



## Correction to: Monogenean parasites infect ornamental fish imported to Australia

A. Trujillo-González<sup>1</sup>  · J. A. Becker<sup>2</sup> · D. B. Vaughan<sup>1</sup> · K. S. Hutson<sup>1</sup>

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The phylogenetic tree (Figure 7) in the published document has incorrect Bayesian analysis posterior probabilities. This error prevents accurate analysis by future research in parasitology. The figure is therefore replaced by the corrected figure below.

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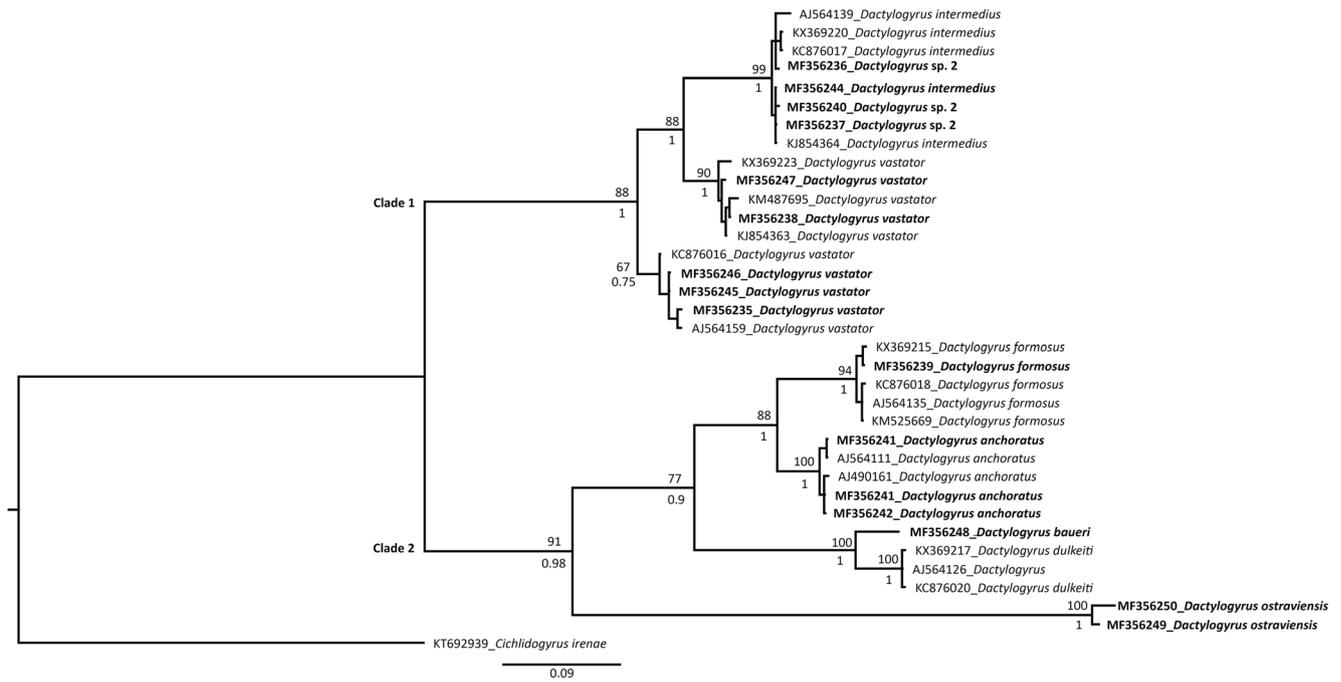
The online version of the original article can be found at <https://doi.org/10.1007/s00436-018-5776-z>

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✉ A. Trujillo-González  
[alejandro.trujillogonzalez@my.jcu.edu.au](mailto:alejandro.trujillogonzalez@my.jcu.edu.au)

<sup>1</sup> Marine Parasitology Laboratory, Centre for Sustainable Tropical Fisheries and Aquaculture, College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia

<sup>2</sup> School of Life and Environmental Sciences, Faculty of Science, University of Sydney, 425 Werombi road, Camden, NSW 2570, Australia



**Fig. 7** Consensus phylogenetic tree of *Dactylogyrus* spp. estimated by Bayesian analysis of gene sequence data of ITS1. *Cichlidogyrus irenae* Gillardin, Vanhove, Pariselle, Huyse and Volckaert, 2011 (Genbank No. KT692939) was used as the outgroup sequence. Nodal support is shown

by bootstrap percentages from the parsimony analysis (above) and Bayesian posterior probabilities (below). Sequences in bold are accessions from this study