**Appendix A**

*Study site:*Tropical dry forest constitutes the predominant vegetation of the study site, and due to the marked seasonality, most of the vegetation drops its leaves during the dry season (November to June). The rainy season provides 80% of the annual precipitation. This region is important because of the high levels of richness and endemism of herpetofauna and other taxa, harboring a third of the species distributed in Mexico (García, 2006). However, the original vegetation has been highly transformed and is currently composed of a landscape matrix with different land covers and uses where pastures for livestock and crop fields predominate. The rest of the landscape consists of a mixture of primary forest and secondary vegetation under different succession stages (Quesada et al., 2009). The landscape around each of the study plots is composed of a mixture of grasslands (approx. 45 %) with few scattered shrubs; corn, bean, and squash crop fields; and fragments of secondary forest under different stages of succession. Two of the plots of primary forest were located within the limits of the Chamela-Cuixmala Biosphere Reserve, and one is closer to the limits of the Reserve but within the original vegetation continuum (Fig. S1).

*Field procedures:*Plots were fenced to prevent them from being altered and their time of abandonment was estimated based on interviews with landowners. Surveys took place across the whole hectare of each plot by five expert field herpetologists from August 2009 to October 2013. In total, each plot was surveyed 13 times (once/month): eight times during the rainy season (July 2010, 2011, 2013; August 2009, 2012; and October 2009, 2010, 2013) and five times during the dry season (May 2010, February 2011, April 2012, March and May 2013). The timing of phylogenetic diversity surveys is important in this and other habitats with dramatic seasonal fluctuations because it can affect the comparability of metrics among areas if conducted at different time periods. Besides, comparing both seasons can provide information regarding the processes that could affect differentially community composition. Organisms were located during the day from 9:00-16:00 and at night from 21:00-04:00 hrs, through visual searches directly in the typical microhabitat used by amphibians and reptiles such as creeping vegetation, bushes, trees, under stones, leaf litter, under logs, and other microhabitats. Individuals were captured and released in the same places after identification. To avoid duplicated sampling, toe tips from frogs and ventral scales from lizards and snakes were removed to permanently mark each individual. We completed a total search effort of 234 person-hours (3 plots x 13 surveys x 5 people x 1.2 hours) in each vegetation succession stage. To assess the efficiency of our sampling, we compared the observed richness per sampling effort with estimated richness through the estimation of the nonparametric species estimators ICE (incidence-based coverage estimator), Chao2, and Bootstrap using EstimateS v. 9.1.0 (Colwell, 2013). To assess sampling completeness for each succession stage of the TDF we calculated the percentage in which the recorded species represented the estimated species richness (Soberón and Llorente, 1993). A sample completeness of at least 50% is considered sufficient sample size (Colwell, 2013).

*Structure and phylogenetic diversity measures:* The phylogenetic diversity index *(*PD) quantifies the total branch length spanned by the phylogenetic tree including all the species of a community (Faith, 1992). The higher the PD values, the longer length of evolutionary pathways connecting an ensemble of taxa. The communities that show a phylogenetically clustered pattern tend to have a lower PD, because species in these communities capture only a small part of the total phylogenetic diversity present in the phylogeny. PD is reported in millions of years and was calculated with the function *pd* in picante. The net relatedness index (NRI) and the nearest taxon index (NTI) measures the standardized effect size of the phylogenetic community structure based on the mean pairwise distance (MPD) between all species in each community (for NRI) and based on the mean nearest taxon distance (MNTD), which is the mean distance separating each species in the community from its closest relative (for NTI; Kembel et al., 2010). These metrics describe the difference between phylogenetic distances in the observed communities versus null communities generated with some randomization methods. These indices determine if a community is phylogenetically overdispersed (negative values of NRI and NTI, indicating greater diversity than expected at random) or is phylogenetically clustered (positive values of NRI and NTI, indicating lower diversity than expected; Webb et al., 2002; Kellar et al*.,* 2015). NTI is more sensitive to patterns of evenness and clustering closer to the tips of the phylogeny (clustering or overdispersion near the tips of the phylogeny), while NRI is more sensitive to tree-wide patterns of phylogenetic clustering and eveness (deeper divergences; Webb *et al.,* 2002; Kembell et al., 2010). NRI was calculated with the picante function *ses.mpd*, and NTI, with the function *ses.mntd* (Webb et al., 2002).

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