# How does habitat filtering affect the detection of conspecific and phylogenetic density dependence?

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Conspecific negative density dependence (CNDD) has been recognized as a Abstract. key mechanism underlying species coexistence, especially in tropical forests. Recently, some studies have reported that seedling survival is also negatively correlated with the phylogenetic relatedness between neighbors and focal individuals, termed phylogenetic negative density dependence (PNDD). In contrast to CNDD or PNDD, shared habitat requirements between closely related individuals are thought to be a cause of observed positive effects of closely related neighbors, which may affect the strength and detectability of CNDD or PNDD. In order to investigate the relative importance of these mechanisms for tropical tree seedling survival, we used generalized linear mixed models to analyze how the survival of more than 10 000 seedlings of woody plant species related to neighborhood and habitat variables in a tropical rainforest in southwest China. By comparing models with and without habitat variables, we tested how habitat filtering affected the detection of CNDD and PNDD. The best-fitting model suggested that CNDD and habitat filtering played key roles in seedling survival, but that, contrary to our expectations, phylogenetic positive density dependence (PPDD) had a distinct and important effect. While habitat filtering affected the detection of CNDD by decreasing its apparent strength, it did not explain the positive effects of closely related neighbors. Our results demonstrate that a failure to control for habitat variables and phylogenetic relationships may obscure the importance of conspecific and heterospecific neighbor densities for seedling survival.

Key words: competition; habitat association; Janzen-Connell hypothesis; mixed models; phylogenetic relatedness; tropical forest.

#### INTRODUCTION

Tree populations are often thought to be regulated by negative density dependence (NDD), thereby making NDD an important mechanism underlying the maintenance of species diversity across multiple life stages (e.g., Wills et al. 1997, Harms et al. 2000, Peters 2003, Volkov et al. 2005, Comita et al. 2010, 2014, Swamy et al. 2011, Johnson et al. 2012). Intraspecific competition and Janzen-Connell effects (Janzen 1970, Connell 1971) via species-specific natural enemies (seed predators, pathogens, and herbivores) are two main drivers of NDD (Wright 2002). Many studies have tried to demonstrate NDD by examining the relationship between plant survival, recruitment, or growth and the densities of conspecific neighbors. Such studies, typically conducted using seedlings, have frequently found conspecific negative density dependence (CNDD) in the species studied (e.g., Webb and Peart 1999, Chen et al. 2010, Comita et al. 2010, Johnson et al. 2012, Lin et al. 2012).

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The effects of intra- and interspecific density on seedlings may be interchangeable if pathogens have wide host ranges where neighborhood density per se drives NDD and it is not necessary to invoke CNDD (Freckleton and Lewis 2006). However, tropical forest investigations that have partitioned their analyses into conspecific and heterospecific effects have often found significant differences in intra- and interspecific effects (e.g., Peters 2003, Comita and Hubbell 2009, Johnson et al. 2012, Lin et al. 2012). This has supported the widespread view that seedling performance is limited more by interactions with conspecific individuals than with heterospecific individuals. If generally valid, the greater strength of negative intraspecific effects relative to negative interspecific effects promotes stable species coexistence (Chesson 2000).

Interestingly, conspecific adult neighbor densities have been found to have a particularly strong negative influence on seedling survival (e.g., Comita and Hubbell 2009, Chen et al. 2010, Johnson et al. 2014). Seedling– seedling interactions, in contrast, are often relatively weak, presumably because the sizes and densities of seedlings in the understory of tropical forests are not typically great enough to generate such large impacts (Paine et al. 2008, Svenning et al. 2008). Further, positive correlations between the probability of seedling survival and heterospecific neighbor densities have been found (Comita and Hubbell 2009), supporting the so-called "species herd protection hypothesis" (Peters 2003). Thus, seedling survival is likely to be lower in an area of high conspecific adult neighbor density and higher in an area with many heterospecific adult neighbors.

Due to the enormous diversity in the tropics, heterospecific neighbors are more common than conspecific neighbors. A simple division of neighbors into conspecifics and heterospecifics may therefore hide the potentially large variation in the degree to which heterospecific species are similar to the focal species. Such thinking led Webb et al. (2006) to characterize heterospecific species in terms of their phylogenetic distance from the focal individual, thereby moving neighborhood analyses beyond a potentially overly simplistic conspecific/ heterospecific dichotomy.

The rationale for considering phylogenetic relatedness in studies of NDD rests on empirical evidence suggesting that there is often a phylogenetic signal in morphological and biochemical traits that dictate host-pest interactions (Mitter et al. 1991). In the most extensive syntheses to date, the probability of sharing a pest or pathogen between two host plants decays strongly with phylogenetic distance (Parker and Gilbert 2004, Novotny et al. 2006, Gilbert and Webb 2007, Gilbert et al. 2012). This pattern is expected to be more pronounced under broader taxonomic samples, and less pronounced under smaller taxonomic samples (e.g., a single genus). Phylogenetic negative density dependence, due to shared natural enemies between closely related species, may therefore be expected to emerge in a tropical forest containing many plant lineages (i.e., a broad taxonomic sample). In such cases, CNDD can be extended across evolutionary distance between two neighboring species (e.g., Webb et al. 2006, Metz et al. 2010, Liu et al. 2012, Paine et al. 2012, Lebrija-Trejos et al. 2014) therefore generating phylogenetic negative density dependence (PNDD).

Beyond biotic interactions, an important driver of local community composition is the abiotic environment (Metz et al. 2010). For example, variation in light availability (Comita et al. 2009, Queenborough et al. 2009, Rüger et al. 2009), soil water availability (Comita and Engelbrecht 2009, Lin et al. 2012), and soil nutrients (Bai et al. 2012) are all well-known drivers of species survival, coexistence, and diversity.

Findings that survival probability is positively correlated with conspecific density are often interpreted as being due to species' habitat preferences (e.g., Comita and Hubbell 2009, Comita et al. 2009, Lin et al. 2012). Indeed, many studies examine species' habitat preferences by analyzing the association between species occurrence and habitat variables (e.g., topography, light, soil nutrients, water availability, etc.) at the seedling stage (e.g., Webb and Peart 2000, Comita et al. 2007, John et al. 2007, Comita and Engelbrecht 2009, Metz 2012). However, we argue that such results do not necessarily indicate a lack of biotic interactions in general or NDD in particular. Specifically, biotic interactions are dictated by the abiotic context, and a shared habitat preference does not negate the possibility of NDD. Rather, it is likely that habitat preferences and NDD operate simultaneously to produce observed species composition and population dynamics (e.g., Comita et al. 2009, Chen et al. 2010, Bai et al. 2012, Piao et al. 2013). In order to elucidate such a scenario, nested models that consider density effects without and with the abiotic context are needed.

In this study, we used a population dynamics data set of 10 316 seedlings for 269 woody plant species for four contiguous one-year census intervals in the 20-ha Xishuangbanna tropical seasonal rainforest dynamics plot in southwest China. Using generalized linear mixed models, we explored the relative importance of CNDD, PNDD, and habitat filtering for seedling survival. Specifically, we built models of seedling survival dependent on the densities of conspecific and heterospecific neighbors and on the phylogenetic dissimilarities between heterospecific neighbors and focal seedlings. Each of these models was built without and with habitat variables to determine the degree to which habitat filtering affected the apparent prevalence of NDD. We specifically ask (1) Does scaling the effects of neighbors by their phylogenetic distances improve model fit? (2) What is the relative importance of CNDD, PNDD, and habitat filtering in our study system? (3) How does habitat filtering affect the detectability of CNDD and PNDD?

## Methods

## Study site

The study was conducted within the 20-ha Xishuangbanna Forest Dynamics Plot (XSBN), located in Mengla, Yunnan Province, Southwestern China (101°34' E, 21°36' N). The elevational range of the plot is from 709 m above sea level (asl) to 869 m asl (Lan et al. 2012; Appendix S1: Fig. S1). There is a rainy season from May to October and a dry season from November to April in the following year. Mean annual precipitation is approximately 1500 mm, of which 80% occurs from May to October (Cao et al. 2006).

The XSBN plot ( $400 \times 500$  m) was established in 2007 and censuses are carried out every five years. All woody stems with a diameter at breast height (DBH)  $\ge 1$  cm are tagged, identified, measured, and mapped (see detailed methods in Condit 1998). A detailed description of the climate, geology, and flora of XSBN can be found in Cao et al. (2008).

## Seedling quadrats

During March 2010, a total of 500 seedling quadrats  $(2 \times 2 \text{ m})$  were established in a regular pattern in the

center of each  $20 \times 20$  m subplot in the 20-ha XSBN plot. Where obstacles such as streams, large trees, rocks or fallen woods prevented the establishment of seedling quadrats in these locations, they were placed instead in nearby  $5 \times 5$  m subplots. In each of the 500 seedling quadrats, all woody (tree, shrub, and liana) seedlings with DBH < 1 cm and height  $\ge$  20 cm were tagged, identified to species, and measured for height. In this study, we used seedlings with height  $\geq 20$  cm as focal seedlings because seedlings with this height can be assumed to be established in our study system, and therefore more likely to be dependent upon relevant biotic and abiotic interactions rather than effects of chance events that drive mortality in younger seedlings. Seedling quadrats were subsequently censused in the late dry season (April and May) 2010, 2011, 2012, 2013, and 2014. In each census, the states (alive or dead) of all the woody seedlings alive at the previous census were recorded and all new recruits to the 20-cm height threshold were identified and tagged.

## Neighborhood variables

At the first (2010) census, we defined total seedling neighbor density of each seedling quadrat as the number of seedlings within the quadrat. Conspecific and heterospecific seedling neighbor densities were defined in the same way. At subsequent censuses, we recalculated seedling neighbor densities by excluding dead seedlings and adding newly recruited seedlings. Tree, shrub, and liana seedlings were monitored at the censuses, and all were included in the calculation of heterospecific seedling neighbor densities, although lianas were not included as focal seedlings in our models. Seedlings that were impossible to classify by species (121 in the 2010 census) were included in heterospecific neighbor counts, but not as focal seedlings.

We calculated the total adult neighbor density (TA) as the summed basal area (BA) of nearby adults weighted by their distances to the focal seedling (Canham et al. 2004)

$$\Gamma \mathbf{A} = \sum_{i}^{N} \frac{\mathbf{B} \mathbf{A}_{i}}{\mathrm{Distance}_{i}}$$

where N is the number of adult neighbors. Conspecific and heterospecific adult neighbor densities were calculated in the same way. Models with densities calculated over a distance of 20 m had stronger support than those with densities calculated over distances of 10 m or 30 m (Appendix S1: Table S1). In the following analyses, we therefore used total, conspecific and heterospecific adult neighbor densities calculated over 20 m. As a result, data from 86 of the 500 seedling quadrats were excluded from the following analyses because these quadrats were within 20 m of the edge of the XSBN plot, and therefore had incomplete adult neighbor density values.

## Construction of phylogenetic tree and indices of phylogenetic dissimilarity

We have previously produced a molecular phylogeny for 428 species in the 20-ha XSBN plot (Yang et al. 2014). A total of 121 species identified in the 20-ha plot and/or the seedling quadrats were added to this phylogeny using the APE package (Paradis 2006) in R software (v. 3.0.2; R Development Core Team 2014). These species were added at the crown node of the most closely related taxonomic level (genus, family, or order) in the original molecular phylogeny. For example, any species missing from the original phylogeny that had a congener in the original phylogeny was manually added to the phylogeny at the node for that genus. If there was no congener in the original phylogeny, then the species was added to the node for its family in the original phylogeny. A total of 18 species could not be added to the phylogeny because they were from orders not in the original phylogeny. These species only constituted < 1% of all individuals in the seedling quadrats and therefore had little influence on our results.

Four phylogenetic diversity indices quantifying phylogenetic dissimilarity between focal seedlings and their heterospecific neighbors were used in our analyses: total phylogenetic diversity (TOTPd), average phylogenetic diversity (AVEPd), relative average phylogenetic diversity (APd'), and relative nearest taxon phylogenetic diversity (NTPd'). The TOTPd and AVEPd are, respectively, the sum and average of the phylogenetic distances between a focal seedling and its heterospecific neighbors. The APd' and NTPd' (proposed by Webb et al. 2006) quantify the deviation of observed average phylogenetic distance between a focal seedling and its heterospecific neighbors from that expected under a null model and the equivalent deviation of observed phylogenetic distance between a focal seedling and its most closely related heterospecific neighbor, respectively. The null model used in this study shuffled the names of species on the phylogeny 999 times to produce a null distribution of neighborhood phylogenetic diversities. Positive APd' and NTPd' indicate that neighbors are less related to the focal seedling than expected under the null model and negative APd' and NTPd' indicate that the neighbors are more related than expected. We recalculated the four phylogenetic diversity indices at each census after 2010 to exclude dead seedlings and add newly recruited seedlings. The indices were calculated separately for heterospecific seedling neighbors and heterospecific adult neighbors (with the adult neighborhood again defined as having a radius of 20 m).

#### Habitat variables

Habitat variables for each of the 414 target seedling quadrats were characterized using measurements of canopy openness, soil properties, and topography.

Canopy openness.—For each seedling quadrat, hemispherical photographs were used to obtain a measure of canopy openness (Comita et al. 2009, Queenborough et al. 2009), which indicated the light condition in the understory. Hemispherical photographs was taken 1.3 m aboveground at the center of each quadrat, using a Nikon Coolpix 4500 camera equipped with a Nikon FC-E8 Fisheye Converter lens (Tokyo, Japan) in January 2014. The camera was arranged horizontally with the aid of a spirit level and pointed to the geographic south. Black and white .jpg images of  $2272 \times 1704$  pixels were produced in accordance with the methods of Queenborough et al. (2009). The high contrast setting increased distinction between sky and foliage. Three to five replicate photos were taken using a fixed aperture of f/7.5 and shutter speeds between 1/1000 and 1/30 s. Photographs were taken in uniformly overcast weather, during either early dawn or late dusk. The photograph showing the highest contrast between sky and foliage for each quadrat was selected. Gap Light Analyser software (GLA, version 2.0) (Frazer et al. 1999) was used to convert photographs to a single canopy openness measure following the protocol of Beaudet and Messier (2002).

Soil properties.—Soils were sampled following the protocol of John et al. (2007). The 20-ha plot was divided into regular grid squares of  $30 \times 30$  m, and two soil samples were taken at depths of 10 cm (without litter and humus) and random distance combinations of 2 and 5 m, 2 and 15 m, or 5 and 15 m in a random direction from the grid point. A total of 765 soil samples were obtained. Soil pH, organic matter content (C), total nitrogen (TN), total phosphorus (TP), total potassium (TK), available nitrogen (AN), available phosphorus (AP), available potassium (AK) and soil bulk density within each sample were measured (for details see Hu et al. 2012). We used the residuals from polynomial trend-surface regressions for these soil variables to compute empirical variograms, to which we fitted variogram models and used ordinary kriging to obtain spatial predictions of soil variables for each seedling quadrat. This kriging interpolation was implemented using the gstat package (Pebesma 2004) in R software (v. 3.0.2; R Development Core Team 2014). The volumetric soil water content (%) was measured in the late dry season of 2013, using the mean values of three replicates taken randomly around the center of each seedling quadrat using a TDR probe (MPM-160B, ICT International Pty Ltd., Armidale, New South Wales, Australia) at a depth of 5 cm (Song et al. 2013).

*Topography.*—The topographic variables used were elevation, convexity, slope, and aspect for each seedling quadrat. As above, the full plot was divided into 500  $20 \times 20$  m subplots with seedling quadrats located at the centers of these subplots. The elevation of each seedling quadrat was taken as the mean of values at each of the four corners of the  $20 \times 20$  m subplots. The convexity of each seedling quadrat was calculated by subtracting the mean of the four corner elevations of the surround-

ing  $20 \times 20$  m subplots from the elevation at its center. The slope was calculated as the mean angular deviation from horizontal of each of the four triangular planes of the  $20 \times 20$  m subplot formed by connecting three of its corners. Aspect was calculated as

Aspect=180 - arctan 
$$\left(\frac{fy}{fx}\right) \times \left(\frac{180}{\pi}\right) + 90 \times \left(\frac{fy}{|fx|}\right)$$

where fx was the elevation difference from east to west in the 20 × 20 m subplot while fy was that from north to south.

To reduce the colinearity of habitat variables in our models, we used a principal components analysis (PCA) in the Vegan package (Dixon 2003) of the R software (v. 3.0.2; R Development Core Team 2014) on the 14 habitat variables (soil pH, C, TN, TP, TK, AN, AP, AK, soil bulk density, soil moisture, elevation, slope, aspect, and convexity). Canopy openness was not included in the PCA and was inserted into models directly. The first two principal components, accounting for 56.96% variation of these 14 habitat variables, were used in the later analysis. The first principal component was associated with high elevation and convexity, and low TN, TP, TK, AN, AP, AK, C, pH, and soil moisture. The second principal component was associated with high TN, AN, C, elevation, and convexity, and low AK, pH, soil bulk density, and soil moisture (Appendix S1: Table S2).

#### Statistical analysis

We conducted analyses separately for all living seedlings in each census interval (2010–2011, 2011–2012, 2012–2013, and 2013–2014). Living seedlings at any one census included survivors from the previous census and new recruits from the most recent census interval.

Generalized linear mixed models (GLMMs) were constructed using the lme4 package (Bates et al. 2014) in R software (v. 3.0.2; R Development Core Team 2014) to model the probability of seedling survival as a function of explanatory variables, with binomial errors (Bolker et al. 2009). Due to the unknown age of seedlings in this study, we included seedling height as a covariate in our models to account for the fact that larger seedlings have higher survival, and therefore to approximately exclude effects of age on survival. The focal seedling height was log-transformed, and all continuous explanatory variables were standardized by subtracting the mean value of the variable (across all individuals in the analysis) and dividing by 1 standard deviation before analyses. This allowed us to directly compare the relative importance of these explanatory variables (Gelman and Hill 2006). The means and ranges of all continuous explanatory variables used in the analysis are listed in Table S3.

It is possible that spatial autocorrelation exists in seedling survival due to unexplored habitat and other factors. However, previous studies have found that spatial autocorrelation in tropical seedling survival is negligible at distances > 5 m (Queenborough et al. 2007), and seedling quadrats in this study were spaced 20 m apart. Therefore, we added random seedling quadrat effects to our models to exclude any effect of spatial autocorrelation within quadrats on our results. Previous studies suggest that this should be sufficient to account for autocorrelation (Comita et al. 2009, Chen et al. 2010). Furthermore, we included species identity as a random effect, because seedlings of different species were expected to respond differently to local neighborhood variables (Lin et al. 2012).

In the simplest, density-independent model, seedling survival depended only on the initial heights of focal seedlings (Table 1, Appendix S1). This model was grounded in evidence that the probability of seedling survival increases with increasing seedling stature (Paine et al. 2012). Given the importance of habitat filtering on seedling survival, we then built a habitat-only model, including habitat variables in addition to initial seedling height (Table 1, Appendix S1). To assess the role of neighbor densities on seedling survival, we then built models in which conspecific and heterospecific neighbor effects were included together and separately. In these densitydependent models, seedling survival depended on initial seedling height, the total seedling neighbor density or conspecific and heterospecific seedling neighbor densities, and the total adult neighbor density or conspecific and

heterospecific adult neighbor densities (Table 1, Appendix S1). To assess the importance of evolutionary relationships in the survival model, we finally constructed phylogenetic density-dependent models in which heterospecific neighbor densities were replaced by the phylogenetic diversity indices described above (Table 1, Appendix S1).

Akaike's information criterion (AIC) was used to compare models, with  $\triangle$ AIC calculated by subtracting the overall minimum value of AIC from each of the models' AIC values. We selected the most parsimonious models among those with  $\triangle$ AIC less than 2, which are thought to be the equally best-fitting models (Burnham and Anderson 2002). We identified the best-fitting densitydependent model (Appendix S1: Table S4) and the bestfitting phylogenetic density-dependent model (Appendix S1: Table S5).

To explore the influence of habitat filtering on the detection of CNDD and PNDD, we compared the best-fitting density-dependent model to the equivalent model in which habitat variables were included (density + habitat model; Table 1, Appendix S1). We also compared the best-fitting phylogenetic density-dependent model with its equivalent phylogenetic + habitat model (Table 1, Appendix S1). We also included interactions between habitat variables and neighborhood variables and used AIC scores to identify the best interaction terms combination in both the density

TABLE 1. Akaikae information criterion (AIC) values for the six classes of model for each of the four one-year census intervals.

|  |           | AIC       |           |           |
|--|-----------|-----------|-----------|-----------|
| Candidate model  | 2010-2011 | 2011-2012 | 2012-2013 | 2013-2014 |
| Density-independent model  |           |           |           |           |
| Н  | 3463.1    | 3213.7    | 4227.3    | 4997.7    |
| Habitat-only model   |           |           |           |           |
| H + light + PCA1 + PCA2  | 3448.3    | 3203.9    | 4225.2    | 4998.8    |
| Density-dependent model <sup>†</sup>   |           |           |           |           |
| $H + \cos + hets + CA + HA$  | 3462.6    | 3214.8    | 4230.2    | 5003.1    |
| Density + habitat model <sup>‡</sup>   |           |           |           |           |
| H + cons + hets + CA + HA + light + PCA1 + PCA2 + cons<br>× PCA1 + cons × PCA2 + CA × PCA1 + CA × PCA2   | 3442.0    | 3201.9    | 4234.0    | 4998.2    |
| Phylogenetic density-dependent model§  |           |           |           |           |
| $H + cons + s_NTPd' + CA + a_NTPd'$  | 3466.0    | 3211.4    | 4230.1    | 5000.4    |
| Phylogenetic +habitat model  |           |           |           |           |
| H + cons + s_NTPd' + CA + a_NTPd' + light + PCA1<br>+ PCA2 + cons × PCA1 + cons × PCA2 + CA × PCA1<br>+ CA × PCA2 + s_NTPd' × PCA1 + s_NTPd' × PCA2<br>+ a_NTPd' × PCA1 + a_NTPd' × PCA2 | 3449.1    | 3196.9    | 4234.7    | 4996.6    |

*Notes; H* is the height of focal seedlings. Neighborhood variables included the density of conspecific seedling neighbors (cons), the density of heterospecific seedling neighbors (hets), sum of conspecific adults' basal areas weighted by the distance between the focal seedling and the adult neighbors at distances up to 20 m (CA), sum of heterospecific adults' basal areas weighted by the distance between the focal seedling and the adult neighbors at distances up to 20 m (CA), sum of heterospecific adults' basal areas weighted by the distance between the focal seedling and the adult neighbors at distances up to 20 m (HA), and two phylogenetic diversity indices: relative nearest taxon phylogenetic diversity between heterospecific adult neighbors and focal seedlings (s\_NTPd') and relative nearest taxon phylogenetic diversity between heterospecific adult neighbors and focal seedlings (a\_NTPd'). Habitat variables included ed percentage of canopy openness (light) and the first two principal components (PCA1 and PCA2) of soil properties and topography.  $\triangle AIC$  is calculated by subtracting the minimum AIC value from each of AIC values of the models. We selected the most parsimonious models among the models with  $\triangle AIC \leq 2$  (AIC in boldface type) (Appendix S1: Table S2).

†The model comparison for density-dependent models is shown in Appendix S1: Table S4.

<sup>‡</sup>The model comparison for density + habitat models with different interaction term combinations is shown in Appendix S1: Table S6. <sup>§</sup>The model comparison for phylogenetic density-dependent models is shown in Appendix S1: Table S5.

The model comparison for phylogenetic + habitat models with different interaction combinations is shown in Appendix S1: Table S7.

+ habitat model (Appendix S1: Table S6) and the phylogenetic + habitat model (Appendix S1: Table S7). In total, we ran six classes of model: (1) density independent, (2) habitat-only, (3) density dependent, (4) density + habitat, (5) phylogenetic density dependent, and (6) phylogenetic + habitat. Equations defining these models can be found in Appendix S1.

We analyzed the above six model classes for each of the four one-year census intervals (Table 1). To explore the effects of habitat filtering on the detection of CNDD and PNDD, we compared the estimated coefficients of neighborhood variables in four of our models: the bestfitting density-dependent model (Model I in Table 2), the density + habitat model with the same neighborhood variables as in the best-fitting density-dependent model (Model II in Table 2), the best-fitting phylogenetic density-dependent model (Model III in Table 2) and the phylogenetic + habitat model with the same neighborhood variables as in the best-fitting phylogenetic densitydependent model (Model IV in Table 2). We labeled Models I and II as density models, and Models III and IV as phylogenetic models. The estimated coefficients represent the relative strength of the variables' effects, and coefficients > 0 indicate positive effects on seedling survival while coefficients < 0 indicate negative effects. Specifically, a positive estimated coefficient for phylogenetic diversity indices indicates a negative relationship between the phylogenetic similarity of heterospecific neighbors and seedling survival (and vice versa). We calculated the variance for each of the models' fixed effects, random effects and for the residuals in each of the above four models (Appendix S1: Table S8).

To determine whether and how habitat filtering affects the detectability of CNDD and PNDD among species, we added species-specific random slopes for each neighborhood variable in the above four models. Differences between these slopes within a model, and across models with and without habitat variables, were used to capture species-specific responses to neighbor densities and the extent to which habitat filtering might obscure these responses. We used likelihood ratio tests to assess the significance of added species-specific random slopes (Appendix S1: Table S9). If P values were less than 0.05, we inferred that the coefficients of neighborhood variables did vary across species. We also used two-sample Kolmogorov-Smirnov tests to compare the distributions of the speciesspecific coefficients of neighborhood variables between the varying-slope models with and without habitat variables.

## RESULTS

# CNDD, PNDD, and habitat filtering for seedling survival in the best-fitting model

In the 414 target seedling quadrats, there were 8324, 7868, 7680, and 8156 living seedlings of 238, 237, 240, and 262 focal woody plant species in the 2010, 2011, 2012, and 2013 censuses, respectively.

Of the six survival models we built, the phylogenetic + habitat model had the best-fit for the 2011–2012 and 2013–2014 census intervals, while the density + habitat model and habitat-only model had the best-fit for 2010-2011 and 2012-2013 respectively (Table 1). Across all four census intervals, seedling survival was mainly influenced by fixed effects for habitat variables, followed by the density of conspecific seedling and adult neighbors and NTPd' of heterospecific seedling and adult neighbors (Fig. 1). The effects of the first principal component of topographic and edaphic variables were significantly positively correlated with seedling survival for three census intervals (2010-2011, 2011-2012, and 2013-2014), whereas canopy openness was significantly negatively related for the 2012-2013 census interval. Conspecific adult neighbors had significantly negative effects on survival for the first three census intervals (Table 2). Across all four census intervals, seedling and adult NTPd' generally had insignificant negative effects.

## How does habitat filtering affect the detection of CNDD?

Across all four census intervals, the coefficients of conspecific seedling and adult neighbor densities were smaller in Models I and III (without habitat variables) than in Models II and IV (with habitat variables) (Table 2). There were also significant positive interactions between habitat variables and conspecific seedling and adult neighbor densities in Models II and IV (Table 2). Furthermore, we found that adding habitat variables increased the variance explained by the densities of conspecific seedling and adult neighbors, while variances explained by random effects remained almost constant (Appendix S1: Table S8). Together, these results indicate that the true extent of CNDD was obscured when not accounting for habitat variables.

Because adult CNDD was significant in the best-fit models for 2010-2011 and 2011-2012 (Table 2), we added species-specific random slopes for conspecific adult neighbor density to these models. The distribution of these species-specific coefficients changed significantly between models with and without habitat variables (Models II and IV vs. I and III; two-sample Kolmogorov-Smirnov test, P < 0.05, Fig. 2). When taking into account habitat variables in Model II, we found that 97.90% and 97.47% of the focal species in the 2010-2011 and 2011-2012 census intervals suffered stronger negative effects of conspecific adult neighbor densities than those in equivalent nonhabitat-informed models (Model I). Similarly, 98.32% and 92.83% of the focal species in Model IV (with habitat variables) suffered stronger negative effects than those in Model III (without habitat variables).

## How does habitat filtering affect the detection of PNDD?

Across all four census intervals, the coefficients of seedling NTPd' and adult NTPd' were generally negative in both Models III (without habitat variables) and IV (with habitat variables; Table 2), indicating that seedlings

|   |                             | 2010                            | 2011                            |                                  |                                   | 2011-                            | -2012                           |                                  |                                    | 2012-                            | -2013                           |                                 |                                      | 2013-                            | -2014                            |                                  |
|---|-----------------------------|---------------------------------|---------------------------------|----------------------------------|-----------------------------------|----------------------------------|---------------------------------|----------------------------------|------------------------------------|----------------------------------|---------------------------------|---------------------------------|--------------------------------------|----------------------------------|----------------------------------|----------------------------------|
| Explanatory                             | _                           | Ш                               | III                             | IV                               | -                                 | П                                | III                             | N                                | I                                  | П                                | H                               | IV                              | I                                    | П                                | H                                | IV                               |
| Intercept 3.6<br>Height 0.6<br>cons 0.6 | 686***<br>698***<br>095NS   | 3.640***<br>0.678***<br>0.006NS | 3.663***<br>0.696***<br>0.042NS | 3.601***<br>0.678***<br>-0.019NS | 3.616***<br>0.783***<br>0.076NS - | 3.581***<br>0.779***<br>-0.038NS | 3.584***<br>0.783***<br>0.075NS | 3.514***<br>0.748***<br>-0.022NS | 2.849***<br>0.323***<br>0.071NS    | 2.830***<br>0.318***<br>0.042NS  | 2.827***<br>0.322***<br>0.052NS | 2.811***<br>0.314***<br>0.034NS | 2.691***<br>-0.037NS -<br>-0.010NS - | 2.633***<br>-0.037NS<br>-0.115NS | 2.644***<br>-0.037NS<br>-0.029NS | 2.599***<br>-0.038NS<br>-0.125NS |
| nets 0.<br>CA -0.<br>HA 0.0             | ) SN9CL<br>110* –(<br>002NS | 0.088NS<br>0.169** -<br>0.035NS | -0.116*                         | -0.187**                         | 0.002NS -<br>-0.127* -<br>0.003NS | -0.020NS<br>-0.166**<br>0.020NS  | -0.125*                         | -0.185**                         | - 0.026NS<br>- 0.091*<br>- 0.026NS | -0.113NS<br>-0.113NS<br>-0.010NS | +060.0-                         | -0.117*                         | 0.04/NS<br>-0.055NS<br>-0.061NS      | 0.026NS<br>-0.095NS<br>-0.045NS  | -0.052NS                         | -0.093NS                         |
| s_NTPd'<br>a_NTPd'                      |                             |                                 | -0.029NS<br>-0.034NS            | -0.025NS<br>0.001NS              |                                   |                                  | -0.100NS                        | -0.137*<br>-0.028NS              |                                    |                                  | -0.016NS<br>-0.071NS            | -0.055NS<br>-0.059NS            |                                      |                                  | -0.016NS<br>-0.157NS             | -0.024NS<br>-0.140NS             |
| Light                                   | Ť                           | 0.084NS                         |                                 | -0.076NS                         | ł                                 | -0.025NS                         |                                 | -0.020NS                         | ·                                  | -0.177**                         |                                 | $-0.170^{*}$                    | ·                                    | -0.059NS                         |                                  | -0.065NS                         |
| PCA1<br>PCA2                            |                             | 0.328***<br>0.261**             |                                 | $0.314^{***}$<br>0 245**         |                                   | 0.299***<br>0.202**              |                                 | 0.272***<br>0.143NS              |                                    | 0.117NS<br>0.103NS               |                                 | 0.106NS<br>0.106NS              |                                      | 0.197**<br>0.025NS               |                                  | 0.201**<br>0.038NS               |
| cons ×<br>PCA1                          |                             | 0.103NS                         |                                 | 0.084NS                          |                                   | 0.056NS                          |                                 | 0.053NS                          |                                    | 0.069NS                          |                                 | 0.056NS                         |                                      | 0.118NS                          |                                  | 0.121NS                          |
| cons ×<br>PCA2                          |                             | 0.029NS                         |                                 | 0.011NS                          |                                   | 0.167*                           |                                 | 0.138NS                          | ·                                  | -0.001NS                         |                                 | -0.015NS                        |                                      | 0.004NS                          |                                  | 0.011NS                          |
| CA ×<br>PCA1                            |                             | $0.150^{*}$                     |                                 | 0.133NS                          |                                   | 0.072NS                          |                                 | 0.088NS                          |                                    | 0.041NS                          |                                 | 0.035NS                         |                                      | $0.164^{**}$                     |                                  | $0.165^{**}$                     |
| CA ×<br>PCA2                            |                             | 0.224**                         |                                 | 0.212**                          |                                   | 0.052NS                          |                                 | 0.055NS                          |                                    | 0.021NS                          |                                 | 0.022NS                         |                                      | SN680.0                          |                                  | 0.083NS                          |
| s_NTPd' ×<br>PCA1                       |                             |                                 |                                 | 0.059NS                          |                                   |                                  |                                 | 0.032NS                          |                                    |                                  |                                 | 0.020NS                         |                                      |                                  |                                  | -0.082NS                         |
| s_NTPd' ×<br>PCA2                       |                             |                                 |                                 | 0.016NS                          |                                   |                                  |                                 | 0.128*                           |                                    |                                  |                                 | $0.115^{*}$                     |                                      |                                  |                                  | 0.063NS                          |
| a_NTPd' ×<br>PCA1                       |                             |                                 |                                 | 0.017NS                          |                                   |                                  |                                 | 0.073NS                          |                                    |                                  |                                 | 0.044NS                         |                                      |                                  |                                  | 0.011NS                          |
| a_NTPd'×<br>PCA2                        |                             |                                 |                                 | 0.051NS                          |                                   |                                  |                                 | 0.093NS                          |                                    |                                  |                                 | -0.041NS                        |                                      |                                  |                                  | -0.086NS                         |

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FIG. 1. Estimated effects (mean  $\pm$  2SE) of neighborhood variables and habitat variables on seedling survival for each of the four one-year census intervals in phylogenetic + habitat model (model IV in Table 2). Solid circles indicate significant effects (P < 0.05). The interactions of neighborhood variables and habitat variables were not shown here and can be found in Table 2. See Table 1 for variable abbreviations. Dash-dot lines mark 0 on the *x*-axis scale.



FIG. 2. A comparison of the frequency distribution of species-specific coefficients of conspecific adult neighbor density between Model I (density model without habitat variables) and Model II (density model with habitat variables), and between Model III (phylogenetic model without habitat variables) and model IV (phylogenetic model with habitat variables) for 2010–2011 and 2011–2012 census intervals. Bars to the left of the dashed zero line indicate species whose survival is reduced by increasing neighborhood variables.

survived significantly better when growing among closely related heterospecific neighbors. In contrast to conspecific neighbor densities, adding habitat variables into the survival models did not substantially affect the coefficients of the phylogenetic diversity indices, and the interactions between habitat variables and s\_NTPd' and a\_NTPd' were insignificant (Table 2). The inclusion of species-specific random slopes for seedling NTPd' and adult NTPd' did not significantly increase the variation explained (Appendix S1: Table S9). Thus, we did not conduct further analyses into how habitat filtering affected the variation of PNDD among species.

#### DISCUSSION

Conspecific negative density dependence (CNDD), phylogenetic negative density dependence (PNDD), and habitat filtering are often cited as prominent mechanisms maintaining the composition and diversity of communities. Some studies have discussed a potentially confounding influence of habitat filtering when attempting to quantify negative density dependence (Comita et al. 2009, Chen et al. 2010, Bai et al. 2012, Piao et al. 2013), but this has not previously been well documented. Our results show that CNDD and habitat filtering simultaneously influence seedling survival. Taking habitat variables into account elucidated more clearly the negative impacts of conspecific neighbors (seedlings + adults) on seedling survival, and made the speciesspecific negative effects of conspecific neighbor densities generally stronger. Our study system showed the opposite effect with respect to PNDD. In the following, we discuss these results in more detail.

## Local neighborhood and habitat effects

Seedling-seedling and seedling-adult interactions may be stronger in tropical forests than in subtropical forests (e.g., Chen et al. 2010) or temperate forests (e.g., Bai et al. 2012). We found these interactions, at the scales we considered, were a significant driver of seedling survival. These results are in line with evidence from other tropical forests (e.g., Queenborough et al. 2007, Comita et al. 2009, 2010, Metz et al. 2010, Kobe and Vriesendorp 2011, Johnson et al. 2012, Lebrija-Trejos et al. 2014). The negative effects of conspecific neighbors on seedling survival are consistent with intraspecific competition and the Janzen-Connell hypothesis (Janzen 1970, Connell 1971). Our results show that seedling survival was significantly influenced by densities of conspecific seedling and adult neighbors, which may be involved in intraspecific competition for shared resources and/or as a source for specialized natural enemies (herbivore and pathogen; e.g., Augspurger 1984, Packer and Clay 2000, 2003, Bell et al. 2006, Freckleton and Lewis 2006, McCarthy-Neumann and Kobe 2008). Another possible explanation for the negative impact of conspecific adult neighbors is that their presence implies that there may be many more conspecific seedling neighbors over the wider area (beyond our seedling quadrats), making competition and mortality due to pests and pathogens even greater than we expect from measured seedling densities.

Recently, several studies focusing on NDD for seedling survival have scaled the effects of heterospecific neighbors by phylogenetic relatedness. For example, Liu et al. (2012) found a phylogenetic Janzen-Connell effect, which might be caused by associated host-specific fungal pathogens in a subtropical forest. Metz et al. (2010) found that seedling survival increased where nearby adult neighbors were more distantly related to focal seedlings. The critical factors affecting a pathogen's infection of a host plant are morphological and biochemical, which are often phylogenetically conserved (Mitter et al. 1991). Further, empirical evidence has shown that closely related species are more likely to share the same or similar pests and pathogens (e.g., Novotny et al. 2006, Gilbert and Webb 2007, Gilbert et al. 2012, Liu et al. 2012), and to have several similar key functional traits (Yang et al. 2014). Thus, the effects of neighbors on a focal plant should depend upon phylogenetic similarities, and should be less negative for less related plants. However, we found a negative effect of phylogenetic diversity, indicating that increased

phylogenetic similarities between heterospecific neighbors and focal seedlings increased seedling survival. Our results therefore do not support PNDD. While these findings are in contrast to those of the studies cited above, they are consistent with several other studies that have shown that plants perform better when heterospecific neighbors are relatively closely related (summarized in Lebrija-Trejos et al. 2014). Our results also suggest that this phylogenetic positive density dependence (PPDD) is a more important determinant of seedling survival than PNDD (see below).

The edaphic and topographic variables in our study had important effects on seedling survival. Specifically, the positive effect of the first principal component of edaphic and topographic variables on seedling survival demonstrated that the availability of belowground resources is also an important driver of tree seedling survival (Comita et al. 2009, Bai et al. 2012, Piao et al. 2013). Many works have also shown that light availability has a strong effect on the performance of shade-tolerant seedlings in tropical forests (e.g., Paz and MartInez-Ramos 2003, Comita et al. 2009, Queenborough et al. 2009). However, light availability had a slight negative effect on seedling survival in our study, even though the range of canopy openness we found was sufficient to produce positive effects (with approximately 90% of seedling quadrats within a range of canopy openness between 0.29% and 3%). This unexpected relationship may indicate a widespread problem with the use of canopy photographs in studies of this kind (e.g., Comita et al. 2009, Lin et al. 2014).

## Habitat filtering and CNDD

The increase in survival driven by favorable habitat may offset the thinning of conspecific trees due to CNDD (Wright 2002). A positive relationship with conspecific densities would therefore be found when hostspecific natural enemies or intraspecific competition do not offset the advantages of occurring in a preferred habitat (at least until the population size becomes too large). A few studies have shown such an interaction between habitat variables and negative density dependence. For example, Piao et al. (2013) suggested that a failure to take into account the confounding effect of habitat heterogeneity may lead to mischaracterization of the role of density dependence in shaping plant communities. Zhu et al. (2010) found that factoring out habitat heterogeneity made most tree species show negative density dependence in a subtropical forest, but did not explore in detail exactly how habitat variables affected density dependence.

Our work clearly shows that taking habitat variables into consideration made the effects of conspecific neighbors appear more negative in both the density models and the phylogenetic models (Table 2). The significant positive interactions between habitat variables and conspecific seedling and adult neighbor densities (Table 2) implied changes in CNDD across different habitat conditions. This is why the variance explained by the densities of conspecific seedling and adult neighbors increased in models with habitat variables (Appendix S1: Table S8).

The impact of habitat filtering on the detection of CNDD can also be seen in the prevalence of specieshabitat associations at both seedling and adult stages in the XSBN plot (Appendix S1: Table S10). Of the species with more than 20 surveyed seedlings, 41.77% and 60.76% showed significant habitat preferences at the seedling stage and the adult stage, respectively. Our results therefore suggest that conspecific negative density dependence is evident at lower densities in marginal habitats and only at higher densities in optimal habitats. Further, the inclusion of habitat variables led to an increase in apparent strength of species-specific negative effects of conspecific neighbors, especially conspecific adult neighbors. In sum, CNDD and habitat filtering both had vital influences on seedling dynamics and the observed effects of conspecific neighbors were the result of an interaction between them.

## Lack of evidence for PNDD

Though more and more ecologists have concluded that phylogenetic density dependence is an important mechanism for seedling dynamics and coexistence (e.g., Webb et al. 2006, Metz et al. 2010, Zhu et al. 2015), the influence of habitat filtering on the detection of phylogenetic density dependence had not been taken into account. As with conspecifics, the impact of natural enemies and the stronger competition for similar resources among closely related neighboring plants should lead to a negative effect of phylogenetic similarity on seedling survival. An apparently positive relationship between phylogenetic similarity and seedling survival might be caused by habitat filtering, because closely related plants may often have similar habitat requirements (Vamosi et al. 2009, Baldeck et al. 2013). We expected that habitat filtering could therefore affect the detection of the negative effect of phylogenetic similarity on seedling survival in the same way that it affected CNDD detectability. However, this expectation was not met in this study. While we did find that the inclusion of phylogenetic relatedness of heterospecific neighbors improved model accuracy, we found no evidence of PNDD. Furthermore, differences in the effects of phylogenetic relatedness between survival models without and with habitat variables were relatively slight. Instead, we found evidence of phylogenetic positive density dependence (PPDD). There appears to be an emerging consensus about the existence of this effect, perhaps due to the shared habitat preferences between closely related individuals (Lebrija-Trejos et al. 2014). However, our results showed that seedling survival was greater among closely related heterospecific neighbors even when habitat variation was controlled (Model IV in Table 2). While it is possible that unobserved habitat factors had

a confounding effect on this analysis, it is not clear what these factors might be, and it seems unlikely that they could be strong enough to reverse the apparent direction of relationships between seedling survival and neighbor relatedness. We therefore suggest that PPDD, as detected here, may be a real and independent effect of some as-yet unrecognized mechanism.

#### CONCLUSIONS

To the best of our knowledge, our study is the first to explore the joint effects of conspecific negative density dependence (CNDD), phylogenetic negative density dependence (PNDD), and habitat filtering and their relative importance for tropical tree seedling survival. Our results demonstrate that replacing heterospecific neighbor densities with phylogenetic diversity indices improved survival models, which is in line with an increasing awareness of the importance of evolutionary relationships in neighborhood dynamics. However, the effect of phylogenetic diversity indices in our study system was opposite to that expected under PNDD, even when we controlled for the effects of habitat. CNDD and habitat filtering played important roles in seedling survival simultaneously. The observed effect of conspecific neighbor densities is primarily a result of an interaction between habitat filtering and conspecific neighbor densities, making CNDD detectable at lower densities in marginal habitats than in preferred habitats. Therefore, adding habitat variables into survival models strengthens the measured negative effects of conspecific neighbors on seedling survival. We conclude that future studies of neighborhood density dependence must take habitat filtering and phylogenetic relationships into account in order to properly assess the effects of conspecific and heterospecific neighbors, and the occurrence and cause of phylogenetic positive density dependence.

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