Supplemental information

Building behaviour does not drive rates of phenotypic evolution in spiders

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Supplemental figures

S1.1. Dynamics of the discrete character (building behaviour), inferred by the stochastic character mapping of equal rates model (n=100). Red colours indicate a high posterior probability for building behaviour, and blue colours for non-building behaviour. A. For the body length-only dataset there were 26 gains and 46 losses of building behaviour, on average. B. For 2-trait dataset there were 22 gains and 41 losses of building behaviour, on average. C. For the 6-trait dataset there were 14 gains and 29 losses of building behaviour, on average.

S1.2. Histogram of the posterior state-dependent rate ζ[builder] for different priors on the estimated number of rate shifts. A. Body length only dataset. B. 2-trait dataset. C. 6-trait dataset.
S1.3. Kernel density estimate (KDE) plot of the posterior rate at the root $\beta^R_2$ for different priors on the estimated number of rate shifts. A. Body length only dataset. B. 2-trait dataset. C. 6-traits dataset.

S1.4. KDE plot of the posterior rate of the building behaviour $\lambda$ for different priors on the estimated number of rate shifts. A. Body length only dataset. B. 2-trait dataset. C. 6-traits dataset.

S1.5. Histogram of the posterior number of state changes for different priors on the estimated number on rate shifts. A. Body length only dataset. B. 2-trait dataset. C. 6-traits dataset.

S1.6. Histogram of the posterior number of rate shifts for different priors on the estimated number of rate shifts. A. Body length only dataset. B. 2-trait dataset. C. 6-traits dataset.
S1.7. Posterior probability of \( H_0 \) (\( \zeta[\text{builder}] = \zeta[\text{non-builder}] \)), \( H_1 \) (\( \zeta[\text{builder}] > \zeta[\text{non-builder}] \)) and \( H_2 \) (\( \zeta[\text{builder}] < \zeta[\text{non-builder}] \)) for different priors on the estimated number of rate shifts. A. Body length only dataset. B. 2-trait dataset. C. 6-traits dataset.
S1.8. Phylogenetic mapping of the posterior branch-specific rates for different priors on the estimated number of rate shifts for the body length only dataset. A. 16 shifts (0.01 nbranches). B. 72 shifts (equal to the mean number of changes in the discrete character). C. 163 shifts (0.1 nbranches).

S1.9. Phylogenetic mapping of the posterior branch-specific rates for different priors on the estimated number of rate shifts on the 2-trait dataset. A. 15 shifts (0.01 nbranches). B. 63 shifts (equal to the mean number of changes in the discrete character). C. 150 shifts (0.1 nbranches).
S1.10. Phylogenetic mapping of the posterior branch-specific rates for different priors on the estimated number of rate shifts on the 6-trait dataset. A. 7 shifts (0.01 nbbranches). B. 43 shifts (equal to the mean number of changes in the discrete character). C. 68 shifts (0.1 nbbranches).