

# Predator phylogenetic diversity decreases predation rate via antagonistic interactions

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## Introduction

How do predators respond in different combinations?

There have been many studies of predator combinations, and many of the effects of phylogenetic diversity on the functioning of food webs. No study has shown results from a direct manipulation of predator phylogenetic diversity.

Decreasing predator richness has been shown to increase herbivory (Byrnes et al. 2006) in a three-level kelp food web. As these authors point out, the effect of diversity on ecosystem functioning is better known for lower trophic levels, rather than predators.

Predator combinations can have many different outcomes. From the perspective of ecosystem function it is important to consider whether these result in more or less top-down control.

Predator effects can be direct via changes in consumption, indirect via non-consumptive effects. In other words, it can be via the effects of predators on each other, or on their prey, and directly or indirectly. Therefore, in our experiment we tracked both predator and prey survival to the end of the experiment

for example, predators can kill each other, or decrease feeding rates.

## Methods

We combined predators together in species pairs that represented a range of relatedness: congeners (two congeneric damselflies, *Leptagrion andromache* and *Leptagrion elongatum*), two insects (a damselfly, *L. elongatum* and a predatory fly (Diptera: Tabanidae)) and two invertebrates (*L. elongatum* and leeches). We also included these four species in monoculture, along with a predator-free control (8 treatments, n=5). Combinations were substitutive, maintaining the same amount of predator metabolic capacity (biomass raised to the power of 0.69, predicting the scaling of metabolism with body mass (Brown et al. 2004)) in each. Response variables included the rate of decomposition of leaves, bromeliad growth and insect emergence. This experiment allows the estimation of the effect of each predator species from monoculture treatments, as well as the detection of non-additive effects in predator combinations.

In February 2011, bromeliads between 90 and 200ml were collected, thoroughly washed and soaked for 12 hours in a tub of water. They were then hung for 48 hours to dry. One bromeliad dissected after this procedure contained no insects.

Each bromeliad was supplied with dried leaves, simulating natural detritus inputs from the canopy. We enriched these leaves with N-15 by fertilizing five (Jabuticaba, *Plinia cauliflora*) plants with 40ml/pot/day of 5g/L ammonium sulphate containing 10 percent atom excess of N15. *duration.* started on 27/1/2011 Whole leaves were then picked from plants and air-dried until constant weight, and then soaked for three days and the water discarded. About 1.5 g of leaves were placed in each bromeliad ( $1.5006 \pm 0.0248$ ).

Each bromeliad was stocked with a representative insect community. The densities of each prey taxon were calculated from a 2008 observational dataset, using data from bromeliads of similar size to those in our experiment (DS Srivastava, upub. data). All densities used were within the range of these calculated abundances, and all experimental bromeliads received the same insect community. Halfway through the experiment, insects were added to bromeliads a second time.

Table 1: densities of each species

<i>Chironomus detriticula</i>	10
<i>Polypedium</i> sp. 1	4
<i>Polypedium</i> sp. 2	2
<i>Psychodid</i> sp. 1	1
<i>Scyrtes</i> sp. A	5
<i>Culex</i> spp.	4
<i>Trentepholia</i> sp.	1

After addition of the prey community, all bromeliads were enclosed with a mesh cage and checked daily for emergence of adults.

## Results

Our central hypothesis is that the phylogenetic relationships among predatory taxa in this system can be used to interpret their ecology. Specifically, we test the hypothesis that phylogenetic relatedness is negatively correlated with probability of co-occurrence, positively with diet similarity. Consequently, we might predict that ecosystem function peaks at some intermediate level of phylogenetic diversity – where predators occur but where their similarity creates complementarity.

Phylogenetic distance was not correlated with similarity in diet ( $F_{1,4}=0.0681, P=0.8071$ ).

### phylogenetic distance

Our phylogenetic relatedness in our community was very different – it ranged from very related organisms – congeneric leptagrion Larvae, which can barely be distinguished – to profound differences between a leech and a damselfly.

All increases in predator phylogenetic diversity beyond damselflies resulted in a reduction of prey mortality, however these did not reduce predator survivorship.

Predator diet breadth is quite similar. To test diet similarity, we compared the similarity in feeding trials between predators who were offered the same prey. This was a lower number for the leech-damselfly comparison than for the damselfly-damselfly comparison. We have data from **NUMBER** feeding trials. (a table, with similarity in diet in each cell and the number of species tested in brackets, with predators along the top and side (lower diagonal only) – how to format this in R?) by calculating a similarity matrix and converting to character, using paste to include sample sizes.

All predators showed a broad diet overlap. The system appears quite nested – but this is possibly due to the difficulty in observing predation by leeches in the lab.

Predator co-occurrence was unrelated to predator phylogenetic distance, as well.

## Discussion

## Works Cited

Brown, James H., James F. Gilgooly, Andrew P. Allen, Van M. Savage, and Geoffrey B. West. 2004. “Toward a metabolic theory of ecology.” *Ecology* 85 (jul): 1771–1789. doi:10.1890/03-9000. <http://www.esajournals.org/doi/abs/10.1890/03-9000>.

Byrnes, Jarrett, John J. Stachowicz, Kristin M. Hultgren, a Randall Hughes, Suzanne V. Olyarnik, and Carol S. Thornber. 2006. “Predator diversity strengthens trophic cascades in kelp forests by modifying herbivore behaviour.” *Ecology letters* 9 (jan): 61–71. doi:10.1111/j.1461-0248.2005.00842.x. <http://www.ncbi.nlm.nih.gov/pubmed/16958869>.

## Figures

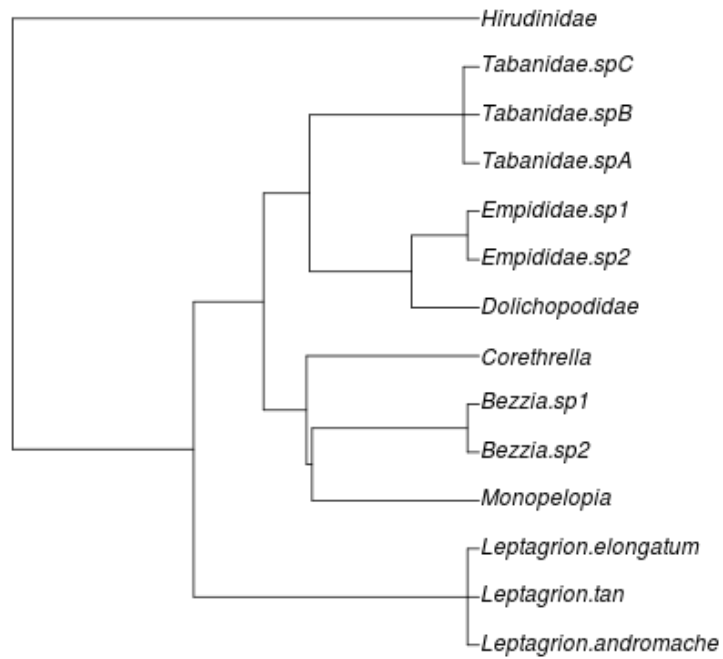


Figure 1: FALSE

## Figure 1

similarity between predators in diet composition in food web trials, as predicted by phylogenetic distance.

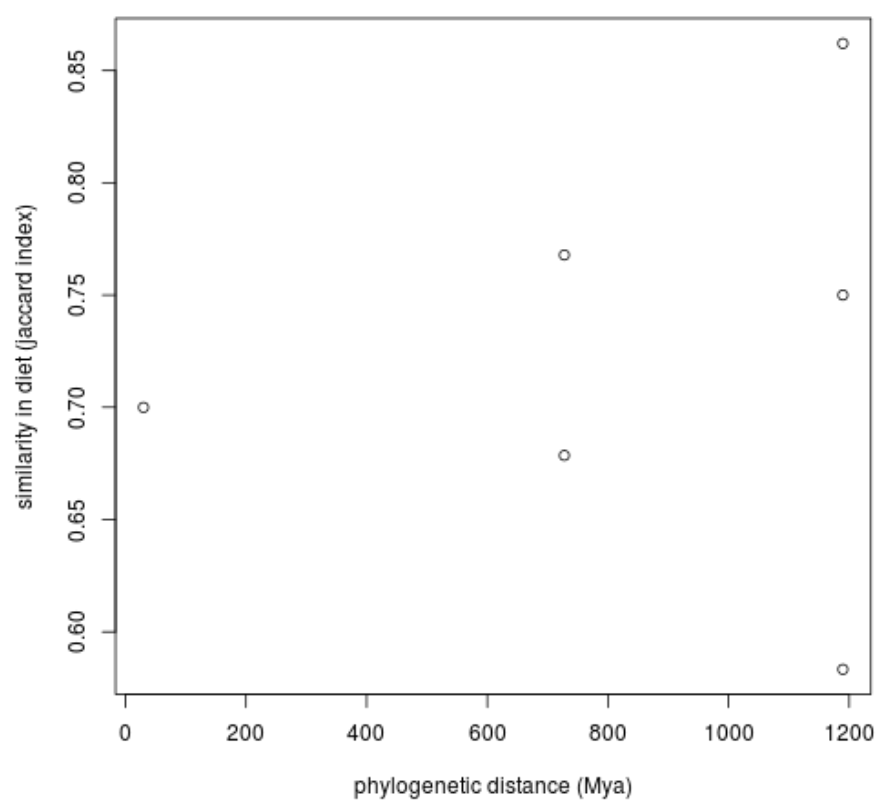


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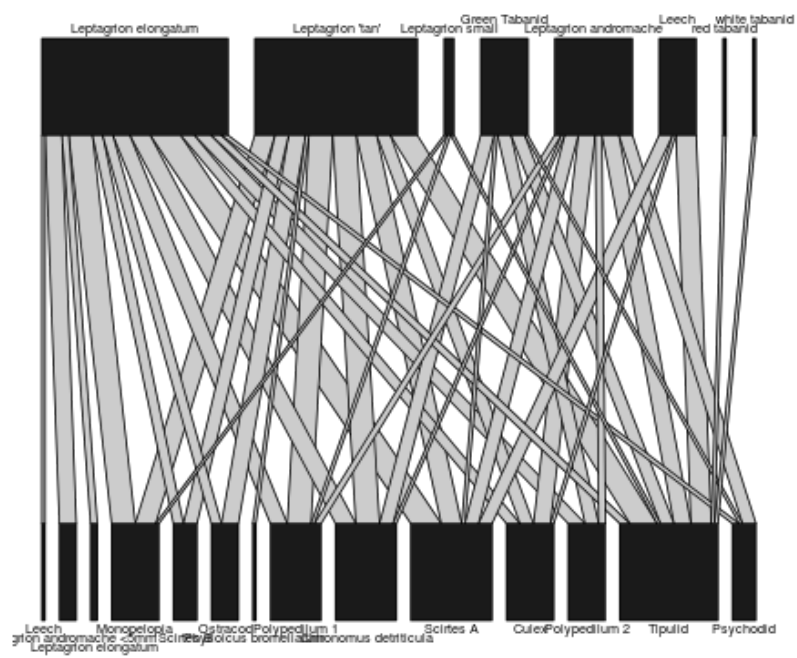


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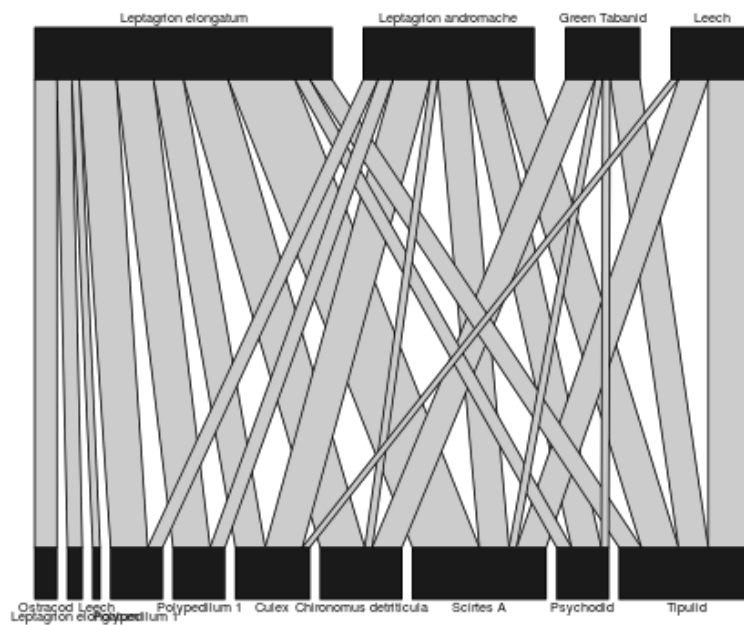


Figure 4: FALSE