

Additional Figure S3. Statistical parsimony network showing the genealogical relationships between the *mclr* haplotypes inferred for nine *Podarcis* species based on 946 sequences retrieved from GenBank [57-60, 80], generated in this study (*P. tiliguerta*), and unpublished (*P. wagleriana*; Salvi et al. in prep). Haplotypes are represented with circles with size proportional to their frequency; small white circle represent 'missing' or extinct haplotypes.

