ERRATUM

Erratum to: Complete genome sequence of longan witches' broom-associated virus, a novel member of the family *Potyviridae*

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The prediction of cleavage sites in the polyprotein derived from the genomic sequence of Longan witches' broom-associated virus (LWBaV), as depicted in Fig. 1C of the article by Seo and colleagues [1], contains a site which does not comply with the standard consensus for the NIa-Pro mediated processing of potyvirus mature gene products [2]. As already mentioned by authors in the text, the site proposed for the cleavage at the NIb/CP junction is located close to another possible site, which could lead to a slightly larger CP with a N-terminal sequence starting with the residues AGEMTD..., and a predicted size of 311 amino acids. Until further experimental evidence can be provided, the annotation of the CP of LWBaV should preferably be derived from the predicted standard processing event (LVIETQ/AG) at position 2775 in the viral polyprotein.

In addition, the numbering corresponding to the position for the P1/HC-Pro cleavage site (EPITYY/SG) in the same Fig. 1C should be corrected to 396. The predicted sizes of the two first gene products of LWBaV should be 396 and 456 amino acids for P1 and HC-Pro, respectively.

References

1. Seo JK, Kim MK, Kwak HR, Kim JS, Choi HS (2017) Complete genome sequence of longan witches' broom-associated virus, a novel member of the family *Potyviridae*. Arch Virol. doi:10.1007/s00705-017-3405-2
2. Adams MJ, Antoniw JF, Beaudoin F (2005) Overview and analysis of the polyprotein cleavage sites in the family *Potyviridae*. Mol Plant Pathol 6:471–487

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