Erratum

VERENA TUNNICLIFFE & CORINNA BREUSING (2022) Redescription of *Bathymodiolus septemdierum* Hashimoto and Okutani, 1994 (Bivalvia, Mytilida, Mytilidae), a mussel broadly distributed across hydrothermal vent locations in the western Pacific and Indian Oceans. *Zootaxa*, 5214 (3): 337–364.

We detect two errors, neither of which affects the results and interpretation in the paper:

1. On page 358, the first six entries in Appendix 2 should read "*B. septemdierum*—NW Pacific" instead of "*B. marisindicus*—Indian Ocean". The identities were correct in the analyses.

The corrected appendix is as follows:

APPENDIX 2. *ND4* sequence accessions for *B. septemdierum* from the NW Pacific, SW Pacific and Indian oceans.

Sample	Morphotype	Region
AY649806	*B. septemdierum*	NW Pacific
KF521941	*B. septemdierum*	NW Pacific
AB485629	*B. septemdierum*	NW Pacific
AB485628	*B. septemdierum*	NW Pacific
AB485627	*B. septemdierum*	NW Pacific
AB485626	*B. septemdierum*	NW Pacific
...	...	...
KP881211	*B. brevior*	SW Pacific
KP881212	*B. brevior*	SW Pacific
KP881213	*B. brevior*	SW Pacific
KP881214	*B. brevior*	SW Pacific
KP881215	*B. brevior*	SW Pacific
KP881216	*B. brevior*	SW Pacific
KP881217	*B. brevior*	SW Pacific
KP881218	*B. brevior*	SW Pacific
KP881219	*B. brevior*	SW Pacific
KP881220	*B. brevior*	SW Pacific
KP881221	*B. brevior*	SW Pacific
KP881222	*B. brevior*	SW Pacific

2. The specimens sequenced from the Indian Ocean were collected from several sites. However, a database entry error switched some specimen designations when sequenced. Thus, the specimens from the holotype location (Kairei) are not correctly presented in the haplotype network in Figure 2 on page 340. The topology and interpretation of the figure is not changed, only the colour distribution for the Indian Ocean specimens.

Note that the specimen presented in Figure 5 was part of a different collection and is, indeed, from the type location.

The corrected Figure 2 is presented on the following page.
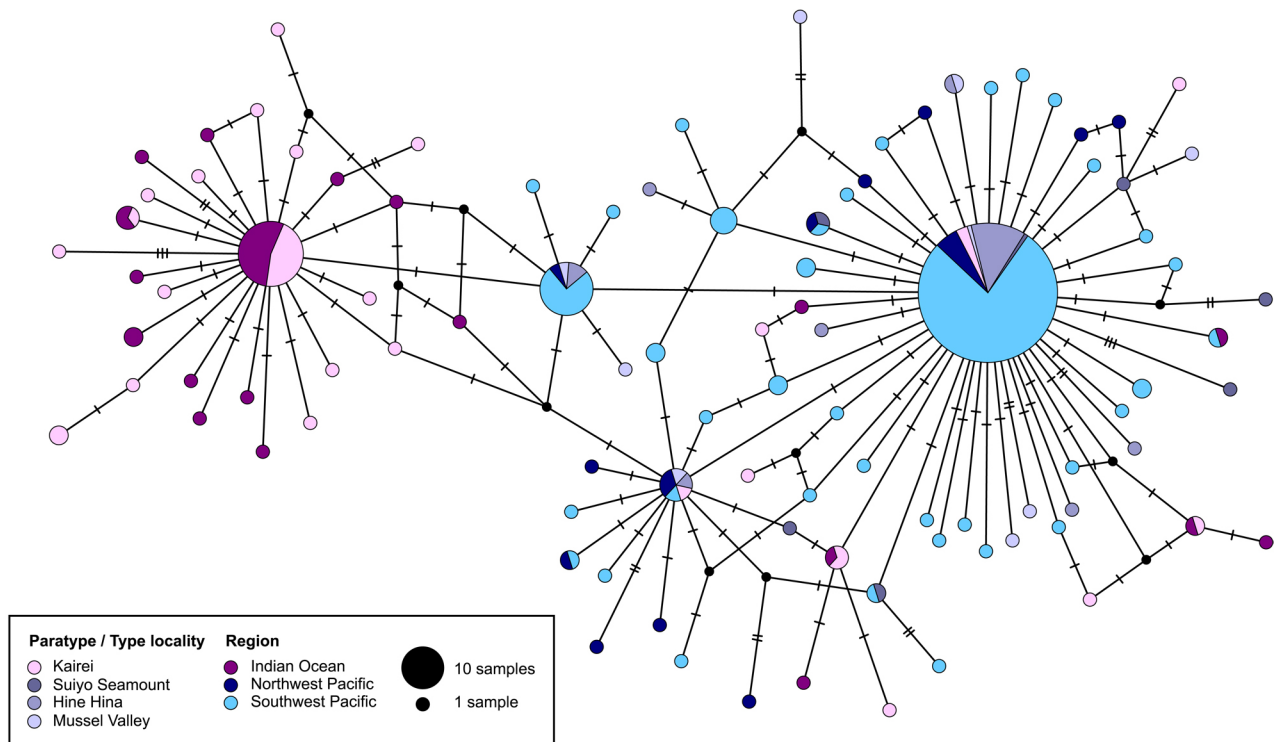
A COI
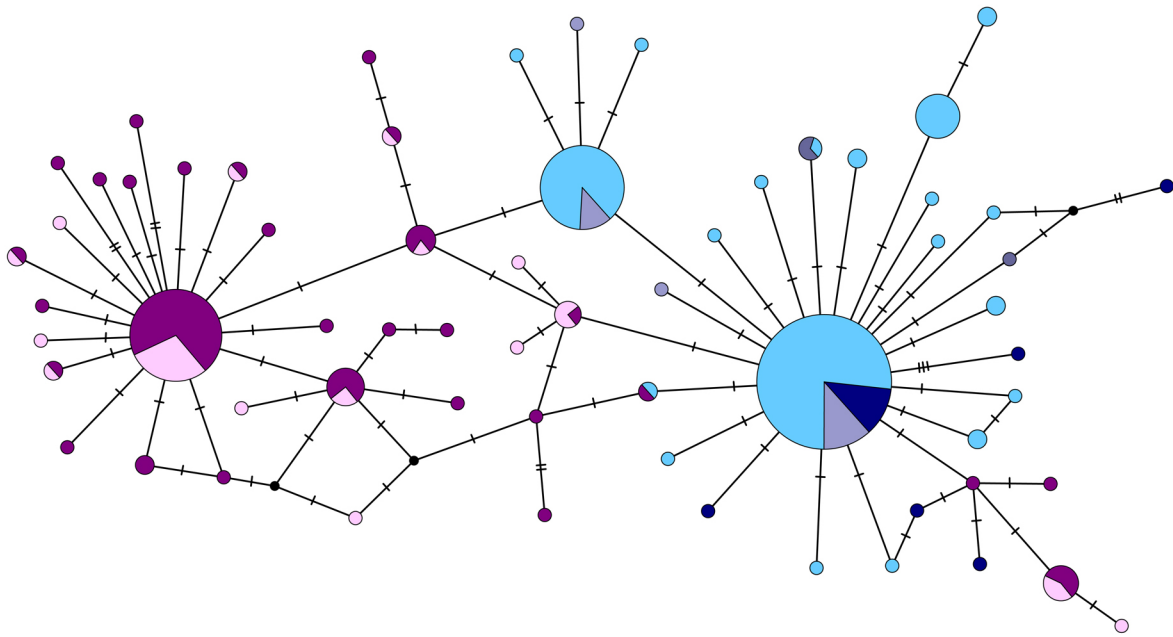
B ND4

FIGURE 2 Haplotype networks for mitochondrial *COI* and *ND4*, with haplotypes coloured by broader geographic region or type / paratype locality. Dot sizes are proportional to haplotype frequency. Dashes on connecting branches indicate number of mutations between haplotypes. Despite shared genetic variation among geographic regions, haplotypes can be broadly grouped into an Indian and western Pacific cluster.