Phylogenetic reconstruction based on ten concatenated nuclear genes.

Coding sequences of the 10 nuclear genes listed in Table S1 were concatenated for tree reconstruction. Of 5801 total characters used, 833 variable characters were parsimony-uninformative, and 1467 were parsimony-informative. Reliability was assessed using bootstrap re-sampling of 20,000 replicates, and bootstrap values are indicated. The species are *Fundulus heteroclitus* (Fundulus), *Oryza latipes* (Medaka), *Gasterosteus aculeatus* (Stickleback), *Tetraodon nigroviridis* (Tetraodon), *Fugu rubipes* (Fugu), *Oncorhynchus mykiss* (Trout), *Salmo salar* (Salmon), *Danio rerio* (Zebrafish), *Poecilia reticulata* (Guppy). The outgroup is the chicken, *Gallus gallus* (Gallus).