Historical contingency in species interactions: towards niche-based predictions

Supplementary Information

Table S1. Regression coefficients for the analyses assessing if phylogenetic distance or ecological similarity predicts the strength of priority effects. Separate regressions were conducted using environmental harshness and either phylogenetic and ecological similarity for all nectar environments combined. In addition, the importance of these predictors was determined for each nectar environment separately. Phylogenetic distance was calculated using patristic distance between species pairs, as in, e.g., Peay et al 2012. Ecological similarity was assessed using standard methods, where principal components are extracted from all physiological data and used as predictors (PC.e1-3). The most parsimonious model was selected using the likelihood ratio test. Adjusted R^2 (R^2_{adj}) indicates the variance explained in the focal model. ΔAIC indicates the difference in AIC values between the best-fit model using niche components (summarized in Table 1), which had an AIC value of 180.7, and the model using phylogenetic distance or ecological similarity (AIC values of 211.7 and 202.9, respectively). Positive ΔAIC values indicate that the focal model is a worse fit than the model in Table 1. N = 12 for each regression analysis. *NR indicates that no predictors were retained in the final model.

Nectar environment	Predictors	Coefficient	SE	P-value	R^2_{adj}	*ΔAIC*
All combined					0.15	+31.1
	Phylogenetic distance	9.33	6.99	0.18		
	Environmental Harshness	-1.82	0.60	0.004		
Harsh, rich	Phylogenetic distance	37.56	14.01	0.02	0.35	
Harsh, poor	Phylogenetic distance	7.76	8.14	0.36	0	
Benign, rich	Phylogenetic distance	7.04	18.70	0.71	0	
Benign, poor	Phylogenetic distance	-15.05	10.06	0.16	0.10	
All combined					0.31	+22.26
	PC1.e	-0.85	0.31	0.009		
	PC2.e	-0.83	0.33	0.01		
	Environmental Harshness	-2.37	0.58	0.00019		
Harsh, rich	PC1.e	-1.73	0.55	0.01	0.43	
Harsh, poor	NR*	-	-	-	0	
Benign, rich	PC1.e	-1.92	0.83	0.04	0.28	
Benign, poor	NR*	-	-	-	0	

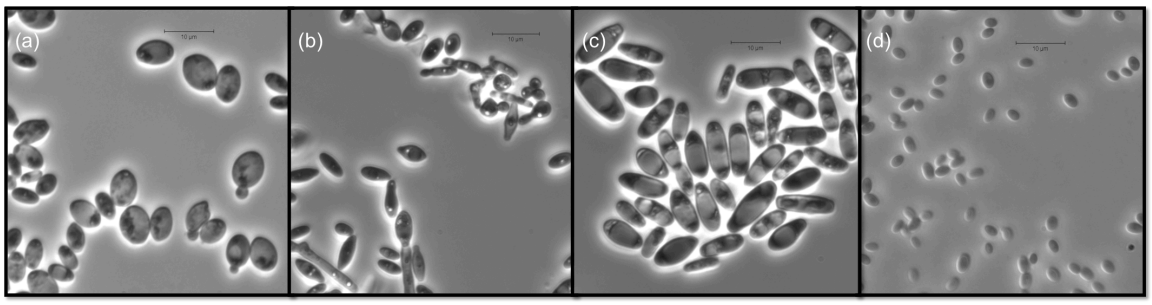

Figure S1. Cell morphology of the species of yeast used in the experiment **a**, *Candida rancensis*, **b**, *Hanseniaspora valbyensis*, **c**, *Metschnikowia reukaufii*, and **d**, *Starmerella bombicola*. Scale bars indicates 10 µm.

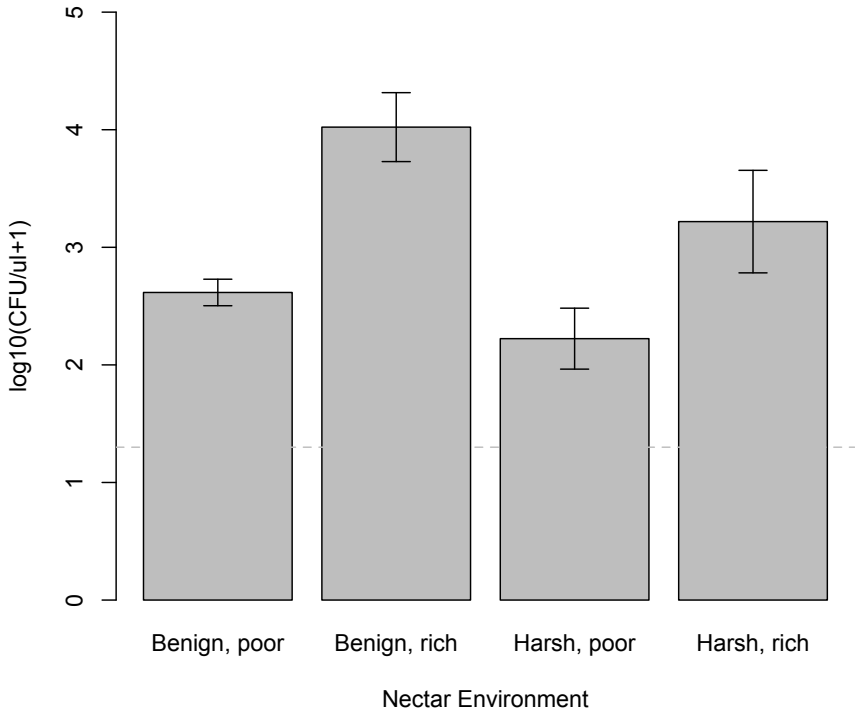

Figure S2. Average yeast density among treatments. Density, measured in $\log_{10}$(CFU/µl nectar), of yeast species after three days of growth when inoculated singly into different nectar environments. Dotted line indicates initial density. Bars indicate mean ± 1 SE for N=16. Harsh environments support a lower CFU density than do benign environments ($F_{1,60}$=4.02, p=0.04), while resource addition strongly increases nectar carrying capacity ($F_{1, 60}$=16.21, p<0.001).

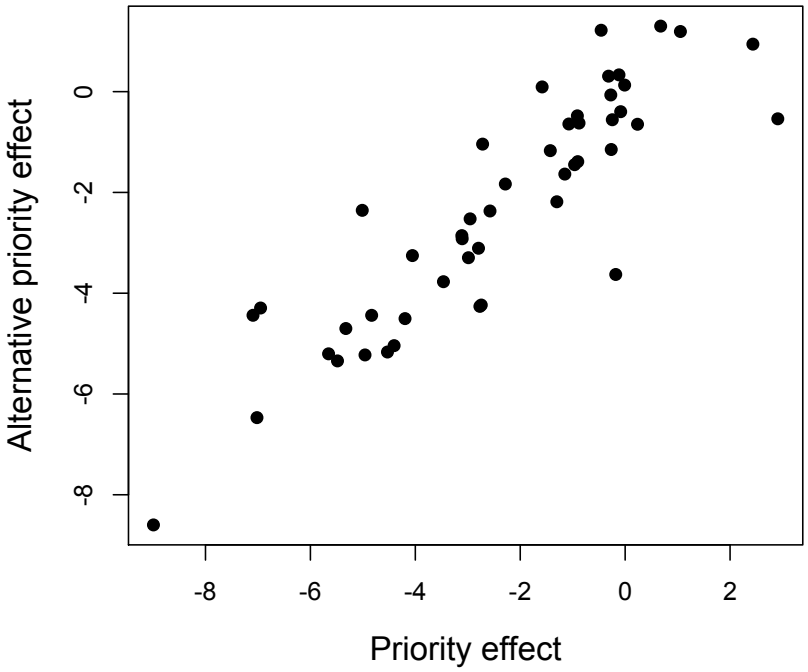

Figure S3. Correlation between the priority effect metric used in the main text and the alternative priority effect metric (see Methods), where R^2 =0.78 and P< 0.0001.

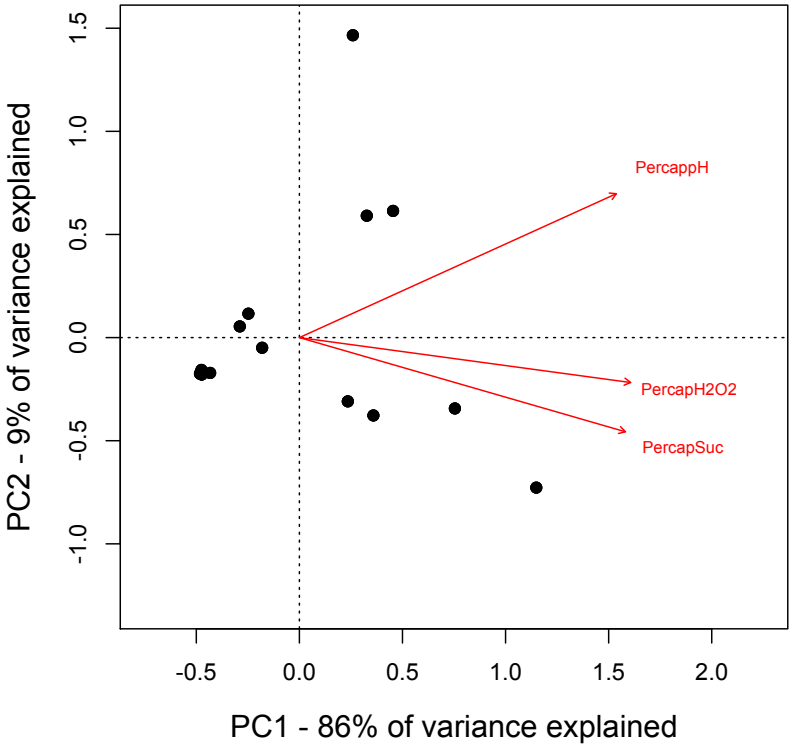

Figure S4. Principal component analysis (PCA) used to generate measures of the non-resource impact niche of yeast species. Per-capita changes in pH, H_2O_2, and sucrose concentrations (indicated as "PercappH," "PercapH2O2," and "PercapSuc" in the figure) were used in the PCA. Data points represent replicate communities. The first two axes from this PCA were used as predictors in the multiple regression. Although yeasts affect multiple nectar characteristics simultaneously, previous work in this system has demonstrated that reduction in pH caused by microbial growth in nectar resulted in lowered yeast growth rate, whereas variation in H_2O_2 levels does not affect yeast growth (authors' unpublished data). Yeast also decreased sucrose concentrations, but this effect is likely not the cause of inhibitory priority effects, because changes in sucrose concentrations were relatively small (<<10% of total) and because high concentrations of sucrose inhibit microbial growth. As a result, priority effects among nectar yeasts are likely to be driven by changes in nectar pH, particularly in benign environments.

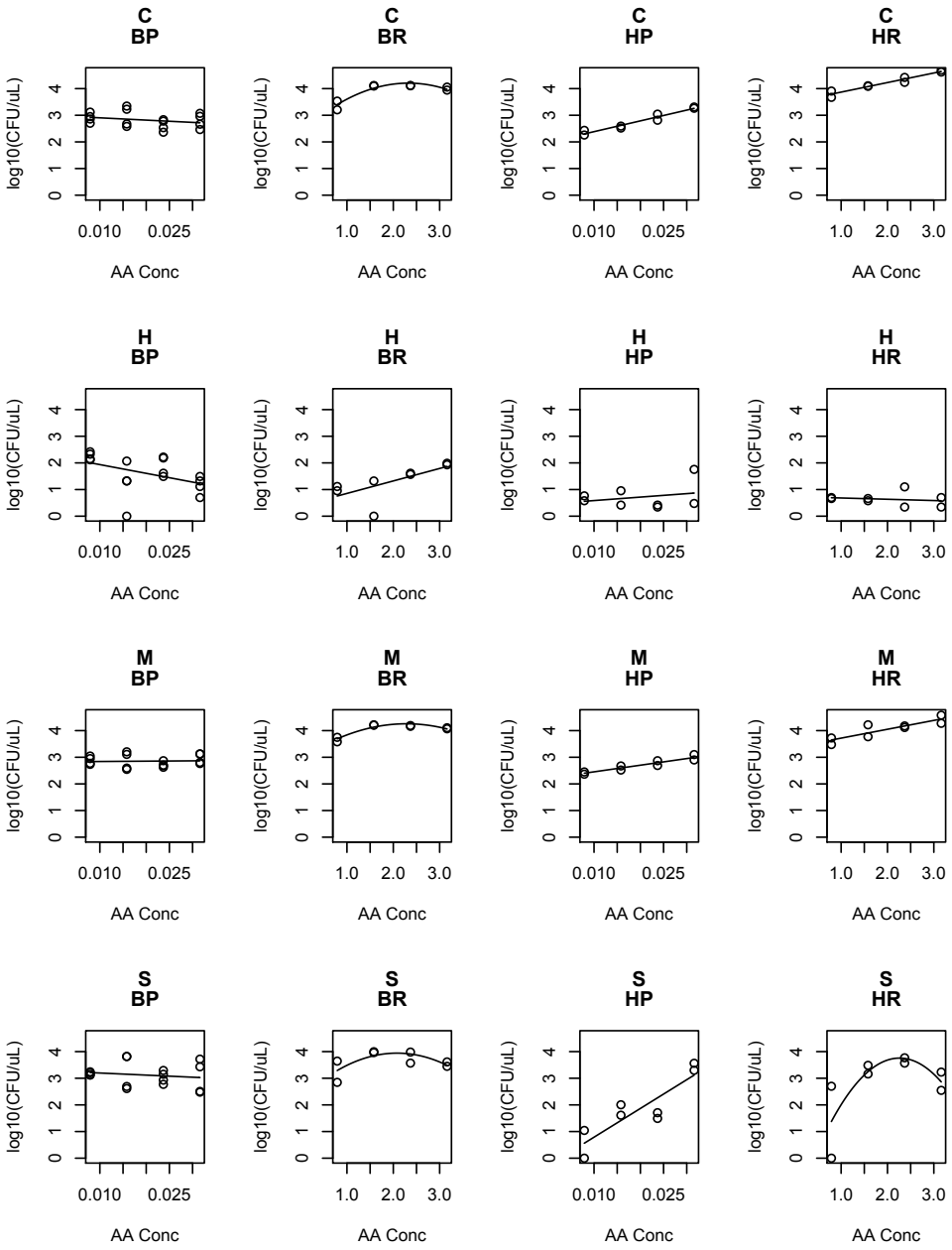

Figure S5. Best-fit lines for the growth responses of each species to variation in amino acid concentration. Y-axis shows final yeast density, and x-axis shows amino acid concentration. Symbols above each panel indicate species, where *Candida rancensis* (C), *Hanseniaspora valbyensis* (H), *Metschnikowia reukaufii* (M), and *Starmerella bombicola* (S). Nectar environmental conditions are below; benign, poor (BP), benign, rich (BR), harsh, poor (HP) and harsh, rich (HR).

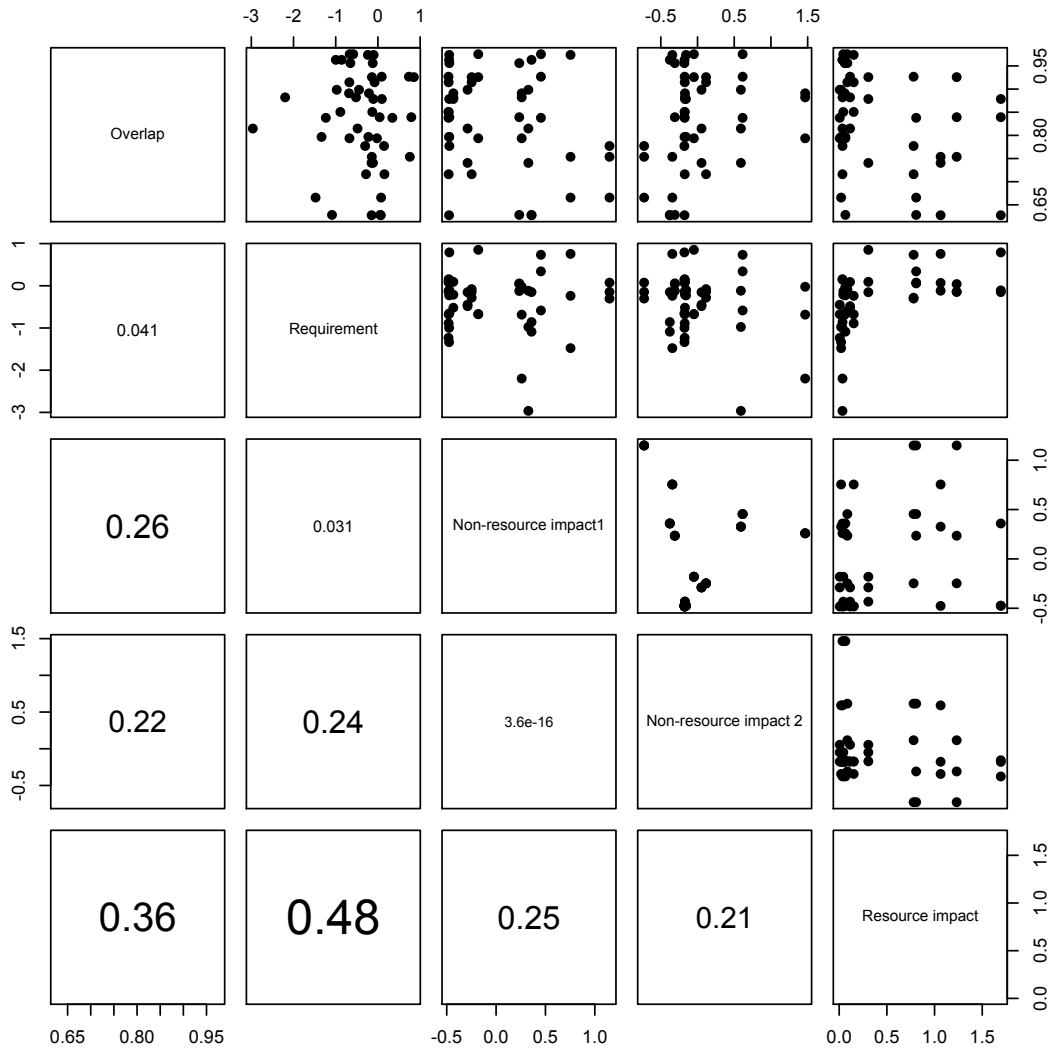

Figure S6. Relationships among niche metrics used as predictors in the full niche component model. Upper panels display correlation plots, while lower panels show r-values for each correlation.