RESEARCH PAPER

Geographic variation in network structure of a nearctic aquatic food web

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ABSTRACT

Aim

that pitchers have smaller openings and tubes (Ellison & Gotelli, 2002), will decrease food chain length and complexity. Fourth, food chain length and complexity will increase with the presence of the larvae of the pitcher-plant mosquito, [illegible] (Coq.), an important filter-feeding predator in this system (Cochran-Stafira & von Ende, 1998; Kneitel & Miller, 2002; Ellison, 2006; Peterson [illegible]., 2008).

In addition to testing these predictions regarding food web structure, we also determined what percentage of the variance in food web structure could be accounted for by a suite of broad-scale climatic variables (a list of climate variables is available in Table 3 and Appendix S1 in Supporting Information14.7e240.0ionT6mem

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positional turnover shows an inverse relationship with latitude (Buckley [illegible]., 2010). We predict that within-site variability in food web structure will track compositional turnover and increase at lower latitudes due to the lack of trophic redundancy in the low-latitude species-poor pools (Baiser & Lockwood, 2011).

METHODS

The *Sarracenia* food web

The food web occupying the aquatic microhabitat in the leaves of the northern pitcher plant comprises microbes, protozoa, the bdelloid rotifer [illegible] Donner (Bledzki & Ellison, 2003) and a suite of obligate arthropods: the mite [illegible] (Nesbitt), aquatic larvae of the pitcher-plant mosquito [illegible], the midge [illegible] (Coq.) and the sarcophagid fly [illegible] (Aldrich) (Addicott, i812.7(abr)e

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the total volume of pitcher fluid for each pitcher (see Buckley [illegible]., 2003, 2010, for detailspiteeepelection, leaf pelection,

web metric for the 20 pitchers at each of the 39 sites) on C-PC1, and the CVs of pitcher volume, mosquito abundance and bacterial abundance. The model for the food web metric ‘Top’ (see Table 1 for definition) included the climate variable CV of precipitation instead of C-PC1 based on the climate variable model selection (see Climatic data). We used the CV of pitcher volume, mosquito abundance and bacterial abundance for this analysis because we were interested in how pitcher-to-pitcher variation of predictor variables within each site was correlated with pitcher-to-pitcher variation in food web metrics across all pitchers within each site.

We built a set of candidate models for each response variable that included a global model, univariate models for each predictor variable and all subsets of variables that had a P-value < 0.1 for the slope coefficient in both the global and univariate models. We ranked models using the AIC, and used this score to select the best fitting model(s) among the candidate set (Burnham & Anderson, 2002). We calculated the adjusted ^{2} to determine the proportion of variance explained by each model.

[illegible]

The correlations among predictor variables had correlation tionship with food web metrics and was not a significant predictor in any of the best-fitting models.

Predator–prey interactions, food chain length and food web complexity

Mosquito abundance was not correlated with food web structure at the pitcher scale. However, variation in mosquito abundance at the site scale was positively correlated with structural turnover in two measures of chain length – mean trophic level and mean chain length (Table 5, Fig. 4a,b). Although the hypothesized relationship between mosquito abundance and chain length was observed at the site scale, food web complexity did not increase with mosquito abundance at the pitcher scale and variation in mosquito abundance within sites did not increase structural turnover in complexity metrics.

Biogeographic correlates of food chain length, and food web complexity

C-PC1, which is positively correlated with latitude (Table 3), was present in all of the best-fitting models that explained more than 5% of the variation in food web structure (Tables 4 & 5). At the pitcher scale, C-PC1 was positively correlated with two measures of food web complexity – linkage density and species richness. Species richness was shown to follow the same pattern and increase with latitude in previous analyses of these data (Bu-0.0012.9(of)]TJ.96.5(va]TJ.u8227.9all)-227J.u838J.u8227.3tr phic–oere138.

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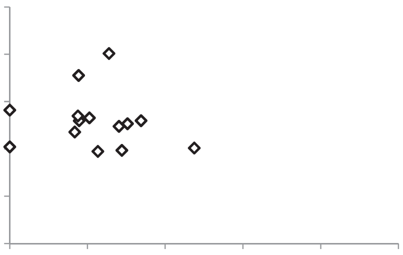

Resource availability showed no relationship with food web structure at the pitcher or site scales. One possibility why the predicted relationship was not observed is that bacterial abundance is not an appropriate measure for resource availability. The true resources are prey items that are captured by the plant. Although a bottom-up effect of prey abundance on bacterial abundance has been demonstrated repeatedly in the [illegible] system (Kneitel & Miller, 2002; Miller *et al*., 2002; Hoekman, 2010a), it is possible that bacterial abundance is a poor surrogate for resource availability due to sampling effects (i.e. only a fraction of the bacterial species can be cultured) or because abundance may not reflect productivity as a result of ongoing consumption of bacteria by higher trophic levels.

Although mosquito abundance had no effect on food web structure at the pitcher scale, increased variation in mosquito abundance between pitchers was positively correlated with

Kitching, R.L. (2001) Food webs in phytotelmata: ‘bottom-up’ and ‘top-down’ explanations for community structure. [illegible], **46**, 729–760.

Kneitel, J.M. (2007) Intermediate-consumer identity and resources alter a food web with omnivory. [illegible]

Appendix S1 Climatic variables (and latitude) used in climate variable principal components analysis and regressions.
Appendix S2 Methods for modelling nitrogen deposition.
Appendix S4 Correlations among climatic variables and latitude.
Appendix S4 Mixed effect models for the pitcher-scale analysis using function lme in package nlme in R v.2.11.1.
Appendix S5 Xu's (2003) method for calculating the variance explained (^{2}) by the fixed effects in a mixed-effects model.

BIOSKETCH

Ben Baiser is a post-doctoral research associate at Harvard Forest. He has interests in community ecology, conservation biology, invasion ecology and understanding the impact of global change on biodiversity.

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