



Correction to: Molecular analysis of maize (*Zea mays* L.)-infecting mastreviruses in Ethiopia reveals marked diversity of virus genomes and a novel species

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Correction to: Virus Genes
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The original version of this article unfortunately contained errors in the “Results” section.

In the “Detection and reconstruction of mastrevirus genomes” subsection, the word ‘third’ and ‘three’ indicating the underlined nucleotide position for C and G should be changed to ‘fourth’ and ‘four’ respectively. Hence, the correct text reads as follows:

“Only the conserved nonanucleotide sequence TAATAT T↓AC is diverse in MSDV with nucleotide mutations at the fourth and the eighth positions (underlined, TAACATT↓GC) of this most conserved sequence in geminiviruses. Interestingly this unusual feature is also evident in *Sweet potato symptomless virus 1* (SPSMV-1) with a nonanucleotide mutation at positions four and eight resulting in TAA GATT↓CC motif.”

In the “Distribution and incidence of mastreviruses infecting maize in Ethiopia” subsection, ‘August’ should be changed to ‘September’. The correct sentence reads as:

“As revealed from PCR results, both MSV (100%) and MSR (36%) have higher incidence in samples collected during September 2015 (late main rain feed cropping season) but ...”

The original article has been corrected.

The original article can be found online at <https://doi.org/10.1007/s11262-019-01655-1>.

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