**Table S1**. Percentage of squamate, lizard, and snake species present in the ancestral reconstruction (i.e., with genetic and distribution data) for each desert, relative to the total number of species in the phylogeny of all squamates (Tonini et al., 2016).

**Table S2**. Categorisation of squamate species with genetic (Tonini et al., 2016) and

distribution data (Roll et al., 2017) into the major arid regions of the world. This was the dataset used for the ancestral reconstruction of desert occupancy (Figure S2).

**Table S3**. Significance values (p-values) of the post-hoc tests showing differences in tip speciation rates (DR metric) between desert regions.

**Table S4**. Average number of biome transitions into and out of each desert region reconstructed in the 100 simulations of the evolution of desert occupancy (Figure S2). Rows show the ancestral state, and columns show the descendant state. For example, the first row shows the frequency of shifts from non-desert conditions (“Out”) to each of the desert regions. Likewise, the first column shows the frequency of shifts from each desert to non-arid conditions (“Out”).

**Table S5**. Results from the correlation tests between environmental variables and grid-cell lizard richness in each desert. For each correlation, 1,000 replicates were implemented, each one with a random sample of 200 grid cells. The table show the mean, the standard deviation (sd), and the 95% confidence interval (low.ci and up.ci) of the correlation coefficients from each analysis.