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**Publisher Correction:****Myzorhynchus series of *Anopheles* mosquitoes as potential vectors of *Plasmodium bubalis* in Thailand**

Yudhi Ratna Nugraheni, Apinya Arnuphappasert, Trang Thuy Nguyen, Duriyang Narapakdeesakul, Hoang Lan Anh Nguyen, Juthathip Poofery, Osamu Kaneko, Masahito Asada & Morakot Kaewthamasorn

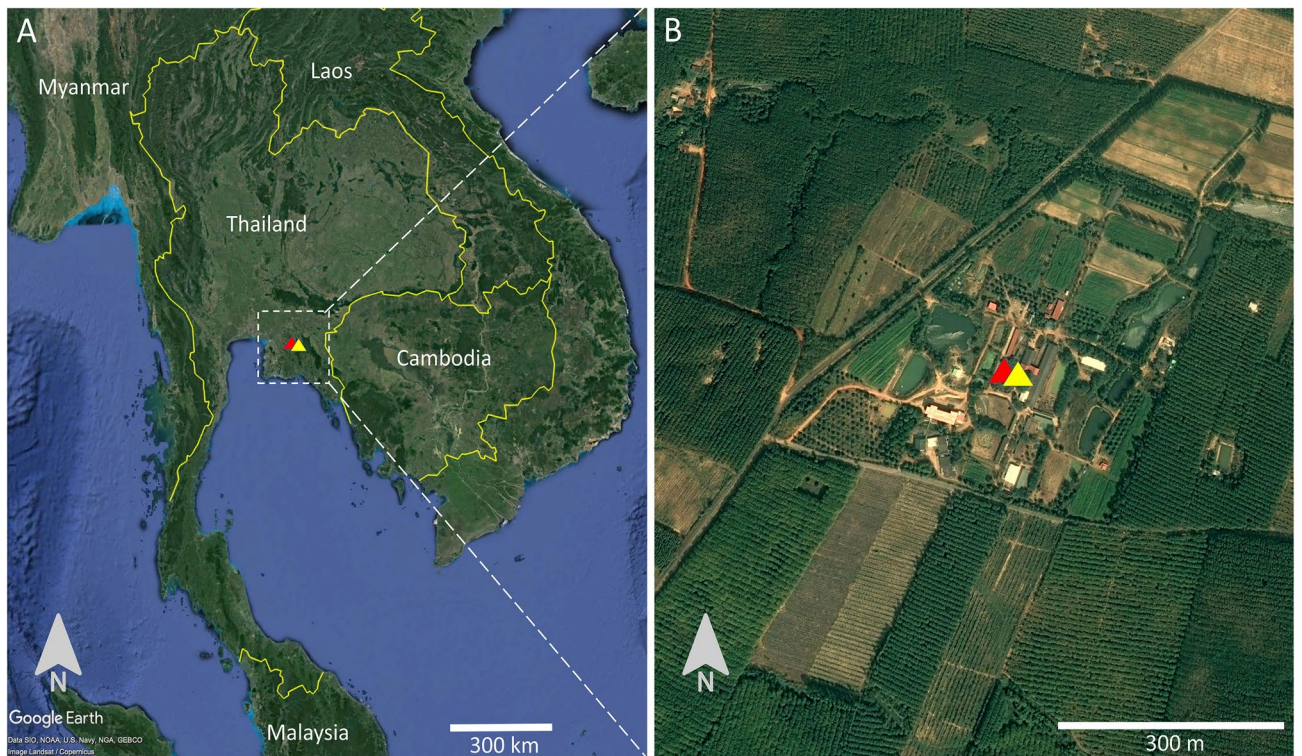
Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-022-09686-9>, published online 06 April 2022

The original version of this Article contained errors in the order of the Figures. Figures 2 and 3 were published as Figures 3 and 2. As a result, the Figure legends were incorrect.

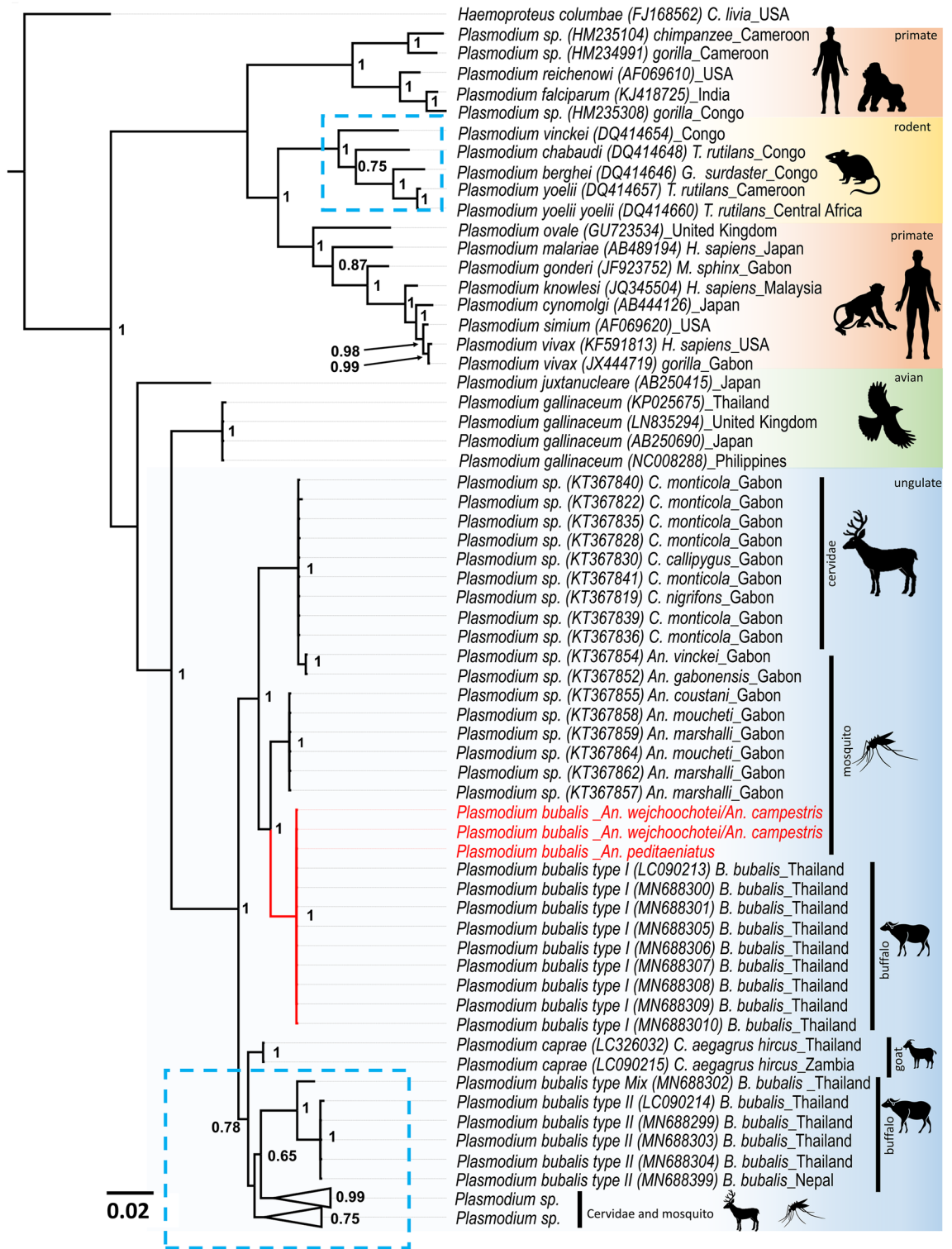
The original Figures 2 and 3 and accompanying legends appear below.

The original Article has been corrected.

Published online: 20 April 2022



**Figure 2.** Phylogenetic positions of *Plasmodium* detected from *Anopheles* mosquitoes in this study. The phylogenetic tree was inferred by Bayesian inference method using partial *cytb* sequences (789 bp). *Haemoproteus columbae* was used to root all sequences. At the nodes, Bayesian posterior probabilities ( $PP \geq 0.65$ ) are indicated. *Plasmodium* sequences obtained in this study are highlighted in red. The length for the substitutions/site (0.02) is indicated.



**Figure 3.** (A) Map depicting a buffalo farm in Chachoengsao for sample collection in Thailand. (B) The landscape of mosquito sampling sites in a buffalo farm in Chachoengsao. The images were obtained and modified from Google Earth Pro version 7.3.4.8248. The red triangle indicates blood sample collection sites, while the yellow triangle indicates mosquito sampling sites.



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