Supplementary Material

Investigating the Bivalve Tree of Life – an exemplar-based approach combining molecular and novel morphological characters

Rüdiger Bieler^{A,N}, Paula M. Mikkelsen^B, Timothy M. Collins^C, Emily A. Glover^D, Vanessa L. González^E, Daniel L. Graf^G, Elizabeth M. Harper^H, John Healy^{A,I}, Gisele Y. Kawauchi^E, Prashant P. Sharma^F, Sid Staubach^A, Ellen E. Strong^J, John D. Taylor^D, Ilya Tëmkin^{J,K}, John D. Zardus^L, Stephanie Clark^A, Alejandra Guzmán^{E,M}, Erin McIntyre^E, Paul Sharp^C and Gonzalo Giribet^E

^AInvertebrates, Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, IL 60605, USA.

^BPaleontological Research Institution, 1259 Trumansburg Road and Department of Ecology & Evolutionary Biology, Cornell University, Ithaca, NY 14850, USA.

^CDepartment of Biological Sciences, AHC 1 Bldg, Rm 319C, Florida International University, Miami, FL 33199, USA.

^DDepartment of Life Sciences, The Natural History Museum, London SW7 5BD, UK.

^EMuseum of Comparative Zoology & Department of Organismic and Evolutionary Biology, Harvard University, 26 Oxford Street, Cambridge, MA 02138, USA.

^FAmerican Museum of Natural History, Division of Invertebrate Zoology, 200 Central Park West, New York City, NY 10024, USA.

^GUniversity of Wisconsin-Stevens Point, Biology Department, 800 Reserve Street, Stevens Point, WI 54481, USA.

^HDepartment of Earth Sciences, University of Cambridge, Downing Street, Cambridge, CB2 3EQ, UK.

^IQueensland Museum, PO Box 3300, South Brisbane, Qld 4101, Australia.

^JDepartment of Invertebrate Zoology, National Museum of Natural History, Smithsonian Institution, PO Box 37012, MRC 163, Washington, DC 20013, USA.

^KBiology Department, Northern Virginia Community College, 4001 Wakefield Chapel Road, Annandale, VA 22003, USA.

^LDepartment of Biology, The Citadel, 171 Moultrie Street, Charleston, SC 29409, USA.

^MStanford University, 300 Pasteur Drive, Stanford, CA 94305, USA.

^NCorresponding author. Email: <u>rbieler@fieldmuseum.org</u>

Fig. S1. Phylogenetic relationships of Bivalvia based on maximum likelihood analysis of nine genes ($-\ln L = 80409.47$). Constituent taxa consist of the subset of terminals that were sequenced for four nuclear protein-encoding genes by Sharma *et al.* (2012). Colours correspond to major lineages, as in Fig. 26. Numbers on nodes indicate bootstrap resampling frequencies.





Fig. S2. Tree file with the estimated dates of diversification for all major clades of bivalves, as inferred by this analysis.

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