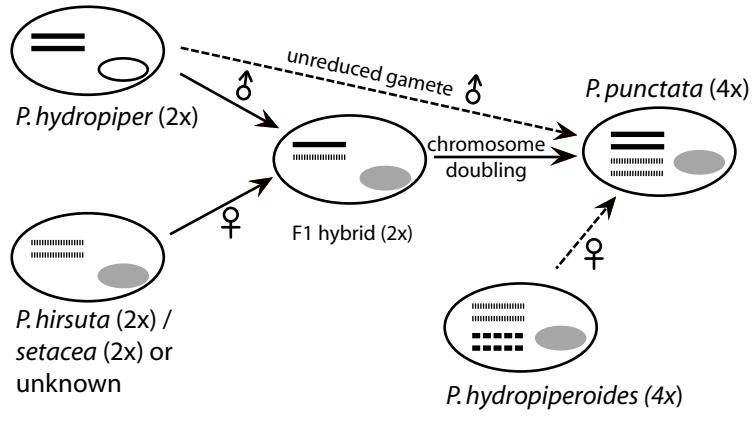


KIM, SANG-TAE AND MICHAEL J. DONOGHUE. 2008. Incongruence between cpDNA and nrITS trees indicates extensive hybridization within *Eupersicaria* (Polygonaceae). *American Journal of Botany* 95(9): 1122-1135.

APPENDIX S1. Summary information from phylogenetic analyses using a 60-taxon combined data set of three chloroplast DNA regions and the nuclear ITS region. BA = Bayesian analysis. hLRT = hierarchical likelihood ratio test (see text). Note: ¹ intergenic spacer region between *psbA* and *trnH*; ² partial *matK* and *trnK* 5' intron; ³ intergenic spacer region between *trnL* and *trnF* and *trnL* intron; ⁴ combined dataset with *psbA*, *matK*, and *trnL*; G = among site rate variation modeled to fit a discrete gamma distribution; *Arithmetic mean of two runs after burn in.

	<i>cp-combined</i>	nrITS
	<i>psbA</i> ¹ , <i>p-matK</i> ² , <i>trnLF</i> ³	
Sequence length (bp)	231 – 396, 578 – 617, 872 – 908	606 - 665
%GC content (all sites)	27.1 – 34.3, 33.4 – 36.9, 33.3 – 35.6	58.2 – 66.2
Aligned sequence length (bp)	2,023	687
No. of variable sites	377	267
No. of parsimony-informative sites (PIS)	249	195
PIS/aligned sequence length (%)	12.3	28.4
PIS/variable sites (%)	66.0	73.0
No. of most parsimonious trees	416	305
Length of most parsimonious tree	480	594
Consistency Index (CI)	0.867	0.647
CI excluding Parsimony-uninformative sites	0.817	0.589
Retention Index (RI)	0.938	0.827
Model selected by hLRT using 'Modeltest'	K81uf + G	TrN + G
-log likelihood in ML analysis	5921.876	4200.498
Model selected by hLRT for BA	F81 + G, K81uf + G, F81 + G	TrN + G
*Mean -log likelihood in BA	6585.224	4290.123



—————> Hypothesis 1 - - - - -> Hypothesis 2