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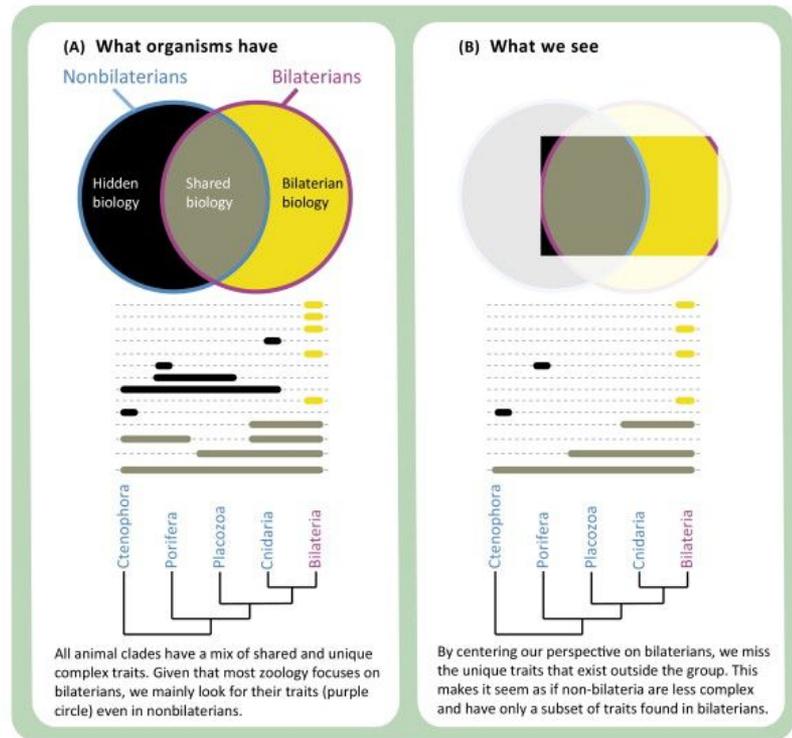
The hidden biology of sponges and ctenophores

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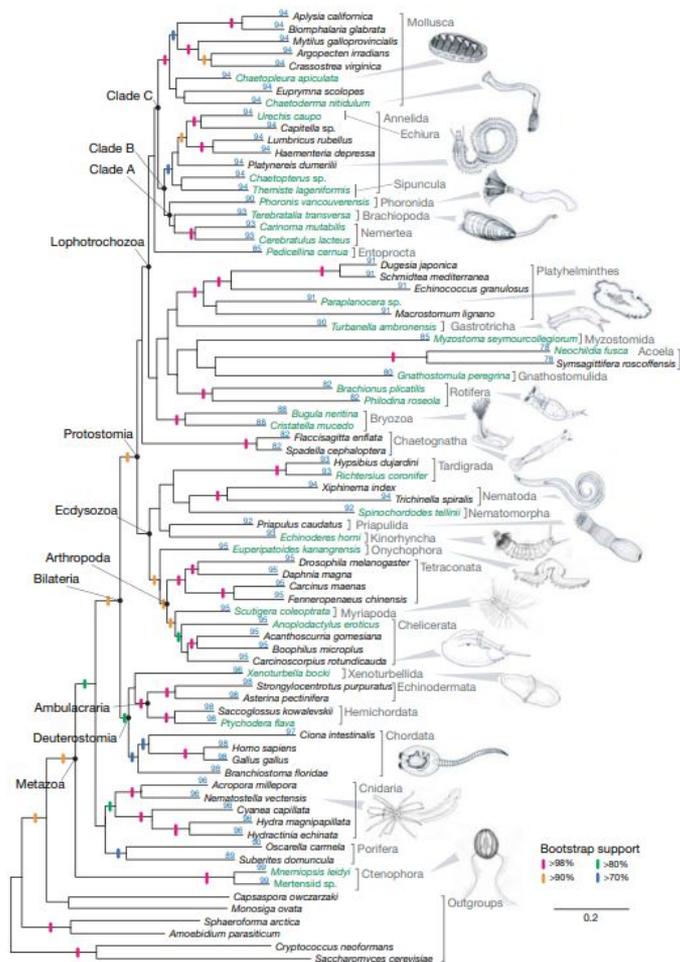


Figure 1 | Phylogram of the 77-taxon RaxML maximum likelihood analyses conducted under the WAG model. The figured topology and branch lengths are for the sampled tree with the highest likelihood (1,000 searches, log

likelihood = 796,399.2). Support values are derived from 1,000 bootstrap replicates. Leaf stabilities are shown in blue above each branch. Taxa for which we collected new data are shown in green.