

Article

Upregulation of Endosymbiont Densities in *Bemisia tabaci* by Acquisition of Tomato Yellow Leaf Curl Virus

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Abstract

Sweetpotato whitefly, *Bemisia tabaci*, is a vector of more than 100 plant-diseased viruses, as well as a serious pest of various horticultural plants. This species harbors a primary endosymbiont *Portiera* along with several secondary endosymbionts such as *Cardinium* and *Hamiltonella*. We investigated whether or not TYLCV acquisition alters the densities of endosymbionts in the body of *B. tabaci* using quantitative real-time PCR. Our results showed that the densities of both *Cardinium* and *Hamiltonella*, but not *Portiera*, increased upon acquisition of TYLCV. In addition, expression of GroEL, a molecular chaperone produced by *Hamiltonella*, was significantly upregulated in TYLCV-infected whiteflies. Our results suggest that endosymbionts may play an important role in TYLCV transmission mechanism within the body of *B. tabaci*.

Keywords : *Cardinium*, GroEL, *Hamiltonella*, TYLCV, Vector insects, Virus transmission

Introduction

Endosymbiotic bacteria have been identified in various arthropod species including insects. It has become increasingly evident that endosymbionts can have major effects on their host's biology, ecological relationships, and evolutionary dynamics (Moran, 2006). The influence of endosymbionts on their hosts can range from beneficial to detrimental, and effects may be conditional on extrinsic factors (Russell and Moran, 2006; Haine, 2008).

Bemisia tabaci harbors primary obligate and secondary facultative endosymbionts (Baumann, 2005). The primary endosymbiont *Portiera* is harbored within bacteriocytes and supplements its insect host with essential amino acids for growth and reproduction (Douglas, 1989; Baumann et al., 2000; Moran et al., 2003). In addition, *B. tabaci* harbors several secondary endosymbionts, including *Arsenophonus* (Thao and Baumann, 2004), *Cardinium* (Weeks et al., 2003), *Fritschea* (Everett et al., 2005), *Hamiltonella* (Moran et al., 2005), *Rickettsia* (Gottlieb et al., 2006), and *Wolbachia* (Zchori-fein and Brown, 2002). In addition to providing essential nutrients to their insect hosts, these endosymbionts bestow functional capabilities such as temperature tolerance (Montlloret et al., 2002), increased resistance to parasites (Oliver et al., 2003), increased resistance to insecticides (Kontsedalov et al., 2008), sex determination (Himler et al., 2011), and other unidentified physiological and

ecological activities.

Endosymbionts play a major role in virus transmission of *B. tabaci* as well as other vector insects. Several studies have shown that a molecular chaperone, GroEL protein, produced from endosymbionts has a protective role by binding to coat protein of viruses in the vector's body. GroEL protein of *Buchnera aphidicola* binds to luteovirus coat protein and prevents virus particles from proteolysis in the gut and hemolymph of *Myzus persicae* (Van den Heuvel et al., 1997). It has also been reported that interrupting the interaction between GroEL and coat protein leads to a dramatic decrease in virus transmission efficiency in *B. tabaci* (Morin et al., 1999, 2000). Tomato yellow leaf curl virus (TYLCV) is exclusively vectored by *B. tabaci*, and its transmission depends on the presence of GroEL protein, which is produced by *Hamiltonella* but not other endosymbionts (Gottlieb et al., 2010). Further, Rana et al. (2012) reported that Cotton leaf curl virus (CLCuV) coat protein strongly interacts with GroEL from *Arsenophonus*, whereas both *Escherichia coli* and *Portiera* GroEL proteins do not interact with CLCuV coat protein. They suggest *Arsenophonus* is highly involved in the transmission of CLCuV in the AsiaII genetic group of *B. tabaci*. Therefore, it is likely that the relationship between virus and endosymbiont is highly specific at a species level within the vector's body. Here, we demonstrated whether TYLCV acquisition influence on the density of different endosymbionts

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in *B. tabaci*.

Materials and methods

Insect collection and rearing

Bemisia tabaci were initially collected from Korean melon (*Cucumis melo* var. *nakuwa*) grown in a greenhouse in Seongju, Korea in 2009 and maintained in the laboratory as a non-viruliferous (NV) colony on tomato plants (*Lycopersicon esculentum* Mill.) in insect-proof cages ($45 \times 60 \times 90$ cm³). A portion of the NV colony was transferred into another cage housing TYLCV-infected tomato plants and maintained as a TYLCV-viruliferous (V) colony. These two colonies were then reared in separate insect-rearing rooms under conditions of $25 \pm 2^\circ\text{C}$, $60 \pm 5\%$ relative humidity, and a 16 h light/8 h dark (16L:8D) photoperiodic cycle. TYLCV infection of both colonies was confirmed by PCR analysis at regular intervals over 1 month (Park *et al.*, 2012). After every month, fresh TYLCV-free tomato plants were put into both cages. Our previous study on the identification of biotype and endosymbiont profile shows that our colony is Q1 biotype (mtCOI GenBank accession number HM488315) (Park *et al.*, 2012).

Clip cage assay

Clip cage was a hand-made instrument, namely a crystal clear, plastic, round-shaped tube (1.5 cm diameter). Specifically, a

tube was cut to a length of 0.5 cm and sealed at one side with a fine insect-proof mesh. A small-sized hole (2 mm diameter) was prepared on the side of the cage in order to allow whiteflies to enter. A lid was prepared from a plastic piece having the same size as the tube, after which both the cage and lid were attached to the clip. The clip cage was then attached to the underside of a tomato plant leaf. To make TYLCV-infected tomato plants, adult V whiteflies (n=50) were collected from the V colony using a fine glass tube (act as an aspirator) and aspirated into the clip cage through the hole, after which they were kept in a mesh acrylic glass box ($30 \times 30 \times 40$ cm³) for up to 48 hours (Fig. 1A). After 48 hours, we removed the clip cage and collected a small part of the leaves in order to confirm TYLCV infection by PCR (Fig. 1B). The leaves were then put into an acrylic box and were considered as TYLCV-infected tomato plants. We used another box to house TYLCV-free tomato plants. Subsequently, we released the same number (n=500) of NV day-0 whiteflies in the two acrylic cages. Every conjugative day (2, 4, 6, and 8), we collected the same number of whiteflies from both cages for DNA and RNA extraction (25 for DNA and 100 for RNA extraction).

Genomic DNA extraction

Total genomic DNA was extracted from 25 individual adult *B. tabaci* whiteflies according to the protocol supplied by the Invitrogen Purelink Genomic DNA mini kit. After collecting

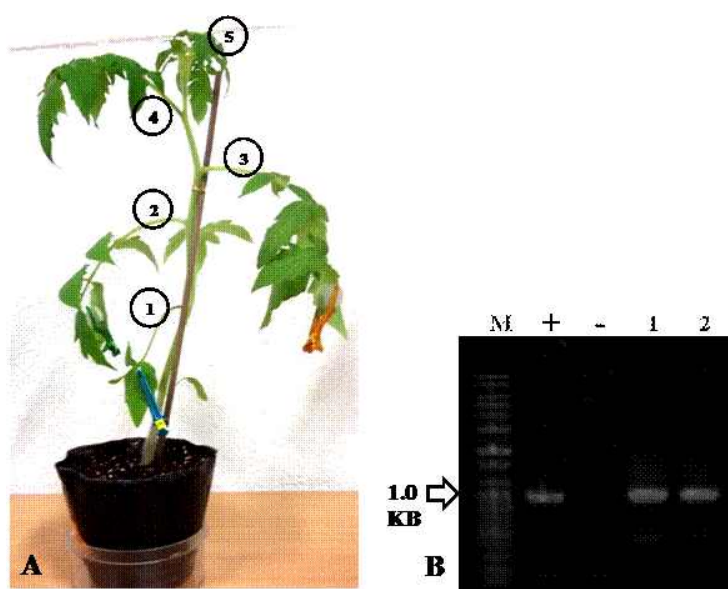


Fig 1. Procedure for construction of TYLCV-infected tomato plants using clip cages with viruliferous whitefly.

Five leaves (1-5) of tomato plant prepared with three clip cages, which were attached to the 1st, 2nd, and 3rd leaves (A). After 48 hours, TYLCV infection was checked using small pieces from the 4th and 5th leaves by PCR (B). DNA marker (M), a positive control (+), a negative control (-), 4th leaf (1), and 5th leaf (2).

the samples from individual NV and V colonies, whiteflies were homogenized in 180 μ l of genomic digestion buffer using a 1.5 ml microcentrifuge tube and micropestle (homogenizer). After the addition of 200 μ l of genomic lysis/binding buffer (1% SDS, 10 mM Tris-HCl, pH 8.0, 25 mM EDTA, 25 mM NaCl, 200 mg/ml of Proteinase K), 200 μ l of absolute ethanol was immediately added. Wash buffer was then added into the genomic column, after which 20 μ l of genomic elution buffer (Invitrogen Purelink, USA) was added. After 1 min of incubation at room temperature, samples were centrifuged at about 12,000 rpm for 1 min. The supernatants and pellets were directly used for PCR detection of secondary endosymbionts or stored at -20°C for later use.

cDNA production

Total RNAs were extracted from whole bodies of 100 adult *B. tabaci* Q1 biotype NV and V whiteflies that were 2, 4, 6, and 8 days old (D2, D4, D6, and D8, respectively) according to the protocol with TRI reagent (MRC Inc., Cincinnati, OH, USA). All extracts were treated with RQ1 DNAase (RNase-free) (Promega, Madison, WI, USA) to avoid DNA contamination. RNAs were subjected to gel electrophoresis and quantified using an IMPLEN Nano photometer (Implen GmbH, Munich, Germany). Two micrograms of RNA was used to synthesize cDNA using a High capacity cDNA reverse transcription kit (Applied Biosystems, Foster city, CA, USA) in a total reaction volume of 20 μ l.

Quantitative real-time polymerase chain reaction (qRT-PCR)

Quantification of the different endosymbionts was performed by amplification using Power SYBR Green PCR Master Mix (Applied Biosystems, USA) and 10 pmol of each primer. Using nucleotide sequences from the NCBI database, gene-specific primers for TYLCV, *Portiera* (primary endosymbiont) 16S rDNA, *Portiera* GroEL, *Cardinium* (secondary endosymbiont) 16S rDNA, *Hamiltonella* (secondary endosymbiont) 16S rDNA, *Hamiltonella* GroEL, and *B. tabaci* actin were designed for quantitative real-time PCR (Table 1). The cDNA samples (0.2 μ l) were run in triplicate on a 7300 Sequence Detection System (Applied Biosystems, USA) for 1 cycle of denaturation (95°C for 15 min), 45 cycles of amplification (95°C for 10 sec; 58°C for 20 sec; 72°C for 30 sec), and 1 cycle of dissociation (95°C for 15 sec; 60°C for 30 sec; 95°C for 15 sec). The expression level of each gene was determined by measuring the relative quantities of cDNAs to their respective mRNAs. The Ct (Threshold cycles) values were used to calculate the mRNA levels. Data were analyzed using the formula: $2^{-\Delta\Delta Ct} = 2^{-(\Delta Ct_{\text{treatment}} - \Delta Ct_{\text{control}})}$. The partial nucleotide sequence of actin from *B. tabaci* (AF071908) was identified from the *Bemisia* EST database in NCBI Genbank. The actin level was used as a reference to normalize the expression levels of the other genes. To ensure validity of the data, the number of bacterial genomes was tested in triplicate in each independent experiment.

Table 1. Oligonucleotide primer sequences used in quantitative real-time PCR

Targeted gene	Primer sequence (5' to 3')	Product size (bp)
TYLCV	F-TCTGTTACGGATTTCGTTG R-GCTGTCGAAGTTCAGCCTTC	182
<i>Portiera</i> 16S rRNA	F-TCAACTAGCCGTTGGATTCTTAAA R-TACTCCCCAGGCGATCAACT	71
<i>Cardinium</i> 16S rRNA	F-GCCGGCGACCGGCGAATG R-CGGAGGCTATCCCCAGTGT	66
<i>Hamiltonella</i> 16S rRNA	F-GTAAACGATGTCGATTTGGAGGT R-GCGGTCGATTTAACGCGT	71
<i>Portiera</i> GroEL	F-GTTGTAGCTGGAGGAGGTAAGTCTT R-TGTTTGGTCTTCGTTGTGTC	71
<i>Hamiltonella</i> GroEL	F-TCTTCGATTTTTACCTGCTCC R-CAATGCAAAACGCGTCGTC	71
<i>B. tabaci</i> Actin	F-GACGGACAGGTCATCATAATCG R-CATACCCAAGAAGGATGGCTG	78
<i>B. tabaci</i> Actin	F-TCA CCA CCA CAG CTG AGA GA R-CTC GTG GAT ACC GCA AGA TT	231

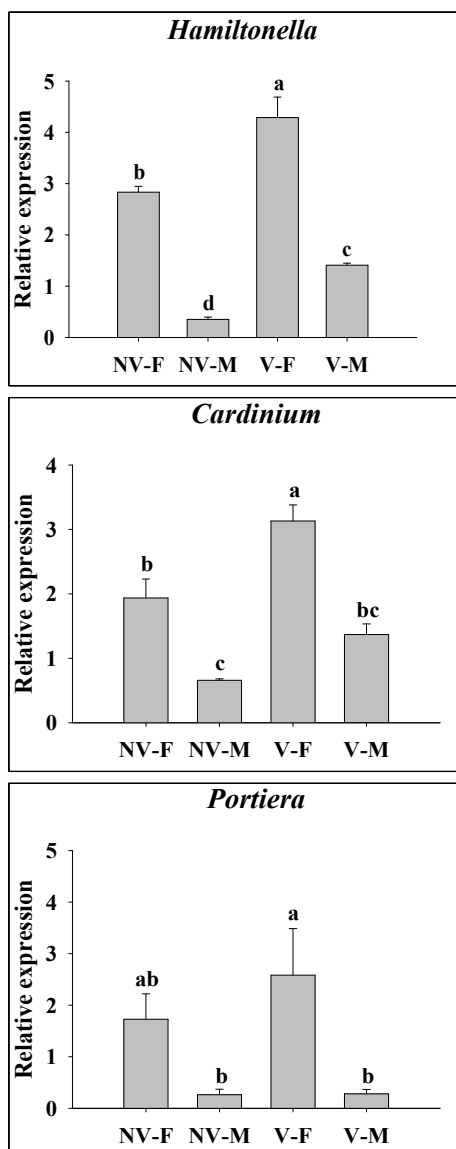


Fig 2. Quantitative real-time PCR analysis of endosymbiont density.

Genomic DNA samples were extracted from female (NV-F) and male (NV-M) of non-viruliferous individuals, and female (V-F) and male (V-M) of viruliferous individuals of *B. tabaci* (n = 100). Different letters above columns indicate statistically significant differences (P < 0.05) using DMRT by SAS.

Statistical analysis

Data were expressed in three individual replicates, and mean values ± standard error were plotted using Sigma plot (Systat software, Inc., Point Richmond, CA, USA). Analysis of variance (ANOVA) was carried out in order to analyze the means by using PROC General Linear Model (GLM) with the Statistical Analysis System (SAS, 2002-2003 SAS Institute Inc., Cary, NC, USA) version 9.1 program. Significant differences among

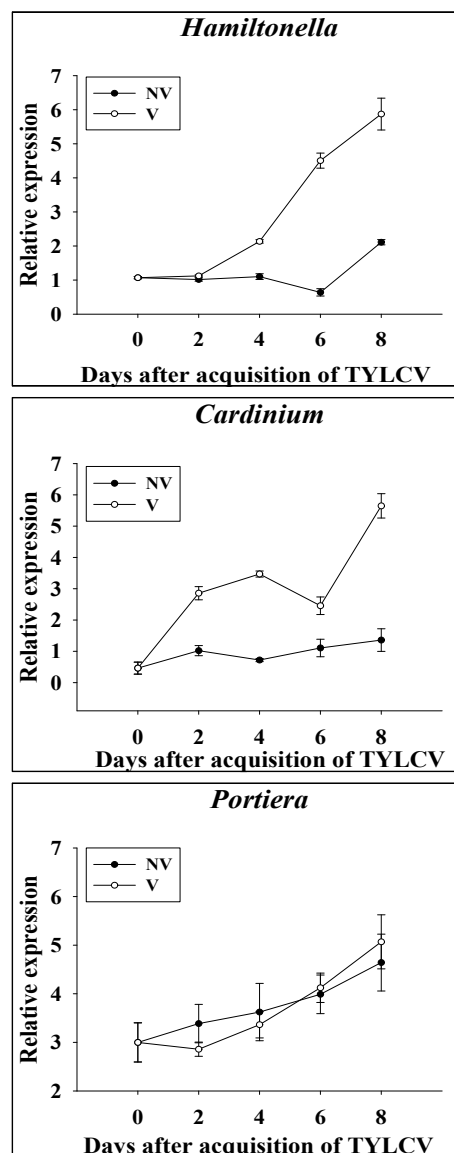


Fig 3. Comparison of densities of three endosymbionts between NV and V *B. tabaci*.

Quantitative real-time PCR analysis was conducted using genomic DNA samples collected from adult *B. tabaci* of 0, 2, 4, 6, and 8 days after TYLCV acquisition.

mean values were determined using Duncan’s Multiple Range Tests (DMRT) at a 95% confidence level. Data were analyzed by using completely randomized design with three individual replications.

Results

Comparison of endosymbiont densities between NV and V whiteflies

Our previous study on the identification of biotype and

endosymbiont profile shows that our colony is Q1 biotype (mtCOI GenBank accession number HM488315) harboring the secondary endosymbionts *Cardinium* and *Hamiltonella*, but not *Arsenophonus*, *Rickettsia*, and *Wolbachia* (Park et al., 2012). Thus, we analyzed one primary (*Portiera*) and two secondary (*Cardinium* and *Hamiltonella*) endosymbionts.

Densities of primary (*Portiera*) and secondary (*Cardinium* and *Hamiltonella*) endosymbionts were significantly different between sexes (Fig. 2). Female whiteflies displayed higher densities of all three endosymbionts compared to males regardless of TYLCV acquisition. In comparing NV with V whiteflies, endosymbiont densities mostly increased in V whiteflies, although the rates slightly differed. For example, the density of *Portiera* slightly increased only in females, whereas the densities of both *Cardinium* and *Hamiltonella* significantly increased in both sexes (Fig. 2). When bacterial densities were analyzed continuously for 8 days, *Portiera* density gradually increased in both NV and V whiteflies. However, both *Cardinium* and *Hamiltonella* densities gradually increased in V whiteflies, whereas they remained at constant levels in NV whiteflies (Fig. 3).

GroEL expression of endosymbionts in NV and V whiteflies

To compare GroEL expression levels between NV and V whiteflies, adult whiteflies (n=100) were collected from NV and V colonies, after which GroEL mRNA levels were determined using quantitative real-time PCR analysis (Fig. 4). GroEL mRNA level of *Portiera* was gradually increased in both NV and V whiteflies. On the other hand, GroEL mRNA level of *Hamiltonella* was increased in V whiteflies from 2 days following TYLCV acquisition, whereas it remained at constant levels in TYLCV-free whiteflies.

Discussion

Similar to a previous report, B and Q1 biotypes of *Bemisia tabaci* are present in Korea. The Q1 biotype is available everywhere in Korea, even Jeju-do island, whereas the B biotype is only restricted to the Goyang region (Park et al., 2012). Both B and Q1 biotypes of *B. tabaci* harbor various secondary endosymbionts with distribution patterns that vary according to biotype. For instance, *Hamiltonella* is common in both B and Q1 biotypes in Korea, whereas other endosymbionts are more selective (Park et al., 2012).

Here, we showed that the densities of both primary (*Portiera*) and secondary (*Cardinium* and *Hamiltonella*) endosymbionts were higher in female compared to male whiteflies. Our results are similar with those of Cohen and Harpaz (1964) and

Muniyappa et al. (2000), who observed that virus diffusion of female whiteflies is higher than males in frequency upon virus transmission from infected to non-infected plants. Namely, females can transmit TYLCV about 5-fold more proficiently than males (Cohen and Harpaz, 1964). Similarly, ToLCV from Bangalore is transmitted by females more efficiently than by males (Muniyappa et al., 2000). Thus, endosymbiont density is sexually differentiated and this is highly significant in virus transmission of vector insects.

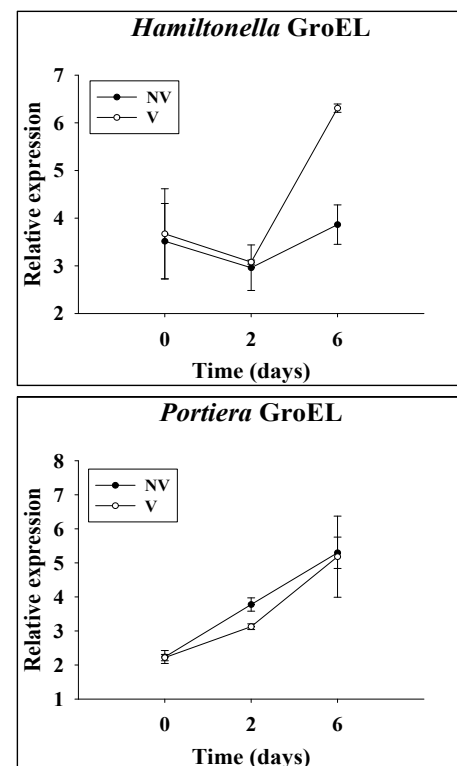


Fig 4. Comparison of GroEL mRNA levels of endosymbionts between NV and V individuals of adult *B. tabaci*.

Quantitative real-time PCR analysis was conducted using cDNA samples collected from 0, 2, and 6 day-old adult whiteflies.

Our genomic DNA analysis showed that endosymbiont densities were increased in both sexes of *B. tabaci* after acquisition of TYLCV. Particularly, this was significant in *Cardinium* and *Hamiltonella* endosymbionts. Otherwise, *Portiera* density was increased at a similar level in both NV and V individuals. Furthermore, GroEL mRNA level of *Hamiltonella* was increased upon TYLCV acquisition, whereas it remained steady in TYLCV-free whiteflies. Our results suggest that TYLCV acquisition induces multiplication of both *Cardinium* and *Hamiltonella* within vector's body. *Hamiltonella* is responsible

to protect TYLCV in the hemolymph by releasing GroEL which binds to coat protein of TYLCV (Gottlieb *et al.*, 2010). TYLCV particles may be more stable in the hemolymph due to the increased amount of *Hamiltonella*. We suppose that this mechanism is highly efficient for the successful transmission of virus.

Similar to *Hamiltonella*, we found that density of *Cardinium* was also increased by the acquisition of TYLCV. This suggests that *Cardinium* may also associate with transmission of TYLCV. However, there is no report on the relationship between *Cardinium* and virus transmission. *Cardinium* is usually located within the reproductive tissues and highly involved in reproduction alteration of various arthropod species (Zchori-Fein and Perlman, 2004). It is also possible that increased *Cardinium* by TYLCV acquisition may influence on the reproductive changes such as cytoplasmic incompatibility, parthenogenesis and feminization (Chigira and Miura, 2005).

In summary, our studies demonstrated that Q1 biotypes of *B. tabaci* increase densities of both *Cardinium* and *Hamiltonella* by the acquisition of TYLCV. We further determined that GroEL expression level was increased in *Hamiltonella*. These results suggest that virus vectoring ability of whiteflies could be increased by upregulated densities of the endosymbionts in viruliferous whiteflies.

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