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Corrigendum: Comparative analysis of the complete mitochondrial genomes of three *Zeugodacus* species (Insecta: Tephritidae: Dacinae) and their phylogenetic relationships with other congeners. Arthropod Systematics & Phylogeny 81: 747–759. doi: 10.3897/asp.81.e105025

Hoi-Sen Yong, Sze-Looi Song, Kah-Ooi Chua, Yvonne Jing Mei Liew, I. Wayan Suana, Phaik-Eem Lim, Kok-Gan Chan, Praphathip Eamsobhana

The article entitled “Comparative analysis of the complete mitochondrial genomes of three *Zeugodacus* species (Insecta: Tephritidae: Dacinae) and their phylogenetic relationships with other congeners”, published in Arthropod Systematics & Phylogeny (DOI: 10.3897/asp.81.e105025), requires two corrections that do not affect the scientific content or integrity of the article. Figures 2 and 3, as presented in this corrigendum, now reflect our original intent.

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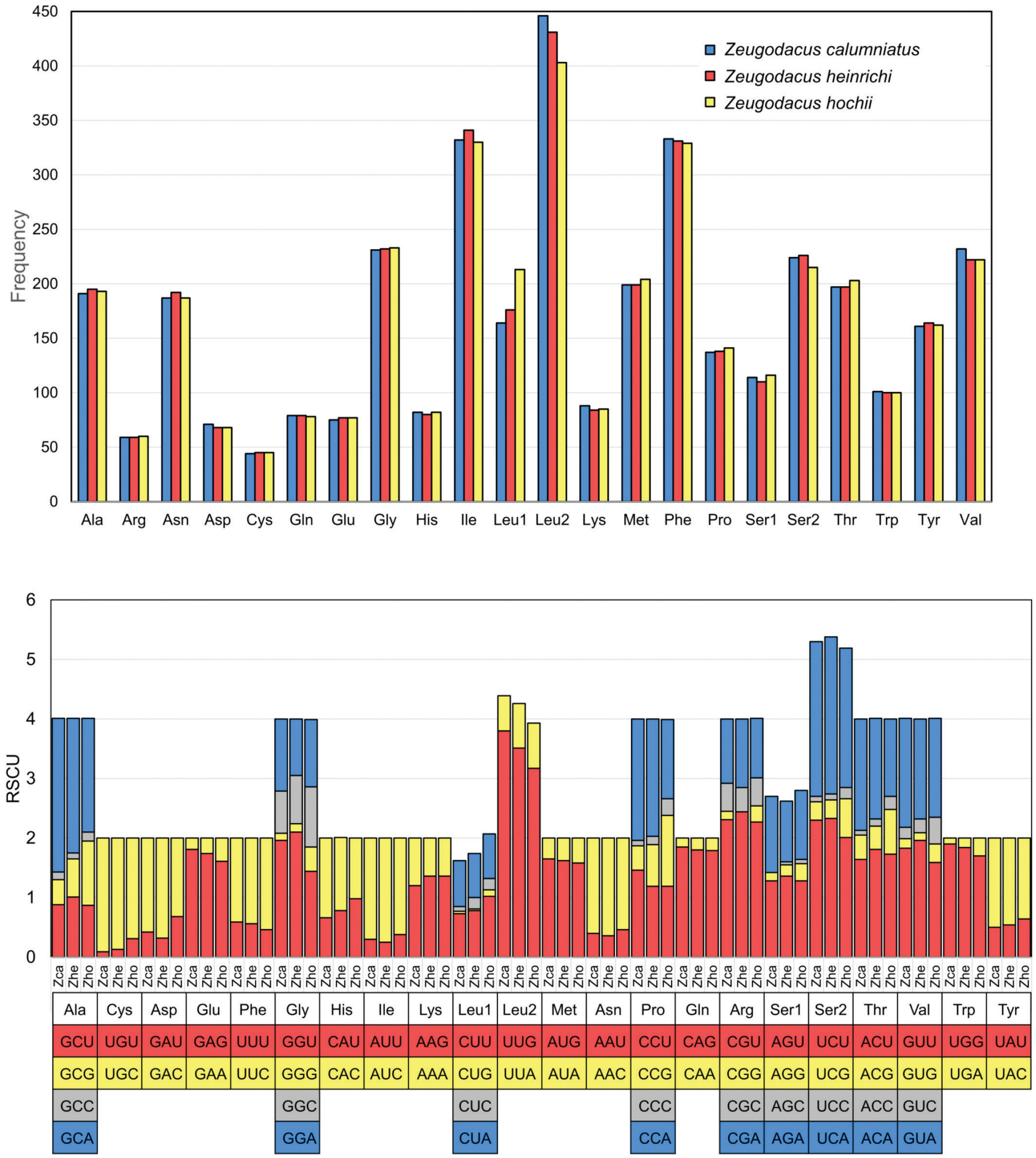

Ala	Cys	Asp	Glu	Phe	Gly	His	Ile	Lys	Leu1	Leu2	Met	Asn	Pro	Gln	Arg	Ser1	Ser2	Thr	Val	Trp	Tyr
GCU	UGU	GAU	GAG	UUU	GGU	CAU	AUU	AAG	CUU	UUG	AUG	AAU	CCU	CAG	CGU	AGU	UCU	ACU	GUU	UGG	UAU
GCG	UGC	GAC	GAA	UUC	GGG	CAC	AUC	AAA	CUG	UUA	AUA	AAC	CCG	CAA	CGG	AGG	UCG	ACG	GUG	UGA	UAC
GCC					GGC				CUC				CCC		CGC	AGC	UCC	ACC	GUC		
GCA					GGA				CUA				CCA		CGA	AGA	UCA	ACA	GUA		

Figure 2. Amino acid frequency (Top) and relative synonymous codon usage (Bottom) of PCGs in the *Zeugodacus* mitogenomes generated using MEGA X (https://www.megasofware.net/). Zca, *Zeugodacus calumniatus*; Zhe, *Zeugodacus heinrichi*; Zho, *Zeugodacus hochii*.

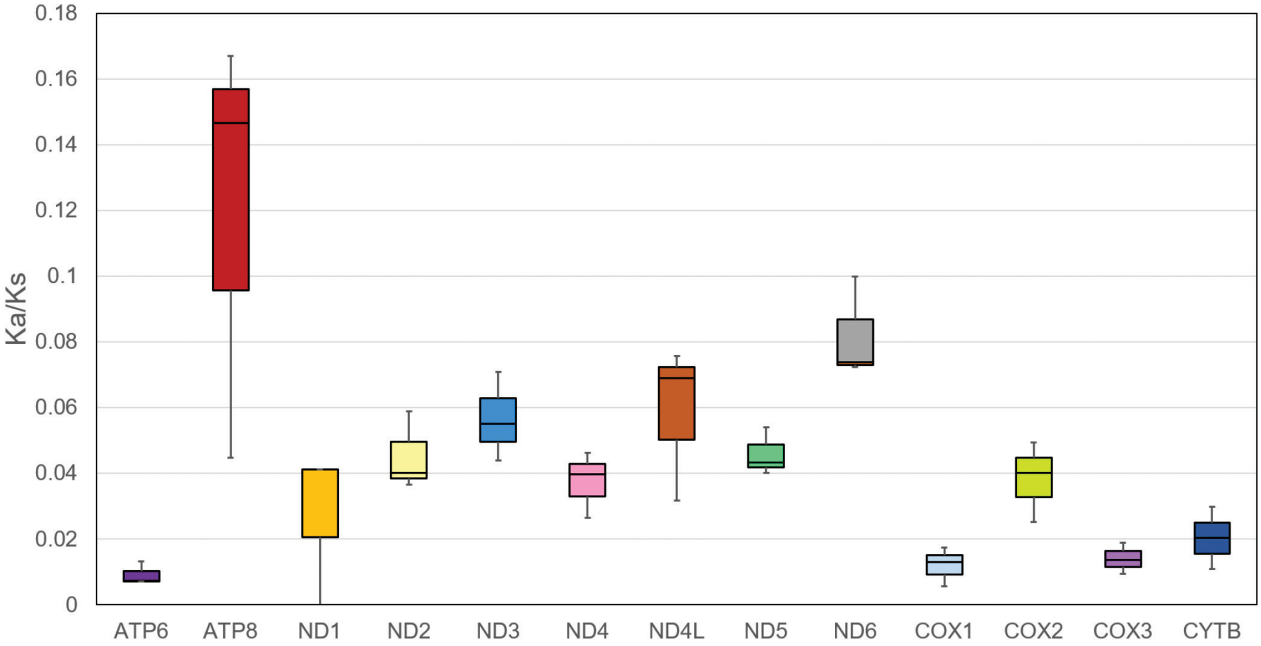

Figure 3. Box plot for pairwise divergence of Ka/Ks ratio (mean ± SD, and range) for 13 protein-coding genes (PCGs) of three *Zeugodacus* mitogenomes (*Z. calumniatus*, *Z. heinrichi*, *Z. hochii*) generated using DnaSP6.0. (http://www.ub.edu/dnasp).

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Autor(en)/Author(s): Yong Hoi-Sen, Song Sze-Looi, Chua Kah-Ooi, Liew Yvonne Jing Mei, Suana I. Wayan, Lim Phaik-Eem, Chan Kok-Gan, Eamsobhana Praphathip

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