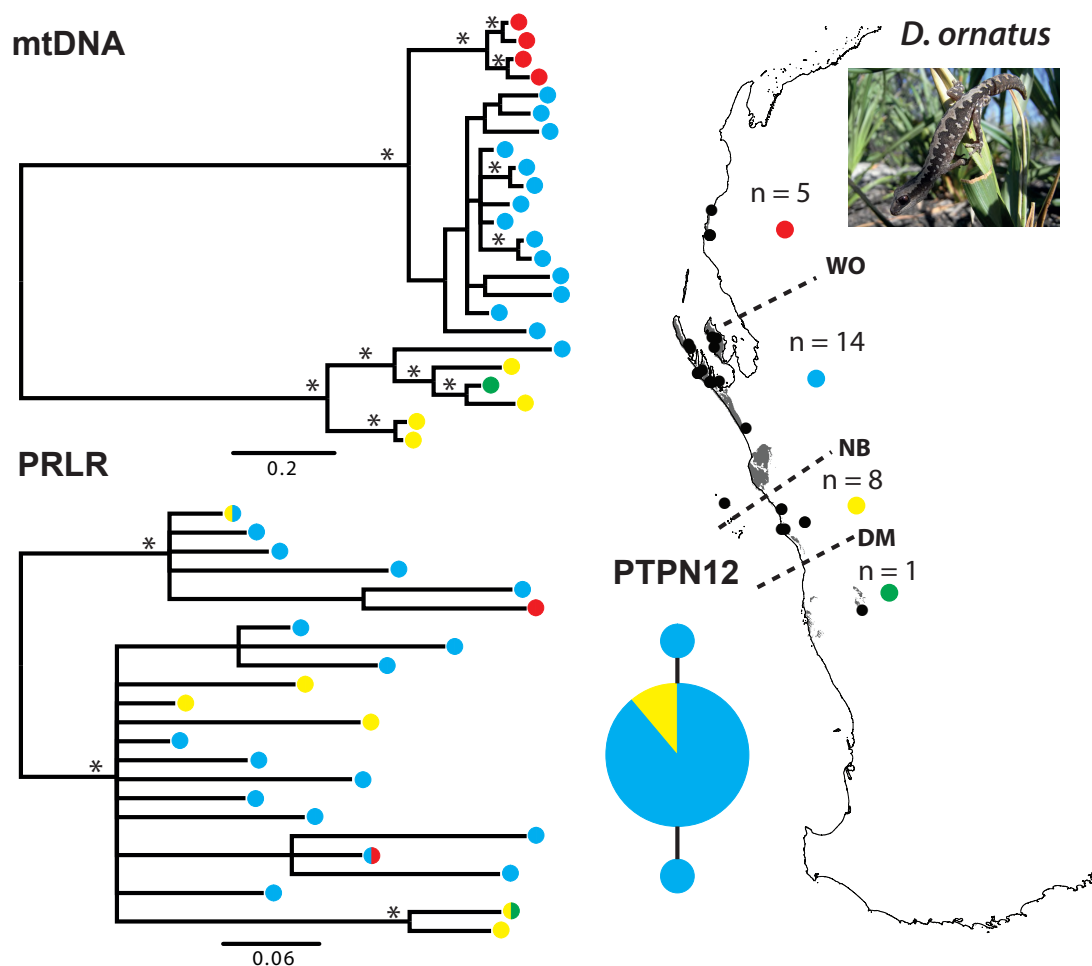
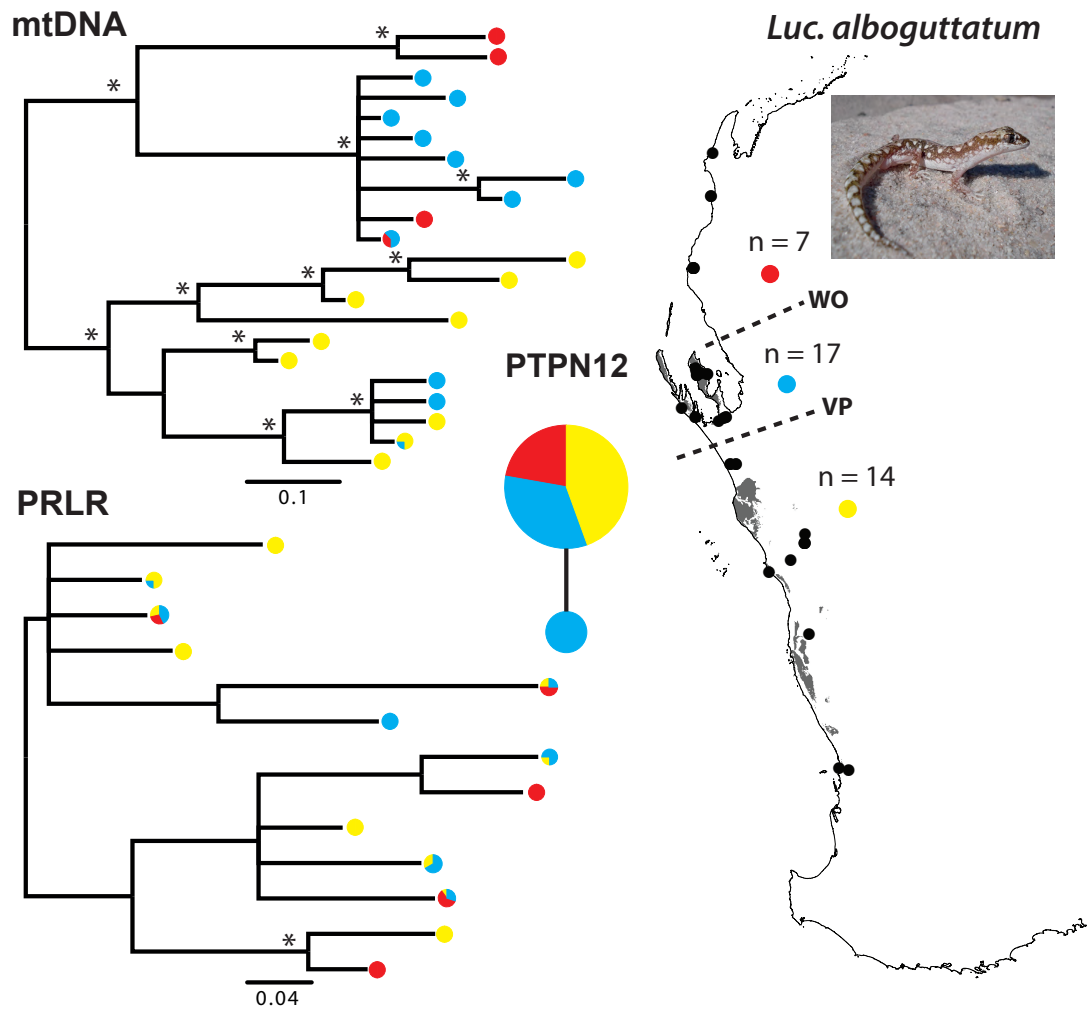


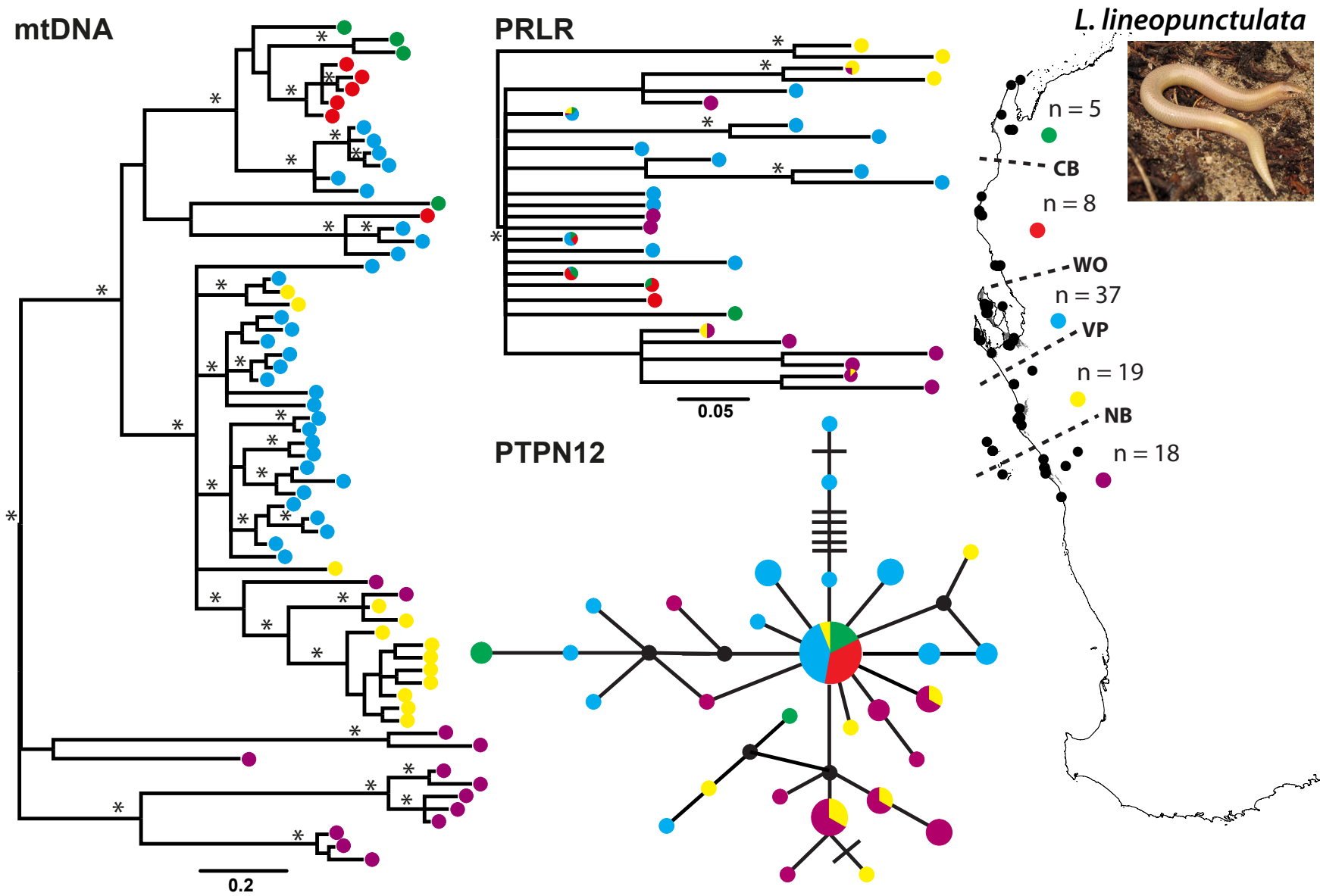
**Supplementary Figure 1:** Presented within are the gene trees/networks, sample distributions, SDM distribution of areas with >70% habitat suitability (shown in gray shading on distribution map), population sizes for each of the SDM defined populations and the location of population breaks inferred from SDMs for each species (A-E – *D. ornatus*, *Luc. alboguttatum*, *L. lineopunctulata*, *L. praepedita* and *M. lineoocellata* respectively). Bayesian analyses were undertaken using MrBayes v3.2 (Ronquist *et al.* 2011) and running for 10 million generations with a 25% burnin. Data were partitioned by codon using GTR + I + G models of evolution as suggested by jModelTest v0.1.1 (Posada 2008). Phylograms are shown for mtDNA (*ND2*) and *PRLR*. Branches with >0.95 posterior probabilities on gene trees are shown with an asterisk. For the *PTPN12* locus gene networks (median-joining networks constructed using Network v4.610 (Bandelt *et al.* 1999)) better represent the diversity within species using this locus. Haplotypes in gene trees and networks are colored by the localities where they occurred – as shown in sampling map to the right of each figure. The size of circles representing haplotypes in the gene networks is reflective of haplotype frequency and inferred missing haplotypes in gene networks are displayed as a cross bar where not forming a connection and a black circle where they form a connection between haplotypes.



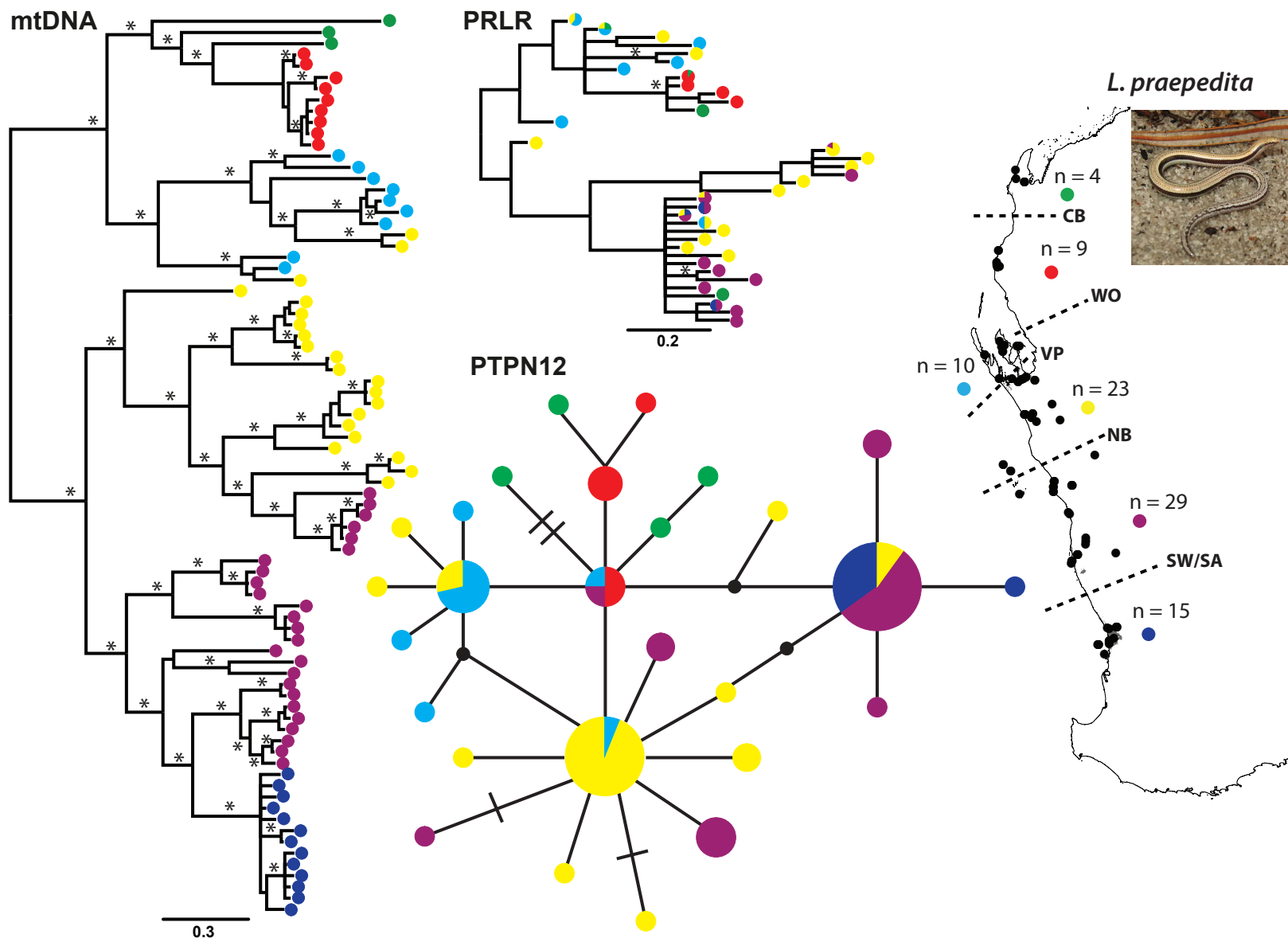
**Supplementary Figure 1A:** Haplotype gene trees/networks, sampling locations, population sample sizes and the distribution of optimal habitat (gray shading on map) for *D. ornatus*. Total samples: 28.



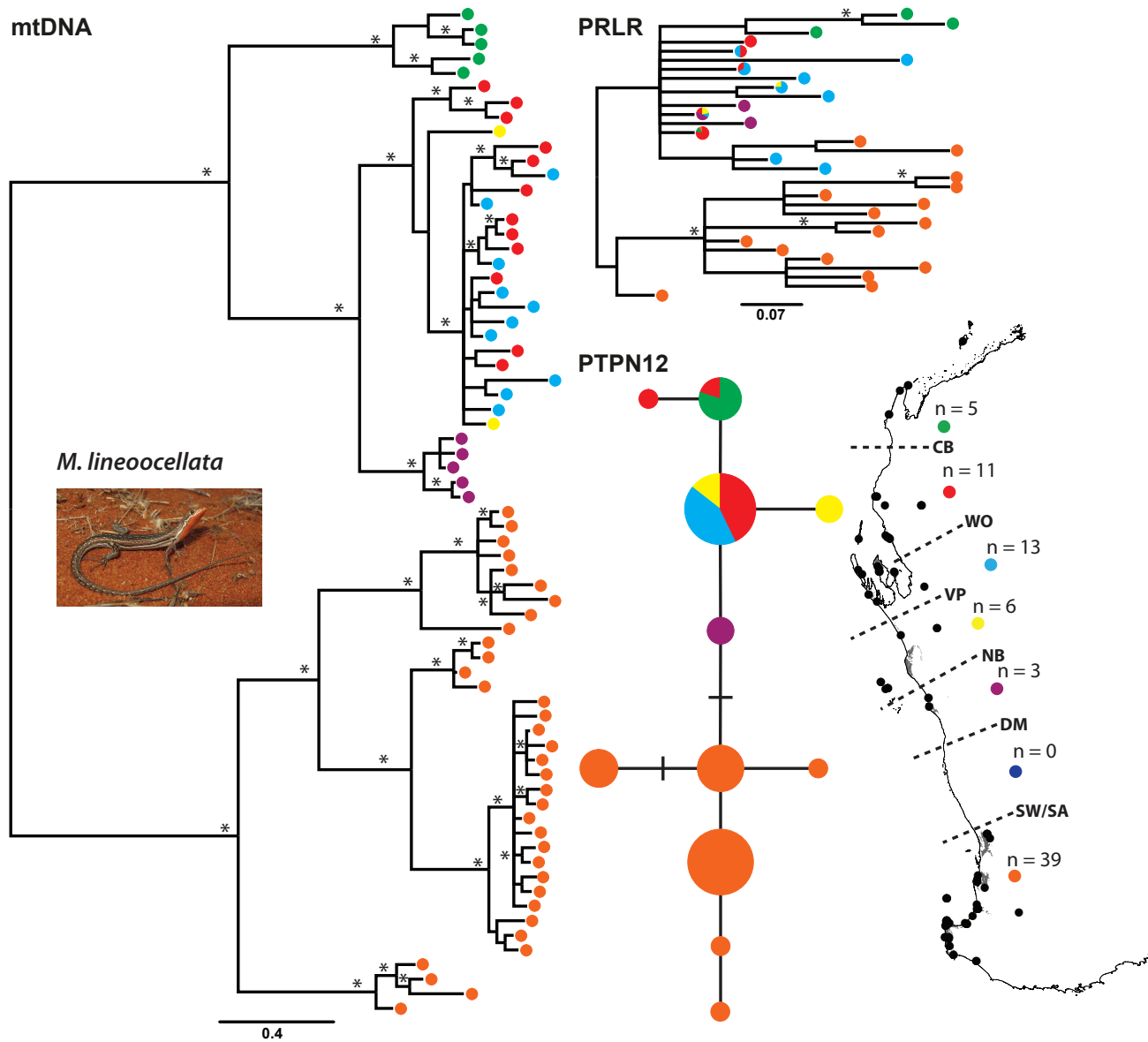
**Supplementary Figure 1B:** Haplotype gene trees/networks, sampling locations, population sample sizes and the distribution of optimal habitat (gray shading on map) for *Luc. alboguttatum*. Total samples: 38.



**Supplementary Figure 1C:** Haplotype gene trees/networks, sampling locations, population sample sizes and the distribution of optimal habitat (gray shading on map) for *L. lineopunctulata*. Total samples: 87.



**Supplementary Figure 1D:** Haplotype gene trees/networks, sampling locations, population sample sizes and the distribution of optimal habitat (gray shading on map) for *L. praepedita*. Total samples: 91.



**Supplementary Figure 1E:** Haplotype gene trees/networks, sampling locations, population sample sizes and the distribution of optimal habitat (gray shading on map) for *M. lineoocellata*. Total samples: 77.

## Literature Cited

Bandelt H-J, Forster P, and Röhl A (1999) Median-joining networks inferring intraspecific phylogenies. *Molecular Biology and Evolution* **16**: 37-48.

Posada D (2008) jModelTest: Phylogenetic model averaging. *Molecular Biology and Evolution* **25**: 1253-1256.

Ronquist F, Huelsenbeck J, and Teslenko M (2011) Draft MrBayes version 3.2 Manual: Tutorials and Model Summaries. <http://mrbayes.sourceforge.net/> (last accessed February 1<sup>st</sup> 2012).