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1 Supplementary material for

2 **“Phylogenetic linkages between composition and structure of tree communities shed light**
3 **on historical processes influencing tropical rainforest diversity”**

4 M. B. Carlucci et al.

5

6 **Appendix 1.** Lists of TEAM Network’s sites (7), Gentry’s sites (74), published studies (34 sites
7 from 32 studies) used to compile rainforest tree species pools for Neotropics, Afrotropics and
8 Madagascar. TEAM data sets are available at <http://www.teamnetwork.org>. Gentry’s transect
9 data is available at <http://www.mobot.org/mobot/research/gentry/welcome.shtml>.

10

11 **(a) TEAM’s sites used:** NEOTROPICS - Volcán Barva (La Selva Biological Station and
12 Braulio Carrillo National Park, Costa Rica), Manaus (three different field stations near the city
13 of Manaus, Brazil) and Caxiuanã (Caxiuanã National Forest, Brazil); AFROTROPICS - Korup
14 (Korup National Park, Cameroon), Bwindi (Bwindi Impenetrable National Park, Uganda),
15 Udzungwa (Udzungwa Mountains National Park, Tanzania); MADAGASCAR - Ranomafana
16 (Ranomafana National Park, Madagascar).

17 We selected seven sites containing information of tree composition and abundance in
18 tropical rainforests. For each site, we used the inventory data that ranged between Aug 2010
19 and May 2011. The TEAM Network sampling design for trees consists of tropical rainforest
20 sites with five to seven 1-ha plots (100 x 100 m), each subdivided in 25 subplots of 400 m² (20
21 x 20 m), where trees with diameter at breast height ≥ 10 cm were recorded. Plots were placed in
22 closed-canopy moist forest habitats. Each of the selected sites was composed by six plots of 1

23 ha, except for Korup and Volcán Barva, which were composed by five and nine plots,
 24 respectively. The data from all these plots were gathered using a defined, shared and therefore
 25 comparable method, which follows quality controls, such as including late successional forests
 26 with little anthropogenic impact. Further information can be found in TEAM Network (2010)
 27 and at <http://www.teamnetwork.org>.

28

29 **(b) Alwyn Gentry's sites (codes in parentheses):** AFROTROPICS – Banyong (Afr1), Belinga
 30 (Afr6), Makokou 1 (Afr7), Makokou 2 (Afr8), Mount Cameroun (Afr3), Ndakan (Afr4), Pande
 31 Forest Reserve (Afr17), Pugu Forest Reserve (Afr18); MADAGASCAR – Nosy Mangabe
 32 (Afr13), Perinet Forestry Station (Afr14); NEOTROPICS - Allpahuayo (SAm89), Alter de
 33 Chao (SAm20), Alto de Cuevas (SAm33), Alto de Mirador (SAm35), Alto Madidi (SAm10),
 34 Alto Madidi – Ridge Top (SAm11), Anchicayá (SAm36), Antado (SAm37), Araracuara
 35 (SAm39), Araracuara - High Campina (SAm38), Bajo Calima (SAm40), Belém-Mocambo
 36 (SAm29), Berbice River (SAm87), Bosque de la Cueva (SAm41), Bosque Nacional von
 37 Humboldt (SAm90), Cabeza de Mono (SAm91), Candamo (SAm108), Carajas (SAm23),
 38 Carara National Park (CAm6), Centinela (SAm70), Cerro de la Neblina 1 (SAm124), Cerro de
 39 la Neblina 2 (SAm125), Cerro El Picacho (CAm24), Cerro Olumo (CAm23), Cochacashu
 40 (SAm96), Constancia (SAm97), Cuangos (SAm71), Curundu (CAm25), Cuzco Amazónico
 41 (SAm99), Dureno (SAm72), Fila de Bilsa (SAm68), Huamaní (SAm75), Indiana (SAm101),
 42 Jatun Sacha (SAm76), Jenaro Herrera (SAm102), La Planada (SAm54), Madden Forest
 43 (CAm26), Maquipucuna (SAm78), Miazi (SAm79), Mishana - Tahuampa (SAm104), Mishana
 44 Old Floodplain (SAm105), Mishana White Sand (SAm106), Murri (SAm59), Osa-Sirena
 45 (CAm8), Pampas del Heath (SAm109), Pipeline Road (CAm27), Quebrada Sucusari
 46 (SAm112), Rancho Quemado (CAm7), Río Manso (SAm61), Río Nangaritza (SAm82), Río

47 Palenque 1 (SAm83), Río Palenque 2 (SAm84), Río Távora (SAm110), San Sebastián
48 (SAm85), Saul (SAm86), Shiringamazú (SAm111), Tambopata Alluvial (SAm114),
49 Tambopata Lateritic (SAm116), Tambopata Swamp Trail (SAm115), Tambopata Upland
50 Sandy (SAm113), Tutunendo (SAm65), Yanamono 1 (SAm120), Yanamono 2 (SAm121),
51 Yanamono Tahuampo (SAm119).

52

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125

126

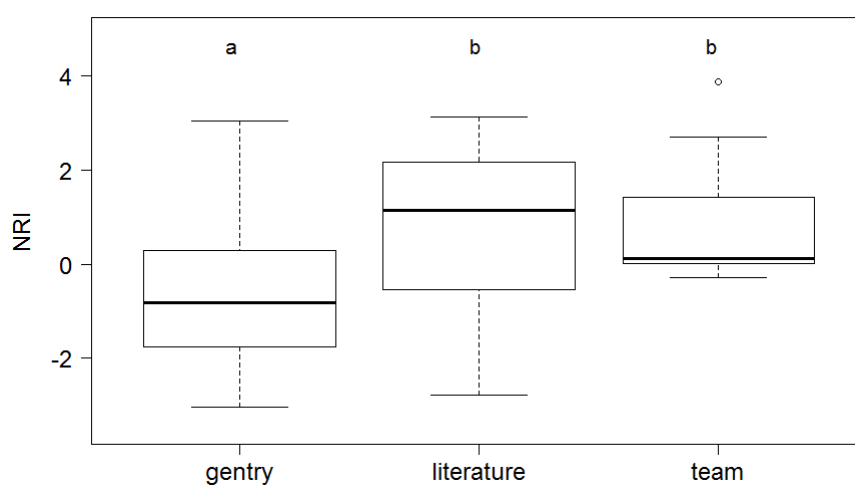
127 **Appendix 2.** Analyses of the influence of data source on phylogenetic structure patterns.

128

129 Considering that our data came from different sources with different sampling sizes, we
 130 tested for the influence of data source on net relatedness index (NRI), our measure of
 131 phylogenetic structure. Among the data sources used, the transects sampled by Alwyn Gentry
 132 had the smallest sampling effort, where each site had one transect with 0.1 ha, while TEAM
 133 Network's sites had 5 to 9 ha sampled and surveys from the literature had variable sampling
 134 effort (mostly 1 ha). Thus, one could wonder about the effect of small sampling effort in
 135 Gentry's sites over NRI.

136 In order to test for this possible sampling effect, we compared NRI values between data
 137 sources. For this, we used a two-way ANOVA, in which the factors were Source (Gentry vs.
 138 TEAM vs. Literature) and Andes (sites in the Andes vs. sites in other regions). Since the design
 139 was unbalanced, we used an ANOVA with randomization tests (Pillar and Orłóci 1996) to test
 140 for significance of the contrasts between groups of each factor. Analyses were performed using
 141 the software MULTIV v. 3.1 by V. Pillar (available at
 142 <http://ecoqua.ecologia.ufrgs.br/software.html>).

143 Gentry's sites had lower NRI values than TEAM's sites and surveys from the literature
 144 (Fig. A3; Table A1). Moreover, Andes sites had lower NRI values than other sites (Fig. A4;
 145 Table A1).

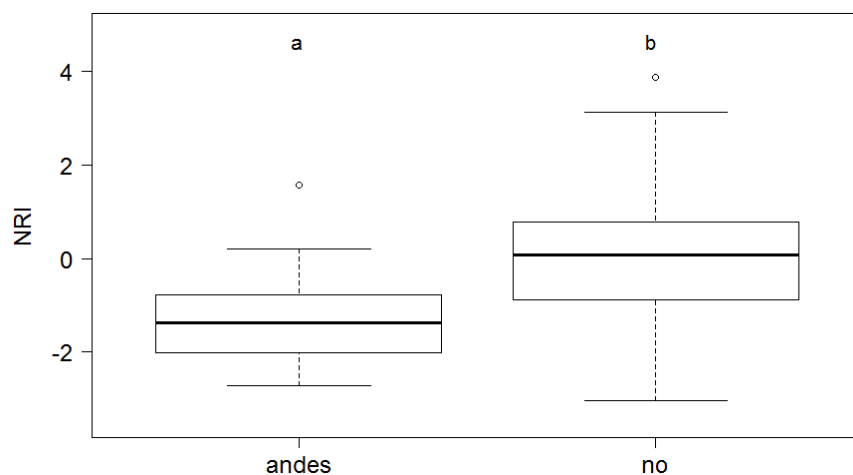


146

147 **Figure A1.** Comparison of NRI values between different sources of data: Gentry's transects, surveys from
 148 the literature, and TEAM Network's plots. Different letter above boxes mean significant differences

149 between data sources ($P < 0.05$).

150



151

152 **Figure A2.** Comparison of NRI values between groups of sites in Andes and in other regions. Different
153 letter above boxes mean significant differences between data sources ($P < 0.05$).

154

155 **Table A1.** Results of the two-way ANOVA with randomization tests, comparing NRI values between
156 Andean and non-Andean sites and between sites from different data sources.

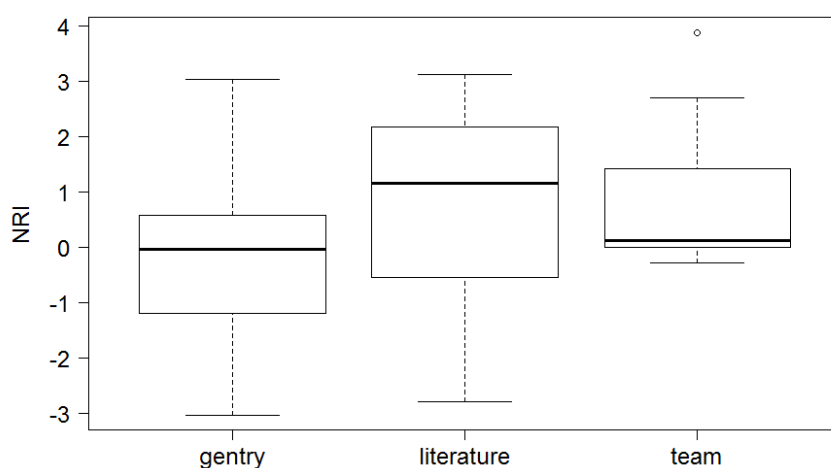
Source of variation	Sum of squares (Q)	$P(Q_{b_{null}} \geq Q_b)$
Factor Andes		
Andean sites vs. other sites	40.721	0.002
Factor Source		
Between groups	30.391	0.034
Contrasts:		
Gentry vs. Literature	17.188	0.048
Gentry vs. TEAM	16.656	0.036
Literature vs. TEAM	0.61308	0.672
Andes vs. Source *	-18.8	0.973
Between groups	52.312	0.001
Within groups	158.17	
Total	210.48	

157 *Note that the interaction between Andes and Source does not contain all the
158 combinations of levels, because all Andean sites came from Gentry's database.

159

160 Given that all data on Andean sites came from Gentry's database, we were not able to
161 decouple the effect of data source from biogeographic causation using only the data from
162 Andean sites. Thus, we compared NRI values between Gentry's non-Andean sites and non-
163 Andean sites from other data sources. If Gentry's sites are not biased toward low NRI values,
164 then there should be no difference in NRI between Gentry's non-Andean sites and all other non-
165 Andean sites.

166 Indeed, there were no significant differences in NRI between non-Andean sites from
167 different data sources (Fig. A5; Table A2). Hence, Gentry's sites in general presented lower
168 NRI values than other data sources because of Andes, which typically had low NRI values (see
169 Results in the main text). Therefore, we conclude that Gentry's sites are unbiased and can be
170 used together with TEAM Network's sites and the surveys from the literature in the analyses.



171

172 **Figure A3.** Comparison of NRI values between non-Andean sites from different data sources. NRI did
173 not differ between groups.

174

175

176

177 **Table A2.** Results of the one-way ANOVA with randomization tests, comparing NRI values between
 178 non-Andean sites from different data sources.

Source of variation	Sum of squares (Q)	P($Q_{b_{null}} \geq Q_b$)
Factor Source		
Between groups	11.591	0.084
Contrasts		
Gentry vs. Literature	5.9116	0.096
Gentry vs. TEAM	7.7806	0.061
Literature vs. TEAM	0.61308	0.669
Within groups	129.01	
Total	140.6	

179

180

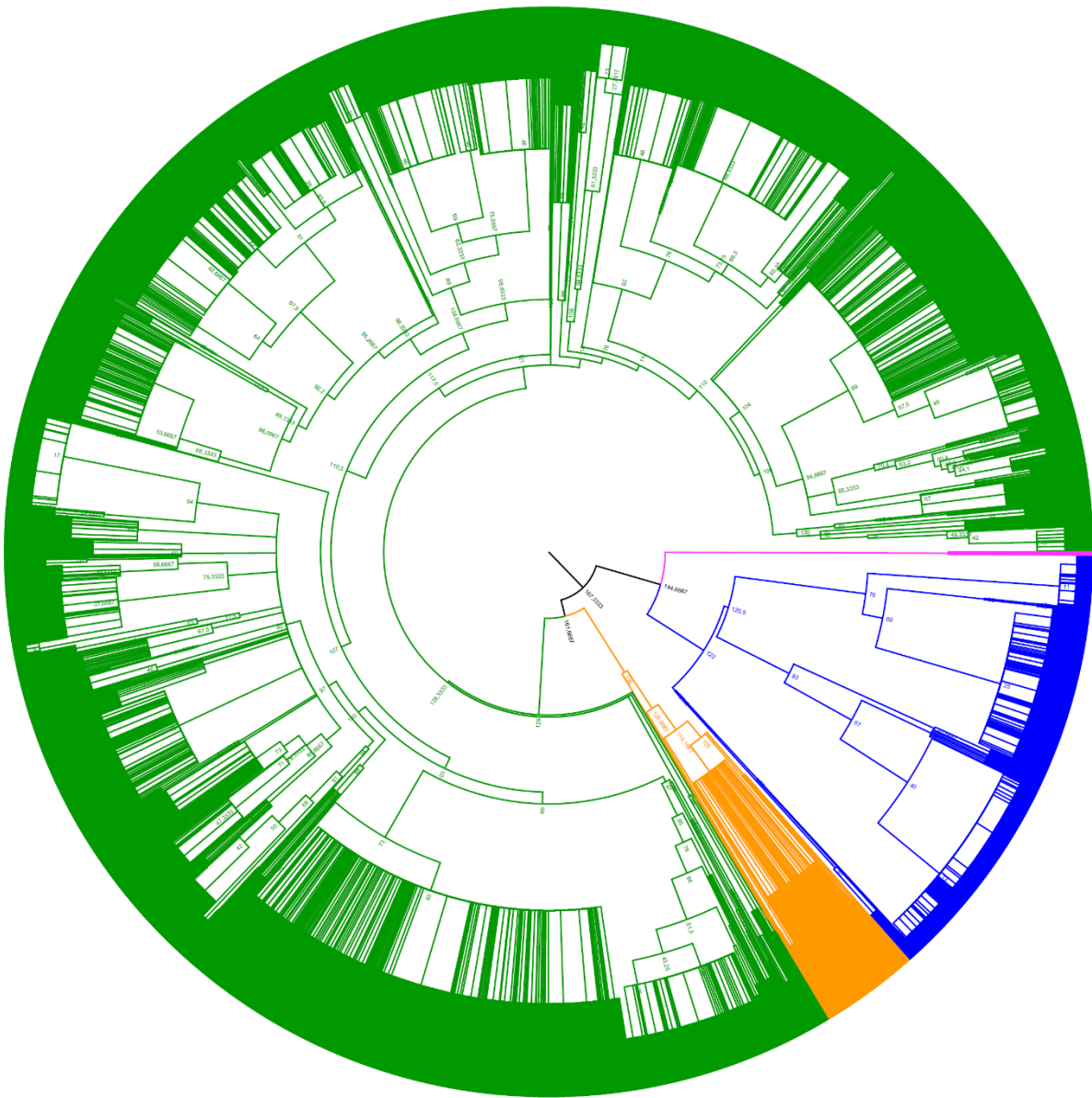
181 **References**

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184

185 **Appendix 3.** Figure of the phylogenetic tree.

186

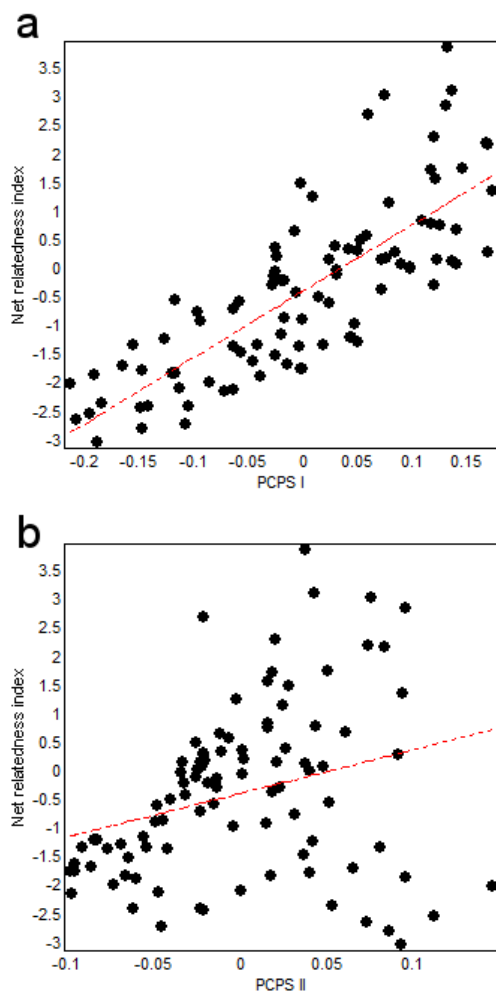


187

188 **Figure A4.** Phylogenetic tree for 6,307 rainforest tree species occurring in 115 Neotropical, Afrotropical
 189 and Malagasy communities (including the 94 with species abundance data and 21 with only species
 190 occurrence data). Pink, Chloranthales; Blue, magnoliids; orange, monocots; Green, eudicots.

191 **Appendix 4.** Correlation between PCPS (principal coordinates of phylogenetic structure) and
 192 NRI (net relatedness index).

193



194

195 **Figure A5.** Scatter plot between phylogenetic composition and structure of tropical rainforest tree
 196 communities ($n=94$), measured using PCPS and NRI, respectively. Pearson's correlation was significant
 197 for the comparisons of NRI with both main phylogenetic composition vectors: (a) PCPS I vs. NRI, $r =$
 198 0.791 , $F_{30,2} = 50.35$, $P < .001$; (b) PCPS II vs. NRI, $r = 0.28$, $F_{52,1} = 4.42$, $P = 0.04$. Correlation statistics
 199 and significance were obtained after accounting for the influence of spatial autocorrelation on the
 200 number of degrees of freedom by using Dutilleul's correction (Dutilleul 1993).

201

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