**Appendix D**

Sears, Snyder, and Rohr. 2015. Host life-history and host-parasite syntopy predict behavioral resistance and tolerance to parasites. *Journal of Animal Ecology*

**Appendix D. Methods and Results for Phylogenetic Analyses**

**Methods**

To test for a phylogenetic signal in our traits, we first generated a phylogeny for the seven tested species using Frost et al. ([2006](#_ENREF_1)) and Roelants et al. ([2007](#_ENREF_3)) (Fig. A1). We then determined the slopes of the relationships between cercarial dose and overall swimming, angled swimming, and mass change for each species. We focused on these three traits because they were the three quantified in all seven species. We then conducted two tests for a phylogenetic signature in these three traits using the ‘fitContinuous’ function in the ‘geiger’ package of R statistical software ([Harmon et al. 2013](#_ENREF_2)). First, we quantified the lambda value for each trait. Lambda values near 0.0 indicate that the trait is evolving among species as if the species were independent, thus indicating that phylogenetic correction is unnecessary. If traits are evolving as expected given the tree topology and a random walk model, lambda values will approach 1.0, with values equaling 1.0 being consistent with the constant-variance or Brownian motion model. Second, we compared the sample-size corrected Akaike information criteria (AICc) of Brownian motion (BM), Ornstein-Uhlenbeck (OU), Early-burst (EB), Lambda, and white-noise (non-phylogenetic) models of evolution. If the white-noise model is best based on AICc, then a phylogenetic correction again would not be necessary.

**Results**

Both tests indicated that a phylogenetic correction was unnecessary. The lambda values for all three traits were all close to zero (Overall swimming: 1.14 x 10-16, Angled swimming: 1.77 x 10-16, Log mass change: 1.81 x 10-16), indicating that the traits were evolving among species as if the species were independent. Moreover, the white-noise or non-phylogenetic model of evolution had the lowest AICc by far (Table S1), indicating that it was the evolutionary model that best fit the data.

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| **Table D1.** Small-sample-size corrected version of Akaike information criterion based on Brownian motion (BM), Ornstein-Uhlenbeck (OU), Early-burst (EB), Lambda, and white-noise (non-phylogenetic) models of evolution for the slope of the relationship between cercarial dose and overall tadpoles swimming, tadpole angled swimming, and tadpole mass change. | | | | | |
| Traita | BM | OU | EB | Lamda | White noise |
| Any swimming | 18.57 | 19.88 | 21.04 | 19.87 | 9.87 |
| Angled swimming | 18.39 | 19.17 | 20.50 | 19.16 | 9.16 |
| Log mass change | 15.88 | 17.14 | 18.29 | 15.86 | 7.13 |
| aTo ensure that all the slopes were positive, 0.5 was added to each slope value for each species. | | | | | |

Phylogeny (S1).tif

**Fig D1.** Phylogeny for seven anuran study species.

**References**

Frost, D. R., T. Grant, J. Faivovich, R. H. Bain, A. Haas, C. F. B. Haddad, R. O. De Sa et al. 2006. The amphibian tree of life. Bulletin of the American Museum of Natural History:8-370.

Harmon, L., J. Weir, C. Brock, B. Glor, W. Challenger, G. Hunt, R. FitzJohn et al. 2013.Package 'geiger': Analysis of evolutionary diversification.

Roelants, K., D. J. Gower, M. Wilkinson, S. P. Loader, S. D. Biju, K. Guillaume, L. Moriau et al. 2007. Global patterns of diversification in the history of modern amphibians. Proceedings of the National Academy of Sciences of the United States of America 104:887-892.