



Corrigendum: Development and Evaluation of Stable Sugarcane Mosaic Virus Mild Mutants for Cross-Protection Against Infection by Severe Strain

Xiao-Jie Xu, Qing Zhu, Shao-Yan Jiang, Zhi-Yong Yan, Chao Geng, Yan-Ping Tian* and Xiang-Dong Li*

Shandong Province Key Laboratory for Agricultural Microbiology, Laboratory of Plant Virology, Department of Plant Pathology, College of Plant Protection, Shandong Agricultural University, Tai'an, China

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Edited and reviewed by:

Wen-Ming Wang,
Sichuan Agricultural University, China

*Correspondence:

Xiang-Dong Li
xdongli@sdau.edu.cn
Yan-Ping Tian
yanping.tian@sdau.edu.cn

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A Corrigendum on

Development and Evaluation of Stable Sugarcane Mosaic Virus Mild Mutants for Cross-Protection Against Infection by Severe Strain

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In the original article, there was a mistake in **Figure 2** and **Figure 3** as published. The pictures of SCMV-GFP in the second column of **Figure 2B** and SCMV in the second column of **Figure 3A** were wrongly used. We have replaced them with the correct ones. The corrected **Figure 2** and **Figure 3** appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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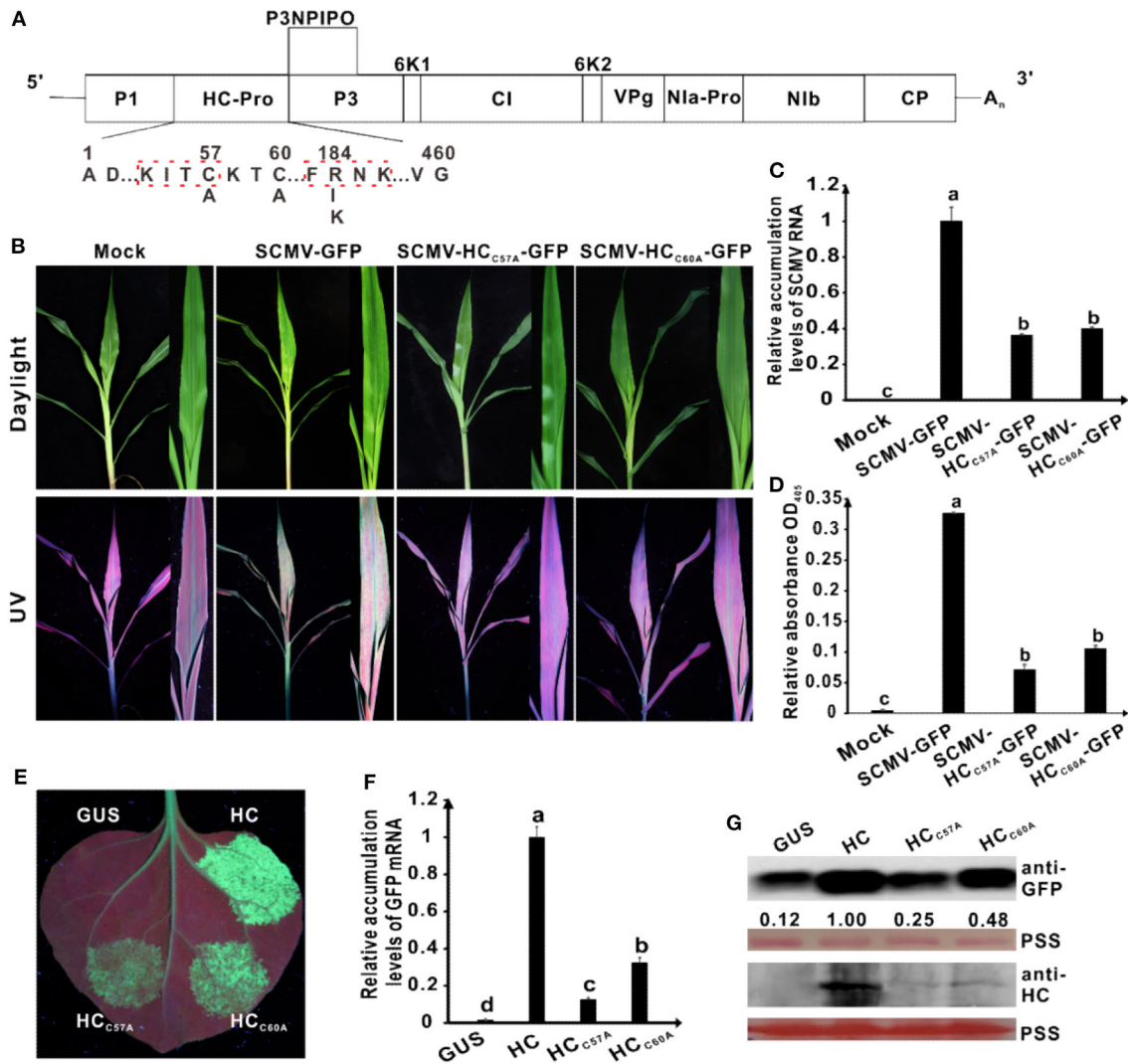


FIGURE 2 | Effects of the mutations in the conserved C⁵⁷ and C⁶⁰ of wild type HC-Pro on its RNA silencing suppression activity and virulence of SCMV. **(A)** Genetic map of SCMV, showing the all mutations in HC-Pro. The numbers above the sequence indicate their position in SCMV HC-Pro and the letters below the sequence showed the substituted residues at that position. The highly conserved KITC and FRNK motifs in SCMV HC-Pro were marked by the red dotted boxes. **(B)** Symptoms of SCMV and two SCMV mutants in maize plants at 10 days post inoculation (dpi). The conserved C⁵⁷ and C⁶⁰ in wild type SCMV HC-Pro were mutated to A residues in HC-Pro of SCMV-HC_{C57A}-GFP and SCMV-HC_{C60A}-GFP, respectively. Mock, the maize plants inoculated with the empty vector pCB301-Rz. SCMV-GFP, the maize plants infected with wild type SCMV with *gfp* reporter gene. **(C)** The wild type and mutant SCMV RNA accumulation levels in the upper leaves of maize plants at 10 dpi. **(D)** ELISA analysis of the wild type and mutant SCMV accumulation levels in the upper leaves of maize plants at 10 dpi. **(E)** The wild type and mutants HC-Pro RSS activity in *Agrobacterium* co-infiltration assay. The *N. benthamiana* 16C leaves were infiltrated with a mixture of *Agrobacterium* cultures carrying pBin-GFP and either wild type or mutant HC-Pro and photographed under long-wavelength UV light at 3 days post agroinfiltration (dpa). The conserved C residues in wild type HC-Pro (HC) were mutated to A residues in HC_{C57A} and HC_{C60A}, respectively. The GUS was used as a negative control. **(F)** The GFP mRNA accumulation levels in agroinfiltrated 16C leaf patches. **(G)** Western blotting analysis of the accumulation levels of GFP and HC in agroinfiltrated leaf patches of 16C. The ponceau S staining (PSS) shows sample loadings. Band intensities were measured using the ImageJ software. Numbers indicate the accumulation levels of SCMV CP normalized to PSS staining. Error bars indicate the means ± standard deviation of three replicates. Statistical significance was determined by employing *Tukey* multiple range test for between-group comparisons. Different letters indicate significant differences (*P* < 0.05). The same below. The experiments were repeated thrice independently.

