

## Supporting Information 3

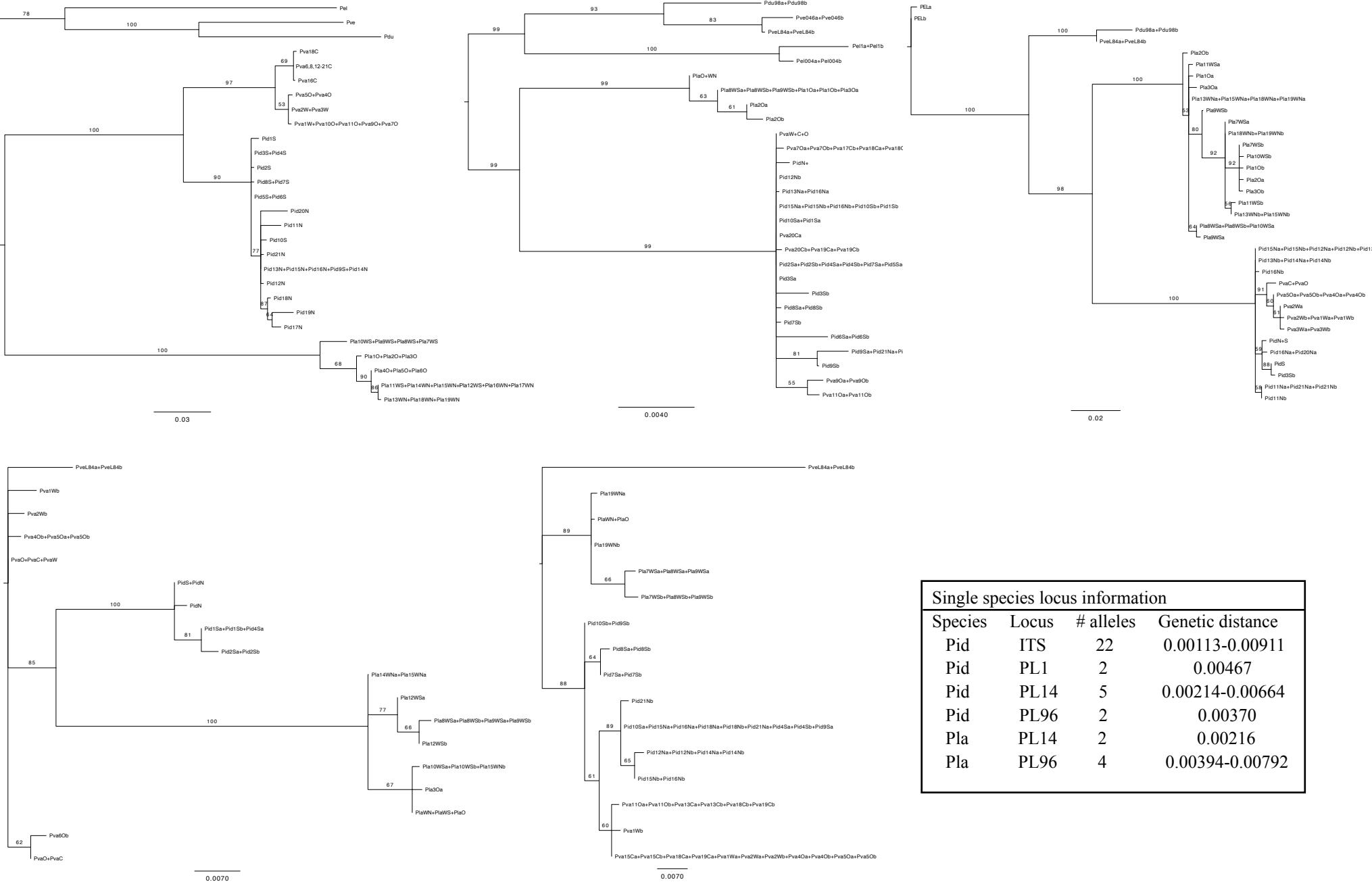
### *Gene tree estimation*

Models of sequence evolution for each locus were selected using DT-ModSel (Minin et al. 2003) and PAUP\* (Swafford 2002). GARLIv2.0 (Zwickl 2006) was used to estimate ML gene-trees for each locus using the unique alleles of each dataset. Nodal support was assessed with 500 bootstrap replicates and combined using SumTrees of the DendroPy package (Sukumaran and Holder 2010). Outgroups chosen based on Kozak et al. (2006).

Estimates of gene trees show extensive allele sharing among populations within, and in some cases between, species. Nodal support values are modest compared to phylogenetic investigations, as is often the case for phylogeographic data. In the cases where only one species was sequenced for a given locus and/or there were few alleles, the genetic distance and number of alleles are present in a table. In instances where there was allele sharing within a region by many individuals the allele was simply labeled as that species of that region to ease readability. For example, PidS represents an allele of *P. idahoensis* from the southern portion of its range that is shared by more than one individual. If an allele was shared between regions it may simply be labeled as PidS+PidN, meaning that individuals from both the northern and southern river drainages of *P. idahoensis* share that allele. Pve=*P. vehiculum*, Pdu=*P. dunni*, Pel=*P. elongatus*, Pva=*P. vandykei*, Pla=*P. larselli*, Pid=*P. idahoensis* (see also Table 1 and Fig. 1).

- Kozak K.H., Weisrock D.W., Larson A. Rapid lineage accumulation in a non-adaptive radiation: phylogenetic analysis of diversification rates in eastern North American woodland salamanders (Plethodontidae: *Plethodon*). Proc. Roy. Soc. Lond. B Bio. 2006;273:539-546.
- Minin, V., Z. Abdo, P. Joyce, and J. Sullivan. 2003. Performance-based selection of likelihood models for phylogeny estimation. Systematic Biology 52:674-683.
- Swafford, D. 2002. Paup\*. Phylogenetic analysis using parsimony (\* and other models). Version 4:b10.
- Sukumaran, J., and M. T. Holder. 2010. DendroPy: a Python library for phylogenetic computing. Bioinformatics 26:1569-1571.
- Zwickl, D. 2006. GARLI: genetic algorithm for rapid likelihood inference. See <http://www.bio.utexas.edu/faculty/antisense/garli/Garli.html>.

## Supporting Information 3 (cont.)

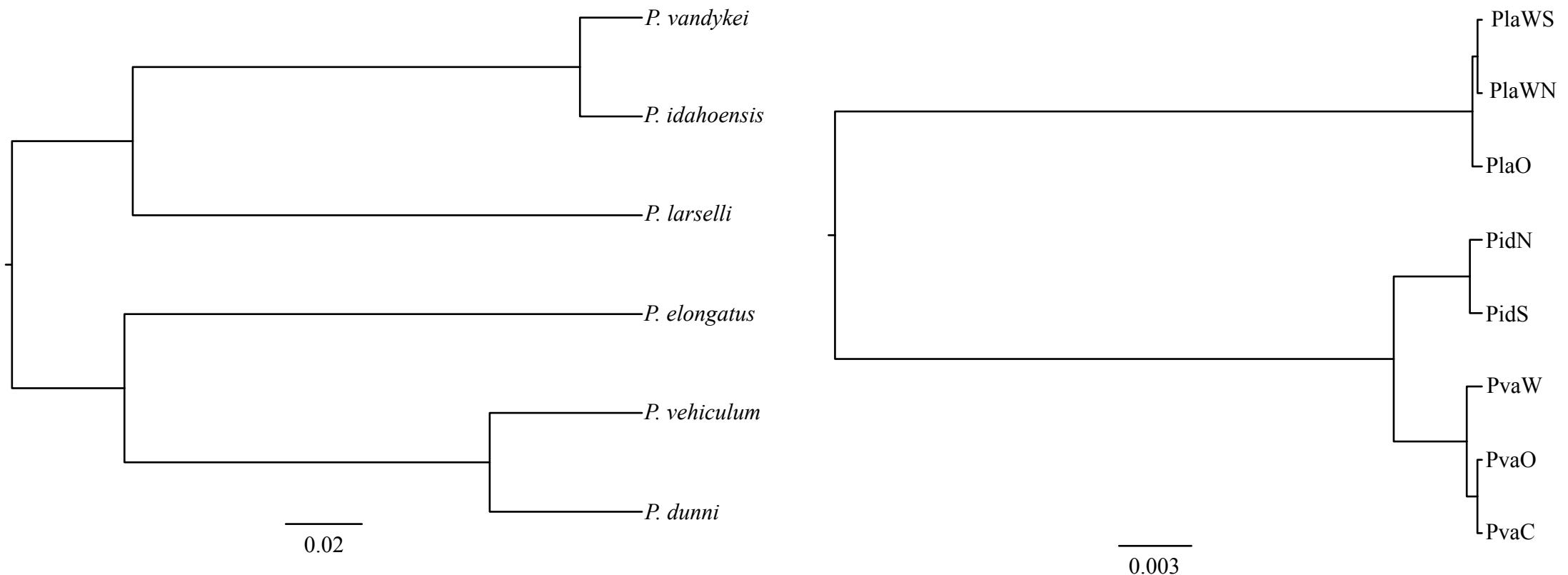


### Single species locus information

Species	Locus	# alleles	Genetic distance
Pid	ITS	22	0.00113-0.00911
Pid	PL1	2	0.00467
Pid	PL14	5	0.00214-0.00664
Pid	PL96	2	0.00370
Pla	PL14	2	0.00216
Pla	PL96	4	0.00394-0.00792

Gene trees ordered from left to right: Cytb, RAG1, GAPD, C32C32, C109C110

### Supporting Information 3 (cont)



\*BEAST results (3 loci) for nominal species and 3 outgroups.

\*BEAST results (5 loci) for 8 potential lineages.