

Biotype identification of *Bemisia tabaci* by acoustical methodHiroki Nakabayashi¹, Koichi Mizutani², Tadashi Ebihara³, Naoto Wakatsuki⁴, Hiroyuki Uga⁵, Kenji Kubota⁶, Masahisa Ishii⁷

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ABSTRACT

Bemisia tabaci has two major biotypes: B and Q. Biotype identification is necessary for whitefly control, since different biotypes have different pesticide resistance. However, slow and expensive techniques are needed for accurate biotype classification. In this paper, we propose a whitefly biotype identification scheme using an acoustic signature, and evaluate its performance. The proposed scheme achieves biotype identification by three steps: signal detection, frequency-domain matching, and classification of biotypes. We evaluated the performance of the proposed scheme by processing actual whitefly sounds obtained in a recording experiment, and calculated the accuracy of the classification. Results showed the proposed biotype identification method achieved a correct detection rate of 92% in *Bemisia tabaci*. This result suggests that the proposed scheme is a viable alternative for biotype identification of whitefly.

1. Introduction

Whitefly (e.g., *Bemisia tabaci* and *Trialeurodes vaporariorum*) is a major pest insect commonly found in greenhouse environments (Brown et al. 1995; Denholm et al. 1998). Once whitefly invade a greenhouse environment, they quickly become distributed over the entire greenhouse, and immediately attack a huge assortment of vegetables, causing millions in damage. Specifically, they transmit more than 100 kinds of virus, in particular the tomato yellow leaf curl virus—one of the most damaging pathogens of tomato, with losses up to 100% in commercial fruit production (Czosnek et al., 2001; Jones, 2003; UC IPM, 2016a). Hence, control of whitefly is an urgent issue for increased crop yield.

Physical, chemical and biological methods have widely been proposed to control whitefly (Denholm et al., 1998; UC IPM, 2016b), and a combination thereof is currently in actual use. In terms of chemical control, species and biotypes of whitefly are important information for determining optimum pesticide, since pesticide sensitivity is different according to whitefly species and biotypes (Horowitz et al., 2005; Prabhaker et al., 2005). To determine species and biotypes of whitefly, appearance check using microscope (Ma et al., 2007) and genetic testing (Ma et al., 2007) are employed, respectively.

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Focusing on biotype testing, however, is slow, high-cost and complicated, since whiteflies with different biotypes have a similar appearance. Nevertheless, to the best of our knowledge, these schemes [e.g. RAPD-PCR method, (Qiu et al. 2009)] are the only alternative for accurate determination, resulting in decreased utilization of biotype testing.

We focus here on the acoustic communication of *Bemisia tabaci*, which are spread globally and cause remarkable economical loss in many countries (De Barro et al. 2011; Perring 2001; Tay et al., 2012). *Bemisia tabaci* have two major biotypes: Middle East-Asia minor 1 (B-biotype) (Bellows et al., 1994; Lima et al 2000;) and Mediterranean (Q-biotype) (Perring 2001; Chu et al. 2006; Ueda and Brown 2006; Boykin et al. 2007). Meanwhile, hybridization of the B- and Q-biotypes has not been reported, which means that the whitefly reproduction and development process is closed within each biotype. It has been reported that whiteflies make unique sounds before reproduction, and one study found that the acoustic communication plays an important role in the mating process (Kanmiya 1996). Thus, one possibility is that whitefly biotypes could be identified from the characteristics of their sound communication. It has been reported that acoustic sounds of whiteflies vary depending on species (Kanmiya et al. 2011; Kashima et al. 2016) and biotype (Nakabayashi et al. 2016). Hence, biotype identification of whitefly could be achieved by acoustic means.

In this paper, we propose a scheme to identify *Bemisia tabaci* using acoustic signature, to provide fast, reliable, and cost-effective biotype identification. More specifically, we design a signal-processing method that can detect the sound of whitefly and determine its biotype automatically. The performance of the proposed scheme is then evaluated by experiments. Section 2 presents an overview of the acoustics sounds of *Bemisia tabaci* and their characteristics. Section 3 describes the biotype identification scheme of *Bemisia tabaci* by acoustic signature. We evaluate the performance of the proposed scheme in experiments in Section 4, and Section 5 contains our conclusions.

2. Acoustic sound of *Bemisia tabaci*

In this section, we present an overview of an acoustic monitoring system that can record the acoustic communication signals of *Bemisia tabaci* (B-biotype and Q-biotype) as naturally as possible (Nakabayashi 2015), and examine the differences in recorded sounds (Nakabayashi 2016) in 2.1 and 2.2, respectively.

2.1. Acoustic monitoring system of *Bemisia tabaci*

Whitefly makes unique sounds before reproduction, and it has been found that acoustic communication plays an important role in the mating process (Kanmiya 1996). However, the sound of whitefly is very faint, and therefore difficult to observe (Kanmiya [1996] amplified the sound of whitefly using a thin resonance film). To monitor the sound of whitefly as naturally as possible (i.e., without the effect of the film), we designed an acoustic monitoring system (Figure 1). As shown in the figure, an insect-breeding box (SPL-310077, SPL Life Sciences) and a highly sensitive microphone (Type4955, B&K) were placed inside a full anechoic chamber. About 20–40 whiteflies were put in the box with a cucumber plant, with the cucumber plant leaf arranged close to the through-hole of the box. This was because the microphone was inserted into the box via the through-hole, and whitefly is often found in thick crowds on the undersides of leaves. Hence, it was expected that whiteflies would stay near the microphone, resulting in successful recording of their natural sound. The recorded sound was amplified with a conditioning amplifier (Type2690, B&K), and then stored to a PC via an analog-to-digital (A-D) converter (USB-6221, National Instruments). The sensitivity of this monitoring system (microphone, preamplifier, and signal-conditioning amplifier system) was set at 10 V/Pa. With this monitoring system, recording experiments to obtain the sounds of *Bemisia tabaci* B- and Q-biotypes were performed for 6 h. The number of whiteflies in each recording experiment was as follows: about 40 in the B-biotype experiment, and about 20 in the Q-biotype experiment. From these recordings, 1,500 and 1,000 sound samples were obtained for the B-biotype and Q-biotype, respectively.

2.2. Overview of acoustic sound of *Bemisia tabaci* and their characteristics

Figure 2 shows the time- and frequency-domains of recorded sounds of *Bemisia tabaci* B-biotype and Q-biotype obtained from experiments. The time-domain of the recorded sounds [B-biotype: Figure 2(a-1) and Q-biotype: Figure 2(b-1)] revealed that the duration of the sounds was about 0.5 s regardless of biotype. However, for the frequency-domain of sounds [B-biotype: Figure 2(a-2) and Q-biotype: Figure 2(b-2)], it was found that the power spectrum shape of the B- and Q-biotypes were different. Specifically, the power spectrum shape of the (B-biotype) whitefly sound had two peaks at over 300 Hz and under 250 Hz, while the (Q-biotype) spreads were mainly under 300 Hz. Figure 3 shows the maximum, minimum, average and standard deviation of frequency peaks of 3,734 or 5,151 sound samples for each biotype. The results indicate that the power spectrum shape of whitefly sound would be a reliable characteristic for the identification of biotype.

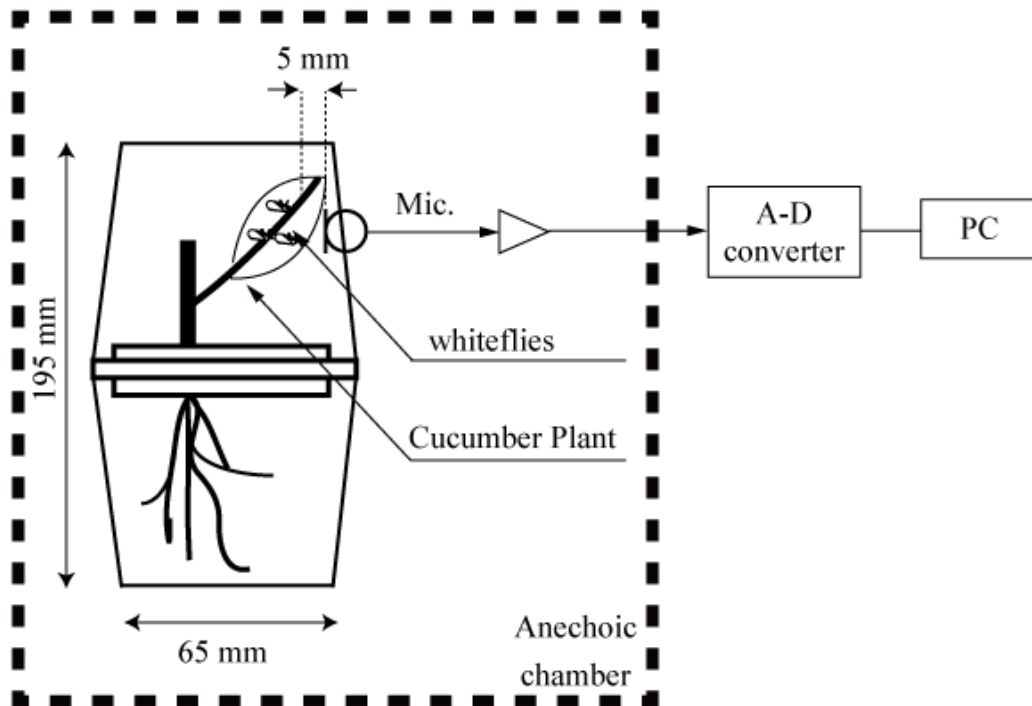


Figure 1. Whitefly acoustic monitoring system

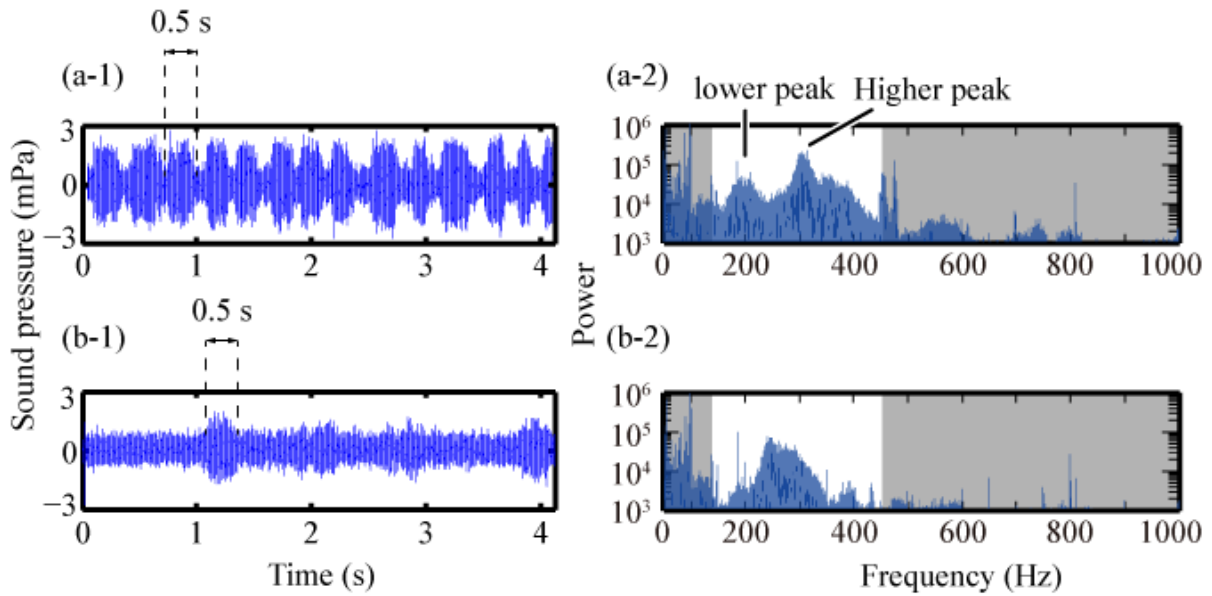


Figure 2. Recorded sound in the time-domain (a-1): B-biotype and (b-1): Q-biotype; and, recorded sound in the frequency-domain (a-2): B-biotype and (b-2): Q-biotype

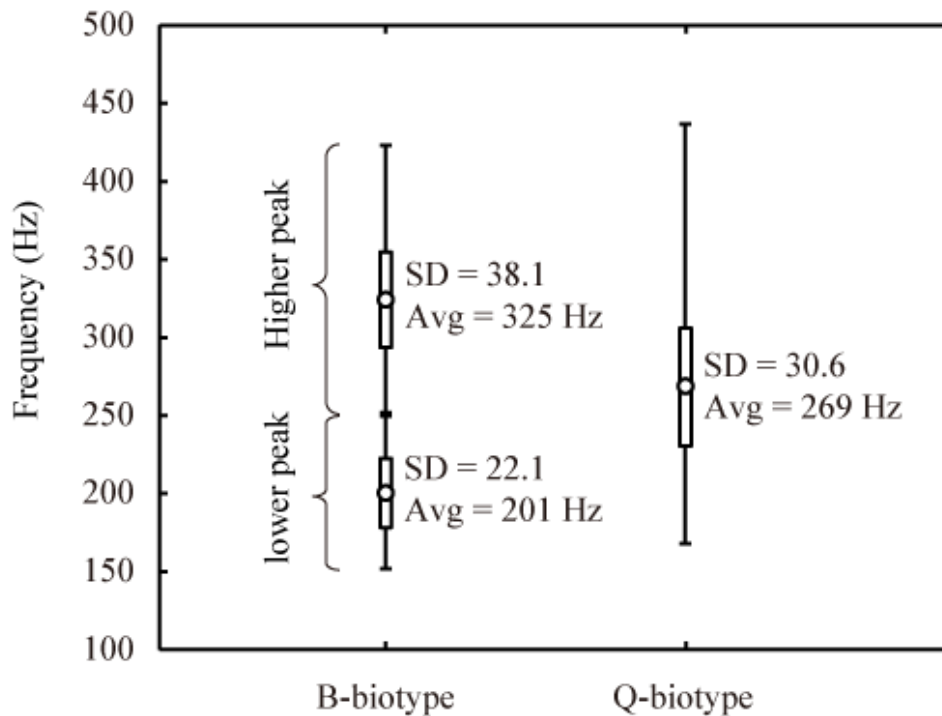


Figure 3. Maximum, minimum, average (circle) and standard deviation of frequency peaks

3. Biotype identification scheme of *Bemisia tabaci* by acoustic signature

Figure 4 shows a block diagram of the scheme for biotype identification of *Bemisia tabaci* proposed in this paper. The proposed scheme is divided into two steps: recording, and signal processing. The

recording step is the same as in our previous study, as shown in Figure 1. The signal processing step consists of three sub-steps; signal detection, frequency-domain matching, and classification of biotype. The details of each sub-step are described in subsections 3.1 and 3.2.

3.1. Automatic detection of whitefly sound

Figure 5 contains a schema that outlines the signal-processing procedure for automatic detection of whitefly sound. The detector first applies a bandpass-filter on the recorded sound [Figure 5(a)]. It then finds an index where the amplitude of the bandpass-filtered signal exceeds the threshold [Figure 5(b)]. After removing the duplicated index, the detector finally samples a specific 0.5-s section that corresponds to whitefly sound [Figure 5(c)].

In the bandpass-filtering process, a bandpass-filter (BPF) of 150-450 (Hz) is applied. Figure 6(a) shows the bandpass-filtered signal of the B-biotype. An index is then created where the power of the bandpass-filtered signal exceeds the threshold [Figure 6(b)]. As shown in this figure, the created index does not correspond to the whitefly sound one-to-one, because there are multiple index elements during a single whitefly sound duration. Hence, index elements whose neighbor difference is within 0.4 s are treated as duplicate records, and duplicates are removed [Figure 6(c)]. Finally, 0.5 s of sound (triggered 0.1 s before each index) is sampled and output as detected whitefly sound [Figure 6(d)].

In this detection process, the value of the threshold determines the performance. Figure 7 shows a relationship between the threshold (0 dB: background noise power) and the number of indexes [blue: index of sound (SUCCESS); red: false alarm (FAIL)] obtained from 5 min of recorded sound. As shown in this figure, it was found that threshold of 20 dB was sufficient to obtain a maximum number of sound indexes in both the B- and Q-biotypes. Hence, the threshold of 20 dB was used. In addition, the number of false alarms increased as the threshold decreased; however, the number of duplicate indexes increased more than the number of false alarms. Hence, the number of false alarms decreased with decreasing threshold after duplication removal.

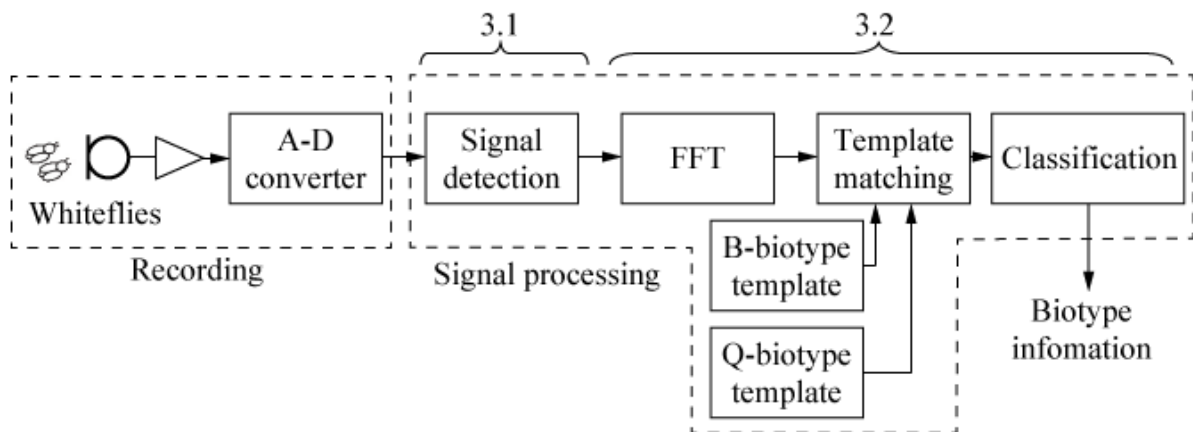


Figure 4. Block diagram of biotype identification scheme for *Bemisia tabaci*

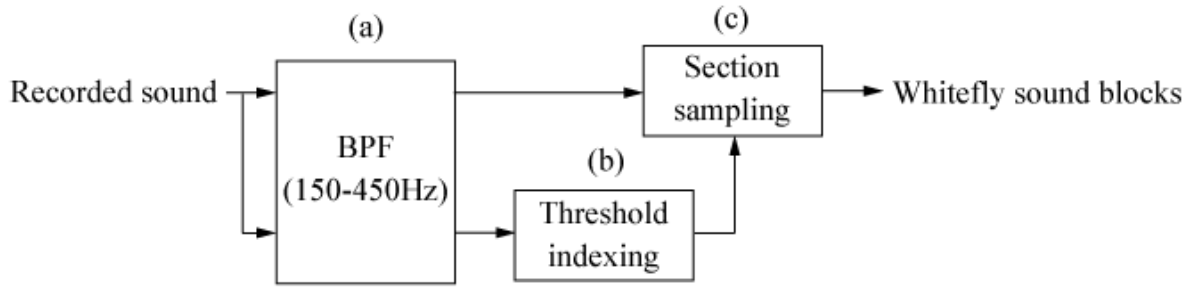


Figure 5. Signal processing for automatic detection of whitefly sound

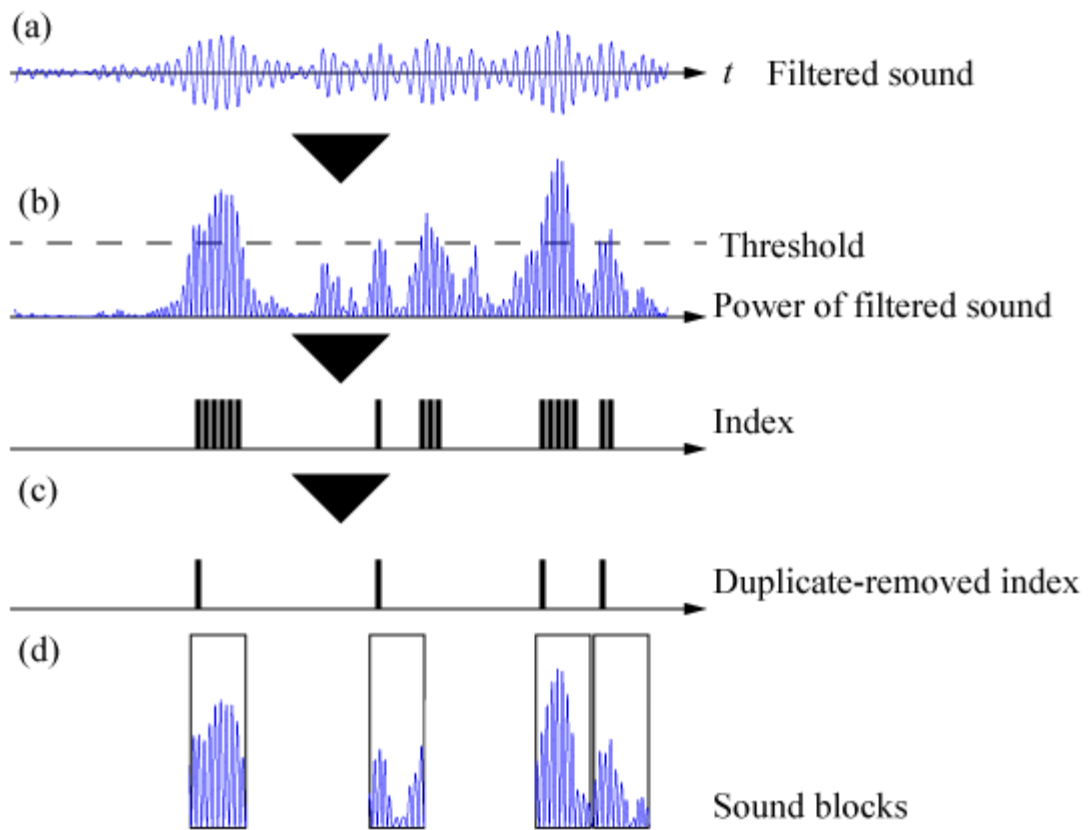


Figure 6. Example of signal processing: (a) bandpass-filtered signal; (b) index that exceeds the threshold; (c) duplicate-removed index; and (d) sampled whitefly sound

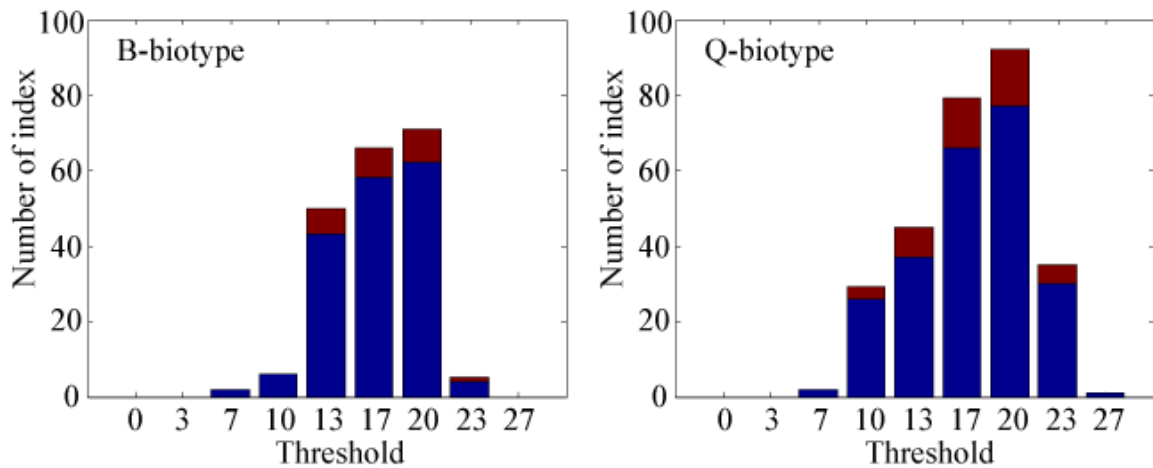


Figure 7. A Relationship between threshold and number of indexes [Blue: Index of sound (SUCCESS); Red: False alarm (FAIL)]

3.2. Frequency-domain matching for biotype identification

Figure 8 presents a schema detailing the signal-processing approach for biotype identification of whitefly. The identifier first converts the detected whitefly sound in the time domain into the frequency domain by calculating a fast Fourier transform (FFT) [Figure 8(a)]. In this paper, the parameters of the FFT calculation are as follows: the sound sampling frequency is 40 kHz, and duration is 0.5 s, therefore sample size is 20,000 samples, and the window function is a rectangular window. The identifier then compares the detected whitefly sound with the known whitefly sound (template) of the B- and Q-biotypes by calculating a spectrographic cross correlation, and outputs the correlation value [Figure 8(b)]. Finally, the identifier identifies the biotype of the whitefly by analyzing a set of correlation values [Figure 8(c)].

Figures 9 and 10 are examples of the detected B-biotype and Q-biotype whitefly sounds, and template sounds in the frequency domain, respectively. As shown in these figures, both the power spectrum shape and template of detected (B-biotype) whitefly sound spreads mainly over 300 Hz. On the other hand, both the power spectrum shape and template of detected (Q-biotype) whitefly sound spreads mainly under 300 Hz. Hence, the identifier calculates two correlation values, c_B and c_Q [c_B/c_Q : correlation value of the detected whitefly sound and that of template (B/Q-biotype) at 150-450 (Hz)], and stores them as C_B and C_Q , respectively. Finally, the identifier compares the mean value of C_B and C_Q , and judges that the detected whitefly sound belongs to the biotype whose template returns the larger correlation value.

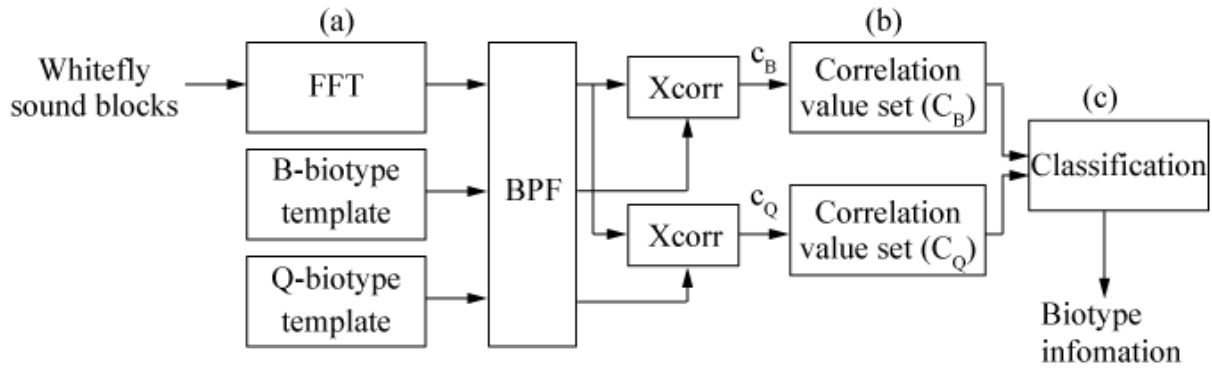


Figure 8. Signal processing for biotype identification of whitefly

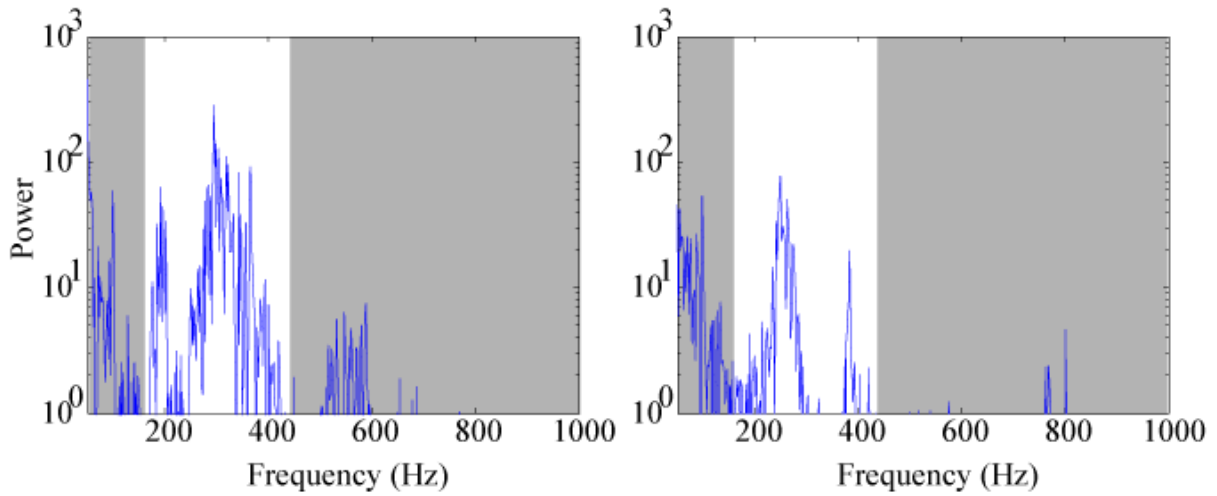


Figure 9. Examples of the detected whitefly sound: (a) B-biotype, and (b) Q-biotype

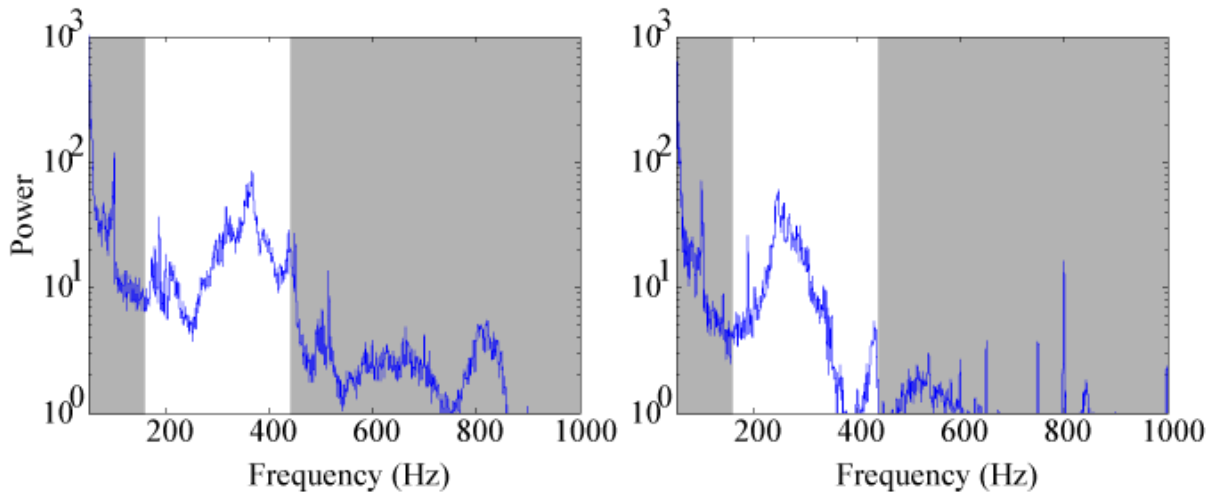


Figure 10. Template sounds in the frequency domain: (a) B-biotype, and (b) Q-biotype

4. Experiments and discussion

The performance of the proposed scheme was evaluated in experiments. The whitefly sound recording was performed using the acoustic monitoring system described in Section 2, and the monitoring and simultaneous biotype identification was performed by software (LabVIEW, National Instruments and MATLAB) on a personal computer (Figure 1).

Prior to the experiment, the template sounds shown in Figure 10 were prepared. Specifically, B-biotype and Q-biotype sounds were recorded for 5 min, and 50 sound blocks of 0.5 s were obtained manually for each biotype. Sound templates for the B- and Q-biotypes were then calculated by averaging the power spectrum of each sound block.

The experiment was performed for 280 min for each biotype, and biotype identification was performed every 5 min. Figure 11 shows an example of the distribution of a correlation value set, C_B and C_Q . The horizontal axis shows relative correlation value [correlation value divided by $\max(C_B \cup C_Q)$], and the vertical axis indicates the frequency (the number of cases in each bin). As shown in this figure, it is clear that the two distributions were separated. Hence, if a suitable threshold were set, biotype identification of *Bemisia tabaci* using acoustic signatures would be successful. Figure 12 shows the distribution of $\text{mean}(C_B)$ and $\text{mean}(C_Q)$, plotted over 280 min, every 5 min. As shown in this figure, when the threshold was 0.41, the biotype identifications of *Bemisia tabaci* were achieved with a correct detection rate of 92% (206/224). This result reveals that the proposed scheme sometimes fails to identify a biotype correctly. This was due to the lack of detected sound. Figure 13 shows the number of detected sounds during the experiment. As may be seen in the figure, biotype identification failed when the number of sounds detected was small. This was because the whitefly had silent periods during the experiment (Nakabayashi 2015); hence, sound detection and processing period would need to be adjusted adaptively by referring the number of detected sounds to improve identification performance.

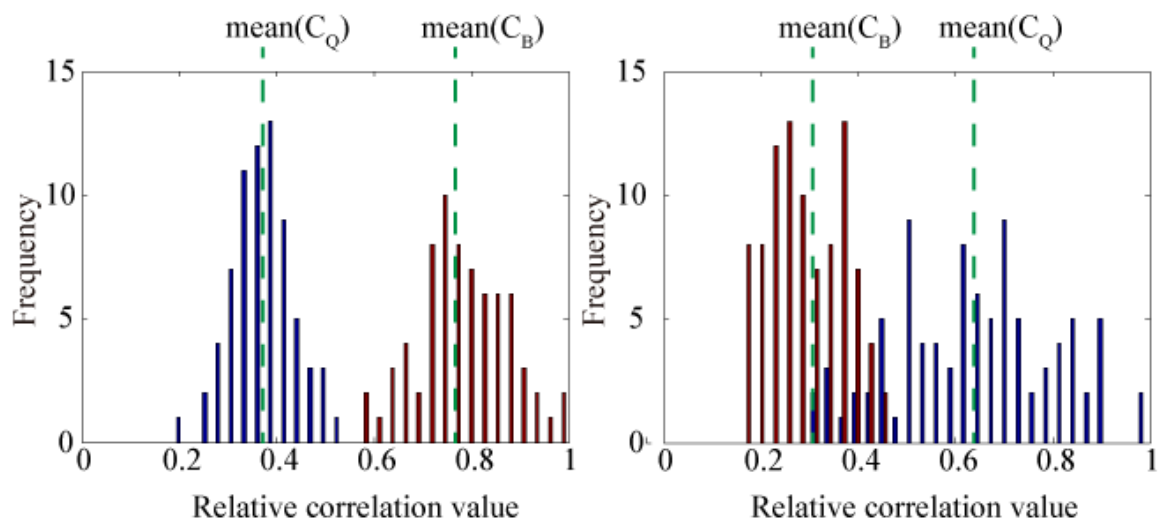


Figure 11. Examples of distribution of correlation value set, C_B (Red) and C_Q (Blue)

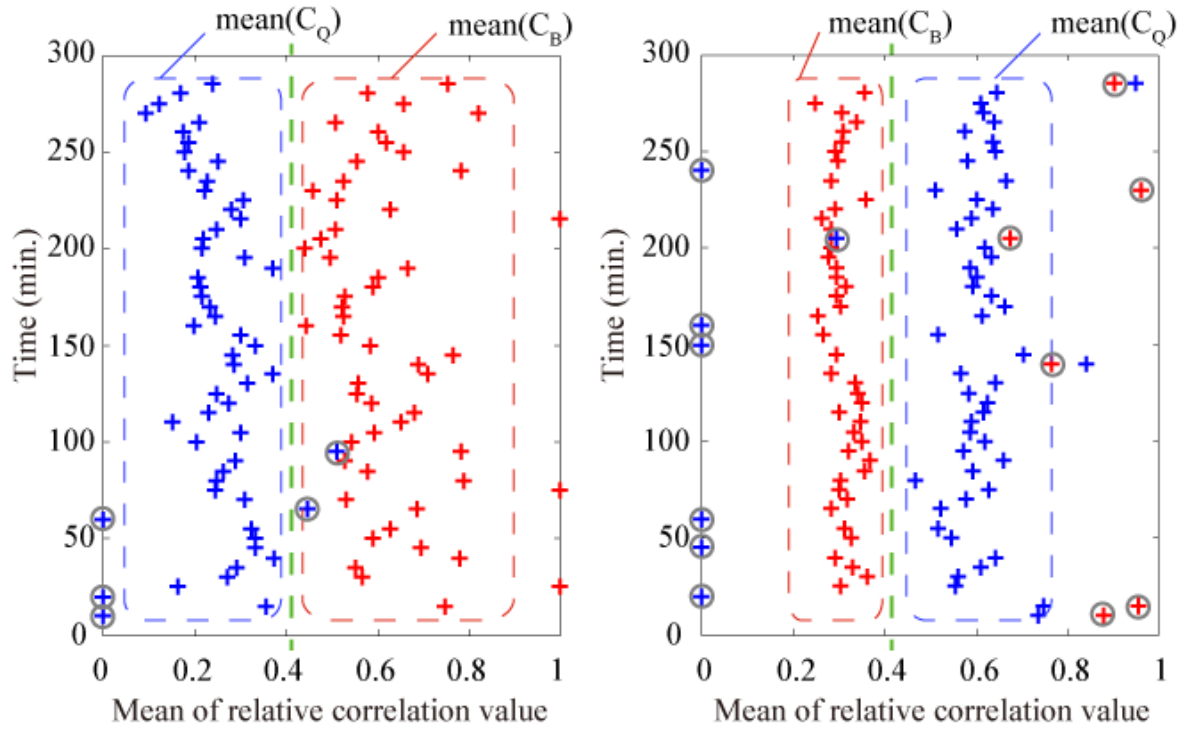


Figure 12. Distribution of $\text{mean}(C_B)$ and $\text{mean}(C_Q)$ obtained through the experiment (circle: failure point of biotype identification)

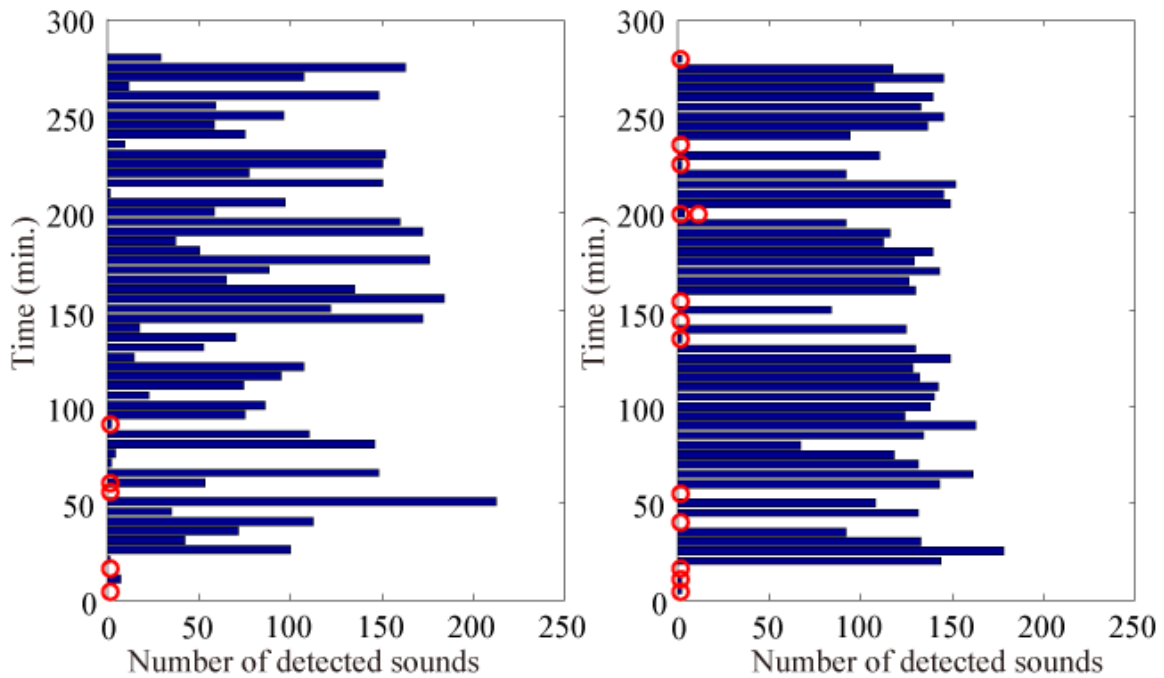


Figure 13. Number of detected sounds during the experiment (circle: failure point of biotype identification)

5. Conclusions

The objective of this paper was to develop a biotype identification system for *Bemisia tabaci*, to enable fast, reliable, and cost-effective biotype testing. To achieve this, a signal-processing method for automatic detection and classification of whitefly biotypes was proposed and designed. Performance of the proposed scheme was evaluated in an experiment. The experiment was performed for 280 min for each biotype, and biotype identification was performed every 5 min. Experimental results showed that biotype identification of *Bemisia tabaci* could be achieved with a correct detection rate of 92%. The obtained results suggest that the proposed scheme is a viable alternative for biotype testing of whitefly. Our future work will seek to improve the identification performance of this proposed scheme by adjusting sound detection and processing period by adaptively referring the number of detected sounds.

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