different strains or genotypes of TYLCV at UCC and Asuansi experimental sites which may have resulted in different resistance reactions at the two locations could be deduced from the PCR test conducted with three degenerate primer pairs. Primers PAR1c496/PAL1v1978 detected the virus from 5 (K027, K005, K202, CV and K042) out of the eight

samples from Asuansi but did not detect the virus from any of the samples from UCC (Figure 1)**.** Primers AV494/AC0148 detected the virus in all the 8 genotypes from UCC farm but, could not detect the virus in genotype K213 from Asuansi farm (Figure 2). Primers PTYv787/PTYc1121 was able to amplify the geminivirus in all the samples from both UCC and Asuansi, however, the DNA amplification generally resulted in stronger bands in the UCC samples, except genotypes K213, and weaker bands with the Asuansi samples except genotypes K213 and K042 (Figure 3). Thus in case of any resistance breaking TYLCV strains or pathotypes, at Asuansi, they would be able to change mild symptoms at UCC farm to moderate, moderate to severe and severe to very severe symptoms, as observed in this study.

The three degenerate primers selected for PCR amplification are known to amplify three sites of the begomovirus genome. The first primer pairs; Av494 and Ac1048, is known to amplify the core coat protein region (Wyatt and Brown, 1996) whereas primer pairs; PALIv1979 and PARIc715 and PARI722 and PALIc1960 are known to amplify the top half and bottom half respectively of the A genome of begomoviruses (Rojas *et al*., 1993). Given that these primers targeted sites are highly conserved regions that cut across begomoviruses, spontaneous changes in viral DNA through peudorecombination and mutations, even at highly conserved sites, can prevent viral detection in infected samples. Variations in DNA sequences could reduce the specifity of the primer annealing sites thus making a false positive perception of viral absence. These could account for the differences in efficiencies at which the various primers were able to amplify viral DNA in the eight tomato genotypes from UCC and Asuansi farm. Thus primers

PTYv787/PTYc1121 was more efficient (100%) and more reliable in detecting TYLCV in a given diseased sample, followed by Primers AV494/AC0148 (83.3%) whilst primers PAR1c496/PAL1v1978 which detected the virus from 5 out of the eight samples from Asuansi but none from UCC, is inefficient and unreliable for detecting the virus from diseased samples. Contrary to the fact that PCR is very sensitive as it's able to detect viral DNA in very low concentrations. Work done by Rotbi, De Castro, Díez, & Elmtili (2014) and Potter (2007) attributed failure of primer amplification to viral concentration accumulated in genotypes not being enough to encourage amplification. Again failure in the detection of viral DNA can be attributed to the absence of sequence of sufficient complementarity at primer annealing sites though these primers have been shown by Rojas *et al*. (1993) and Osei *et al* .(2008) to be effective in the detection of begomoviruses. Variation in primer annealing sites can be a possible reason in terms of the primer's failure in detecting viral DNA (Acquah, 2012). What this suggests is the emergence of possibly new strain of begomoviruses with high levels of variation with respect to primer annealing sites.

The commercial variety *Fadzebegy tires* (CV) which is an improved *S. pimpinellifolium* showed moderate symptoms and was therefore stable during the period of evaluation in terms of yield. This could probably explain the reason for its wide cultivation in the region.

In general, the yields of the tomato genotypes recorded during the evaluation were less than that during the screening. The variations in the yields of the genotypes in effect with different seasons probably suggest the effect of time of infection and season on the severity of TYLCV and yield of

the genotype as reported by Stuckey, Niblack, Nyvall, Krausz, & Horne (1993).

Eventhough infection was early, genotypes K100 and K005 had yields that were greater than the average yieldof 7.5 t $ha^{-1}$reported by MoFA (2011). It can therefore be concluded that even in the season and location when disease pressure is high K100 and K005 can still give yields greater than the average yield. Genotype K100 and K005 that are highly consistent in terms of yield and disease reaction across different agro ecological zones are stable can therefore be said to possess a stable source of resistance or tolerance to TYLCV infection, and hence ideal to be released to farmers after possible further evaluation at farmers' fields multilocationally (Adu *et al.,* 2013).

Generally, it could be said that the genotypes that were not able to maintain their reaction group but became worse in terms of severity and yield in the two agro ecological zones are not stable under different zones. Whereas those that were able to maintain their reaction group are stable in terms of disease severity and mean fruit weight.

# CHAPTER SIX

# SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

## Summary

The study has revealed high prevalence of TYLCV disease in the Central Region. The highest incidence and severity of the disease were recorded at KEEA (52.9 ± 2.7) (26.9 ±1.2), followed by Efutu Municipal (49.5 ±1.2) and (25.3 ± 0.9) whereas Mfantseman district had the lowest (42.1 ± 2.7) and 21.4 ± 0.8 respectively.

Tomato farmers in these districts were aware of the symptoms of the disease but not the causes. They rather attributed the disease to climatic conditions such as rain, drought etc. but not to viral infection.

The major management practices employed by farmers were the pesticides application (26.7% out of 76) and rouging (20.7% out of 76) with only a few (7.3%) covering with net at the nursery. Most farmers (39.3%) however do not adopt any control measure.

The phenotypic screening of the 36 genotypes revealed five tolerant varieties (K005, K100, K042 and K116 and K213) with mild symptoms at 60 DAT.

In terms of mean yield, genotype K100 had the highest of 12.6 t/ha followed by K116, K005 and K042 with fruit yield of 11.8 t $ha^{-1}$, 11.8t $ha^{1}$and 10.8 t $ha^{-1}$ respectively, which are greater than the national average yield of 7.5 t $ha^{-1}$.

Genotype K213 which expressed mild symptoms at 60DAT had low yield of 2.6 t $ha^{-1}$whereas genotype K027 with severe symptoms had an appreciable fruit yield of 9.0 t $ha^{-1}$.

Yield correlated negatively with incidence and severity of TYLCV disease and whitefly population. Whitefly population was positively correlated and highly significant with incidence and severity of TYLCV disease ($P < 0.01$).

Overall, incidence and severity of TYLCV disease in the eight tomato genotype tested were significantly higher in Asuansi than UCC. Genotype K042 showed moderate symptoms at both locations while Genotype K116 showed moderate symptoms at UCC but severe symptom at Asuansi. Genotypes K202 and K027showed severe symptoms at UCC and very severe symptoms at Asuansi. Genotypes K005, K100 and K213 maintained their mild symptoms in both locations.

Significantly higher fruit yield was recorded at UCC than Asuansi. The study also revealed a significant interaction between tomato genotypes and location with respect to the mean fruit yields. The mean fruit yield recorded for K027, K042 and K116 at UCC were significantly higher than Asuansi ($P \leq 0.01$).

Genotypes K100 and K005 had the highest yield of 8.8 t/ha and 8.0 t/ha, respectively at UCC and 8.6 t $ha^{-1}$and 8.2 t $ha^{-1}$respectively at Asuansi which are greater than the national average yield of 7.5 t $ha^{-1}$.

. Genotype K213 which had mild severity had low yield of 1.2 t $ha^{-1}$and 1.4 t $ha^{-1}$ at UCC and Asuansi respectively.

The molecular screening using the three degenerate primers revealed the presence of the virus in all the genotypes at both locations. The primers differed in their relative abilities in the detection of the TYLCV from diseased samples. Primer PTYv787/PTYc1121 which amplified the viral DNA in all the samples from both UCC and Asuansi was found to be the most efficient and polymorphic for the detection of TYLCV in diseased samples than primer pairs AV494/AC0148 and PAR1c496/PAL1v1978. Primers PAR1c496/ PAL 1v1978 detected the virus from 5 out of the eight samples from Asuansi and none from UCC. Primers AV494/AC0148 detected the virus in all the eight genotypes from UCC but seven from Asuansi.

**Conclusions**

1. Farmers in the surveyed areas were aware of the symptoms of the disease but not the cause. They attribute weather parameters like temperature and rainfall as the cause of TYLCV disease. The main management practice employed by farmers was rouging or by the use of insecticide with few covering seedlings at nursery.
2. TYLCV disease symptoms was seen and reported by farmers in the three districts and all the fifteen farms assessed. The lowest mean incidence was recorded in Mfantseman district however the mean incidence in the region was more than fifty percent. Severity on the

other hand was generally lower in all the districts with a mean of 24.5± 0.9.

3. All the 36 genotypes showed different levels of severity from mild to severe symptoms but not complete resistance. Genotypes K005 and K100 showed low level of severity and high yield (t $ha^{-1}$).
4. Genotype K005 and K100 continued to show mild symptoms at both coastal and forest zone whereas genotype K213 showed low level of TYLCV but had low yield (t $ha^{-1}$).
5. Genotype K207, K202, K116 and K042 were not stable since they had different reactions in the two locations. The reaction of the commercial variety was stable in both zones.
6. There was no complete resistance to TYLCV following field and molecular screening.

**Recommendations**

Intensive education on the causes and management on TYLCV disease should be carried out in tomato growing areas.

The Integrated Pest Management strategy (covering of seedlings at nursery) should be intensified.

Genotypes with higher mean fruit weight and slight TYLCV infection should be studied for resistance. Tomato genotypes with appreciable yield but demonstrated susceptibility to TYLCV infection could be crossed with those that were tolerant.

Further screening with specific primers should be done to identify possible strains and even new strains in the region, also advanced screening sequencing and phylogenetic studies or research in other tomato growing areas

in the southern Ghana should be done, so that Ghana's array of tomato viruses could be established.

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## APPENDICES

## APPENDIX A: SURVEY QUESTIONNAIRE

**UNIVERSITY OF CAPE COAST**
**SCHOOL OF AGRICULTURE**
**CROP SCIENCE DEPARTMENT**

This questionnaire is designed to know about disease (TYLCV disease) you encounter during the production of your tomato crop. I would therefore ask you few questions about your tomato production practices especially disease control measure.

**NAME OF COMMUNITY**……

***Please provide information about your 2012 tomato management practices***

1. Gender 1) Male 2) Female
2. Age 1) 10-20 2) 21-30 3) 31-40 4) 41-50 5) 51-60 6) 61-70
3. Highest Education level 1)Non formal 2)Primary 3)JHS 4)SHS
4. How many years have you grown Tomato?.....1) < 1year 2) 1 – 5 years 3) above 5 year
5. What was the size of your land?.....1) < acre 2) 1 – 2 acres 3) above 3 acres
6. What farming practices did you employ? 1) Mixed cropping 2) Mono cropping 3) others
7. What crops do u intercrop 1) Pepper 2)Garden eggs 3) Cassava 4) Others
8. What time did you plant your crop?..... 1)Minor season 2) Major season
9. What nursery practices did you engage in?
   i.....ii.....iii.....
10. Do you crop on the same land? 1) Yes 2) No ***If yes answer 8***
11. For how long have you been cropping on the same field?
    1) Just started 2)1 year 3) Over a year
12. What variety did you plant? 1) Local 2) Improved 3) Exotic
13. Where did you obtain your seeds? 1) Market 2) Farmers 3) Seed dealer 4)Research 5) MoFA 6) N.G.O 7) Others
14. Did you encounter any disease? 1)Yes 2) No ***If No answer 21- 29***

15. Can you give the symptoms
    a. ……
    b. ……..
    c. ……

16. Do you know the name of the disease? 1) Yes 2) No ***If yes answer 14-15***
17. Mention them…….
18. What do you see when the plant is attacked by the disease?.....
19. Which of the seasons do you encounter the symptoms or the disease?.... 1)Minor season 2) Major season 3) Both season

20. Can you give the estimation of the loss after disease infest
    1) < 10%  2) 11 – 50 %  3) >50
***21.*** Did you control? 1) Yes  2) No ***If yes answer 19-20***
22. How did you control the disease in your field?
    1)Pesticide application  2) Removal of infected plant  3) Others
***23.*** Did the control work? 1) Yes  2) No
***24.*** Have you heard of TYLCV before?  1) Yes  2) No***Explain the symptoms to the farmer***
25. Do you know what causes the disease?  1.Yes  2.No
26. If yes, state the
    cause…….
27. What growth stage do you encounter the disease?
    1) Seedling  2) Flowering  3) Fruiting
28. What effect does the disease have on the
    plant?.....
29. Did you control  1)Yes  2)No
30. If no, why
31. High cost of pesticide
32. No effect after use
33. No reason
34. How did you control the disease?
    1)Pesticide application  2) Removal of infected plant
    3)Other
35. Did the control measure worked?  1) Yes  2) No
36. What percentage loss did the TYLCV cause?1) < 10% 2) 10-20% 3) 21- 40% 4) 41-50% or more
37. How has the disease affected your livelihood?
    ……..

## APPENDIX B
## Phenotypic screening of 36 genotypes
### Incidence

Variate: trans_30

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 15386.0 | 7693.0 | 26.98 | |
| Block.*Units* stratum | | | | | |
| Name_of_Genotype | 35 | 39917.6 | 1140.5 | 4.00 | <.001 |
| Residual | 70 | 19961.2 | 285.2 | | |
| Total | 107 | 75264.9 | | | |

Variate: trans_45

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 5920.2 | 2960.1 | 7.66 | |
| Block.*Units* stratum | | | | | |
| Name_of_Genotype | 35 | 37735.7 | 1078.2 | 2.79 | <.001 |
| Residual | 70 | 27067.2 | 386.7 | | |
| Total | 107 | 70723.1 | | | |

Variate: trans_60

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 5868.1 | 2934.0 | 9.39 | |
| Block.*Units* stratum | | | | | |
| Name_of_Genotype | 35 | 32805.3 | 937.3 | 3.00 | <.001 |
| Residual | 70 | 21863.8 | 312.3 | | |
| Total | 107 | 60537.1 | | | |

**Severity**
Variate: trans_30

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 5.1776 | 2.5888 | 8.17 | |
| Block.*Units* stratum | | | | | |
| Name_of_Genotype | 35 | 635.4260 | 18.1550 | 57.27 | <.001 |
| Residual | 70 | 22.1897 | 0.3170 | | |
| Total | 107 | 662.7933 | | | |

Variate: trans_45

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 1.3163 | 0.6582 | 3.42 | |

| | | | | | | |
|---|---|---|---|---|---|---|
| Block.*Units* stratum | | | | | | |
| Name_of_Genotype | 35 | 216.4742 | | 6.1850 | 32.16 | <.001 |
| Residual | 70 | 13.4630 | 0.1923 | | | |
| Total | 107 | 231.2535 | | | | |

Variate: trans_60

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 1.4733 | 0.7367 | 3.62 | |
| Block.*Units* stratum | | | | | |
| Name_of_Genotype | 35 | 201.8361 | | 5.7667 | 28.36 | <.001 |
| Residual | 70 | 14.2320 | 0.2033 | | | |
| Total | 107 | 217.5414 | | | | |

**Whitefly population**

Variate: trans_30

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 2.5604 | 1.2802 | 6.19 | |
| Block.*Units* stratum | | | | | |
| Genotype | 35 | 14.3234 | 0.4092 | 1.98 | 0.008 |
| Residual | 70 | 14.4854 | 0.2069 | | |
| Total | 107 | 31.3692 | | | |

Variate: trans_45

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 0.3567 | 0.1783 | 0.63 | |
| Block.*Units* stratum | | | | | |
| Genotype | 35 | 14.3309 | 0.4095 | 1.45 | 0.093 |
| Residual | 70 | 19.7496 | 0.2821 | | |
| Total | 107 | 34.4372 | | | |

Variate: trans_60

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 0.4994 | 0.2497 | 0.86 | |
| Block.*Units* stratum | | | | | |
| Genotype | 35 | 8.3379 | 0.2382 | 0.82 | 0.737 |
| Residual | 70 | 20.3454 | 0.2906 | | |
| Total | 107 | 29.1827 | | | |

**Variate: Mean fruit WT**

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Reps_Blks stratum | 2 | 47.1449 | 23.5724 | 35.93 | |
| Reps_Blks.*Units* stratum | | | | | |
| Genotypes | 35 | 203.9457 | 5.8270 | 8.88 | <.001 |
| Residual | 70 | 45.9221 | 0.6560 | | |
| Total | 107 | 297.0127 | | | |

## APPENDIX C
## Evaluation of eight genotypes
## Interaction between genotypes and location

**Incidence**

Variate: trans_30

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 219.5 | 109.8 | 0.61 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 2444.0 | 2444.0 | 13.67 | <.001 |
| Name_of_Genotype | 7 | 21334.8 | 3047.8 | 17.05 | <.001 |
| Location.Name_of_Genotype | 7 | 568.2 | 81.2 | 0.45 | 0.859 |
| Residual | 30 | 5362.8 | 178.8 | | |
| Total | 47 | 29929.3 | | | |

Variate: trans_45

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 579.2 | 289.6 | 1.95 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 1951.7 | 1951.7 | 13.17 | 0.001 |
| Name_of_Genotype | 7 | 19896.1 | 2842.3 | 19.18 | <.001 |
| Location.Name_of_Genotype | 7 | 1647.0 | 235.3 | 1.59 | 0.177 |
| Residual | 30 | 4446.1 | 148.2 | | |
| Total | 47 | 28520.2 | | | |

Variate: trans_60

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 877.9 | 439.0 | 3.79 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 195.9 | 195.9 | 1.69 | 0.203 |
| Name_of_Genotype | 7 | 27383.9 | 3912.0 | 33.79 | <.001 |
| Location.Name_of_Genotype | 7 | 570.2 | 81.5 | 0.70 | 0.669 |
| Residual | 30 | 3472.9 | 115.8 | | |
| Total | 47 | 32500.8 | | | |

**Severity**

Variate: trans_30

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|

| | | | | | |
|---|---|---|---|---|---|
| Block stratum | 2 | 0.6566 | 0.3283 | 0.44 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 5.1210 | 5.1210 | 6.94 | 0.013 |
| Name_of_Genotype | 7 | 162.5113 | 23.2159 | 31.46 | <.001 |
| Location.Name_of_Genotype | 7 | 8.3883 | 1.1983 | 1.62 | 0.167 |
| Residual | 30 | 22.1362 | 0.7379 | | |
| Total | 47 | 198.8134 | | | |

Variate: trans_45

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 0.4914 | 0.2457 | 0.77 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 1.5988 | 1.5988 | 5.03 | 0.033 |
| Name_of_Genotype | 7 | 157.7320 | 22.5331 | 70.83 | <.001 |
| Location.Name_of_Genotype | 7 | 7.2594 | 1.0371 | 3.26 | 0.011 |
| Residual | 30 | 9.5441 | 0.3181 | | |
| Total | 47 | 176.6257 | | | |

Variate: trans_60

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 3.4109 | 1.7055 | 3.17 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 5.8175 | 5.8175 | 10.81 | 0.003 |
| Name_of_Genotype | 7 | 134.3623 | 19.1946 | 35.66 | <.001 |
| Location.Name_of_Genotype | 7 | 4.8437 | 0.6920 | 1.29 | 0.291 |
| Residual | 30 | 16.1486 | 0.5383 | | |
| Total 47 164.5830 | | | | | |

**Whitefly population**

Variate: trans_30

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 0.4076 | 0.2038 | 1.06 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 3.0478 | 3.0478 | 15.79 | <.001 |
| Name_of_Genotype | 7 | 1.2887 | 0.1841 | 0.95 | 0.482 |
| Location.Name_of_Genotype | 7 | 2.8584 | 0.4083 | 2.12 | 0.073 |
| Residual | 30 | 5.7908 | 0.1930 | | |
| Total 47 13.3932 | | | | | |

Variate: trans_45

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 0.1264 | 0.0632 | 0.15 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 30.9660 | 30.9660 | 71.42 | <.001 |
| Name_of_Genotype | 7 | 12.5064 | 1.7866 | 4.12 | 0.003 |
| Location.Name_of_Genotype | 7 | 13.0905 | 1.8701 | 4.31 | 0.002 |
| Residual | 30 | 13.0077 | 0.4336 | | |
| Total | 47 | 69.6970 | | | |

Variate: trans 60_days

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| Block stratum | 2 | 0.3346 | 0.1673 | 1.44 | |
| Block.*Units* stratum | | | | | |
| Location | 1 | 62.1141 | 62.1141 | 532.95 | <.001 |
| Name_of_Genotype | 7 | 3.3181 | 0.4740 | 4.07 | 0.003 |
| Location.Name_of_Genotype | 7 | 0.3000 | 0.0429 | 0.37 | 0.914 |
| Residual | 30 | 3.4964 | 0.1165 | | |
| Total | 47 | 69.5632 | | | |

Variate: **Mean fruit WT**

| Source of variation | d.f. | s.s. | m.s. | v.r. | F pr. |
|---|---|---|---|---|---|
| blocks stratum | 2 | 0.13653 | 0.06826 | 0.72 | |
| blocks.*Units* stratum | | | | | |
| Locatio | 1 | 4.57567 | 4.57567 | 47.95 | <.001 |
| Genotype | 7 | 79.45539 | 11.35077 | 118.94 | <.001 |
| Locatio.Genotype | 7 | 6.38172 | 0.91167 | 9.55 | <.001 |
| Residual | 30 | 2.86307 | 0.09544 | | |
| Total | 47 | 93.41239 | | | |

## APPENDIX D

## Climatic Data

| Climatological data | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Month | Aug | Sep | Oct | Nov | Dec | Jan | Feb | Mar | Apr | May | Jun |
| Mean Maximum Temperature | 28.8 | 29.6 | 30.4 | 31.7 | 31.3 | 32.5 | 32.4 | 32.8 | 32.1 | 32.5 | 30.6 |
| Mean Minimum Temperature | 17.3 | 18.1 | 18.2 | 18.9 | 18.5 | 18.7 | 18.6 | 19.4 | 19.2 | 19.9 | 18.4 |
| Month | Aug | Sep | Oct | Nov | Dec | Jan | Feb | Mar | Apr | May | Jun |
| Rainfall(mm) | 30 | 82.6 | 48.4 | 83.4 | 38.5 | 36.8 | 16.3 | 74.1 | 98.9 | 321.6 | 84.4 |
| Month | Aug | Sep | Oct | Nov | Dec | Jan | Feb | Mar | Apr | May | Jun |
| Mean Relative Humidity | 86 | 84 | 85 | 83 | 85 | 82 | 81 | 81 | 82 | 83 | 84 |

| Asuansi Climatological data | Mar | Apr | May | Jun |
|---|---|---|---|---|
| Month | | | | |
| Mean Maximum Temperature | 32.6 | 32.9 | 32.2 | 29.7 |
| Mean Minimum Temperature | 23 | 22.9 | 29 | 22.9 |
| Rainfall(mm) | 110.4 | 121.6 | 175.1 | 105.4 |
| Mean Relative Humidity | 81 | 81 | 81 | 85 |