Correction to: Analysis of the complete genome sequence of a potyvirus from passion fruit suggests its taxonomic classification as a member of a new species

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Recently, we carefully checked the original Sanger sequencing data for the assembly of TeMV-PasFru genome (GenBank accession no. MG944249). Unfortunately, we found an error existed in this genome sequence. The genome sequence starting from nt position 191 should be “GCTTTTACTGTG...”, rather than “GCTTTACTGTG...”. As a result, the entire genome of TeMV-PasFru should be 10050 nts in length, 5' UTR should correspond to nts 1 to 169, P1 coding region should start from nt 170, and each of the remaining Arabic numbers shown in Fig. 1C should increase by 1. Also, the corresponding statements throughout the manuscript should be adjusted. Nevertheless, the main conclusions/novelty are still maintained after these corrections: (i) This study represents the first report of complete genome sequence of TeMV isolate from passion fruit. (ii) Compared with the previous TeMV isolate Hanoi from *Telosma cordata*, the only documented isolate with the entire genome sequence annotated, TeMV-PasFru has an extra 127 aa residues at the N-terminus of the P1 protein. (iii) Pairwise sequence comparisons showed that TeMV-PasFru shares 73.90% nt and 79.75% aa sequence identity with the TeMV-Hanoi at

the whole-genome and polyprotein level, respectively, and these values are below the corresponding threshold values for species demarcation in the family *Potyviridae*.

Again, we sincerely apologize for all resulting misunderstandings/confusions to ARVI readers.

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