Appendix 1: Detailed sampling procedure of fish species and environmental variables

Plot sampling

Plots were sampled monthly during the flood season in 2009, between January and July and once in March on the years of 2008, 2010 and 2011. Due to variability in the duration and amplitude of flood, the number of the plots sampled in each month from 2009 varied: 17 plots for January, 20 to February, 21 plots for March and April, 10 plots in May, three plots in June and two in July. The number of plots flooded in March 2008, 2010 and 2011 were 23, 18 and 22 respectively.

Fish were collected using two methods: throw traps and gill nets. A throw trap consist of a cubic metal structure (1m³) with the four sides covered by a 1.5 mm nylon mesh and was employed six times along the strip-like plot at every 50 meters (from 0 m up until 250 m). Individuals captured in this trap were collected with the aid of a triangular fish trap that was used until no additional fish specimen was revealed after 10 consecutive sweeps. Moreover, seven gill nets (20.0 x 1.5m) were distributed (mesh size of 12, 15, 18, 20, 25, 30 and 50 mm between opposite knots) along each plot between 1600 and 1700 hours and removed the following day between 0800 and 0900 hours, remaining exposed for about 16 hours. Each technique was used on a different day, so that they did not interfere with one another. The combination of active and passive sampling methods allowed the capture of both mobile and sedentary species as well as individuals from different size classes (Lapointe et al. 2006). Individuals captured were euthanized with Eugenol, fixed in 10% formalin solution and preserved in 70% ethanol and were identified to the species level.
Environmental variables

Elevation data was acquired with geodetic Global Position System (GPS) with simple frequency, adopting minimal time tracking of 10 minutes or maximum error of 50 mm. As each plot has approximately the same topographical elevation along its length, only one measure was enough to represent the entire plot. Water depth was measured using a measuring tape fixed to a pole and the patch depth was represented by the average value of six measurements performed across them, one at each location where the throw trap was launched. Patch age was estimated as the number of days a patch has been inundated, starting from the first sampling date.

Information on the vegetation cover was extracted from Google Earth™ and transformed into a raster grid. Based in the vegetal structure and inundation, six types of vegetation cover were identified: wet grassland, wet forest, wet pasture, wet grassland with pasture, dry forest and dry pasture. While grassland and pasture include mainly grasses and aquatic macrophytes (submerged, emergent and floating), forest are composed by shrubs and trees without undergrowth. The percentage of each vegetation type was measured using 450 m circular buffer around the center of each plot.

Vegetation cover types were highly correlated among each other, thus we applied a principal components analysis (PCA) to reduce the dimensionality of the data. Two axes were extracted (using the broken stick model, Jackson et al. 1993) and accounted for 61.8% of the variation in vegetation data. The first axis was positively related to wet grasslands, dry forests and negatively related to dry and wet pastures while the second axis was positively correlated with wet forests and presented a negative relationship with wet grassland-pastures (Table A1).
Table A1 - Coefficients and p-values for the correlation between the first and second axis of the PCA and different types of the vegetation cover.

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<tr>
<th>Vegetal cover</th>
<th>PCA1 (36.9%)</th>
<th>PCA2 (24.9%)</th>
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<td>Wet pasture</td>
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References not found in the main text


Appendix 2: Analysis of Metacommunity Structure

The EMS algorithm analyzes the metacommunity structure using an incidence matrix (presence-absence data), which is first ordinated via a correspondence analysis (CA). Each CA axis is a gradient construct describing patterns of variation across species and sites within metacommunities by maximizing the positioning of sites along axes based on the degree to which their communities share species compositions and the positioning of species sharing similar ranges (Leibold and Mikkelson 2002). For each month (i.e. each incidence matrix), species and sites were ranked according to their position along the primary CA axis (i.e., the one that summarizes most of the variation in the incidence matrix). The EMS framework is based on three statistics, namely coherence, turnover and boundary clumping. By assessing the significance of these statistics and their values, we can determine in a hierarchical manner which metacommunity pattern (checkerboard, nestedness, Clementsian gradients, Gleasonian gradients, evenly-spaced gradients and random) best describes the major pattern of species variation (i.e., first CA axis). Here, significance of each statistics was assessed via a null model that permutes species across sites 1000 times within the incidence matrix while maintaining site richness, which has been shown to have acceptable levels of Type I error (Gotelli and Graves 1996, Presley et al. 2009). Each permuted matrix is ordinated via correspondence analysis, which is in turn used to calculate the values of the three elements for the random incidence matrices. P-values were calculated to assess how extreme the observed value was among the random values and for each of the three statistics, significance was assessed on the basis of an $\alpha = 0.05$.

Coherence was evaluated by counting the number of embedded absences in all species ranges and community compositions for each month (see Fig. 1 in Henriques-Silva et al. 2013 for more details). Significant negative coherence (i.e. more embedded absences than the null
distribution) indicates that a checkerboard distribution (Diamond 1975) is the pattern that best fits
the data. If coherence is non-significant, then the metacommunity is randomly structured
regarding the gradient analyzed (Leibold and Mikkelsen 2002). Finally, a significantly positive
coherence (i.e. less embedded absences than the null distribution) suggests that species are
distributed according to the same gradient (Leibold and Mikkelsen 2002), which is further
differentiated by evaluating the species range turnover and boundary clumping. Note that these
two elements were analyzed using the species perspective, which contrasts turnover and
boundary clumping among species ranges rather than community compositions (see Presley et al.
2009 for a discussion on this matter). Turnover is calculated by counting the number of
replacements (i.e. the number of times a species replace another at the edge of their ranges; see
Fig 1 in Henriques-Silva et al. 2013 and Presley et al. 2010 for further details on rationale). The
observed number of replacements is then compared to the ones generated by each null
metacommunity. A lower number of observed replacements (i.e. negative range turnover)
suggests that nestedness (Patterson and Atmar 1986) characterizes the metacommunity structure
whereas if the observed metacommunity exhibits a higher number of replacements (i.e. positive
turnover across species ranges) the data is further contrasted to range boundary clumping. Note
that if range turnover is not significant the metacommunity will exhibit quasi structures (e.g.
quasi-nested, quasi-Gleasonian, quasi-Clementsian and quasi-evenly-spaced; sensu Presley et al.
2010). These quasi-structures have the same characteristics as their associated idealized
structures but with weaker structuring processes (see Presley et al. 2010 for a discussion). This
last element is tested using the Morisita’s Index which has an expected value of 1. If the observed
index is not significantly different than 1, range boundaries are randomly distributed, indicating a
Gleasonian gradient. Conversely, if the observed value is significantly higher or lower than 1, it
shows that the species range boundaries are clumped or overdispersed as in a Clementsian or
Evenly-spaced distributions, respectively (Leibold and Mikkelson 2002). We highlight that nested metacommunities may exhibit clumped, stochastic or hyperdispersed species loss among sites, which are analogous to Clementsian, Gleasonian and evenly-spaced gradients with the difference that these patterns of range dispersion are found only at one side of the distributional gradient (see Presley et al. 2010 for further details). Gleasonian and Clementsian structures differ regarding the response of species to the major gradient of variation defined by the CA: in the former the species respond independently from one another whereas in the latter groups of species respond similarly (Leibold and Mikkelson 2002). Finally, evenly-spaced gradient suggests that species exhibit a trade-off between environmental tolerance and competitive ability along the gradient of variation (Tilman 1982). Significance for the observed Morisita index is evaluated using a Chi-squared goodness-of-fit test that compare the observed distribution to an expected distribution of range boundary locations (Presley et al. 2009).

References not found in the main text


Appendix 3: List of species with codes (from Fig. 2) and regional abundances across the four sampling periods in 2009.

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