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Supplementary Data S1. Standard vs phylogenetic and selective inference.

Phylogenetic and selective Inference: We report the results of the SO *vs*. Traits model based on standard, phylogenetic, and selective inferences to know whether, and how, accounting for non-independence of data or the use of a model selection tool alters effect sizes and/or significance patterns. For this model, we know that both our response and our predictors have a high phylogenetic signal (see S2), so we performed an analysis of the covariance of residuals, which is the only meaningful information to know whether a phylogenetic correction is needed (Revell 2010). We did this through 1000 simulations of regression residuals and then performing an analysis of "spatial autocorrelation" based on the phylogenetic distance matrix through the simulateResiduals and testSpatialAutocorrelation of the DHARMa package (Hartig 2022). The test is performed by Moran's I, an index of autocorrelation that ranges from –1 (absolute negative autocorrelation, like a checkerboard; or in our case, residuals of observations belonging to related species being much more dissimilar than expected by chance) to 1 (absolute positive autocorrelation, with residuals of related species being much more similar than expected by chance). We obtained a Moran's I of 0.01 (P-value = 0.02). Hence, we implemented a phylogenetic correction searching for the evolutionary model that could better explain the correlation structure of our data; this was done by searching the model with the best AIC among the phylogenetic correlation options available in the phylolm function of the phylolm R package (Ho & Ane 2014). The selected model was based on Pagel's evolutionary model with $\lambda = 0.264$, indicating a small but non-negligible degree of non-independence.

At the same time, the use of model selection tools such as the LASSO requires the use of more conservative confidence intervals for inference (Taylor & Tibshirani 2015). Selective inference is still an active field of research (Yates et al. 2023). Fortunately, for simple linear models, there are already options available in off-the-shelf software libraries. Specifically, we used the methods defined by Taylor & Tibshirani (2016) through the selectiveInference R package (Tibshirani et al. 2019)

In Supplementary Fig. S4 it can be seen that the two types of corrections do not make any large change to the inferences on the traits. Bud Bank Size is only significant under standard inference and Height is not under selective inference. However, the effect size estimates and their ordering remain unchanged (with small exceptions in the effect sizes of LDMC and Parasitism, that are respectively increased and decreased under the phylogenetic correction), the conclusions in the text are justified.

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