

Methods

Study site

This study was done in a neotropical lowland rainforest on the Osa Peninsula at the Greg Gund Conservation Center (approx. 8.3778176, -83.2935426) near the Piro Biological Station run by Osa Conservation. (See *Taylor et al. (2015)* for a broader ecosystem description of the region.) The study site was a regrowing 20 ha timber plantation of *Bombacopsis quinata* abandoned in ~1990 after the dry-adapted species from the Guanacaste region (*Pérez Cordero and Kanninen 2002; Hulshof and Powers 2020*) grew poorly in very wet conditions. This focal secondary forest area was roughly triangular, surrounded by primary forest on the two S and NW sides (Fig 1) and a wide service road on the third NE border, with primary forest beyond it. This census was done in 2013 during the rainy season months between June and August.

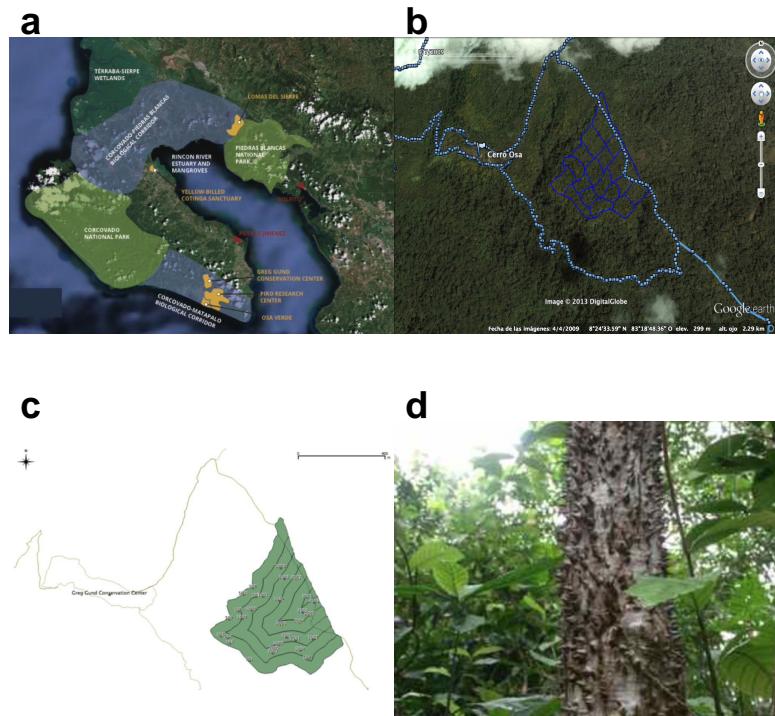


Figure 1: Map of (a) conservation areas and (b) study site (c) showing plot design among distance strata, and focal plantation timber taxon (c) *Bombacopsis quinata* on Osa Peninsula, Costa Rica. Map image data © 2009 Google, © 2022 Osa Conservation. Photo credit: Nicholas Medina.

Census design

Edge effects were studied by dividing the secondary forest area into six 50 m strata spanning 0 - 300 m away from the primary forest edge on the S and NW sides, going inward to the E (Fig 1), using available GIS

software (*ArcGIS 10*, esri.com, and *QGIS 2*, qgis.org). Each stratum was randomly filled with a number of 21 x 21 m square census plots oriented N that was proportional to its area—specifically with 11, eight, five, three, two, and one plot(s), respectively, as distance away from primary forest increased. The total area of the 30 census plots equaled ~1 ha or 5% of the total secondary forest stand area, which is comparable to similar studies (*Onyekwelu and Olabiwonnu 2016*).

Plot measurements

Light reaching the forest floor was measured at the center of each plot at chest height using a densiometer (*Forestry Suppliers, Inc.*), as an average of four readings taken facing each cardinal direction.

The slope of the forest floor was measured using a rangefinder (*Bushnell, Forestry Suppliers, Inc.*) to measure the distance the diagonal between two plot corners and triangulate the observation angle.

The diameter of all stems >10 cm wide were recorded in each census plot, totaling over 1,000 trees. Following common forestry guidelines, in cases where a tree split into 2 or more stems below breast height, each stem was measured separately; in cases where a stem split only above breast height, it was measured as a single stem. Tree height was recorded by measuring distances to both the crown and the stem at chest height (~2.7 m) using a rangefinder (*Bushnell, Forestry Suppliers, Inc.*) and triangulating the missing side length. Taxa were identified with localized knowledge and field guides matching common names to Latin binomials, and trait information was gathered from the literature.

Aboveground biomass (AGB) was estimated per stem using the allometric equation by *Jérôme Chave et al. (2015)*. The equation specifically for wet tropical forests was used, which has performed slightly better compared to both pantropical and previous other models by *J. Chave et al. (2005; Alvarez et al. 2012; Ngomanda et al. 2014)*. The equation version with height was used since height was accessibly measurable and has shown improved local accuracy (*Domke et al. 2012; Khan et al. 2020*). Wood density (or specific gravity) values when available also improve biomass estimates even more than height (*Van Breugel et al. 2011*). The equation used was:

$$AGB = 0.0673(pD^2H)^{0.976}$$

with diameter D in cm, height H in m, and wood density or specific gravity p in $g\ cm^{-3}$. DBHs and heights were measured in the field and wood densities were extracted from available literature. Where information was limited, values at the genus level were used and unrepresented taxa were assumed to be 0.58 following World Agroforestry Database guidelines (worldagroforestry.org). Original values found and recorded were later updated to modern values using the pipeline developed in the *BIOMASS 2.1.8 R* software package by *Réjou-Méchain et al. (2017)*, which notably replaced unknown wood density values with plot-level averages instead during stem biomass calculations.

Traits including successional stage and main dispersal mode were matched to species with *Werden et al. (2020)* data, and wood tissue carbon matched to genera with the GLOWCAD database (*Doraisami et al. 2022*) given high alignment at species levels (*Jérôme Chave et al. 2006*).

Statistical analyses

For all response variables, data were analyzed using plot or distance strata medians and subject to linear regression with distance to forest edge as the only independent variable, after assumption checks of residual normality with Shapiro-Wilk tests and equal variance with Levene tests, using base R version 4.2.0 (2022-04-22) and *rstatix 0.7.0* package functions (*R Core Team 2022*).

Non-linear regressions were run using the function *poly()* in the base R package *stats 4.2.0*, which was only ultimately recorded for stem density and richness variables, based on significance and explained variance over linear models. All trees censused were included in each analysis including unidentified taxa that represented a single group in taxa-specific analyses. Community analysis and ordination was done as a PERMANOVA with the *adonis()* function from the *vegan 2.6.2 R* package (*Dixon 2003*). Data and code were organized

with R packages *here* (Müller 2020), *bookdown* (Xie 2022), and *grateful* (Rodríguez-Sánchez, Jackson, and Hutchins 2022), and internal pipeline *oir* (Medina 2022a) are stored at github.com/nmedina17/osa (Medina 2022b).

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