Detection and epidemic dynamic of ToCV and CCYV with Bemisia tabaci and weed in Hainan of China

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Abstract

Background: In recent years, two of the crinivirus, Tomato chlorosis virus (ToCV) and Cucurbit chlorotic yellows virus (CCYV) have gained increasing attention due to their rapid spread and devastating impacts on vegetable production worldwide. Both of these viruses are transmitted by the sweet potato whitefly, Bemisia tabaci (Gennadius), in a semi-persistent manner. Up to now, there is still lack of report in Hainan, the south of China.

Methods: We used observational and experimental methods to explore the prevalence and incidence dynamic of CCYV and ToCV transmitted by whiteflies in Hainan of China.

Results: In 2016, the chlorosis symptom was observed in the tomato and cucumber plants with a large number of B. tabaci on the infected leaves in Hainan, China, with the incidence rate of 69.8% and 62.6% on tomato and cucumber, respectively. Based on molecular identification, Q biotype was determined with a viruliferous rate of 65.0% and 55.0% on the tomato and cucumber plants, respectively. The weed, Alternanthera philoxeroides near the tomato and cucumber was co-infected by the two viruses. Furthermore, incidence dynamic of ToCV and CCYV showed a close relationship with the weed, Alternanthera philoxeroides, which is widely distributed in Hainan.

Conclusion: Our results firstly reveal that the weed, A. philoxeroides is infected by both ToCV and CCYV. Besides, whiteflies showed a high viruliferous rate of ToCV and CCYV. Hainan is an extremely important vegetable production and seed breeding center in China. If the whitefly can carry these two viruses concurrently, co-infection in their mutual host plants can lead to devastating losses in the near future.

Keywords: Tomato chlorosis virus; cucurbit chlorotic yellows virus; Bemisia tabaci; Molecular identification, Q biotype, Alternanthera philoxeroides

Background

Plant virus causes serious threat in the growth and product of crops and vegetables in the world [1]. Plant viruses depend on insect vectors for transmission in a non-persistent, semi-persistent and persistent manner, respectively [2]. The prevalence of plant viruses is closely related to the dynamics of insect vectors [3, 4].

The whitefly, Bemisia tabaci (Gennadius) (hemiptera; Aleyrodidae) is a main vector for plant virus transmission in greenhouse, which has rapidly increased all over the world followed by outbreaks of whitefly-transmitted viruses, causing great losses in agricultural production [5–7]. The most destructive vector in China is B. tabaci B (MEAM1) and Q (MED) [8]. B. tabaci B has been documented in China since the mid-1990’s, but Tomato yellow leaf curl virus (TYLCV) was not detected until Q became established in 2003 [9, 10], and epidemic of TYLCV is associated with the increasing number of Q [10, 11]. Plant virus can be transmitted by whiteflies in a persistent or semi-persistent manner. Up to now, most research has been focused on the persistent-transmitted virus such as TYLCV but less attention is
paid on semi-persistent transmitted viruses. To note, research on the relationship between epidemiology of the crinivirus and whitefly is important to prevent virus outbreak.

Tomato chlorosis virus (ToCV), genus crinivirus, family *closteroviridae* [12], is transmitted by *B. tabaci* in a semi-persistent manner [1, 13]. The disorder and yellow symptoms such as the interveinal chlorosis, the leaf brittleness, and the limited necrotic flecking can be used to determine the virus [1, 14, 15]. ToCV was first reported in Florida [16], and then it transmitted to Spain [17], Africa [18, 19], the Middle East [17], and Asia [20, 21]. ToCV can be infected in 24 species of 7 family plants [1]. In Spain Q whiteflies has been determined on ToCV-infected leaves [17]. In Costa Rica Q whiteflies has also been detected on ToCV-infected leaves [22]. In China ToCV was first found in Taiwan [23], and then was found in Shandong [21] and many other northern places, such as Shanxi, Beijing and Neimenggu [24]. Up to now, there is still lack of report in the south of mainland China such as Hainan. With the increasing number of whiteflies in recent years, the potential threat should be noticed.

Cucurbit chlorotic yellows virus (CCYV) belongs to genus crinivirus, family *closteroviridae* [25]. CCYV can cause chlorotic leaf spots and yellowing of leaves in pumpkin, melon, watermelon, and tobacco [25, 26]. CCYV is transmitted by *B. tabaci* B and Q in a semi-persistent manner. It was first determined in Japan in 2010 [27], and then it was found in China [28], Sudan [29], Greece [30] and Iran [31]. CCYV was also found in many northern places in China, such as Beijing, Hebei, and Anhui provinces (unpublished data). There is still lack of reports on whitefly biotype detection on virus-infected plants, which has an important role in research of the relationship between epidemiology of the crinivirus and whitefly.

In this research, we found the severe typical chlorotic symptoms on tomato and cucumber in many vegetable growing areas in Hainan province—the south of China. We found that numerous whiteflies gathered on infected plant leaves in cultivated places. We then collected the whiteflies and infected leaves with typical symptoms and then brought them into laboratory to detect the whitefly biotype and to determine the virus. ToCV and CCYV were identified, and *B. tabaci* Q was determined in all infected leaves. The weeds, *Alternanthera philoxeroides* nearby were also collected and determined, and the dynamics of ToCV and CCYV were then determined on tomato, cucumber and weeds in four growth stages in Yongfazhen where ToCV and CCYV showed a high virus incidence. Our results provide a basis for monitoring and prevention of viral diseases.

**Methods**

**Field survey**

To determine the incidence of the chlorosis disease in tomato and cucumber crops, a survey was undertaken in the Hainan province. Five sites (Yunlongzhen, Xinzhuzhen,
Yongfazhen, Tianyzhen, and Yachengzhen), representing the main vegetable-growing areas were surveyed (Fig. 1). For each site, over 200 to 300 plants including tomato and cucumber were surveyed and the incidence of the chlorosis disease was calculated. At each site, the chlorosis tomato and cucumber plants were selected and taken to the laboratory for molecular detection. Meanwhile, whiteflies on the symptomatic plants were collect randomly with aspirating equipment and taken to the laboratory for molecular detection.

**Whitefly biotype and viruliferous rate detection**

The whitefly samples were divided into four parts, of which two parts were used to detect the whitefly biotype on tomato and cucumber, and the other two parts were used to detect the viruliferous rate of ToCV and CCYV. The whitefly biotype was detected using the CAPS-cleavage amplified polymorphic sequence of mitochondrial cytochrome oxidase I gene (*mtCOI*) with the restriction endonuclease *AseI* [32]. The viruliferous rate detection method was described in section of virus detection in plants. In each part, 20 whiteflies were detected, and each of the detection was repeated three times.

**RNA extraction and reverse transcription from infected leaves**

Total RNA was extracted separately from 0.1 g infected tomato and cucumber leaves using the total RNA extraction kit (Tiangen Biotech, Beijing, China) following the manufacturer’s instruction. Each of 20 samples was extracted from tomato and cucumber respectively. Each of the detection was repeated three times. Reverse transcription of RNA from the total nucleic acid extracts was performed using cDNA synthesis kit (Takara, Beijing, China), following the manufacturer’s instruction.

**Virus detection in plants**

ToCV detection: We selected 60 chlorosis tomato leaves for detection, of which 20 leaves were detected each time, and all the leaves were detected for 3 times. Reverse transcript–polymerase chain reaction (RT-PCR) was carried out using the primers designed in the HSP70h gene of ToCV using Primer Premier 5 software (Table 1). The PCR of ToCV was performed in 20 μl of reaction mixtures containing 7 μl of ddH₂O, 10 μl of mix, 1 μl of each primer, and 1 μl of cDNA. The PCR procedures are as follows: initial denaturation at 94 °C for 2 min, followed by 35 cycles of 94 °C for 15 s, 56 °C for 30 s and 72 °C for 30s, and a final elongation step at 72 °C for 10 min. The PCR products of ToCV were obtained and then separated by electrophoresis using 1.0% agarose gels.

CCYV detection: We selected 60 chlorosis cucumber leaves for detection, of which 20 leaves were detected each time, and all the cucumber leaves were detected for 3 times. The PCR of the cucumber samples was carried out using the primers designed in the coat protein (CP) gene of CCYV using Primer Premier 5 software (Table 1). The PCR of CCYV was performed in 20 μl of

| Virus | Host plants | Geographic locations | Number of plants surveyed | Number of infected plants | Incidence of chlorosis disease (%) | Average incidence of chlorosis disease (%) |
|-------|-------------|----------------------|---------------------------|---------------------------|-----------------------------------|--------------------------------------------|
| ToCV  | Tomato      | Yunlongzhen          | 145                       | 0                         | 0.0                               | 69.8                                       |
|       |             | Xinzhuzhen           | 146                       | 93                        | 63.7                              |                                            |
|       |             | Yongfazhen           | 154                       | 117                       | 76.0                              |                                            |
|       |             | Yachengzhen          | 165                       | 0                         | 0.0                               |                                            |
|       |             | Tianayzhen           | 150                       | 0                         | 0.0                               |                                            |
| CCYV  | Cucumber    | Yunlongzhen          | 92                        | 0                         | 0.0                               | 62.6                                       |
|       |             | Xinzhuzhen           | 90                        | 48                        | 53.3                              |                                            |
|       |             | Yongfazhen           | 84                        | 62                        | 73.8                              |                                            |
|       |             | Yachengzhen          | 66                        | 40                        | 60.6                              |                                            |
|       |             | Tianayzhen           | 81                        | 0                         | 0.0                               |                                            |
| ToCV  | Weed        | Yongfazhen           | 60                        | 9                         | 15.0                              | 15.0                                       |
| CCYV  | Weed        | Yongfazhen           | 60                        | 7                         | 11.7                              | 11.7                                       |

**Table 1 Primes of the ToCV, CCYV and whitefly**

| Name        | Primer | Sequence          |
|-------------|--------|-------------------|
| ToCV        | F      | AAACCTGCTGATGAAATGCTTC|
|             | R      | GGTGTGATTGTGTACTACATTCAAGT |
| CCYV        | F      | CGCAATGATAAGGGCGGGACC |
|             | R      | ACTACAACCTCAGGTCGGCAACT |
| Whitefly    | F      | TTGATTATTTCGTATCCAGAAGT |
|             | R      | CTGAATATCGRCGAGGCACTTCC |

**Table 2 Incidence of ToCV and CCYV**
reaction mixtures including 7 µl of ddH2O, 10 µl of mix, 1 µl of each primer, and 1 µl of cDNA. The PCR procedures are as follows: initial denaturation at 94 °C for 5 min, followed by 35 cycles of 94 °C for 15 s, 53 °C for 30 s and 72 °C for 1 min, and a final extension at 72 °C for 10 min. The PCR products of CCYV were obtained and then separated by electrophoresis using 1.0% agarose gels.

ToCV and CCYV detection on weeds: In Yongfazhen, where ToCV and CCYV were detected with a high incidence, we collected the weeds, *A. philoxeroides* which are close to the infected tomato and cucumber to detect ToCV and CCYV. We collected 60 weed leaves for detection of ToCV and CCYV in three replicates.

**Nucleotide sequencing analysis**

The target PCR products were purified by the AxyPrep DNA gel extraction kit (Axygen, Zhejiang, China), following the manufacturer's instructions. The purified products were then sequenced at the Sangon biotech (Shanghai, China). The sequence data of the whiteflies, ToCV and CCYV on tomato, cucumber and weeds were analysed using the BioEdit software. Sequences were compared with the NCBI nucleotide database via the BLAST tools on NCBI online server.

**Virus incidence dynamic on tomato, cucumber and weeds**

The incidence dynamics of ToCV and CCYV were determined on tomato, cucumber and the weeds nearby: In four growth stages, transplanting, seedling, flowering and ripening of tomato and cucumber, plants were collected to our lab to detect the viruliferous rate of ToCV and CCYV. The weed, *A. philoxeroides* that was grown near the tomato and cucumber plants was also collected to detect the viruliferous rate of ToCV and CCYV. In each of the five sites of Yongfazhen where ToCV and CCYV were detected with a high incidence, 100 tomato leaves were collected for detection of ToCV, and 100 cucumber leaves were collected for detection of CCYV. The tomato plants and cucumber plants were adjacent, therefore 100 weed leaves nearby were collected for detection of ToCV and CCYV. That is to say, 500 tomato leaves, 500 cucumber leaves and 500 weed leaves were collected in one growth stage.

**Table 3** Whitefly biotype and viruliferous rate

| Virus | Number of whiteflies | Whitefly biotype | Number of viruliferous whiteflies | Viruliferous rate |
|-------|----------------------|------------------|-----------------------------------|-----------------|
| ToCV  | 60                   | Q                | 39                                | 65.0%           |
| CCYV  | 60                   | Q                | 33                                | 55.0%           |
Data analysis
Statistical analyses were performed with SPSS (version 19.0, Chicago, IL, USA). One-way ANOVA was used to compare the viruliferous rate of plants in different growth stages and weeds.

Results
Incidence of chlorosis disease
The total number of 300 tomato plants and 240 cucumber plants was counted in infected places of Xinzhuzhen, Yongfazhen and Yazhouzhen to calculate the virus incidence. The total number of 210 tomato plants and 150 cucumber plants was observed to show chlorosis symptom, with the average incidence of 69.8% and 62.6%, respectively (Fig. 1, Table 2). In Yongfazhen, the viruliferous rate of ToCV and CCYV on the weed was 15.0% and 11.7%, respectively (Fig. 1, Table 2).

Whitefly biotype and viruliferous rate detection
PCR amplification confirmed that all the whiteflies gathered in symptomatic tomato and cucumber plants were B. tabaci Q. The percentage of viruliferous whitefly was 65.0% and 55.0%, respectively (Fig. 2; Table 3).

Virus detection in plants
The size of 804 bp based on amplification of CP (coat protein) gene of CCYV was amplified, which revealed that the symptomatic cucumber plants collected in Xinzhuzhen, Yongfazhen and Yazhouzhen and the weeds collected in Yongfazhen of Hainan province was infected by CCYV (Figs. 3 and 5a).

The size of 466 bp based on amplification of heat shock 70-like protein (HSP70h) gene of ToCV was amplified, which showed that the chlorosis tomato plants collected in Xinzhuzhen and Yongfazhen and the weeds collected in Yongfazhen of Hainan province was infected by ToCV (Figs. 4 and 5b).

Nucleotide sequencing analysis
The sequencing results were shown in Table 4. The sequence of the whitefly samples shows a similarity of 99% with the cytochrome oxidase subunit I (COI) gene of B. tabaci Q (KT265875.1). Virus samples in tomato were 100% similar with the RNA1 of ToCV (KC887999.1), and the virus samples in cucumber showed 97% similar with the CP gene of CCYV (KX118632.1). The virus samples in weed showed a similarity of 99% and 97%
with the RNA1 of ToCV (KC887999.1) and the CP of CCYV (KX118632.1), respectively.

Virus incidence dynamic on tomato, cucumber and weeds
Virus incidence dynamic of ToCV on tomato, and the weed, A. philoxeroides and CCYV on cucumber and A. philoxeroides changes significantly in the four growth stages of plants (ToCV on tomato: $F_{3,16} = 160.737$, $P < 0.001$; ToCV on weed: $F_{3,16} = 91.701$, $P < 0.001$; CCYV on cucumber: $F_{3,16} = 136.496$, $P < 0.001$; CCYV on weed: $F_{3,16} = 75.522$, $P < 0.001$). In the transplanting stage, viruliferous rate of both ToCV on tomato and CCYV on cucumber was 0%. However, in the ripening stage, viruliferous rate of ToCV and CCYV on tomato and cucumber was highest, with the viruliferous rate of 77% and 62.4%, respectively. Viruliferous rate of ToCV and CCYV on A. philoxeroides showed an opposite trend, which was highest in the transplanting stage of plants and lowest in the ripening stage of plants. In the transplanting stage, the viruliferous rate of ToCV and CCYV on A. philoxeroides was 76.8% and 66.6%, respectively. In the ripening stage, the viruliferous rate of ToCV and CCYV on A. philoxeroides was 15.4% and 12.6%, respectively. Notably, the weed A. philoxeroides that was adjacent from tomato and cucumber can carry both ToCV and CCYV at the same time, with the co-infection viruliferous rate of 32.2% and 6.4% in the transplanting stage and ripening stage, respectively (Fig. 6).

Discussion
B. tabaci is a most important insect vector in agricultural areas and has caused great losses in economy and crop production worldwide [25, 33]. The indirect damage caused by virus transmission is much serious than the direct feeding on the host. For example, TYLCV is transmitted by whitefly in a persistent manner, which causes destructive damage in China [9, 34]. In recent years, TYLCV has attracted the large attention and a series of measure has been used to prevent the disease by researchers in China [11, 35–37]. However, up to now, we still pay less attention to most of the semi-

**Table 4** Nucleotide sequencing analysis of B. tabaci and plant viruses

| Sample | Sequencing description | Accession     | Max score | Total score | Query cover | E value | Identities |
|--------|-------------------------|---------------|-----------|-------------|-------------|---------|------------|
| Tomato | Tomato chlorosis virus isolate ToCV-BJ segment RNA2 | KC887999.1 | 863       | 863         | 45%         | 0.0     | 100%       |
| Cucumber | Cucurbit chlorotic yellows virus isolate GX-BH capsid protein gene | KX118632.1 | 1354      | 1354        | 97%         | 0.0     | 99%        |
| B. tabaci | Bemisia tabaci biotype Q cytochrome oxidase subunit 1 (COI) gene | KT265875.1 | 1062      | 1062        | 99%         | 0.0     | 99%        |
| Weed | Tomato chlorosis virus isolate ToCV-BJ segment RNA2 | KC887999.1 | 856       | 856         | 41%         | 0.0     | 99%        |
| Weed | Cucurbit chlorotic yellows virus isolate GX-BH capsid protein gene | KX118632.1 | 1055      | 1055        | 77%         | 0.0     | 97%        |
persistent viruses transmitted by the whitefly. Furthermore, those plant viruses such as ToCV and CCYV are huge potential crises to agricultural production.

In our research, we found that high density rates of Q at open field in Hainan province and at the same areas we determined that the leaves were infected by ToCV and CCYV, with the incidence of 69.8% and 62.6% on tomato and cucumber plants, respectively. Besides, the viruliferous rate of Q was 65.0% and 55.0% on the tomato and cucumber plants, respectively. Plant virus disease prevalence is closely related to the spread of insect vector. Although B. tabaci B has been shown to be an effective vector of ToCV [1], recently, Q has become a major threat to the quality and yields by transmitting ToCV [22]. Besides, B. tabaci Q plays more roles than B in carrying CCYV [38]. In this research, we notice that the prevalence of CCYV in cucumber and ToCV in tomato was high which was consistent with the high viruliferous rate of Q. Therefore we can speculate that high viruliferous rate of Q may facilitate transmission of ToCV and CCYV.

The weed A. philoxeroides, which was grown near the infected tomato and cucumber, was also infected by ToCV and CCYV. The virus dynamic was then detected on tomato, cucumber and the weeds nearby. In the four growth stages, virus showed a different dynamic on plants and on weeds. On tomato and cucumber plants, viruliferous rate of ToCV and CCYV increased gradually from transplanting stage to ripening stage. On weeds, viruliferous rate of ToCV and CCYV decreased gradually from ripening stage to transplanting stage. Furthermore, both of the ToCV and CCYV were detected on the weed, A. philoxeroides, which is a widely distributed weed in Hainan. To our knowledge, this is the first report of ToCV and CCYV on the weed, A. philoxeroides. From our results we can see that the weed, A. philoxeroides is co-infected and may promote the virus transmission, it’s a pity that we didn’t detect whether the whiteflies were co-infected on weeds, and this needs further confirmation. Notably, Hainan is the mainly vegetable production and breeding center especially for breeding tomato and cucumber in China. In winter season, vegetables in Hainan are transported to all of the north provinces of China because of the low temperature in north provinces. Therefore, the break out of these two viruses may cause fast transmission of ToCV and CCYV to other places via infected seed or viruliferous whiteflies.

**Conclusion**

This report firstly shows ToCV and CCYV detected in the same area with a high incidence in Hainan province, with a high viruliferous rate of Q on infected leaves. Furthermore, the virus dynamic shows a close relationship with the weed nearby, and the weed is infected by both ToCV and CCYV. Hainan is an extremely important vegetable production and seed breeding center in China. If the whitefly can carry these two viruses concurrently, co-infection in their mutual host plants can lead to devastating losses in the near future. Further research should be done to investigate the role of weed in the transmission of virus.

**Abbreviations**

CCYV: Cucurbit chlorotic yellows virus; CP: Coat protein; HSP70h: Heat shock 70-like protein; RT-PCR: Reverse transcript–polymerase chain reaction; ToCV: Tomato chlorosis virus; TYLCV: Tomato yellow leaf curl virus

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Availability of data and materials
The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

Authors’ contributions
XT, XBS, XGZ and YL designed the experiments. XT and XBS performed the experiments. XT analyzed the data. XT and XBS wrote the manuscript. DY2, FL, FY and YIZ contributed reagents/materials. All authors read and approved the final manuscript.

Ethics approval and consent to participate
Not applicable.

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Competing interests
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