

## Supplementary Materials

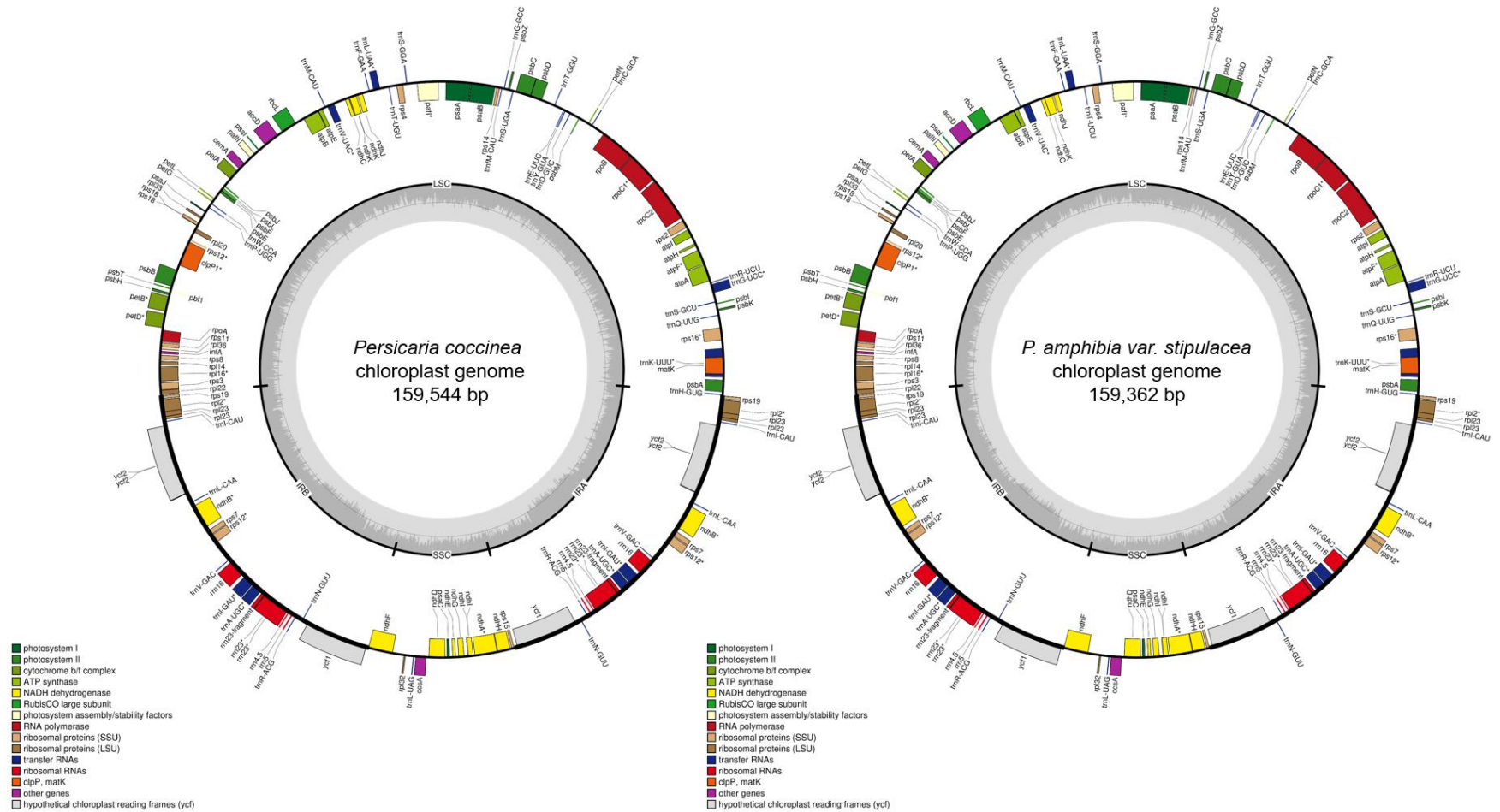


Figure S1. The structure of plastid genome of *P. coccinea* (= *P. amphibia* var. *emersa*) from Potsdam population (left) and *P. amphibia* var. *stipulacea* from Watertown (right). Two representative plastome structures were shown, as no structural variations were observed among the individuals investigated here.

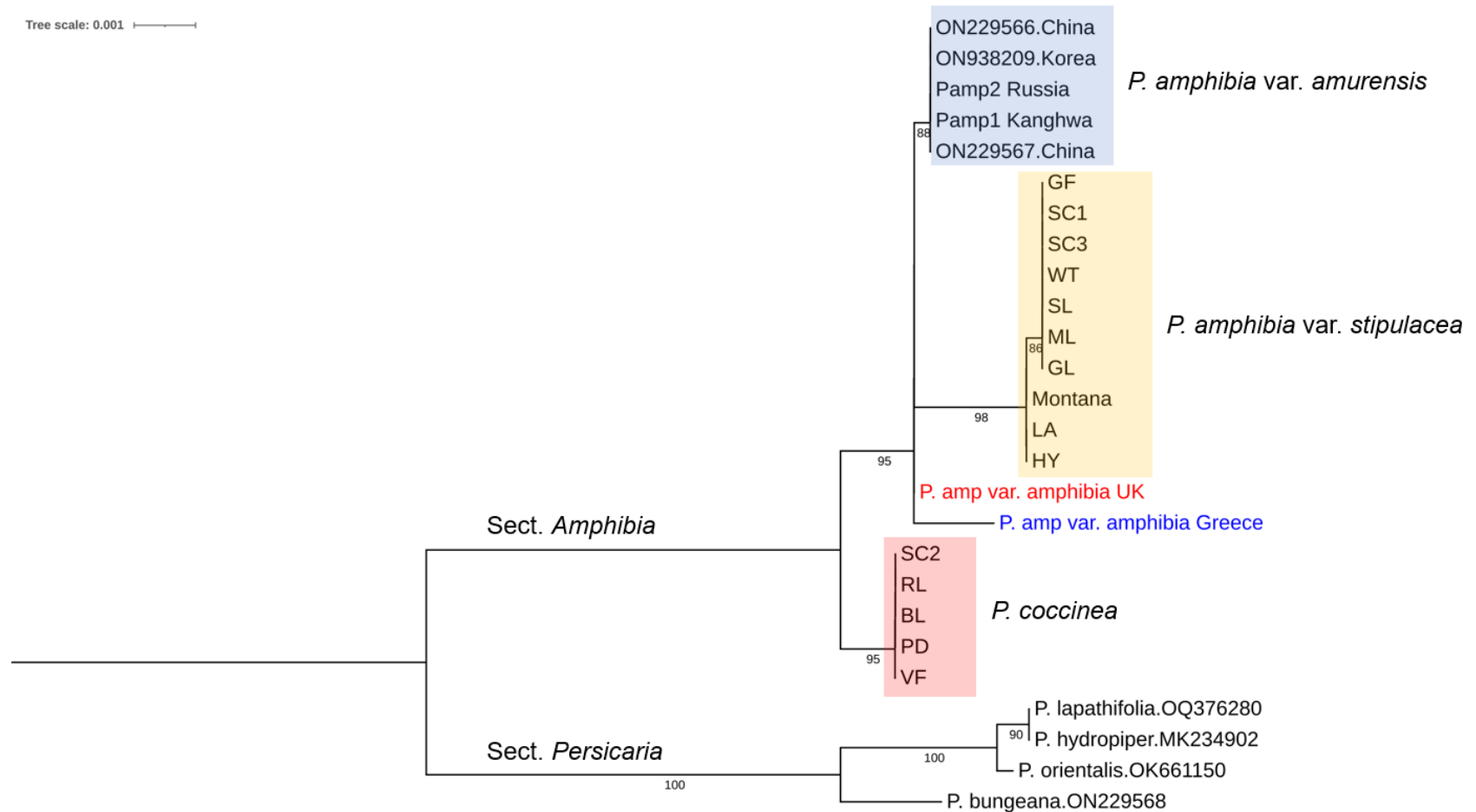


Figure S2. A maximum-likelihood tree inferred from the partial chloroplast sequences with the best fit model of K3Pu+F. The sequences of Greece individual were obtained from Gitsopoulos *et al.* (2013)'s study. The aligned length was 3,897 bp, of which 97.7% (3,808 bp) were constant across taxa and 79 sites were parsimony informative. The number below the branch shows the bootstrap support value. Two European elements (blue and red text) failed to form one clade.

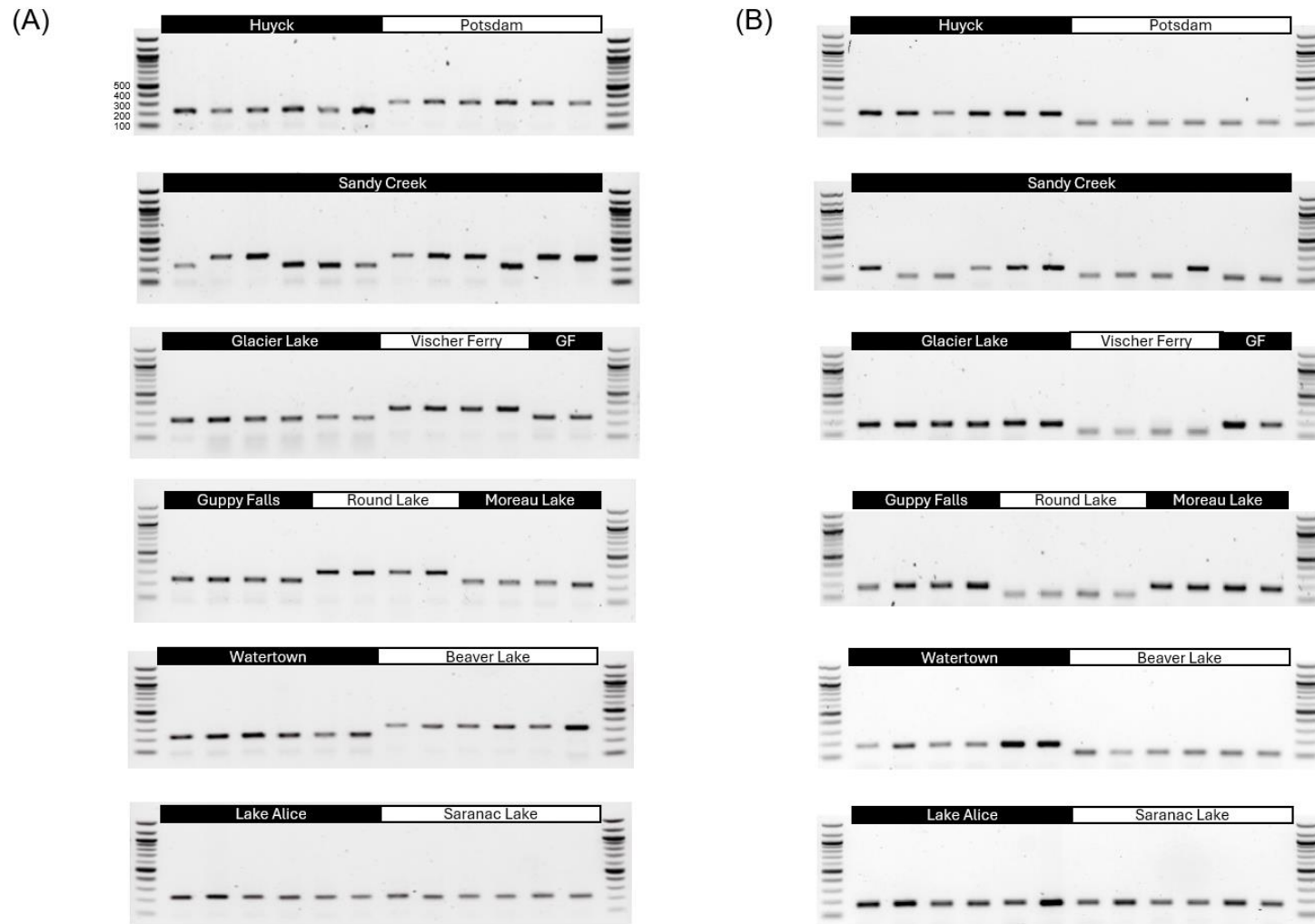


Figure S3. Genotyping results using two chloroplast regions. (A) *rpl20-rpl12* intergenic spacer (240 in *P. amphibia* var. *stipulacea* vs. 311 bp in *P. coccinea*), (B) *rpl33-rps18* intergenic spacer (171 in *P. amphibia* var. *stipulacea* vs. 108 bp in *P. coccinea*). Note that Sandy Creek population shows co-occurrence of two chloroplast genomes.

Table S1. Seven chloroplast regions which show differences between two American elements. Asterisk (\*) indicates the chloroplast regions used in genotyping each population.

Chloroplast region	Primer sequences (5'→3')	Amplicon size (bp) in <i>P. coccinea</i>	Amplicon size (bp) in <i>P. amphibia</i> var. <i>stipulacea</i>	Difference in amplicon sizes
<i>psbA-trnK</i> IGS	F: CAGTATAACATGACTTATATGC R: TCATATCGAAGTCATATGTG	130	124	6 bp
<i>atpF</i> intron	F: TGCTATGGTTCTTCCATATG R: CAAGAATAGACTGGATTCAAC	127	120	7 bp
<i>rpoCl</i> intron	F: ACTACTCCTTACTCAAGTTC R: GGAAGTAGACTACTCAAG	131	123	8 bp
<i>trnE-trnA</i> IGS	F: CTTGGTTCATTGAAGTGATAG R: CTATGCGGATAAGCTATCTC	159	144	15 bp
<i>trnT-trnL</i> IGS	F: CATTCCAATCCTAACAATTAG R: GATAGAACTCATAATTGAATTCA	172	148	24 bp
<i>rpl20-rpl12</i> IGS*	F: TCGAACGTCTGTATATCAC R: AGATCCGACCGAAATAGG	311	240	71 bp
<i>rpl33-rps18</i> IGS*	F: TCATACGCAATAGATGAATATG R: GCCGAGGAACATGTACTAG	108	171	63 bp