

Ecography

ECOG-00527

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Supplementary material

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

706 **Plot sampling**

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

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

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728 **Environmental variables**

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

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

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

749 Table A1 - Coefficients and p-values for the correlation between the first and second axis of the
 750 PCA and different types of the vegetation cover.

Vegetal cover	PCA1 (36.9%)		PCA2 (24.9%)	
	r	p	r	p
Wet grassland	0.80	<0.001	-0.35	0.095
Dry forest	0.70	<0.001	-0.29	0.170
Dry pasture	-0.62	0.001	-0.27	0.211
Wet forest	-0.007	0.972	0.89	<0.001
Wet grassland with pasture	-0.05	0.800	-0.62	0.001
Wet pasture	-0.83	<0.001	-0.07	0.740

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765 Appendix 2: Analysis of Metacommunity Structure

766 The EMS algorithm analyzes the metacommunity structure using an incidence matrix
767 (presence-absence data), which is first ordinated via a correspondence analysis (CA). Each CA
768 axis is a gradient construct describing patterns of variation across species and sites within
769 metacommunities by maximizing the positioning of sites along axes based on the degree to which
770 their communities share species compositions and the positioning of species sharing similar
771 ranges (Leibold and Mikkelsen 2002). For each month (i.e. each incidence matrix), species and
772 sites were ranked according to their position along the primary CA axis (i.e., the one that
773 summarizes most of the variation in the incidence matrix). The EMS framework is based on three
774 statistics, namely coherence, turnover and boundary clumping. By assessing the significance of
775 these statistics and their values, we can determine in a hierarchical manner which
776 metacommunity pattern (checkerboard, nestedness, Clementsian gradients, Gleasonian gradients,
777 evenly-spaced gradients and random) best describes the major pattern of species variation (i.e.,
778 first CA axis). Here, significance of each statistics was assessed via a null model that permutes
779 species across sites 1000 times within the incidence matrix while maintaining site richness, which
780 has been shown to have acceptable levels of Type I error (Gotelli and Graves 1996, Presley et al.
781 2009). Each permuted matrix is ordinated via correspondence analysis, which is in turn used to
782 calculate the values of the three elements for the random incidence matrices. P-values were
783 calculated to assess how extreme the observed value was among the random values and for each
784 of the three statistics, significance was assessed on the basis of an $\alpha = 0.05$.

785 Coherence was evaluated by counting the number of embedded absences in all species
786 ranges and community compositions for each month (see Fig. 1 in Henriques-Silva et al. 2013 for
787 more details). Significant negative coherence (i.e. more embedded absences than the null

788 distribution) indicates that a checkerboard distribution (Diamond 1975) is the pattern that best fits
789 the data. If coherence is non-significant, then the metacommunity is randomly structured
790 regarding the gradient analyzed (Leibold and Mikkelsen 2002). Finally, a significantly positive
791 coherence (i.e. less embedded absences than the null distribution) suggests that species are
792 distributed according to the same gradient (Leibold and Mikkelsen 2002), which is further
793 differentiated by evaluating the species range turnover and boundary clumping. Note that these
794 two elements were analyzed using the species perspective, which contrasts turnover and
795 boundary clumping among species ranges rather than community compositions (see Presley et al.
796 2009 for a discussion on this matter). Turnover is calculated by counting the number of
797 replacements (i.e. the number of times a species replace another at the edge of their ranges; see
798 Fig 1 in Henriques-Silva et al. 2013 and Presley et al. 2010 for further details on rationale). The
799 observed number of replacements is then compared to the ones generated by each null
800 metacommunity. A lower number of observed replacements (i.e. negative range turnover)
801 suggests that nestedness (Patterson and Atmar 1986) characterizes the metacommunity structure
802 whereas if the observed metacommunity exhibits a higher number of replacements (i.e. positive
803 turnover across species ranges) the data is further contrasted to range boundary clumping. Note
804 that if range turnover is not significant the metacommunity will exhibit quasi structures (e.g.
805 quasi-nested, quasi-Gleasonian, quasi-Clementsian and quasi-evenly-spaced; *sensu* Presley et al.
806 2010). These quasi-structures have the same characteristics as their associated idealized
807 structures but with weaker structuring processes (see Presley et al. 2010 for a discussion). This
808 last element is tested using the Morisita's Index which has an expected value of 1. If the observed
809 index is not significantly different than 1, range boundaries are randomly distributed, indicating a
810 Gleasonian gradient. Conversely, if the observed value is significantly higher or lower than 1, it
811 shows that the species range boundaries are clumped or overdispersed as in a Clementsian or

812 Evenly-spaced distributions, respectively (Leibold and Mikkelson 2002). We highlight that
813 nested metacommunities may exhibit clumped, stochastic or hyperdispersed species loss among
814 sites, which are analogous to Clementsian, Gleasonian and evenly-spaced gradients with the
815 difference that these patterns of range dispersion are found only at one side of the distributional
816 gradient (see Presley et al. 2010 for further details). Gleasonian and Clementsian structures differ
817 regarding the response of species to the major gradient of variation defined by the CA: in the
818 former the species respond independently from one another whereas in the latter groups of
819 species respond similarly (Leibold and Mikkelson 2002). Finally, evenly-spaced gradient
820 suggests that species exhibit a trade-off between environmental tolerance and competitive ability
821 along the gradient of variation (Tilman 1982). Significance for the observed Morisita index is
822 evaluated using a Chi-squared goodness-of-fit test that compare the observed distribution to an
823 expected distribution of range boundary locations (Presley et al. 2009).

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

Species	Family	Code	January	February	March	April
<i>Acestrorhynchus pantaneiro</i>	Acestrorhynchidae	1	0	7	4	2
<i>Aequidens plagiazonatus</i>	Cichlidae	2	0	0	1	4
<i>Anadoras weddellii</i>	Doradidae	3	18	21	2	2
<i>Aphyocharax anistsi</i>	Characidae	4	1	1	20	49
<i>Aphyocharax paraguayensis</i>	Characidae	5	0	0	0	9
<i>Apistogramma borellii</i>	Cichlidae	6	0	0	0	1
<i>Astyanax asuncionensis</i>	Characidae	7	0	3	7	6
<i>Brachyhyopomus</i> spB	Hypopomidae	8	0	0	0	1
<i>Bujurquina vittata</i>	Cichlidae	9	3	8	0	3
<i>Callichthys callichthys</i>	Callichthyidae	10	0	9	1	0
<i>Chaetobranchopsis australis</i>	Cichlidae	11	0	0	1	2
<i>Characidium</i> aff. <i>Zebra</i>	Crenuchidae	12	0	0	1	1
<i>Cichlasoma dimerus</i>	Cichlidae	13	5	17	48	168
<i>Corydoras aeneus</i>	Callichthyidae	14	17	24	5	3
<i>Corydoras hastatus</i>	Callichthyidae	15	3	14	47	36
<i>Corydoras latus</i>	Callichthyidae	16	1	0	0	0
<i>Crenicichla lepidota</i>	Cichlidae	17	0	0	0	15
<i>Cyphocharax gillii</i>	Curimatidae	18	1	0	1	20
<i>Gymnocorymbus ternetzi</i>	Characidae	19	1	2	3	8
<i>Gymnogeophagus balzanii</i>	Cichlidae	20	0	0	1	1
<i>Gymnotus carapo</i>	Gymnotidae	21	0	0	1	0
<i>Hemigrammus tridens</i>	Characidae	22	9	23	37	195

<i>Hoplerythrinus unitaniatus</i>	Erythrinidae	23	26	36	64	108
<i>Hoplias malabaricus</i>	Erythrinidae	24	10	30	56	63
<i>Hoplosternum littorale</i>	Callichthyidae	25	62	67	108	79
<i>Hyphessobrycon elachys</i>	Characidae	26	0	1	5	41
<i>Hyphessobrycon eques</i>	Characidae	27	0	0	1	0
<i>Laetacara dorsigera</i>	Cichlidae	28	2	0	0	16
<i>Leporinus lacustris</i>	Anostomidae	29	0	3	9	26
<i>Lepthoplosternum pectoralle</i>	Callichthyidae	30	1	10	11	12
<i>Loricariichthys platymetopon</i>	Loricariidae	31	0	0	1	1
<i>Markiana nigripinnis</i>	Characidae	32	26	9	11	9
<i>Megalechis personata</i>	Callichthyidae	33	25	28	9	14
<i>Megalechis picta</i>	Callichthyidae	34	0	0	0	1
<i>Megalechis thoracata</i>	Callichthyidae	35	0	3	0	0
<i>Merodoras nheco</i>	Doradidae	36	5	7	4	3
<i>Metynnis mola</i>	Characidae	37	0	1	0	2
<i>Moema heterostigma</i>	Rivulidae	38	2	0	0	0
<i>Moenkhausia bonita</i>	Characidae	39	0	1	1	5
<i>Moenkhausia sanctaefilomenae</i>	Characidae	40	0	0	0	1
<i>Neofundulus parvipinnis</i>	Rivulidae	41	32	17	11	3
<i>Parauchenipterus striatulus</i>	Auchenipteridae	42	0	1	3	1
<i>Phenacogaster tegatus</i>	Characidae	43	0	0	0	1
<i>Plesiolebias glaucopterus</i>	Rivulidae	44	39	119	49	39
<i>Poptella paraguayensis</i>	Characidae	45	0	0	1	3
<i>Pyrrhulina australis</i>	Lebiasinidae	46	0	0	0	10

<i>Rhamdia quelen</i>	Heptapteridae	47	1	3	3	2
<i>Roeboides</i> sp.	Characidae	48	0	0	1	0
<i>Satanoperca pappaterra</i>	Cichlidae	49	0	0	0	1
<i>Serrapinnus</i> spp.	Characidae	50	2	47	214	612
<i>Serrasalmus maculatus</i>	Serrasalmidae	51	0	0	4	3
<i>Serrasalmus marginatus</i>	Serrasalmidae	52	0	0	1	0
<i>Steindachnerina conspersa</i>	Characidae	53	0	0	1	1
<i>Stenolebias damascenoi</i>	Rivulidae	54	145	87	52	20
<i>Synbranchus marmoratus</i>	Synbranchidae	55	0	1	10	11
<i>Trachelyopterus coriaceus</i>	Auchenipteridae	56	16	16	4	4
<i>Trigonectes balzannii</i>	Rivulidae	57	0	4	4	8
<i>Triportheus nematurus</i>	Characidae	58	7	3	6	5

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