SI 4 - Additional Results

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This appendix details the results of additional analyses to support the results in the main text.

A. Full results from model comparison

B. Median estimates for model parameters

C. Full posterior distribution of model parameters

D. Diagnostic plots for the model fitting, including posterior predictive plots

E. Results from maximal model including predation effects on competitive terms

A. Model comparison

	Δ ELPD	Standard Error of Difference	Effective Number of Parameters	Standard Error
model2	0.0000	0.0000	48.5480	2.7322
model3	-34.0281	8.1397	43.6685	2.6892
model1	-43.0215	10.1924	76.6309	5.2007

Table S4.1 Results from model comparison through expected log-pointwise predictive density (ELPD), computed using Pareto-smoothed importance sampling with the loo R package (Vehtari *et al* 2019). Models differ in the degree of divergence in fitted parameters between parasitism treatments. Model 1: separate α and r values (representing the hypothesis that parasitism affects both growth rate and competition terms between species.) Model 2: joint α values, but variable r (the hypothesis that parasitism affects growth rates, but not competition terms), Model 3: joint α and r values (the hypothesis that parasitism has no effect). Differences in ELPD suggest strongest support for Model 2.

B. Median Parameter Values

Despite a major point of the paper being that the full posterior is essential to fully understand the uncertainties in parameter estimates, we appreciate that for some purposes a single point estimate is useful. Table S4.2 and Table S4.3 therefore present median estimates for the key model parameters.

Species	Parasitism	Safe
BIR	6.135	6.865
PAL	10.647	14.053
PAN	4.198	5.822
PSA	4.467	5.612
SIM	12.396	13.951
SUL	8.419	13.875

Table S4.2 Median values for growth rates (r) in the two treatments

	BIR	PAL	PAN	PSA	SIM	SUL
BIR	0.0869	0.2495	0.1388	0.0250	0.2316	0.1348
PAL	0.0517	0.1566	0.0516	0.0319	0.1000	0.0987
PAN	0.0058	0.0437	0.0356	0.0406	0.0146	0.0388
PSA	0.0175	0.1723	0.0477	0.0564	0.0850	0.1613
SIM	0.0601	0.0446	0.0352	0.0654	0.1147	0.0806
SUL	0.0518	0.1307	0.0511	0.0346	0.0375	0.1773

Table S4.3 Median values for competition coefficients (α) laid out in standard matrix form ($\alpha_{row,col}$).

C. Parameter posterior distributions (selected model)

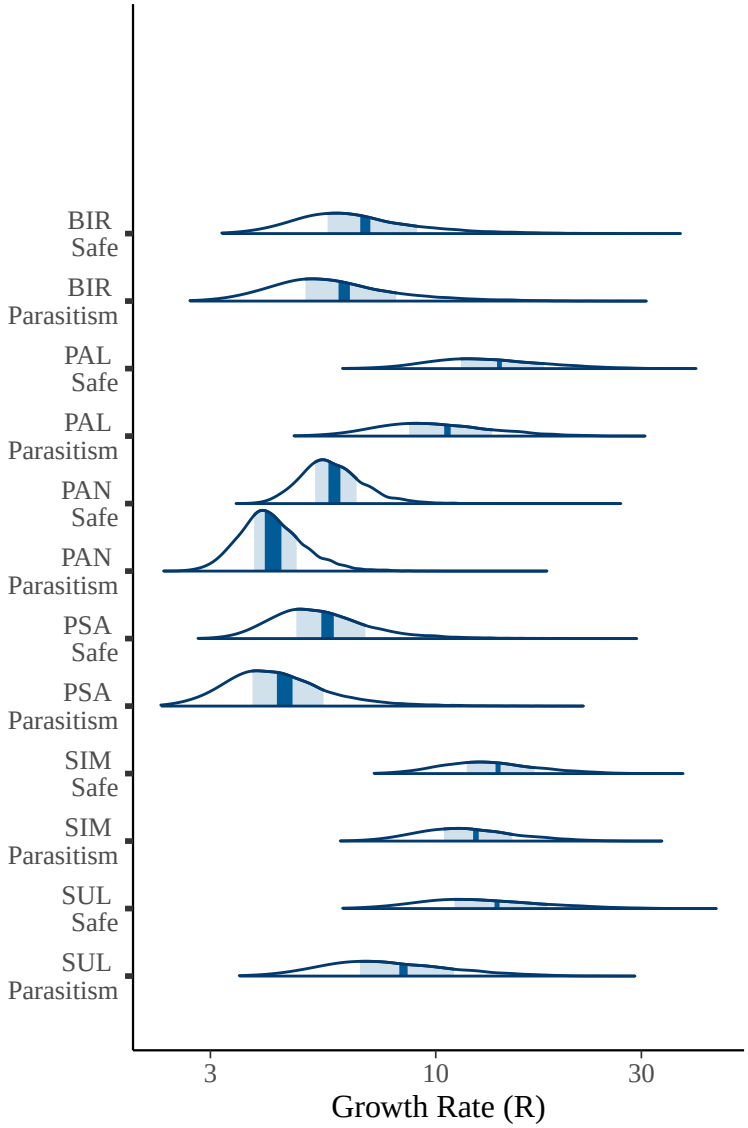


Figure S4.1 Posterior distribution of growth rates under the two treatments. Shaded area shows 50% inner interval. N.B. log-scale.

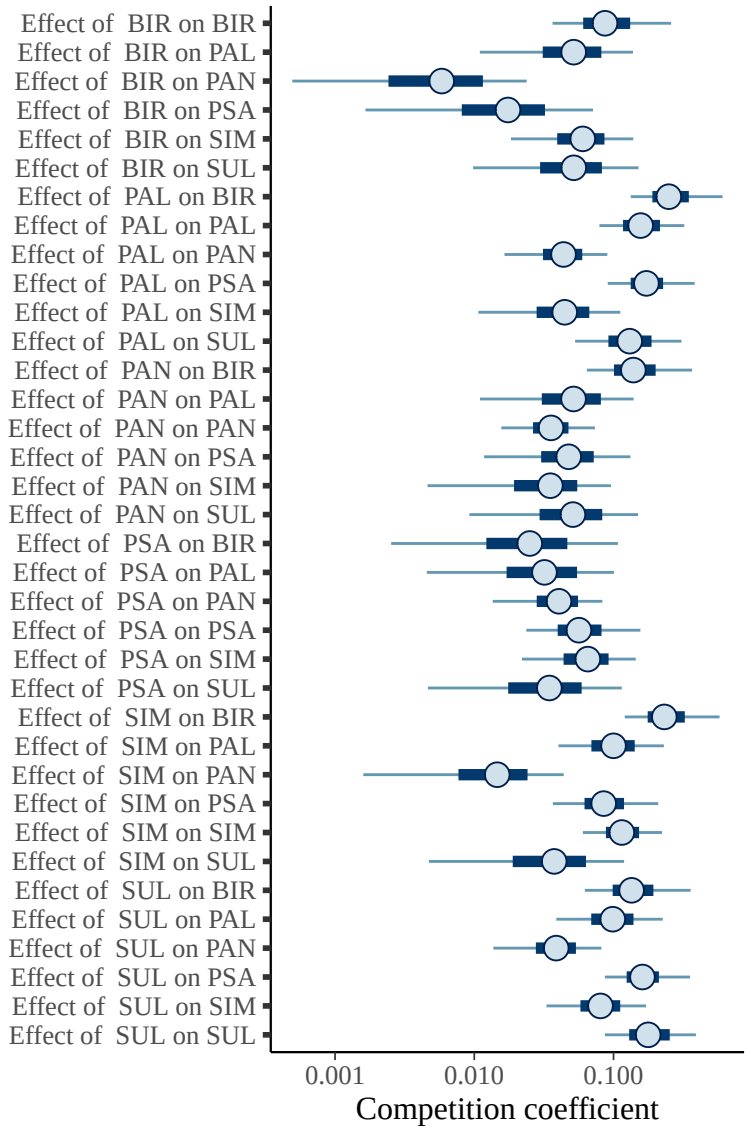


Figure S4.2 Posterior distribution of competition parameters. Wide bar shows 50% inner interval, line shows 90% interval, circle shows median value. N.B. log-scale.

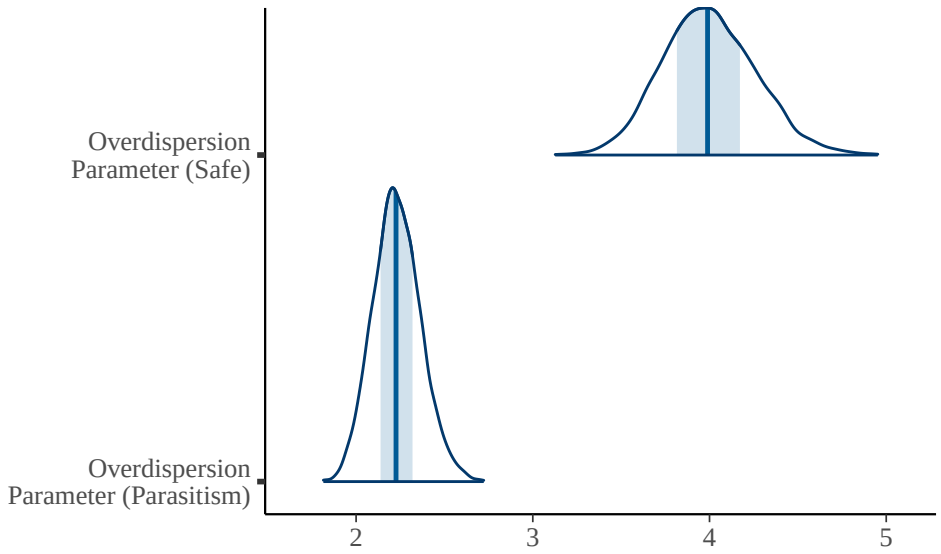


Figure S4.3 Posterior distribution of the ϕ parameters, where the shaded area shows 50% inner interval. Note that in the parameterisation we used (`neg_binomial_2()`), the variance is defined as $\mu + \frac{\mu^2}{\phi}$. Therefore the inverse of ϕ controls the overdispersion, which is scaled by the mean value. ϕ is lower in the parasitoid treatment, suggesting that parasitism increases the variance in the next generation.

Relative uncertainty in components of fitness differences

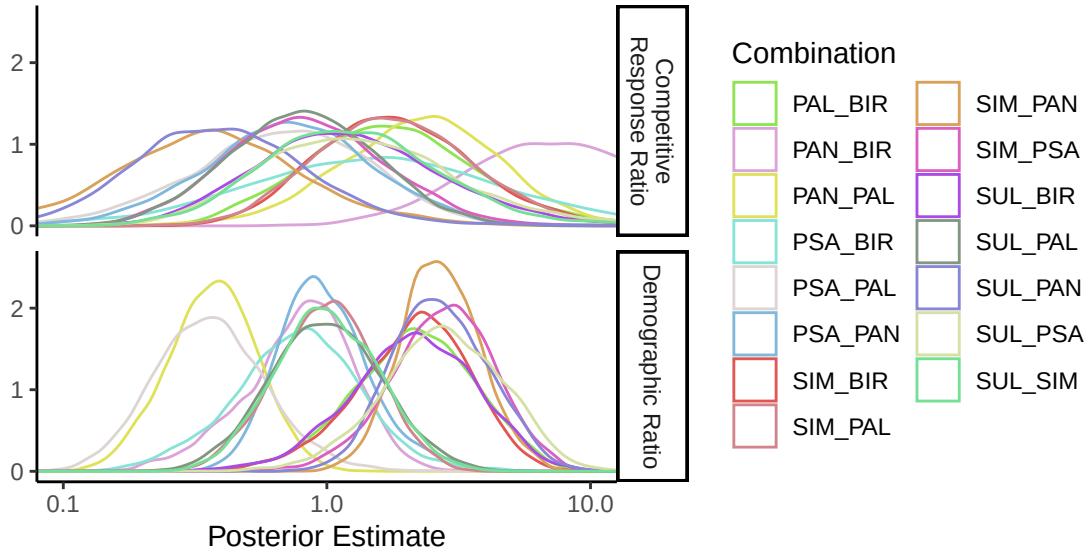


Figure S4.4 Posterior distribution of the two components of the fitness difference. The uncertainty in the 'competitive response ratio' $\sqrt{\frac{\alpha_{ij}\alpha_{ii}}{\alpha_{ji}\alpha_{jj}}}$ is much larger than the demographic ratio $\frac{r_j - 1}{r_i - 1}$ (mean coefficient of variation 32x larger).

D. Model Diagnostics

Overall Predictive Capacity

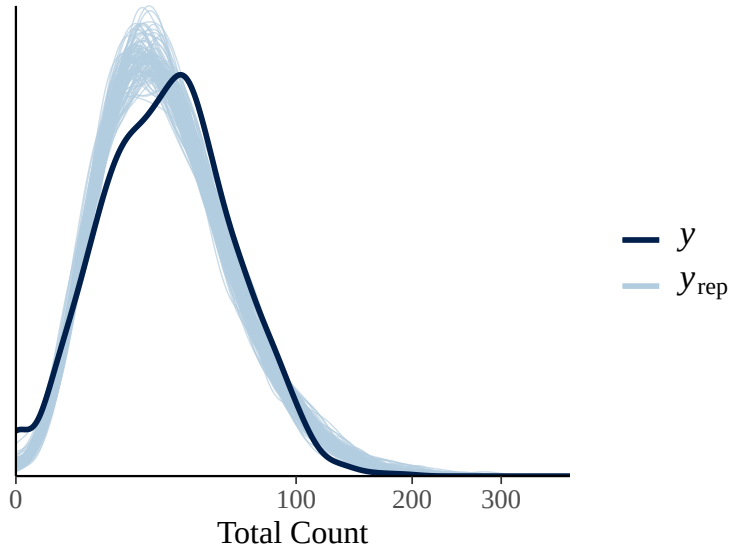


Figure S4.5 Overall predictive capacity of best fit model. 100 sets of predictions from the posterior (blue), are compared to observed values (black). It can be seen that the model captures the overall spread of the data well, but does not pick up the low-growth rate observations (i.e. those cases where no adults were observed to emerge). N.B. the square-root X-scaling to magnify small values.

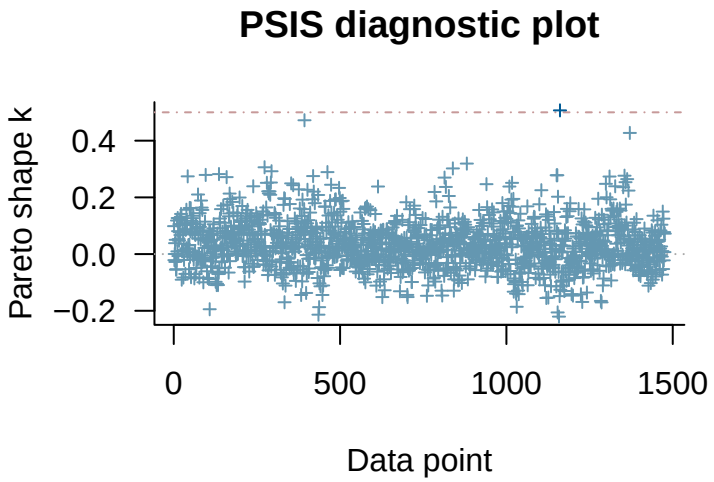
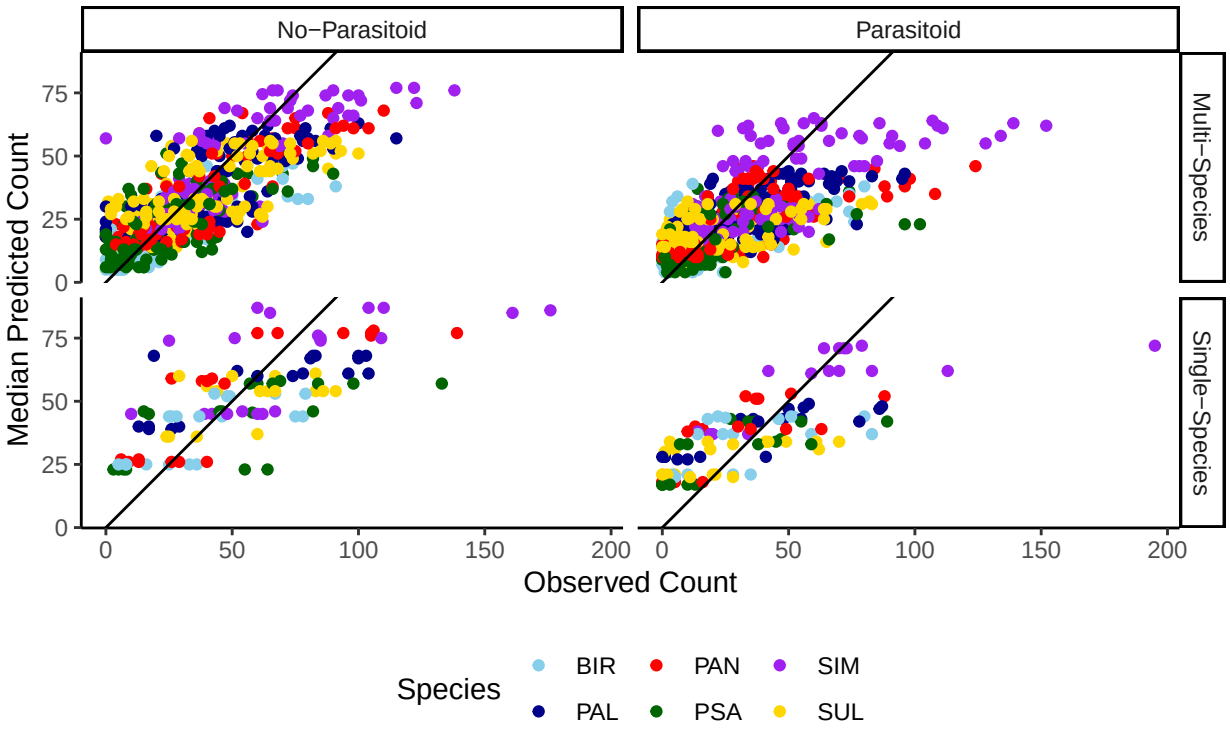


Figure S4.6 Test for model miss-specification, using Pareto-smoothed Importance Sampling to test for strongly outlying data points. No points exceeded the threshold of 0.7 (Gabry *et al.* 2019).

Species-level Predictive Capacity

Figures S4.7 to S4.12 present predictions of the selected model against the raw observations. Because of the multi-dimensional nature of the data, the observations are partitioned by parasitoid treatment, and by the type of competition.



FigS4.7 Overall model predictive accuracy using median posterior values. Plot is faceted by treatment and whether the count was from a single-species or a multi-species trial. Focal species are coloured. In general the model performs well given the inevitable variation, but struggles to capture outlier values across all species.

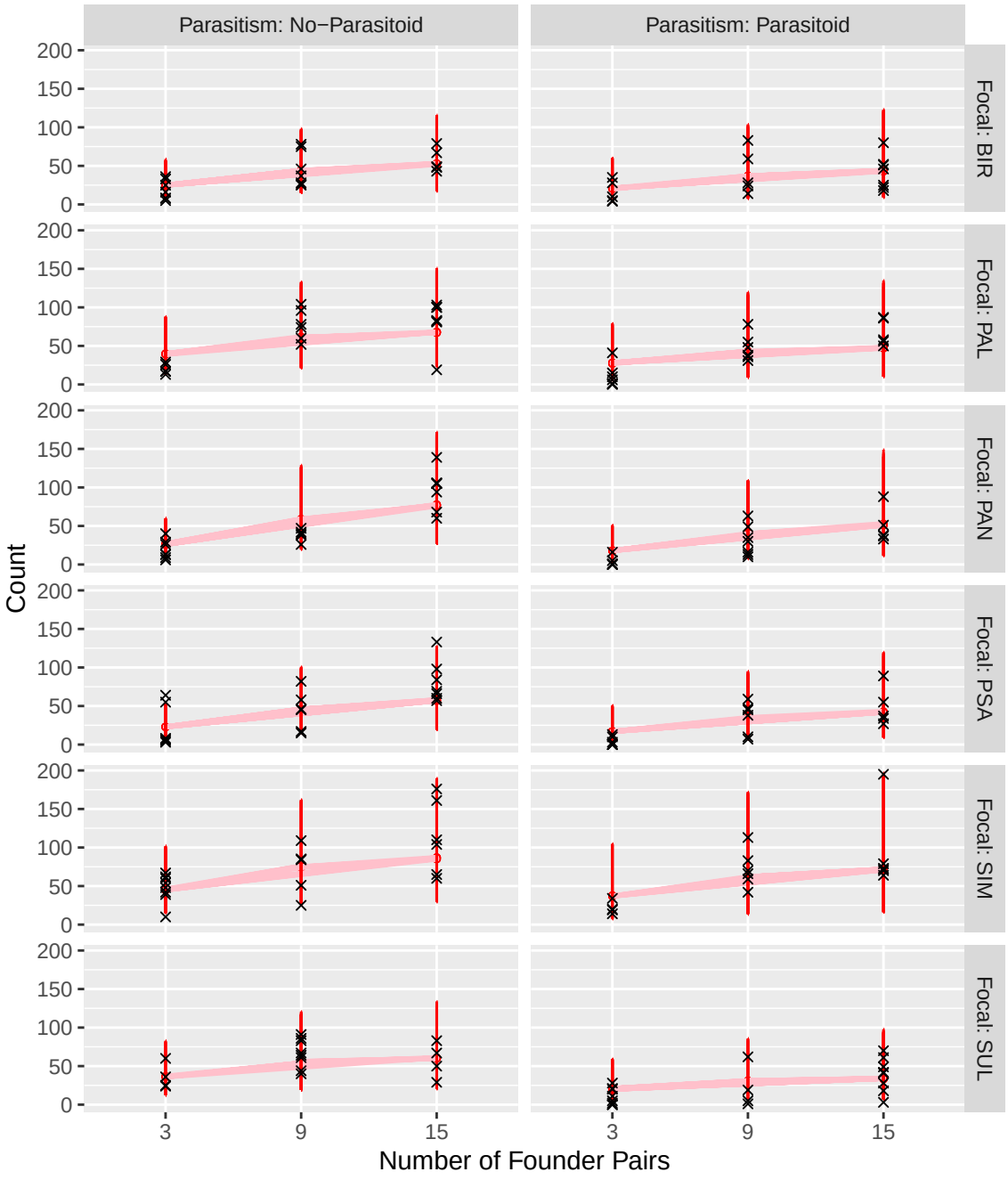


Figure S4.8 Posterior predictions of intraspecific competition. Red dots show median predictions, red lines span central 90% of posterior distribution. Black crosses show observations.

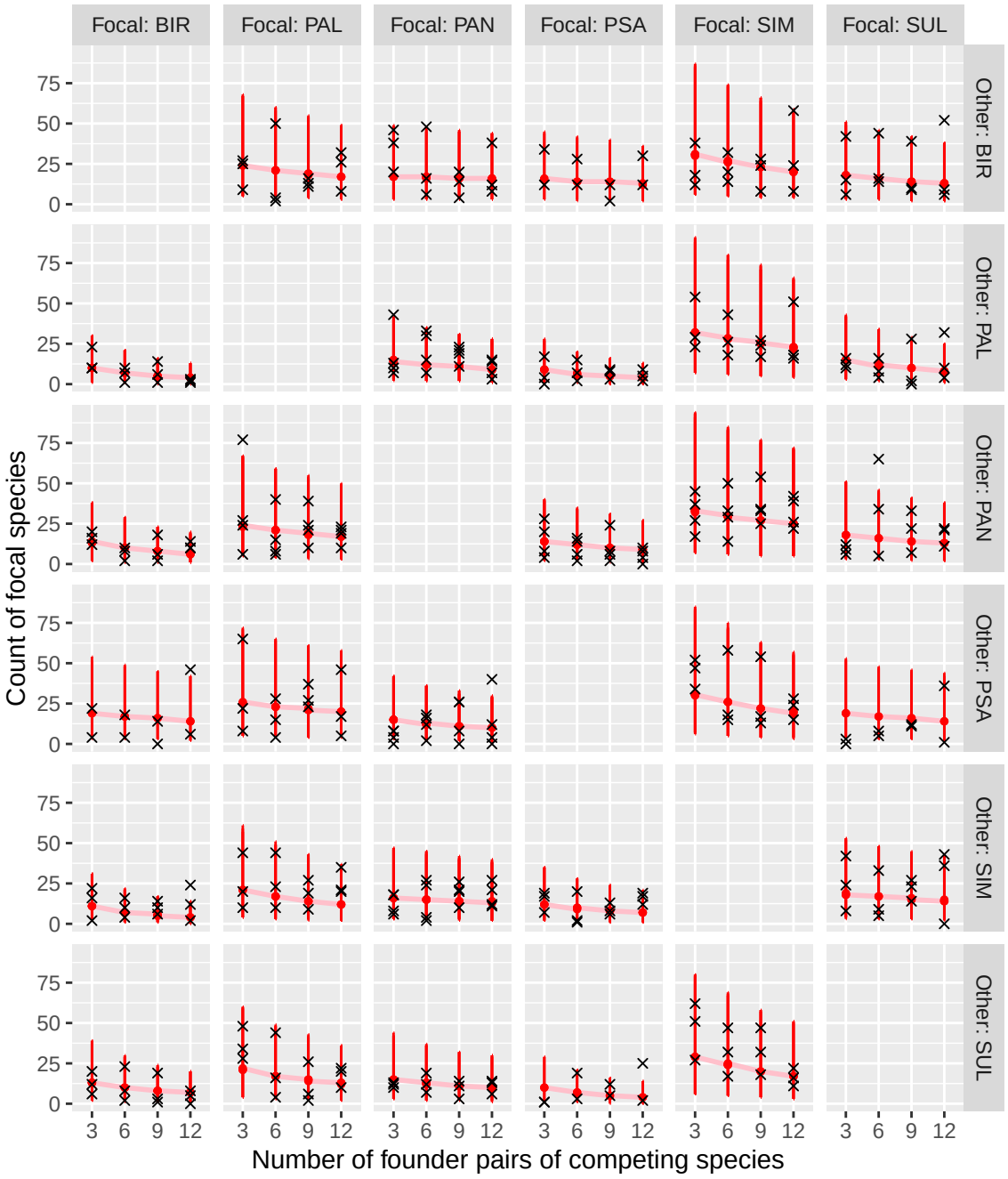
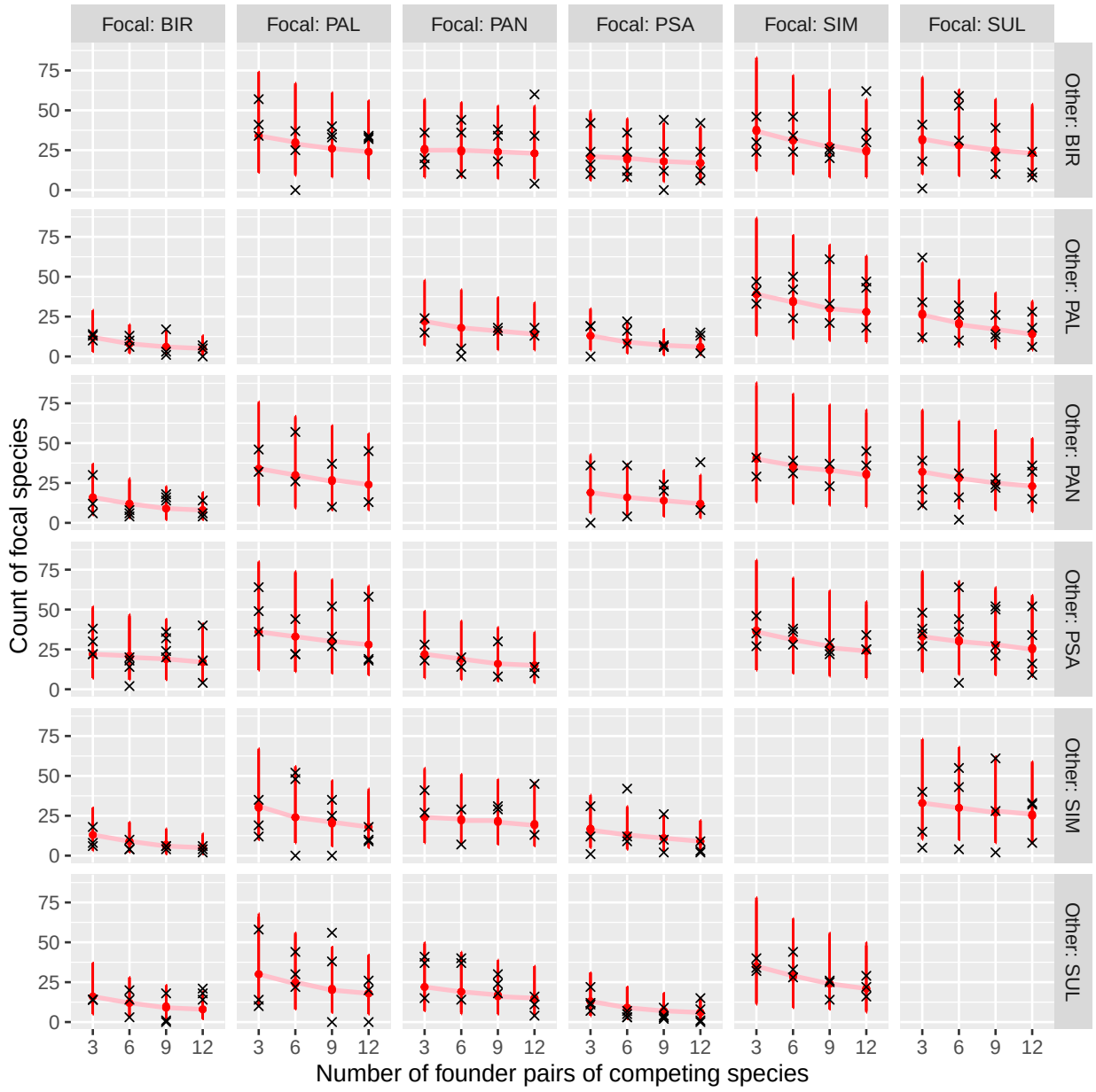
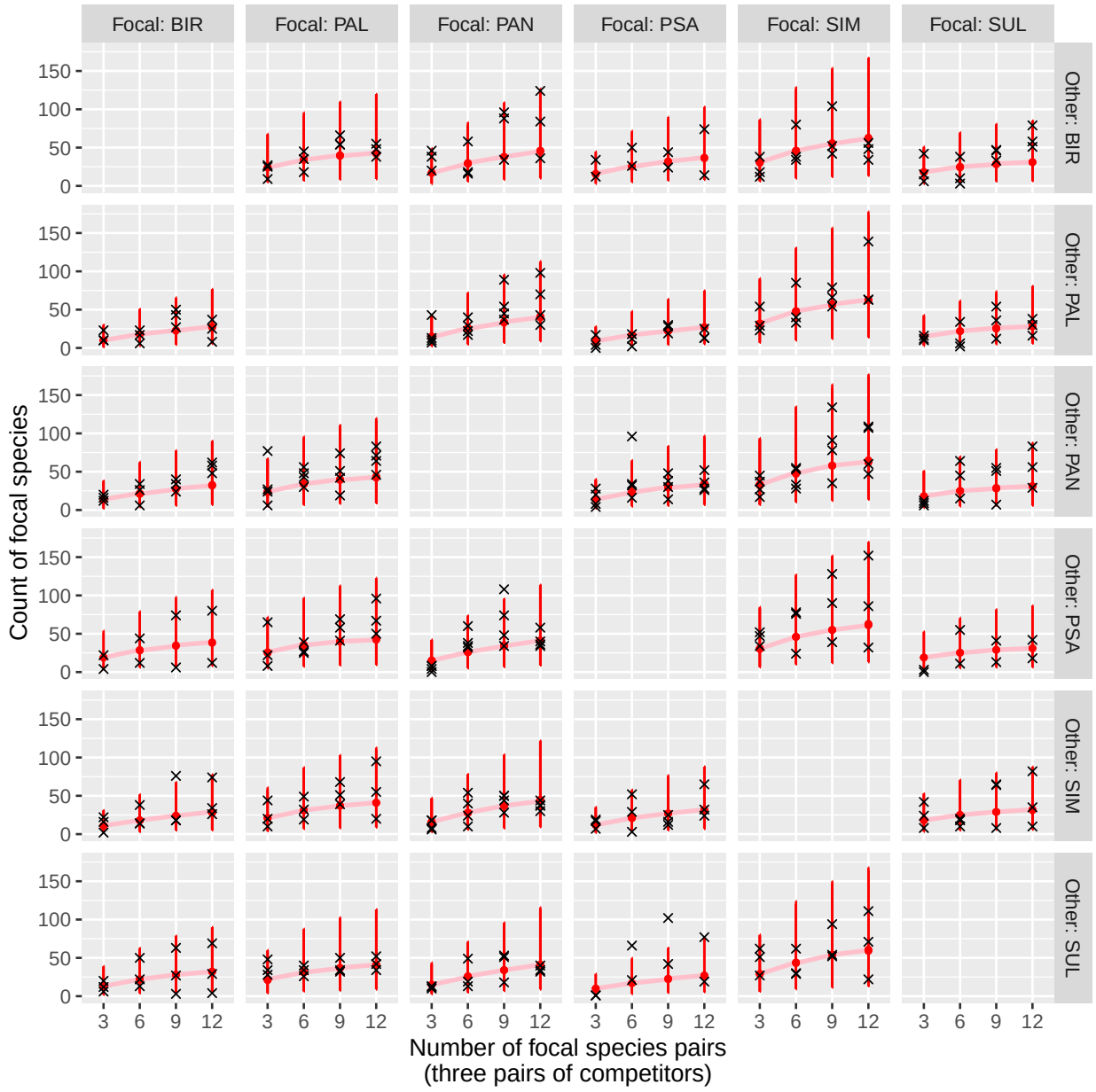


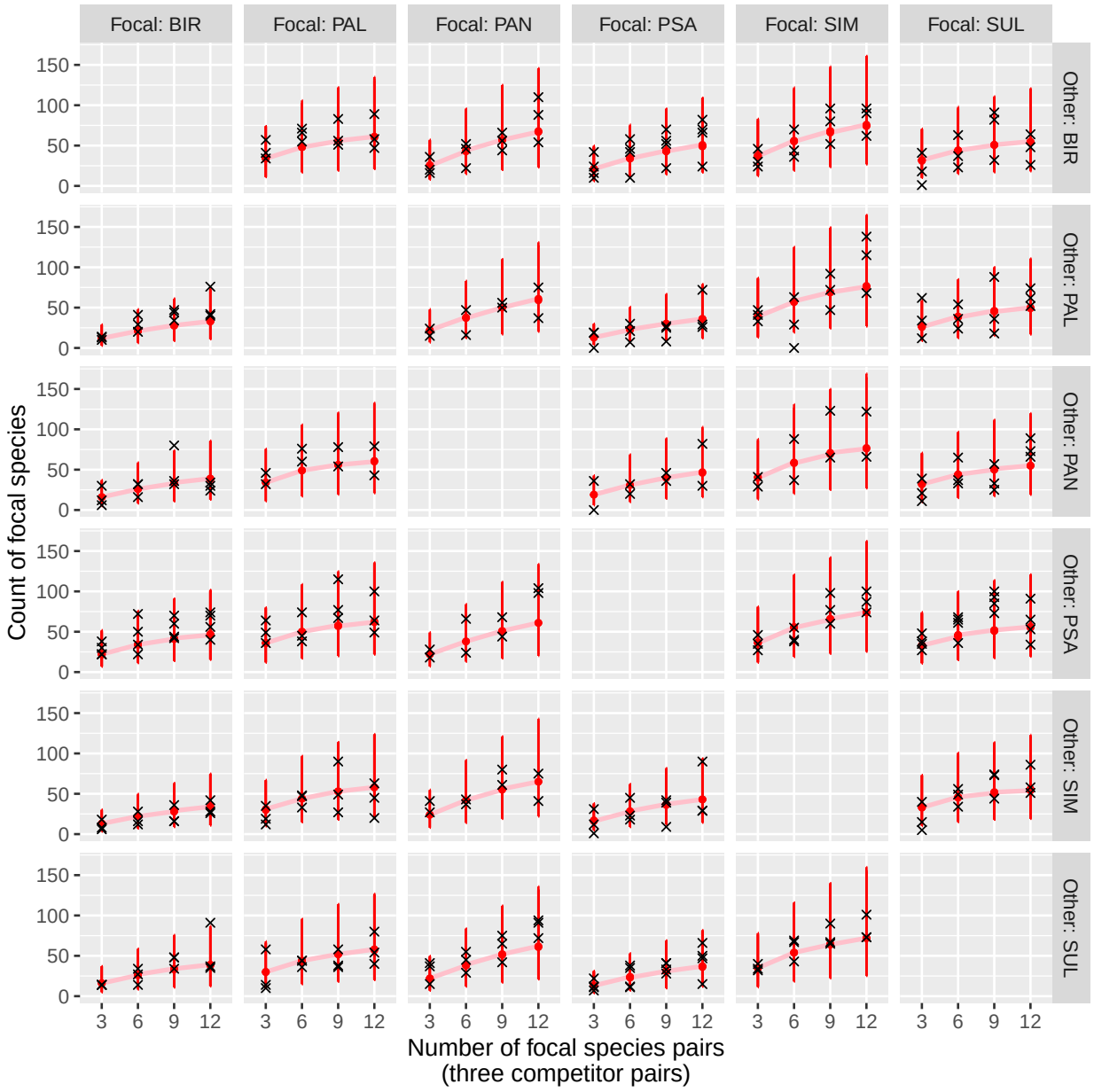
Figure S4.9 Posterior predictions of interspecific competition in the presence of the parasitoid. Red dots show median predictions, red lines span central 90% of posterior distribution. Black crosses show observations.



FigS4.10 Posterior predictions of interspecific competition without the parasitoid. Red dots show median predictions, red lines span central 90% of posterior distribution. Black crosses show observations.



FigS4.11 Posterior predictions covering remaining observations from the parasitoid treatment not easily displayed in previous plots, where the density of the focal species varies and the competing species is represented by 3 founder pairs. Red dots show median predictions, red lines span central 90% of posterior distribution. Black crosses show observations.



FigS4.12 Posterior predictions covering remaining observations from the no-parasitoid treatment not easily displayed in previous plots, where the density of the focal species varies and the competing species is represented by 3 founder pairs. Red dots show median predictions, red lines span central 90% of posterior distribution. Black crosses show observations.

E. Maximal model

Model comparison indicates that there is little support for fitting changes in competitive coefficients due to the parasitism treatment. For completeness, we explore this 'maximal' model here. As discussed in the main text, it is possible that an intermediate model, where some competition terms vary, but others are fixed. Fig. S4.13-14 show the divergences in fitted α values between treatments. On average, competition coefficients are larger under parsistism than without.

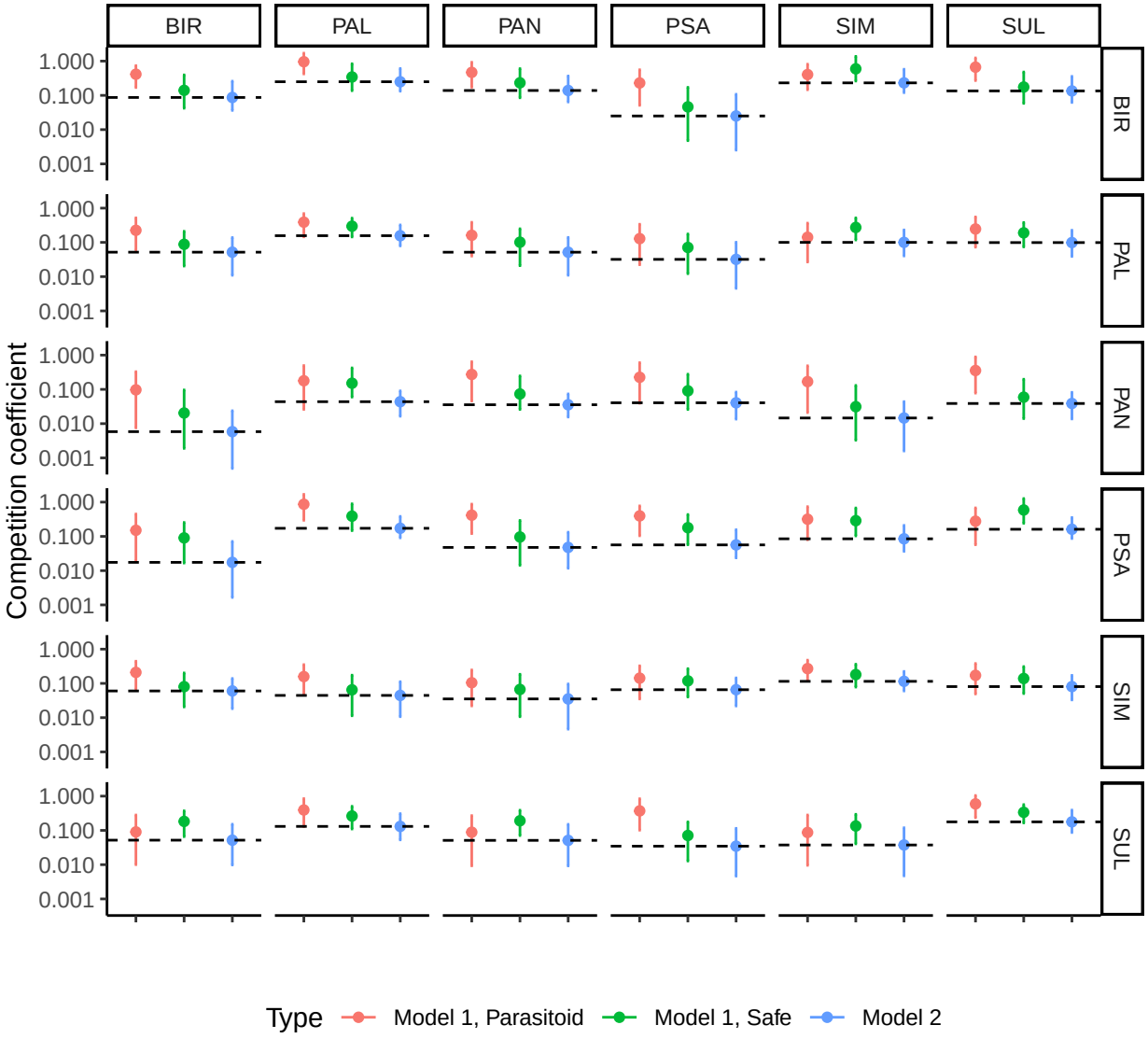


Fig S4.13 Comparison of fitted α values between Model 2 (where a single A matrix is fitted across both treatments) and Model 1 (where a separate A matrix is fitted for each treatment). Dotted line shows median value for Model 2 to allow easier comparison. Error bars show 90% CI.

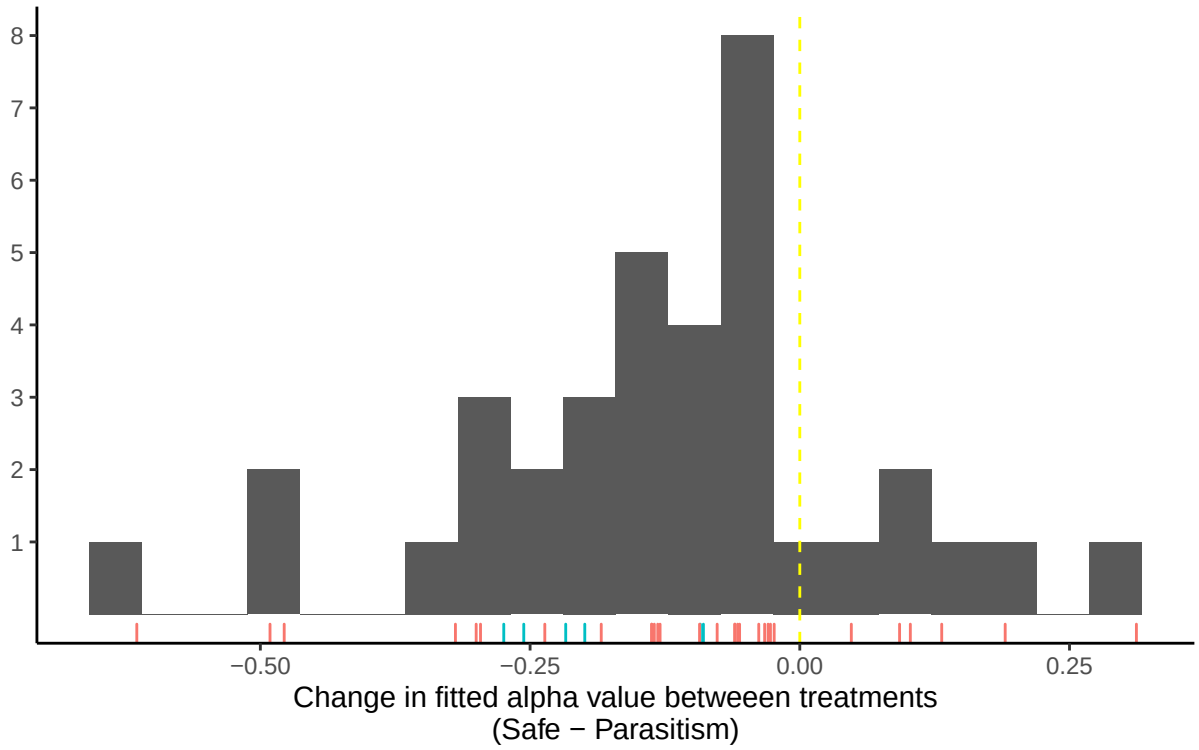


Figure S4.14. Distribution of shifts in median fitted α value between treatments in Model 1. Intraspecific terms are shown in blue, interspecific in red.')

References

1. Gabry, J., Simpson, D., Vehtari, A., Betancourt, M. & Gelman, A. *Visualization in Bayesian workflow.* J. R. Stat. Soc. Ser. A Stat. Soc. 182, 389–402 (2019).