

CORRECTION

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Correction to: Detection and epidemic dynamic of ToCV and CCYV with *Bemisia tabaci* and weed in Hainan of China

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Correction to: Virol J

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In the original publication of this article [1], the author found the legends of Fig. 3 and Fig. 4 were incorrect. The original ones were:

Fig. 3 ToCV detection from tomato plants. CK1 positive control; CK2 negative control; CK3 black control. The size of 466 bp based on amplification of HSP70h gene of ToCV was used. Results of 20 samples were shown in this figure

Fig. 4 CCYV detection from cucumber plants. CK1 positive control; CK2 negative control; CK3 black control. The size of 804 bp based on amplification of CP (coat protein) gene of CCYV was used. Results of 20 samples were shown in this figure

The correct ones should be:

Fig. 3 CCYV detection from cucumber plants. CK1 positive control; CK2 negative control; CK3 black control. The size of 804 bp based on amplification of CP (coat protein) gene of CCYV was used. Results of 20 samples were shown in this figure

Fig. 4 ToCV detection from tomato plants. CK1 positive control; CK2 negative control; CK3 black control. The size of 466 bp based on amplification of HSP70h gene of ToCV was used. Results of 20 samples were shown in this figure

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1. Tang, et al. Detection and epidemic dynamic of ToCV and CCYV with *Bemisia tabaci* and weed in Hainan of China. *Virol J.* 2017;14:169. <https://doi.org/10.1186/s12985-017-0833-2>.

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