Metabolic differentiation facilitates coexistence in two coral reef fish species

Simon J. Brandl1,2,3,4, Calvin N. Quigley5, Jordan M. Casey2,3,Alexandre Mercière3, Nina M.D. Schiettekatte2,3, Tommy Norin6, Valeriano Parravicini2,3, Isabelle M. Côté1

*1 Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada*

*2 PSL Université Paris: EPHE-UPVD-CNRS, USR 3278 CRIOBE, Université de Perpignan, 66860 Perpignan, France*

*3 Laboratoire d’Excellence “CORAIL,” Perpignan, France*

*4 CESAB, Centre for the Synthesis and Analysis of Biodiversity, Institut Bouisson Bertrand, 34000 Montpellier*

*5 School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand*

*6 DTU Aqua: National Institute of Aquatic Resources, Technical University of Denmark, 2800 Kgs. Lyngby, Denmark*

Email: Simon J. Brandl ([simonjbrandl@gmail.com](mailto:simonjbrandl@gmail.com))

Appendix S2

We performed the analyses using the software *R* (R Core Team 2019) and the following packages: *drake* (Landau 2018), *tidyverse* (Wickham et al. 2019), *rstan* (Stan Development Team 2016), *brms* (Bürkner 2017), *bipartite* (Dormann et al. 2008), *iNEXT* (Hsieh et al. 2016), (Pollock et al. 2014), and *fishualize* (Schiettekatte et al. 2019). All code and data necessary to fully reproduce the results presented in this paper are available with the submission and will be made publicly available via a public repository and the lead author’s GitHub page (<https://github.com/simonjbrandl>). The appended .zip file contains a README.md document that provides guidance on how to reproduce the results. The supplementary tables below are output from the analyses and can also be found as separate documents in the “outputs” folder.

Table S1: Model summary for standard metabolic rate. The model was run for 5,000 iterations using the default brms priors.



Table S2: Model summary for maximum metabolic rate. The model was run for 5,000 iterations using the default brms priors. 

Table S3: Model summary for horizontal gape. The model was run for 2,000 iterations using the default brms priors.



Table S4: Model summary for vertical gape. The model was run for 2,000 iterations using the default brms priors.



Table S5: Model summary for girth. The model was run for 2,000 iterations using the default brms priors.



Table S6: Model summary for gastrointestinal tract. The model was run for 2,000 iterations using the default brms priors.

Table S7: Model summary for number of bites. The model was run for 2,000 iterations using the default brms priors and a negative binomial error distribution with a log link-function.



Literature cited

Bürkner, P.-C. 2017. brms: An R package for Bayesian multilevel models using Stan. Journal of statistical software 80:1–28.

Dormann, C. F., B. Gruber, and J. Fründ. 2008. Introducing the bipartite package: analysing ecological networks. interaction 1.

Hsieh, T., K. Ma, and A. Chao. 2016. iNEXT: an R package for rarefaction and extrapolation of species diversity (Hill numbers). Methods in Ecology and Evolution.

Landau, W. 2018. The drake R package: A pipeline toolkit for reproducibility and high-performance computing. Journal of Open Source Software 3:550.

Pollock, L. J., R. Tingley, W. K. Morris, N. Golding, R. B. O’Hara, K. M. Parris, P. A. Vesk, and M. A. McCarthy. 2014. Understanding co‐occurrence by modelling species simultaneously with a Joint Species Distribution Model (JSDM). Methods in Ecology and Evolution 5:397–406.

R Core Team. 2019. R: A language and environment for statistical computing.

Schiettekatte, N. M., S. J. Brandl, and J. M. Casey. 2019. fishualize: Color palettes based on fish species. CRAN.

Stan Development Team. 2016. RStan: The R interface to Stan. R package version 2.14. 1.

Wickham, H., M. Averick, J. Bryan, W. Chang, L. McGowan, R. François, G. Grolemund, A. Hayes, L. Henry, and J. Hester. 2019. Welcome to the Tidyverse. Journal of Open Source Software 4:1686.