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The mangroves of Araçá Bay through time: An interdisciplinary approach for conservation of spatial diversity at large scale

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ABSTRACT

The Araçá Bay is a complex mosaic of interacting ecosystems, such as sandy beaches, rocky shores, muddy bottoms, and mangroves. We describe mangrove stands within an interdisciplinary framework based on structural and functional studies, coverage, historical ecology, and species phenotypic and genetic diversity. Plant coverage in six "overwashed" nuclei was 463 living individuals, among them black mangroves (*Avicennia schaueriana*), white mangroves (*Laguncularia racemosa*), and red mangroves (*Rhizophora mangle*). These mangrove stands had an aggregate area of 3644 m² (6% of the bay's total area). Above and belowground biomass was found to be 50.6 Mg representing about 21.7 Mg of blue carbon storage. Although spatially limited, the mangrove subsystem's confers the capacity to persist in spite of extreme changes in sedimentology and hydrodynamics. A historical analysis briefly summarizes local environmental and societal trends through time, proposing a historical-ecological narrative. The PCA analysis revealed high levels of genetic diversity of both black and white mangrove plants. Here we suggest that scientists can help resolve the mismatch between cultural and environmental concerns by shifting perspectives to an appropriately broader conservation framework.

1. Introduction

Mangroves are intertidal ecosystems characterized by the occurrence of plants and associated fauna adapted to tides and salinity (Schaeffer-Novelli et al., 2000). These specialized ecosystems perform diverse functions many of which are of economic importance to humankind (Costanza et al., 1997, 2014; Holling, 2001), and to hemispheric level migratory bird flyway phenomena (Mancini et al., 2017, in this issue).

Plant-dominated coastal ecosystems, such as mangroves, salt marshes and seagrass meadows, play a critical role in global carbon sequestration (McLeod et al., 2011), and atmospheric CO_2 regulation. The high carbon storage capacity coupled with a pan-tropical distribution highlights mangroves as globally important for both above and belowground sequestration (Donato et al., 2011). Nevertheless, mangroves are among the most vulnerable ecosystems in the world, on the verge of destruction (Ghosh et al., 2015). Brazil is the fourth country with the highest potential increase in gross annual CO_2 emissions due to

mangrove deforestation (Atwood et al., 2017). This exacerbates the loss of sequestration capacity.

Human populations have long depended on mangroves, particularly traditional fishing communities. The current economic development model is bringing increasing pressure to coastal ecosystems on a global scale. The mangroves in the Araçá Bay, Southeast Brazil, are no exception. Changes in the configuration of the bay have taken place throughout the past centuries, and particularly during the middle 20th century. One of the results of these changes is genetic diversity loss through deforestation and fragmentation.

The genetic diversity is positively correlated to natural populations' survival to changes in weather, pathogens, competition, and soil conditions (Basey et al., 2015), as well as evolutionary potential, so lower genetic diversity decreases ecological fitness (Reed and Frankham, 2003). Knowledge about a population's genetic diversity can improve conservation efforts in terms of structure and function (Kettenring et al., 2014).

Mangrove conservation can take place through preservation,

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restoration, or natural regeneration. Concerted efforts blending these three approaches makes conservation more effective (Possingham et al., 2015). Araçá Bay has suffered large alterations associated with changes in forcing functions such as hydrodynamics and sedimentary processes (Siegle et al., in this issue; Alcantara-Carrió et al., in this issue). The bay's mangroves require greater efforts for their conservation and restoration, including genetic diversity management in order to avoid further losses of biodiversity, genetic diversity, and carbon stocks. For this to take place, a characterization of functional diversity of the mangrove stands is the main goal of this study.

The aim was to study the mangrove ecosystem using a broad array of tools, all of them focused on the coastal domain scale - both temporal and spatial. This effort included (1) ecosystem characterization; (2) biomass and carbon stock estimation; (3) analysis of genetic diversity; (4) historical-ecological analysis; and (5) an assessment of strategies for the conservation of the Araçá Bay.

The hypotheses considered are: (1) the mangroves remain healthy and performing services and functions that are fundamental to the Araçá Bay as an ecosystem; (2) ecologic-economic cycles and, more recently, the construction and expansion of the port have reshaped the mangrove coverage in the bay; and (3) the genetic diversity of the plants in the area of Araçá Bay is low due to deforestation and strong human.

2. Study area

Araçá Bay $(23^{\circ}49'S, 045^{\circ}24'W)$ is a $534,500 \,\mathrm{m}^2$ shallow complex mosaic of interacting natural ecosystems, namely sandy beaches, rocky shores, muddy bottoms, and mangroves (Amaral et al., 2010). The setting is microtidal, semi-diurnal tides vary between $2.06 \,\mathrm{m}$ and $-0.04 \,\mathrm{m}$ (Gubitoso et al., 2008); mean annual rainfall of 2600 mm; mean annual temperatures of 20° C. According to oral reports, the current embayment was once a mangrove-dominated open-roadstead. The total mangrove-vegetated area has been significantly altered by human occupation and activities, such as the establishment of the marine outfall and the Port of São Sebastião landfills, which has continuously encroached on the bay (Fig. 1).

3. Methods

3.1. Ecosystem characterization

The six different mangrove nuclei were considered individually as parts of the whole. The mangroves were characterized in terms of coverage, structural development. Locations and area were determined using a portable Garmin eTrext30 GPS by geolocating points along the perimeter of each nucleus. Mangrove structure was described measuring diameter at breast height (DBH), tree height, and species composition, according to the methodology by Cintrón and Schaeffer-Novelli (1984) and Schaeffer-Novelli et al. (2017). Both living and dead trees were measured.

3.2. Biomass and carbon stocks

The aboveground plant biomass were estimated using allometric equations for mangrove species (Chave et al., 2005). The belowground plant biomass was estimated from the dry weight of root samples previously collected by the Benthos project (Checon et al., 2017). The sediment corers were 20 cm in diameter, penetrating 20 cm deep in the sediment within the reach of the mangrove root system. Aerial carbon stock were calculated after a 0.45 conversion factor for a biomass-carbon relation was applied as suggested by Twllley et al. (1992). Similarly a 0.39 conversion factor was used to estimate the belowground root carbon stock (Kauffman and Donato, 2011; Fourqurean et al., 2014). Belowground data are expressed to a depth of 50 cm.

3.3. Analysis of genetic diversity

Leaves of white (Laguncularia racemosa (L.) Gaertn. f.) and black mangroves (Avicennia schaueriana Stapf. & Leechman) were sampled for the analysis of genetic diversity. We analyzed 16 white mangrove individuals and 27 black mangrove individuals, sampled at nuclei 1 and 2 of Araçá Bay. The genetic diversity was assessed by the methodology of Inter-Simple Sequence Repeats (ISSR) of molecular markers, after Ge et al. (2005). The ISSR fragments were separated through electrophoresis in agarose gel, and similar size fragments were considered as belonging to the same locus. All fragments were counted manually based on the agarose gel pictures. We considered each present fragment as 1 and each absent as 0 and found 10 polymorphic loci for white mangrove (of 41 loci) and 102 polymorphic loci for black mangrove (of 106 loci). We used nine primers designed by the University of British Columbia (UBC), primer set #9 (808, 809, 810, 811, 834, 835, 840, 841, 842, Life Technologies, Inc) in this procedure (Table 1).

Genetic diversity indices were obtained by Bayesian analysis, using Hickory v-1.1 (Holsinger et al., 2002). We used the "full model" method with 5000 burn-in and 50,000 replicates. The full model is the most complete for species with uncertainties in the inbreeding values, and it showed lower Deviance Information Criterion (DIC) than other methods (Holsinger et al., 2002). The Bayesian method is the most efficient to estimate the genetic diversity and differentiation between small populations because it ignores the allele frequency using Markov chain Monte Carlo (MCMC) simulation to bypass Hardy-Weinberg Equilibrium assumptions (Holsinger et al., 2002; Lira-Medeiros et al., 2015). Hickory calculated the indices of differentiation between areas (G_{ST}) , mean genetic diversity of Araçá Bay (H_S), and the whole-species genetic diversity (H_T). Because this is a local genetic analysis, the indices Hs and H_T were very similar, so we considered only the main genetic diversity index (H_S) for results and discussion. All indices are shown with the standard deviations (SD). PCA analysis and the differentiation index (βST) were carried out with ADE4 (Thiolouse et al., 1996), a package for R 3.2.0 (R Development Core Team, 2008).

3.4. Historical-ecological analysis

For the assessment of this particular historical and ecological setting, we consulted a series of historical documents (Almeida, 1959; CGG, 1919), and others, including photographs from various sources as well a photograph collection (from 1930 to 2016), nautical charts (1936, 1968 and 2013), books on the history of the São Sebastião Municipality (CGG, 1919; Almeida, 1959), news articles and other written media that could help put together the pieces of this landscape's changing configuration through time. In addition to the investigation of printed documents and imagery, a series of semi-structured interviews were carried out with individuals of the local community such as fishers, 'caiçaras' (people from the traditional coastal communities), and other residents who were familiar with the history of the Araçá Bay.

This analysis relies on geoprocessing tools, using Quantum GIS 2.14, and visual analysis comparing satellite data LANDSAT 5 and LANDSAT 7, and high-resolution satellite data as LANDSAT/Copernicus from 2002 to 2016, available within the enhanced version of Google Earth pro. We found the coastal domain scale to be the most appropriate to fully visualize, interpret, and understand the history of the area. This scale was coherent with the scale adopted by the Mangrove Ecosystem project.

The collaborative interacting framework was adopted to generate insights that might promote creative thinking to avoid or mitigate contemporary problems through the adoption of strategies appropriate to local environments and emerging social-cultural trends. It entrains the belief that environmental prudence is grounded on four disciplinary pillars: Ecology, History, Geography, and Anthropology (Cintrón and Schaeffer-Novelli, 1984; Simmons, 1993; Crumley, 1994; Diegues, 2001; Soffiati, 2006; Schaeffer-Novelli et al., 2017). Each one of them

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