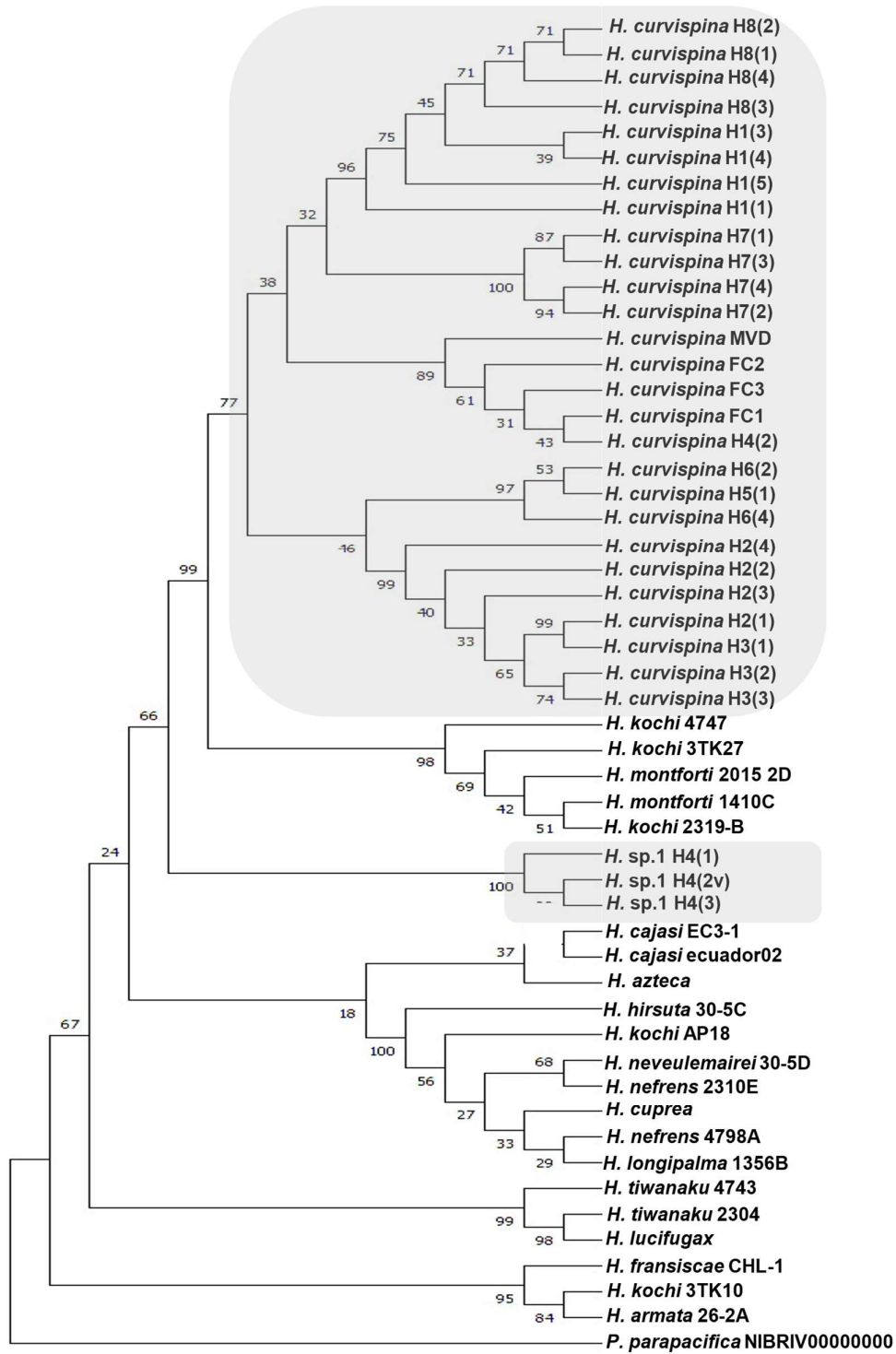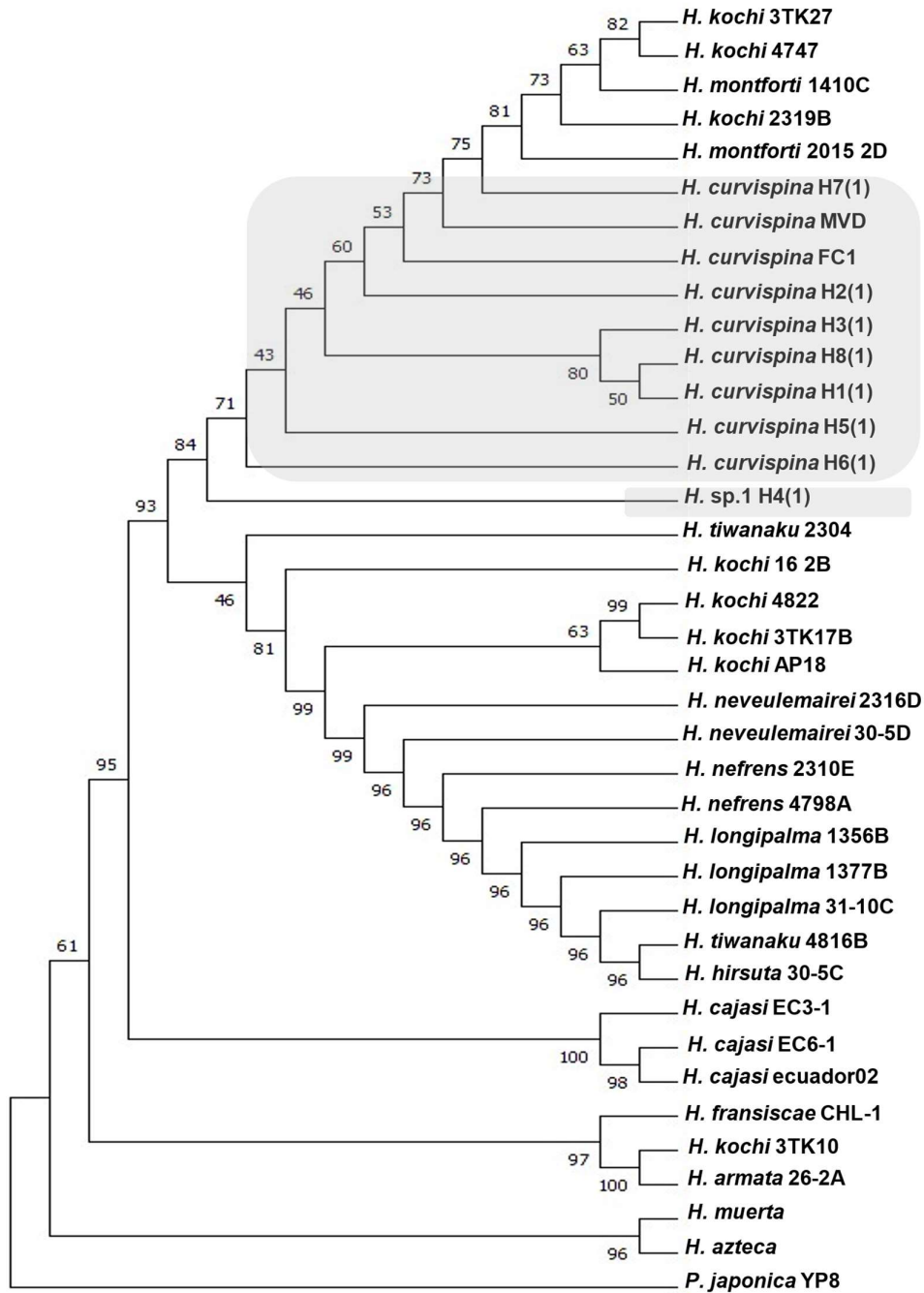**Figure S1**. Maximum parsimony phylogeny of a partial COI sequence of *Hyalella*, using *Platorchestia japonica* as outgroup taxon. Uruguayan samples, "curvispina complex" are denoted in grey color. Bootstrap values are next to the nodes.

Figure S2. Maximum parsimony phylogeny of a partial 12S sequence of *Hyalella,* using *Platorchestia parapacifica* as outgroup taxon. Uruguayan samples, "curvispina complex," are denoted in grey color. Bootstrap values are next to the nodes.
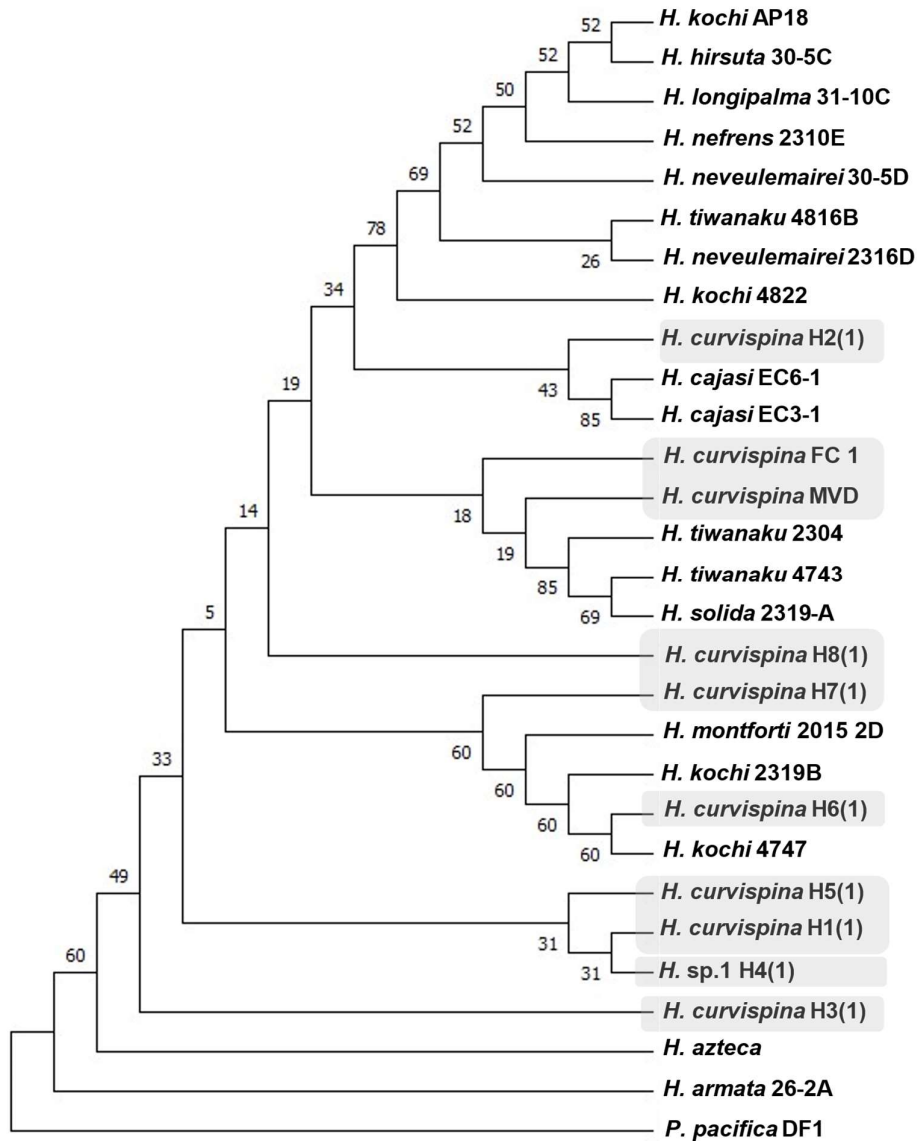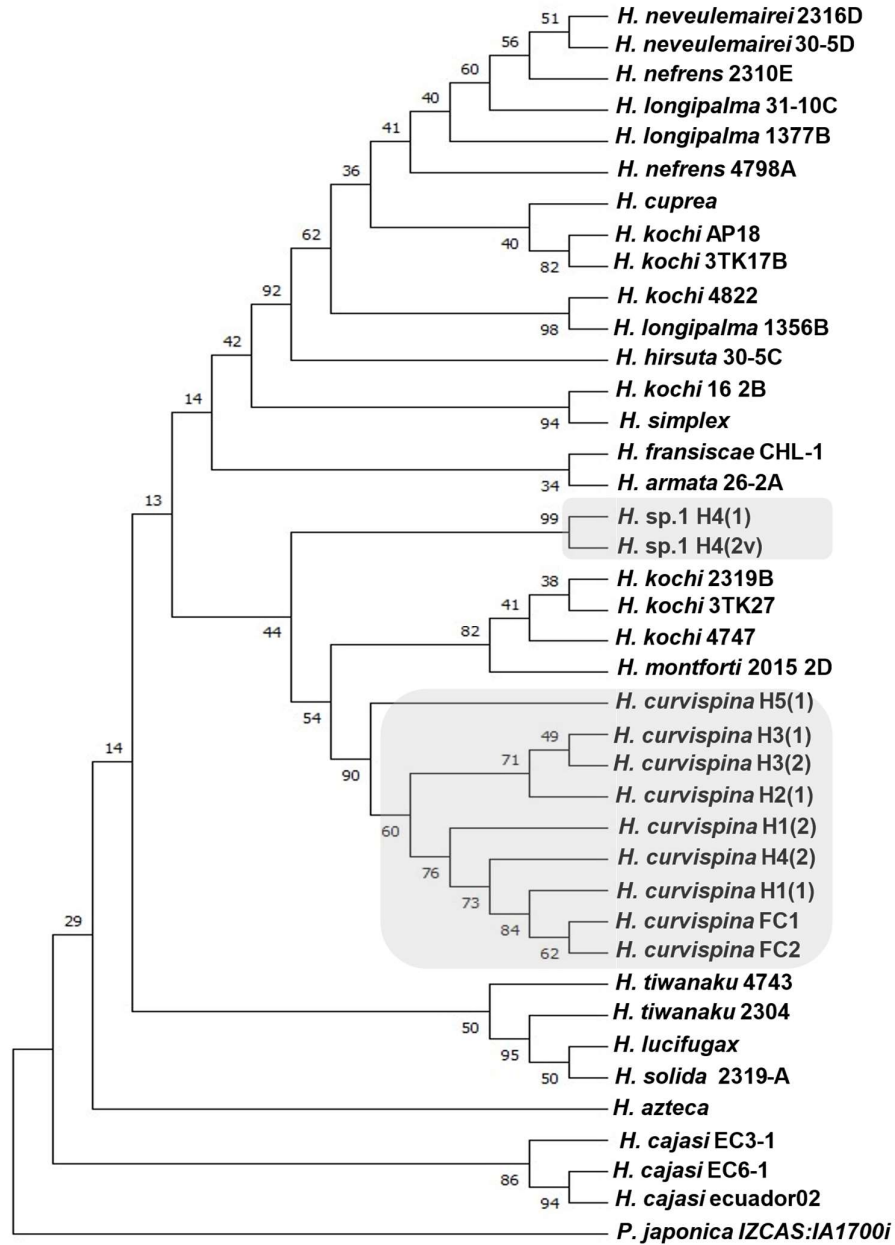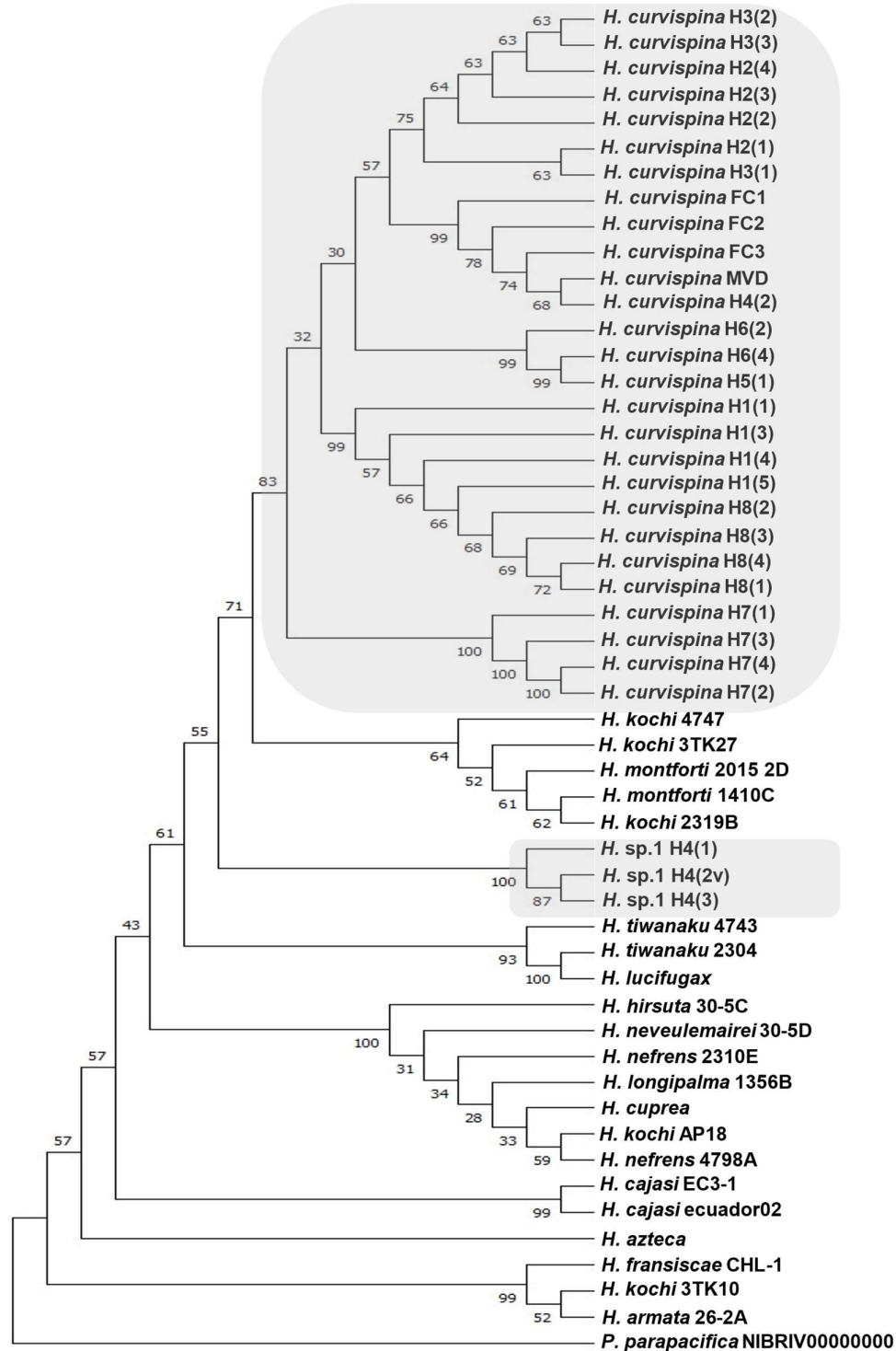
Figure S3. Maximum parsimony phylogeny of a partial 28S sequence of *Hyalella*, using *Platorchestia japonica* as outgroup taxon. Uruguayan samples, "curvispina complex," are denoted in grey color. Bootstrap values are next to the nodes.
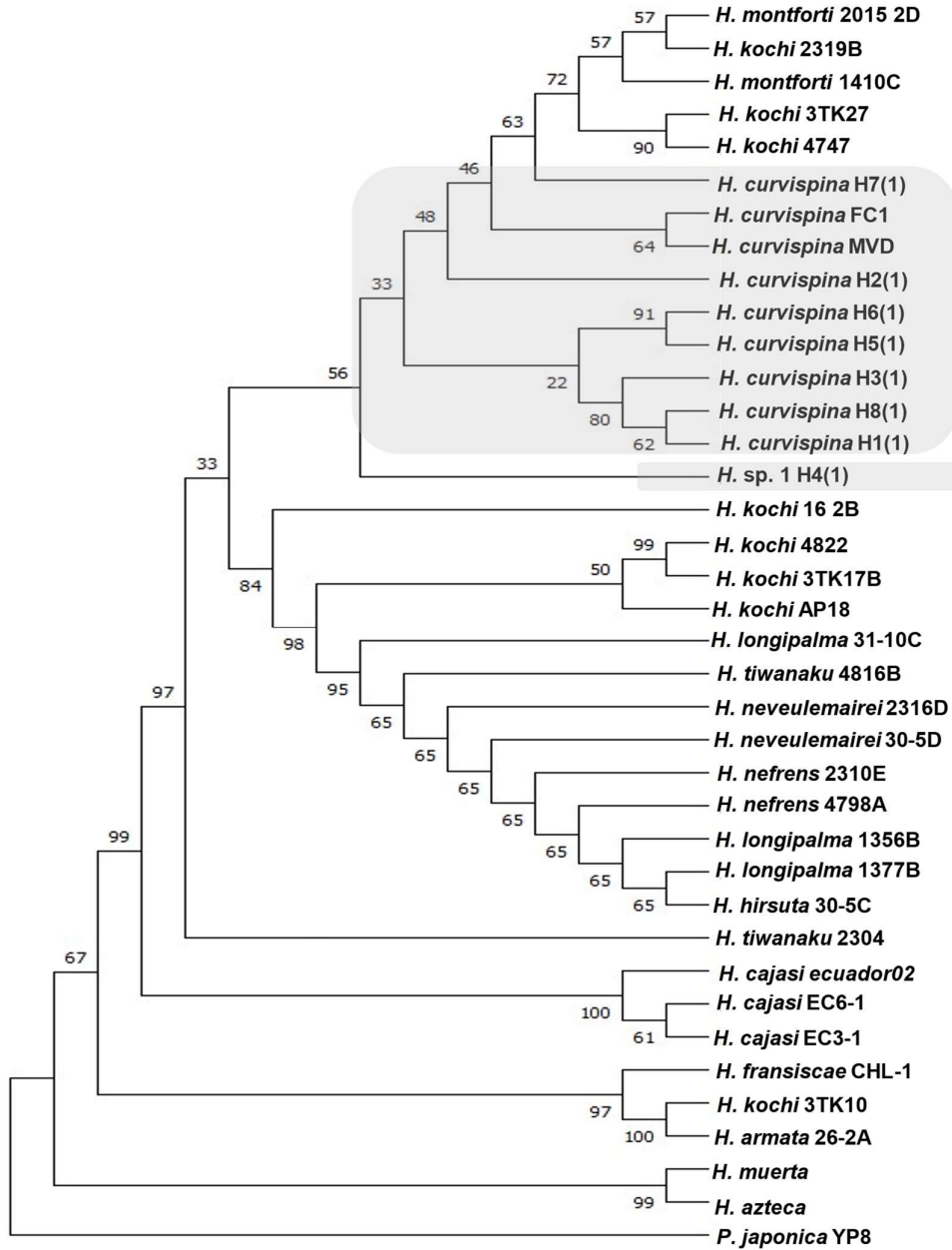
Figure S4. Maximum parsimony phylogeny of a partial H3 sequence of *Hyalella*, using *Platorchestia pacifica* as outgroup taxon. Uruguayan samples, "curvispina complex," are denoted in grey color. Bootstrap values are next to the nodes.

Figure S5. Neighbor-joining phylogeny of a partial COI sequence of *Hyalella*, using *Platorchestia japonica* as outgroup taxon. Uruguayan samples, "curvispina complex," are denoted in grey color. Bootstrap values are next to the nodes.

Figure S6. Neighbor-joining phylogeny of a partial 12S sequence of *Hyalella*, using *Platorchestia parapacifica* as outgroup taxon. Uruguayan samples, "curvispina complex," are denoted in grey color. Bootstrap values are next to the nodes.
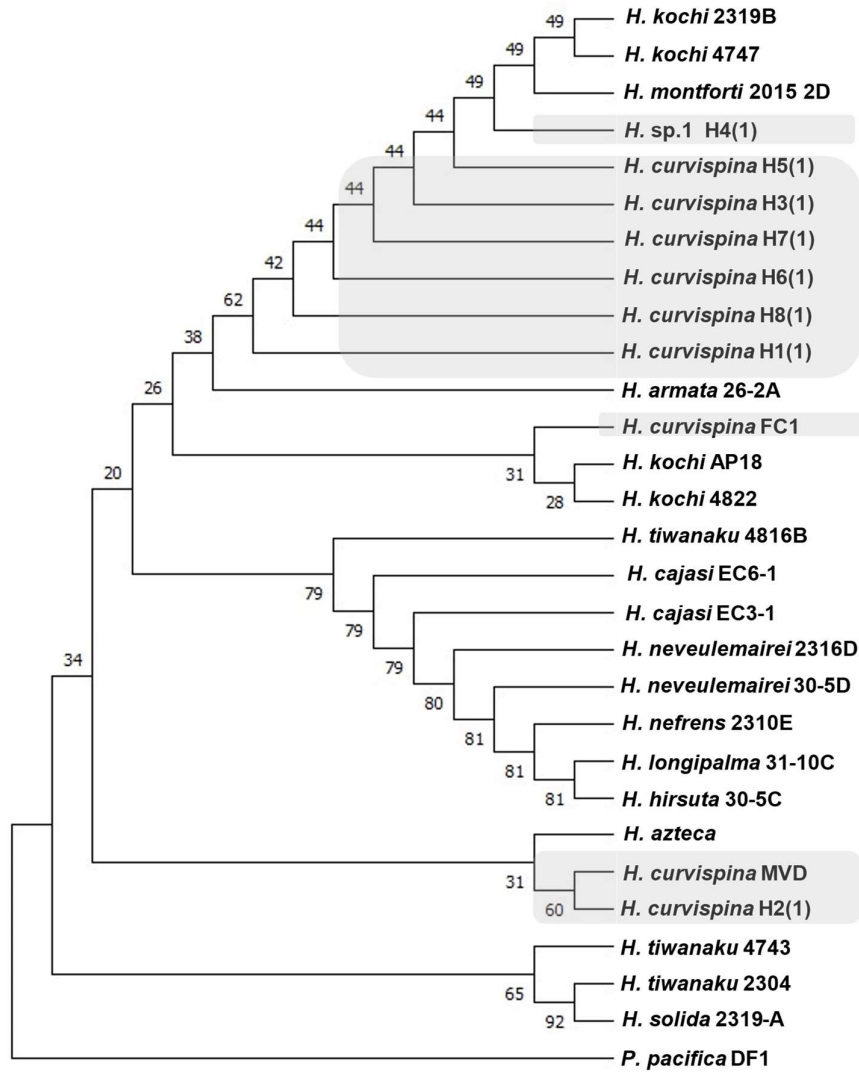
Figure S7. Neighbor-joining phylogeny of a partial 28S sequence of *Hyalella,* using *Platorchestia japonica* as outgroup taxon. Uruguayan samples, "curvispina complex," are denoted in grey color. Bootstrap values are next to the nodes.

Figure S8. Neighbor-joining phylogeny of a partial H3 sequence of *Hyalella*, using *Platorchestia pacifica* as outgroup taxon. Uruguayan samples, "curvispina complex," are denoted in grey color. Bootstrap values are next to the nodes.
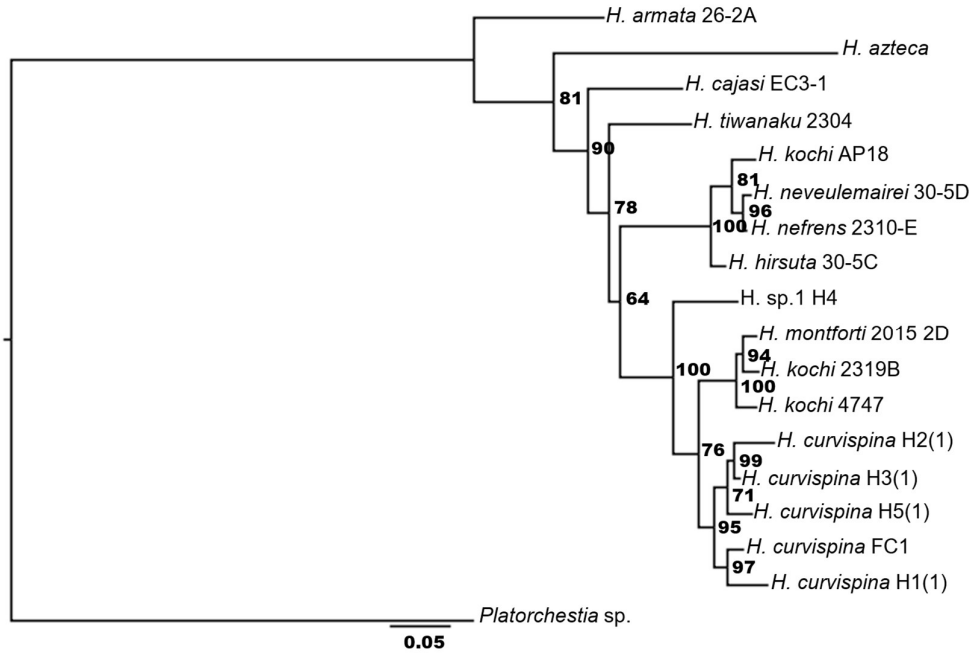
Figure S9. Phylogeny of *Hyalella* reconstructed by maximum likelihood implemented by IQ-tree based on 1758 bp from COI, 12S, 28S, and H3 concatenated datasets, including six Uruguayan samples (*H. curvispina* FC1, H1(1), H2(1), H3(1), H5(1) and H. sp.1 H4(1)) and eleven sequences from North and South America, and using *Platorchestia* sp. as outgroup taxon. Bootstrap values are next to the nodes.
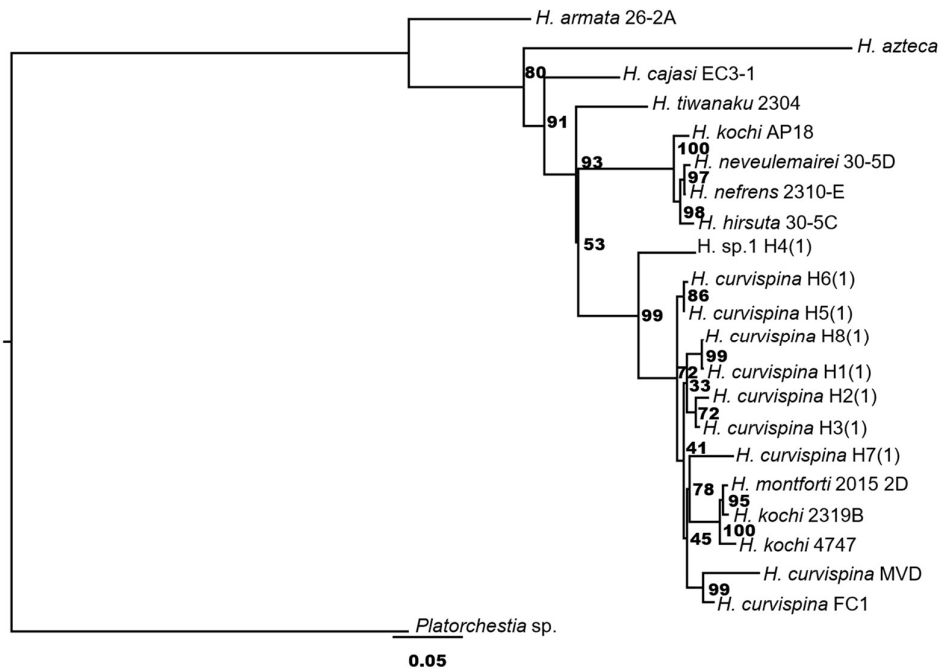
Figure S10. Phylogeny of *Hyalella* reconstructed by maximum likelihood implemented by IQ-tree based on 1389 bp from 12S, 28S, and H3 concatenated datasets, including ten Uruguayan samples (*H. curvispina*

FC1, MVD, H1(1), H2(1), H3(1), H5(1), H6(1), H7(1), H8(1) and H. sp.1 H4(1)) and eleven sequences from North and South America and using *Platorchestia* sp. as outgroup taxon. Bootstrap values are next to the nodes.
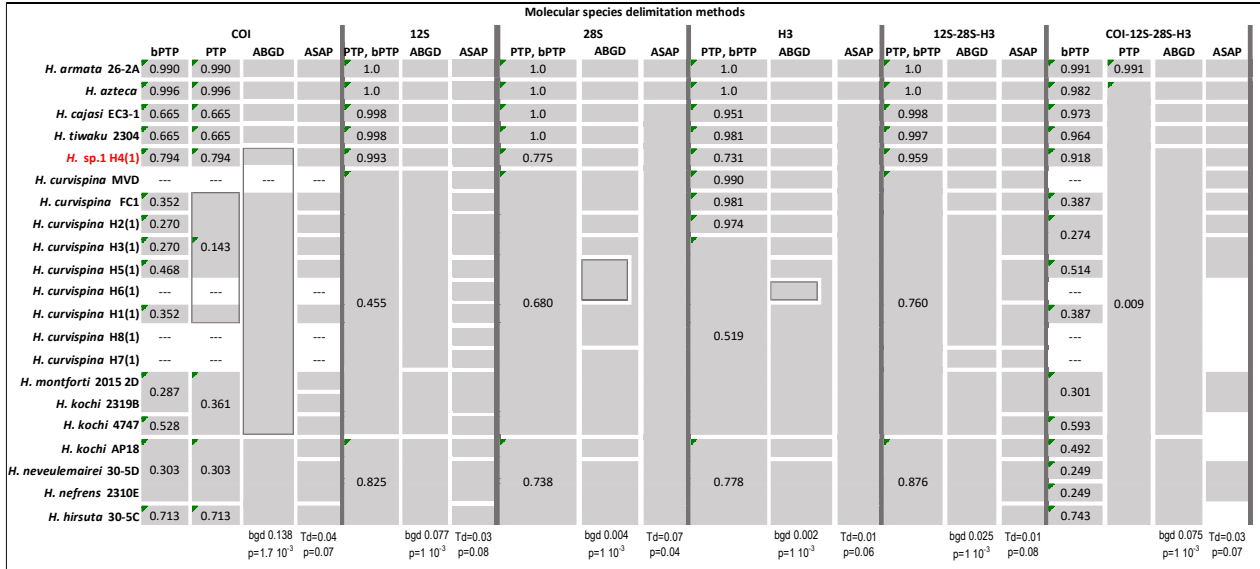
Figure S11. Molecular species delimitation methods (bPTP, PTP, ABGD, and ASAP) were applied to genes COI, 12S, 28S, and H3 individually and concatenated in the *Hyalella* genus. Samples *H. curvispina* FC1, MVD, H1(1), H2(1), H3(1), H5(1), H6(1), H7(1), H8(1) and H. sp.1 H4(1) are Uruguayan samples. The gray blocks or gray boxes represent the groups of samples identified by these methods as a single species. The values inside are the statistical supports of these groupings by maximum likelihood (PTP) or Bayesian (bPTP). For ABGD, the Barcode gap distance (bgd) and the initial Partition with prior maximal distance (p) were specified. For ASAP, p-value (p) and Treshold distance (Td) for each partition were specified. Blank cells (---) are those that were not analyzed for that marker.