versus locations with their pairwise phylogenetic distances. Principal coordinate (PCO) analyses (in MultiVariate Statistical Package v3.13; Kovach Computing Services) on resulting location versus location matrices showed that the MPPD matrices had almost no explanatory power (generally the first five PCO axes explained less than 5% of data variance), meaning that detected patterns were mostly random. The MNTD matrices, however, explained considerable amounts of data variance in the first five axes of the PCO. Therefore, we used only MNTD for further analysis.

Correcting for Taxon Richness Bias in MNTD. Taxon richness differed considerably between locations, varying between 4 and 1,466. MNTD may be sensitive to such differences in taxon richness because the chance of finding a close relative between two locations may increase when their taxon richness increases. Applying MNTD to determine phylogenetic distance between locations with differing taxon numbers could therefore result in taxon-rich locations being grouped together in the cluster analysis simply because they are more taxon-rich. To determine the impact of this effect, we created five "location-by-taxon" matrices, each with a lower number of taxa per location (320, 160, 80, 40, and 20 taxa per location), using the 41 locations containing more than 320 taxa. For each location, taxa were ranked according to abundance, so that the location-by-taxon matrix based on, for example, 320 taxa consisted only of the 320 most abundant taxa per location. Where tied abundances exceeded the predefined number of taxa, we randomly selected the appropriate number of taxa from among those with tied minimum abundance. We then calculated the MNTD matrices for each of these five location-by-taxon matrices and found that with increasing taxon richness of locations, MNTD (as averaged over all locations) decreased with increasing taxon richness per location following a power function [$y = 310.4x^{-0.194}$ (Fig. S4)], demonstrating that MNTD is indeed sensitive to taxon richness.

Determining the Optimal Number of Taxa per Location for Further Analysis. To avoid taxon richness bias when using MNTD, locations had to be compared based on similar numbers of taxa. Minimum variance clustering, based on the five location-by-taxon matrices described earlier, consistently recovered the same major clusters in the same configuration (African and American locations clustered on one main branch and Asian locations clustered on the other), although the relationships between locations within these main clusters could vary (Fig. S5). Only in the 20-taxon analysis was one American location (location no. 165 from the Brazilian Atlantic Forest) placed in the Asian cluster. The amount of variance captured in the first five axes of a PCO analysis (using the same MNTD matrices) declined by only ∼20%, from 83.3 to 60.7%, between the 320- and 20-taxon analyses, respectively. We decided to use 20 taxa per location in the final analyses (Table S1) because of this limited loss of information in the PCO and similarity of cluster results. In addition, we were able to use most of our locations (406 of the initial 439), including locations on remote islands and extreme habitats that would have been excluded if we had set the minimum number of taxa too high.

Forest Classification Analyses. For the final analyses, we produced 20 location-by-taxon datasets. In these datasets, each location was represented by 20 randomly drawn taxa (from that location). Random draws were irrespective of taxon abundance, as abundance is a spatially and temporally labile taxon trait that likely reflects contemporary environmental conditions rather than historical biogeographic signal. For each of these 20 location-by-taxon datasets, we calculated the corresponding symmetrical location-by-location matrices with their pairwise phylogenetic distances (MNTD). These matrices were then used as input for cluster analyses.

Locations were grouped in clusters using Ward's minimum variance method (30), using MultiVariate Statistical Package v3.13. This is a centroid-based clustering technique that identifies cluster centers (centroids) by minimizing the overall squared distances of the objects (in this case locations) to the centroids at each cluster level. This clustering technique identified spatially clearly defined location groupings (Fig. S2). The optimal number of clusters for defining floristic regions across the tropics was determined by calculating the cophenetic correlation coefficient at each cluster level, starting at the first split (K2) in the dendrogram. The cophenetic correlation coefficient calculates the correlation between the distance of the clusters as calculated by the clustering algorithm and the distance based on observed MNTD values between clusters. The higher the cophenetic correlation, the better the cluster result reflects the patterns present in the original distance matrix. We applied this method to each of our 20 datasets, calculated the average cophenetic correlation coefficient for each cluster level, and found a steep increase in cophenetic correlation up to K5, after which it slowly declined (Fig. S6). Therefore, we chose K5 as the optimum level for defining our main floristic regions across the tropics.

For each location, at cluster level K5, we determined the cluster in which it was classified for each of the 20 cluster analyses that we performed. The location was then assigned to the cluster in which it had the highest proportion of observations. A single proportion test (31), which calculates the probability of an observed (sample) proportion (in the range 0 to 1) against a hypothetical proportion, was then used to determine if the observed proportions were significantly higher than expected by random [Paleontological Statistics (PAST) v3.08; https://folk.uio.no/ohammer/past/]. For example, for K5, the expected random proportion of locations per cluster is 0.2. For a sample size of 20, a proportion has to be at least 0.38 to be significantly higher ($P < 0.05$) than the random expectation. The resulting classification success rates of locations for K5 are shown in Fig. S3 and Table S1. The final classification (K5) of the clusters was based on the majority consensus rule (Fig. 1).

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Correction

ECOLOGY

Correction for "Phylogenetic classification of the world's tropical forests," by J. W. Ferry Slik, Janet Franklin, Víctor Arroyo-Rodríguez, Richard Field, Salomon Aguilar, Nikolay Aguirre, Jorge Ahumada, Shin-Ichiro Aiba, Luciana F. Alves, Anitha K, Andres Avella, Francisco Mora, Gerardo A. Aymard C., Selene Báez, Patricia Balvanera, Meredith L. Bastian, Jean-François Bastin, Peter J. Bellingham, Eduardo van den Berg, Polyanna da Conceição Bispo, Pascal Boeckx, Katrin Boehning-Gaese, Frans Bongers, Brad Boyle, Fabian Brambach, Francis Q. Brearley, Sandra Brown, Shauna-Lee Chai, Robin L. Chazdon, Shengbin Chen, Phourin Chhang, George Chuyong, Corneille Ewango, Indiana M. Coronado, Jurgi Cristóbal-Azkarate, Heike Culmsee, Kipiro Damas, H. S. Dattaraja, Priya Davidar, Saara J. DeWalt, Hazimah Din, Donald R. Drake, Alvaro Duque, Giselda Durigan, Karl Eichhorn, Eduardo Schmidt Eler, Tsutomu Enoki, Andreas Ensslin, Adandé Belarmain Fandohan, Nina Farwig, Kenneth J. Feeley, Markus Fischer, Olle Forshed, Queila Souza Garcia, Satish Chandra Garkoti, Thomas W. Gillespie, Jean-Francois Gillet, Christelle Gonmadje, Iñigo Granzow-de la Cerda, Daniel M. Griffith, James Grogan, Khalid Rehman Hakeem, David J. Harris, Rhett D. Harrison, Andy Hector, Andreas Hemp, Jürgen Homeier, M. Shah Hussain, Guillermo Ibarra-Manríquez, I. Faridah Hanum, Nobuo Imai, Patrick A. Jansen, Carlos Alfredo Joly, Shijo Joseph, Kuswata Kartawinata, Elizabeth Kearsley, Daniel L. Kelly, Michael Kessler, Timothy J. Killeen, Robert M. Kooyman, Yves Laumonier, Susan G. Laurance, William F. Laurance, Michael J. Lawes, Susan G. Letcher, Jeremy Lindsell, Jon Lovett, Jose Lozada, Xinghui Lu, Anne Mette Lykke, Khairil Bin Mahmud, Ni Putu Diana Mahayani, Asyraf Mansor, Andrew R. Marshall, Emanuel H. Martin, Darley Calderado Leal Matos, Jorge A. Meave, Felipe P. L. Melo, Zhofre Huberto Aguirre Mendoza, Faizah Metali, Vincent P. Medjibe, Jean Paul Metzger, Thiago Metzker, D. Mohandass, Miguel A. Munguía-Rosas, Rodrigo Muñoz, Eddy Nurtjahy, Eddie Lenza de Oliveira, Onrizal, Pia Parolin, Marc Parren, N. Parthasarathy, Ekananda Paudel, Rolando Perez, Eduardo A. Pérez-García, Ulf Pommer, Lourens Poorter, Lan Qi, Maria Teresa F. Piedade, José Roberto Rodrigues Pinto, Axel Dalberg Poulsen, John R. Poulsen, Jennifer S. Powers, Rama Chandra Prasad, Jean-Philippe Puyravaud, Orlando Rangel, Jan Reitsma, Diogo S. B. Rocha, Samir Rolim, Francesco Rovero, Andes Rozak, Kalle Ruokolainen, Ervan Rutishauser, Gemma Rutten, Mohd. Nizam Mohd. Said, Felipe Z. Saiter, Philippe Saner, Braulio Santos, João Roberto dos Santos, Swapan Kumar Sarker, Christine B. Schmitt, Jochen Schoengart, Mark Schulze, Douglas Sheil, Plinio Sist, Alexandre F. Souza, Wilson Roberto Spironello, Tereza Sposito, Robert Steinmetz, Tariq Stevart, Marcio Seiji Suganuma, Rahayu Sukri, Aisha Sultana, Raman Sukumar, Terry Sunderland, Supriyadi, H. S. Suresh, Eizi Suzuki, Marcelo Tabarelli, Jianwei Tang, Ed V. J. Tanner, Natalia Targhetta, Ida Theilade, Duncan Thomas, Jonathan Timberlake, Márcio de Morisson Valeriano, Johan van Valkenburg, Tran Van Do, Hoang Van Sam, John H. Vandermeer, Hans Verbeeck, Ole Reidar Vetaas, Victor Adekunle, Simone A. Vieira, Campbell O. Webb, Edward L. Webb, Timothy Whitfeld, Serge Wich, John Williams, Susan Wiser, Florian Wittmann, Xiaobo Yang, C. Yves Adou Yao, Sandra L. Yap, Rakan A. Zahawi, Rahmad Zakaria, and Runguo Zang, which was first published February 5, 2018; 10.1073/pnas.1714977115 (*Proc Natl Acad Sci USA* 115:1837–1842).

The authors note that, due to a printer's error, an author name published incorrectly. The author name Lan Qi should instead appear as Lan Qie. The online version has been corrected.

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CORRECTION