ERRATUM

Erratum to: Complete genome sequence of Colocasia bobone disease-associated virus, a putative cytorhabdovirus infecting taro

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Unfortunately, Fig. 1 was incorrectly published in the original publication of the article. The correct version of Fig. 1 is given here:

The online version of the original article can be found under doi:[10.1007/s00705-015-2713-7](https://doi.org/10.1007/s00705-015-2713-7).

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Fig. 1 a) Similarity between sequences corresponding to predicted 3' ends of CBDaV mRNAs, intergenic sequences (IS) and 5' end of the next mRNA. The sequences are provided in the 3'-5' sense of the viral mRNAs. Dashes indicate gaps introduced to optimise the alignment, while conserved nucleotides are highlighted in grey. b) Consensus sequences of the gene junction regions of CBDaV compared with other plant rhabdoviruses [3, 9]. c) Maximum-likelihood analysis

using the GTR + G + I model, of plant rhabdovirus L polymerase open reading frame nucleotide sequences. The tree is rooted at the midpoint, the insect vectors for each virus are shown, and nucleorhabdovirus and cytorhabdovirus clades are indicated by brackets. Bootstrap values greater than 50 are shown for the major nodes, and the scale indicates the number of substitutions per site. Virus abbreviations are as noted in the text