



Corrigendum: Validation and Development of COI Metabarcoding Primers for Freshwater Macroinvertebrate Bioassessment

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A corrigendum on

Validation and Development of COI Metabarcoding Primers for Freshwater Macroinvertebrate Bioassessment

by Elbrecht, V., and Leese, F. (2017). *Front. Environ. Sci.* 5:11. doi: 10.3389/fenvs.2017.00011

In the original article, the reference for Bista et al. (2017) was incorrectly written as “Carvalho, G. R., Walsh, K., Seymour, M., Hajibabaei, M., Lallias, D., Christmas, M., et al. (2017). Annual time-series analysis of aqueous eDNA reveals ecologically relevant dynamics of lake ecosystem biodiversity. *Nat. Commun.* 8, 1–11. doi: 10.1038/ncomms14087.” It should be “Bista, I., Carvalho, G. R., Walsh, K., Seymour, M., Hajibabaei, M., Lallias, D., et al. (2017). Annual time-series analysis of aqueous eDNA reveals ecologically relevant dynamics of lake ecosystem biodiversity. *Nat. Commun.* 8, 1–11. doi: 10.1038/ncomms14087.”

In the original article, there was a mistake in **Table 2** as published. “Ephemeroptera” and taxa abundance (8) are missing in the table. The corrected Table appears below. The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way.

REFERENCES

- Elbrecht, V., and Leese, F. (2015). Can DNA-based ecosystem assessments quantify species abundance? Testing primer bias and biomass—sequence relationships with an innovative metabarcoding protocol. *PLoS ONE* 10:e0130324. doi: 10.1371/journal.pone.0130324
- Elbrecht, V., Taberlet, P., Dejean, T., Valentini, A., Usseglio-Polatera, P., Beisel, J.-N., et al. (2016). Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. *PeerJ* 4, e1966–e1912. doi: 10.7717/peerj.1966

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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TABLE 2 | Number of species recovered with the newly developed primers and data on 16S and Folmer primers from previous tests (Elbrecht and Leese, 2015; Elbrecht et al., 2016).

Taxonomic group	Number of specimens	Number of specimens recovered with specific primer combination					
		LCO1490+HCO2198	16S ins	BF2+BR2	BF2+BR1	BF1+BR2	BF1+BR1
Ephemeroptera	8	7 (88%)	8 (100%)	8 (100%)	8 (100%)	8 (100%)	8 (100%)
Plecoptera	4	4 (100%)	4 (100%)	4 (100%)	4 (100%)	4 (100%)	4 (100%)
Trichoptera	15	13 (86%)	15 (100%)	15 (100%)	15 (100%)	15 (100%)	15 (100%)
Diptera	8	7 (88%)	7 (88%)	8 (100%)	8 (100%)	8 (100%)	8 (100%)
Other insects	7	7 (100%)	7 (100%)	7 (100%)	7 (100%)	7 (100%)	6 (86%)
Other metazoa	10	5 (50%)	2 (20%)	7 (70%)	6 (60%)	9 (90%)	6 (60%)
Σ All insects	42	38 (91%)	41 (98%)	42 (100%)	42 (100%)	42 (100%)	41 (98%)
SD*		1.01	0.62	0.54	0.65	0.71	0.84
Precision**		0.72	0.37	0.28	0.35	0.49	0.58
Σ All taxa	52	43 (83%)	43 (83%)	49 (94%)	48 (92%)	51 (98%)	47 (90%)

*Mean standard deviation (SD) of \log_{10} read abundance from each insect taxon that was detected (specimens with $<0.003\%$ read abundance discarded).

**Precision defined as the SD of the mean \log_{10} distance to the expected read abundances, calculated for each morphotaxon (all taxa).