

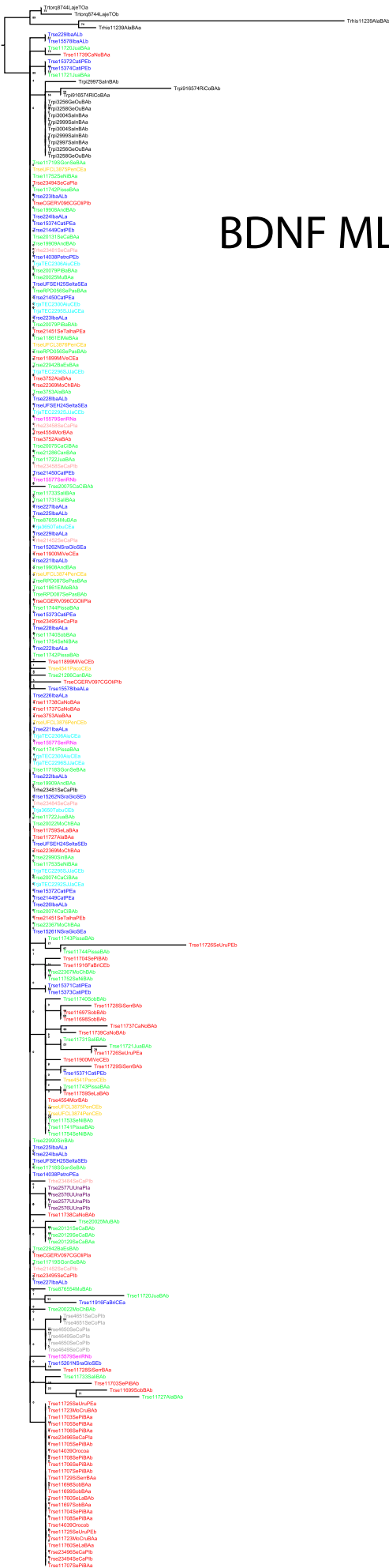
**Supporting Info for the paper**

Biogeographic history and cryptic diversity of saxicolous Tropicuridae lizards endemic to the  
semiarid Caatinga

Fernanda P. Werneck, Rafael N. Leite, Silvia R. Geurgas & Miguel T. Rodrigues

Figure S1: Mitochondrial DNA (cytb + 16S), BDNF and Pho gene trees for the *Tropidurus semitaeniatus* species group, as estimated by maximum likelihood (ML). Colors correspond to localities and clades colors in Fig 1 and Fig. 2.





# BDNF ML gene tree



Figure S2: *Tropidurus semitaeniatus* species group BDNF and Pho haplotype networks build with HaploViewer. Clade colors are the same as in Fig. 1 and 2. Numbers inside the proportionally sized circles represent the number of alleles sharing that particular haplotype.

- T. torquatus*
- T. hispidus*
- T. pinima*
- T. helenae*
- T. semitaeniatus* Seridó
- T. semitaeniatus* Serra Confusões
- T. semitaeniatus* Uruçui-Una
- T. semitaeniatus* Northern Ceará
- T. jaguaribanus*
- T. semitaeniatus* Northwest
- T. semitaeniatus* Northeast
- T. semitaeniatus* South

## BDNF haplotype network

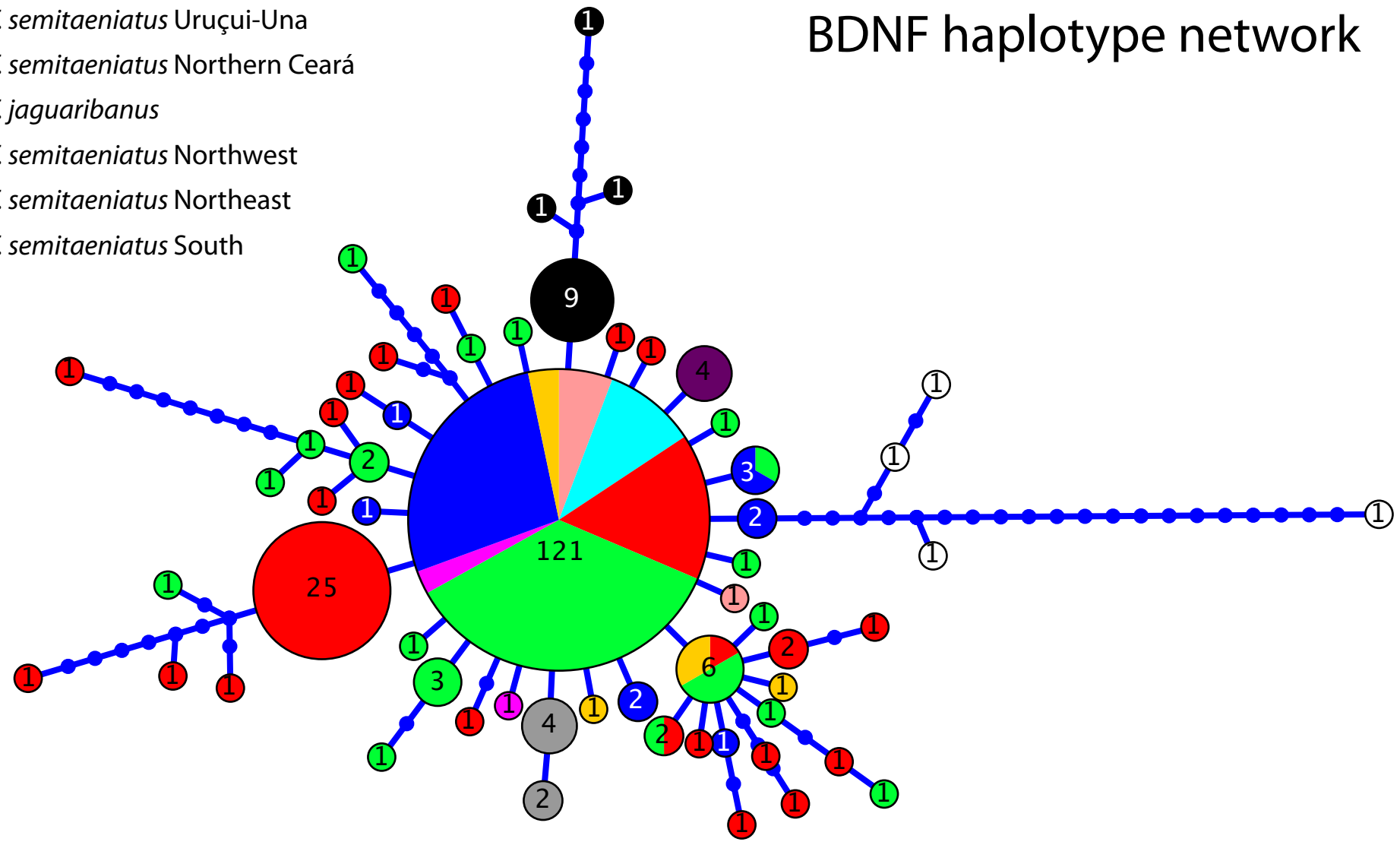






Figure S3: Species tree and divergence times for the *Tropidurus semitaeniatus* species group and outgroups based on the less inclusive species assignments from the mtDNA haploclades. The maximum clade credibility tree was inferred under a coalescent model based on all three independent loci with \*BEAST. Posterior probability (pp) values are indicated by colored circles in the nodes; nodes with no indicative of support have  $pp < 0.75$ .

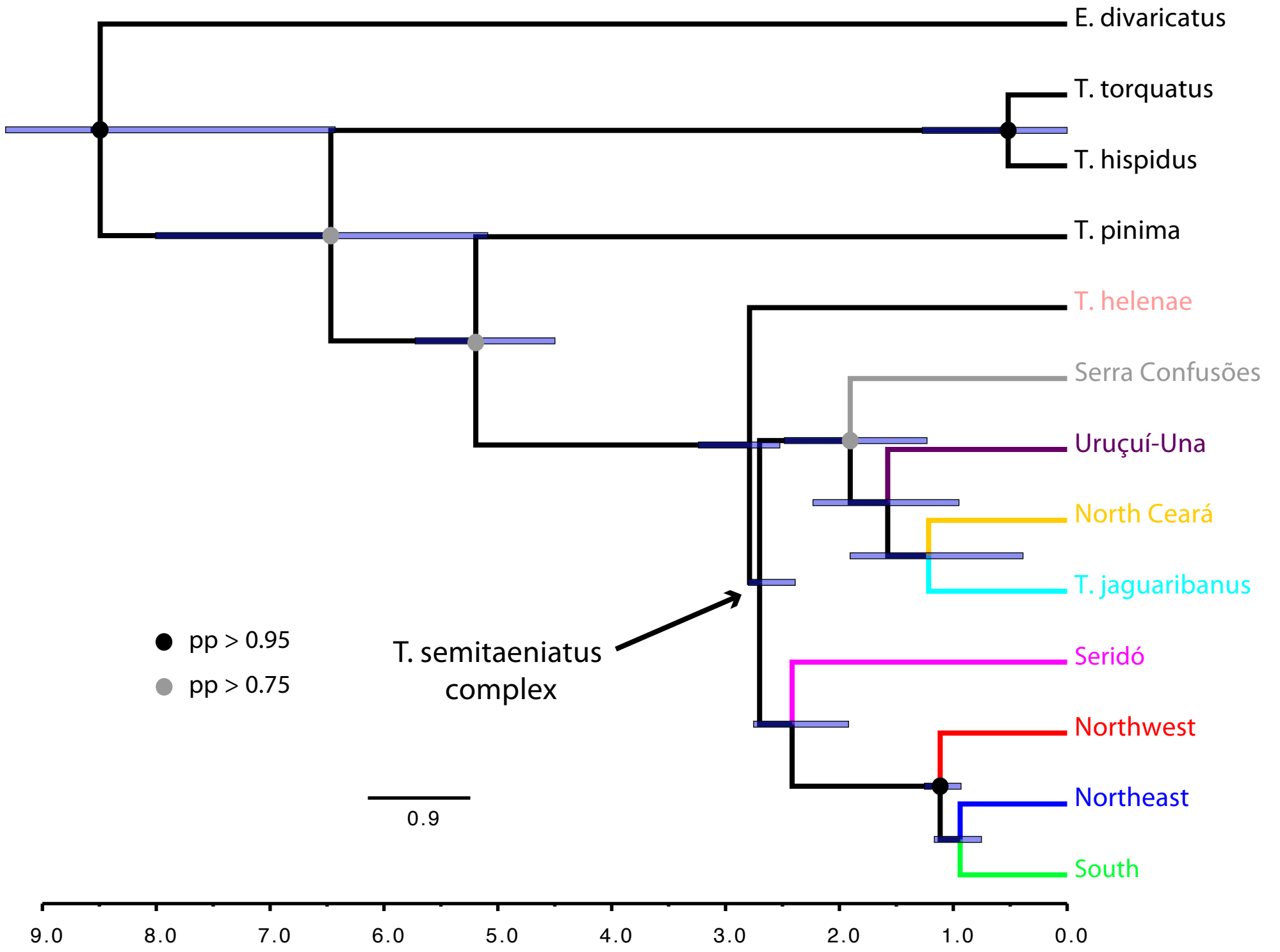


Figure S4: Effective population sizes through time based on the Bayesian Skyride as estimated for each of the three main population strains (Clade C) for the *T. semitaeniatus* complex. Area delimited by the blue line represented the 95%-HPD interval.

