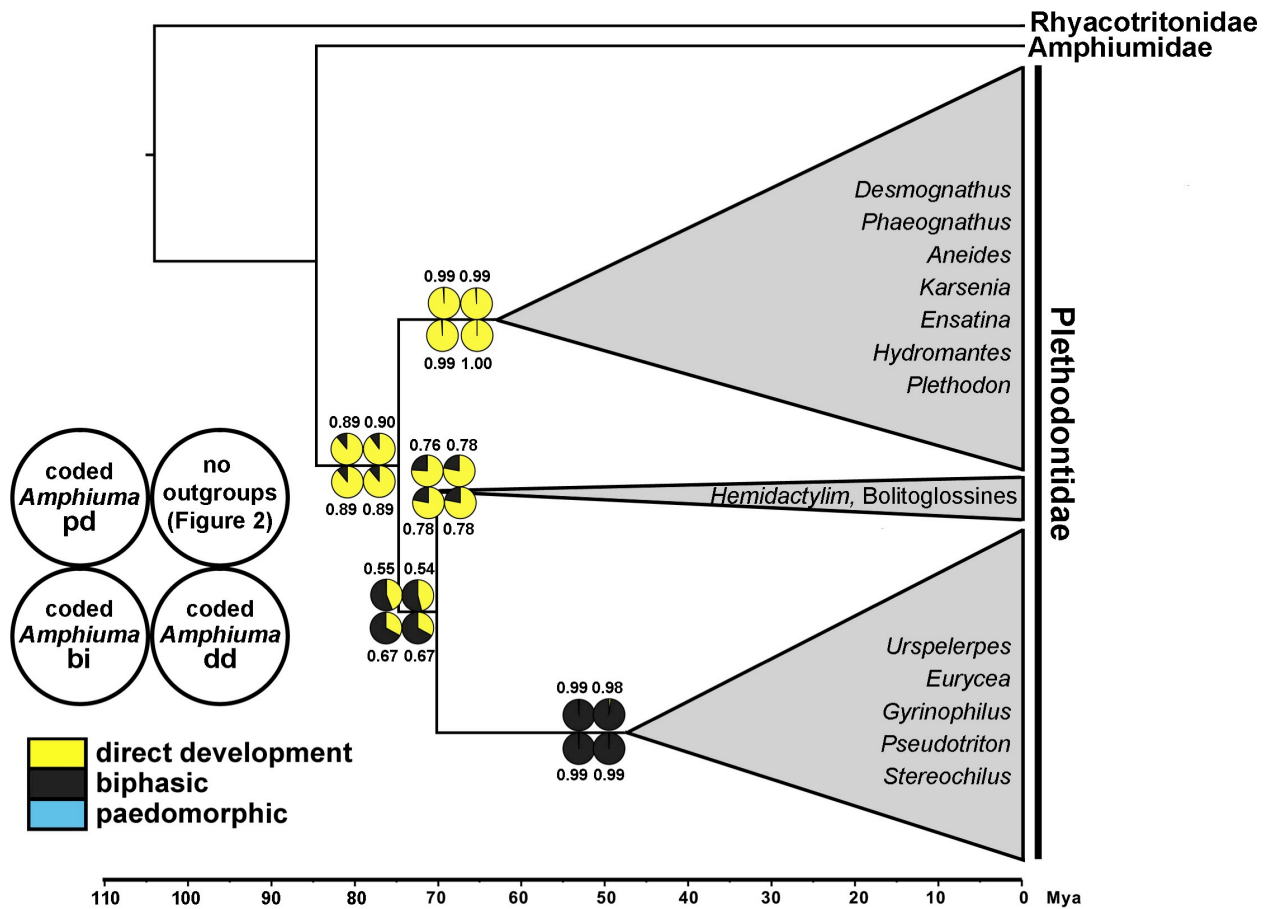**Categorical ancestral state reconstruction of plethodontid life histories including outgroups.**
Bayesian reconstructions were performed using the same methods as described in the main
manuscript (for Figure 2) except for the inclusion of the outgroup families (Amphiumidae and
Rhyacotritonidae) in the three additional analyses presented here. These families are resolved as
the closest relatives to plethodontids in most molecular phylogenetic studies over the last decade.
For diagrammatic purposes only, three major plethodontid clades were collapsed to simplify the
phylogeny, which is intended to highlight the basal nodes within the family. Pie diagrams
subtending major nodes show the proportional probability of each life history state: direct
development (dd), biphasic (bi), and paedomorphic (pd). The value adjacent to the pie is the
proportional probability of the most probable state (highest value). The upper right pie diagram at
each node is from the analysis in Figure 2 (without outgroups). For the three analyses with
outgroups, *Rhyacotriton* were always coded as biphasic, whereas *Amphiuma* were coded as direct
developers (lower right pie), biphasic (lower left pie), or paedomorphic (upper left pie). Note:
including these outgroups (and regardless of how *Amphiuma* was coded) had almost no effect on
the ancestral life history estimates for plethodontids. Maximum Likelihood reconstructions also
performed in BayesTraits yield almost identical values; with and without outgroups.