UNIVERSIDADE ESTADUAL PAULISTA
"JÚLIO DE MESQUITA FILHO"
Instituto de Biociências
Campus do Litoral Paulista

RODRIGO FRANCISCO JUSTINO

DISPERSÃO DE ÁRVORES DE MANGUE REVELADA POR DADOS GENÉTICOS, GENÔMICOS E POR SIMULAÇÃO OCEANOGRÁFICA: UMA ABORDAGEM MULTI-TAXONÔMICA NO HEMISFÉRIO OCIDENTAL

SÃO VICENTE - SP

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Orientador: Prof. Dr. Gustavo Maruyama Mori

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ATA DA DEFESA PÚBLICA DA DISSERTAÇÃO DE MESTRADO DE RODRIGO FRANCISCO JUSTINO, DISCENTE DO PROGRAMA DE PÓS-GRADUAÇÃO EM BIODIVERSIDADE DE AMBIENTES COSTEIROS, DO INSTITUTO DE BIOCIÊNCIAS - CÂMPUS DO LITORAL PAULISTA.

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Nada mais havendo, foi lavrada a presente ata, que após lida e aprovada, foi assinada pelo(a) Presidente(a) da Comissão Examinadora.

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Resumo

A dispersão é um processo biológico fundamental que permite a conectividade entre diferentes áreas, o que permite, por exemplo, a recuperação e a manutenção de populações. Alguns organismos, como os manguezais, têm um alto potencial de dispersão, com evidências que apoiam a dispersão a longa distância. No entanto, estudos de conectividade de manguezais em larga escala frequentemente se baseiam apenas em marcadores moleculares para poucas espécies e não consideram a dinâmica oceanográfica. Este estudo teve como objetivo avaliar a contribuição das correntes oceânicas para a dispersão de linhagens distintas de árvores de manguezal no Hemisfério Ocidental. Utilizamos 15 conjuntos de dados de microssatélites e seis de polimorfismos de nucleotídeo único (SNP) de estudos anteriores para inferir a estrutura populacional e, com base no agrupamento inferido, estimamos as taxas de migração recentes, realizamos simulações oceanográficas biofísicas e testamos sua associação. No geral, observamos baixas taxas de migração recentes que não foram associadas ao deslocamento oceanográfico nem à estrutura genética, uma indicação de que processos de longo prazo provavelmente influenciam a conectividade dos manguezais. Observamos associação entre migração recente e movimento oceanográfico em três dos 21 conjuntos de dados, sugerindo que outros fatores além das correntes oceânicas, como distância pelo mar, adaptação local, dispersão de pólen e processos costeiros, são mais relevantes na formação da conectividade dos manguezais. Nosso estudo exige inferência temporal de migração de maior duração, para complementar nossos resultados de curto prazo. A associação limitada entre correntes oceânicas e fluxo gênico recente revelou que processos locais ou regionais desempenham um papel relevante na conectividade dos manguezais. Essa descoberta pode contribuir para planos de manejo e conservação mais eficazes, visando processos de menor escala que podem aumentar a probabilidade de persistência e expansão das árvores de mangue.

Palavras-chave: Fluxo gênico recente, Plantas, BayesAss, Modelagem biofísica

Abstract

Dispersal is a key biological process that enables connectivity between different areas, which allows, for example, population recovery and maintenance. Some organisms, such as mangroves, have a high dispersal potential with evidence supporting long-distance dispersal. However, large-scale mangrove connectivity studies often rely only on molecular markers for one species and do not consider oceanographic dynamics. This study aimed to evaluate the contribution of ocean currents to the dispersal of distinct lineages of mangrove trees in the Western Hemisphere. We used 15 microsatellite and six single nucleotide polymorphism (SNP) dataset from previous studies to infer population structure and, based on the inferred grouping, we estimated recent migration rates, performed biophysical oceanographic simulations and tested their association. Overall, we observed low recent migration rates which were not associated with oceanographic displacement nor genetic structure, an indication that long-term processes are likely to influence mangrove connectivity. We observed association between recent migration and oceanographic movement for three datasets, out of the 21, a suggestion that factors other than ocean currents, like distance by the sea, local adaptation, pollen dispersal and coastal processes, are more relevant in shaping mangrove connectivity. Our study calls for longer temporal migration inference, to complement our short-term results. The limited association between ocean currents and recent gene flow revealed that local or regional processes play a relevant role in mangrove connectivity. This finding can contribute to more effective management and conservation plans by targeting smaller scale processes that may increase the likelihood of persistence and expansion of mangrove trees.

Keywords: Gene flow, Plants, BayesAss, Biophysical modeling

Introdução Geral

Mangues são florestas amplamente distribuídas por regiões tropicais e subtropicais, que sofrem uma combinação de fatores encontrados em ambientes costeiros, como água do mar, correntes costeiras e oceânicas, ondas e vento (Duke, 2017; Duke et al., 1998). A distribuição geográfica das espécies de mangue é resultado não apenas de fatores climáticos e geográficos atuais, mas também de eventos e condições passados, de acordo com barreiras naturais de temperatura, distância por massas de água e terra (Duke, 2017).

Com relação ao clima, os limites geográficos dessa distribuição são influenciados por fatores climáticos específicos da região, como a temperatura mínima absoluta do ar no leste da América do Sul, a precipitação média anual no oeste da América do Norte e os extremos de temperatura do ar no inverno no leste da Ásia. Há também uma relação entre a temperatura mínima absoluta do ar ou a precipitação média e a riqueza de espécies de manguezal em diferentes regiões (Osland et al., 2017). Independentemente da distribuição onde o ecossistema de florestas de mangue está, ele fornece uma gama de serviços ecossistêmicos, como sequestro de carbono, manutenção da pesca e proteção costeira, e estão envolvidos em uma ampla rede de interações ecológicas (Primavera et al., 2019).

No entanto, processos, principalmente antropogênicos, alteraram sua distribuição. Embora tenha havido uma redução na taxa líquida de perda de manguezais entre 2000 e 2016, o ecossistema pode ter perdido até 35% de sua área total desde 1980 (Goldberg et al., 2020). Um estudo recente sobre a perda global de áreas de manguezais apresenta dados baseados em dados históricos de satélite entre 1996 e 2020, mostrando uma perda líquida global de 3,4% (Bunting et al., 2022). O Sudeste Asiático, onde se encontram as maiores áreas de manguezais do mundo, teve a maior perda líquida absoluta, principalmente devido à aquicultura, embora o cultivo de arroz e o plantio de dendezeiros sejam dominantes em alguns países (Richards & Friess, 2016). A Ásia Ocidental, a Ásia Oriental e o Caribe tiveram as maiores perdas percentuais (13,8%, 11,5% e 7,9%, respectivamente) (Bunting et al., 2022; Spalding & Leal, 2022). Um mecanismo essencial para as espécies de manguezais responderem às mudanças antropogênicas repovoando áreas degradadas ou colonizando novas áreas é a dispersão. Entretanto, em algumas regiões, a dispersão pode ser limitada e não atingir áreas potencialmente colonizáveis, como mostram os estudos que combinaram modelagem de distribuição de espécies com modelagem oceanográfica na Costa Oeste dos Estados Unidos e na África do Sul, respectivamente (Cavanaugh et al., 2024; Raw et al., 2023).

A dispersão permite conexões entre diferentes áreas, o que possibilita que organismos repovoem áreas perdidas ou degradadas, colonizem novos ambientes e mantenham populações. Ela envolve três etapas (Bowler & Benton, 2005; Van der Stocken et al., 2019): emigração, que corresponde à saída de propágulos de manguezal (unidades de dispersão) transportados pela água da árvore parental; transferência, o movimento do propágulo para outro local; e imigração, a chegada e o estabelecimento do propágulo (Van der Stocken et al., 2019). Propágulos de manguezal são frutos e sementes que podem flutuar e sobreviver por longos períodos em água salgada (Clarke et al., 2001; Rabinowitz, 1978), permitindo a dispersão e a conectividade de uma escala local para uma intercontinental por meio do transporte oceânico (Van der Stocken et al., 2019).

Eventos de dispersão de longa distância (DLD) envolvendo transporte transoceânico são raros, mas não menos importantes, e têm profundas implicações evolutivas e biogeográficas (Nathan, 2006; Wu et al., 2023). Para que a DLD em manguezais ocorra, fatores como predação e retenção na matriz da paisagem (nas raízes e copas das árvores, por exemplo) devem ser superados para que os propágulos possam alcançar águas abertas, onde o transporte por correntes oceânicas pode ocorrer. Embora a dispersão próxima à costa e ao longo da costa tenha maior probabilidade de dominar o transporte de propágulos, sistemas de vórtices em larga escala e correntes oceânicas podem permitir a dispersão por milhares de quilômetros (Van der Stocken et al., 2019). No entanto, a detecção de eventos de (Wu et al., 2023) e a identificação de rotas de dispersão em diferentes escalas geográficas continuam sendo um desafio para manguezais e organismos costeiros.

O método de liberação e recaptura considera características realistas, como a dinâmica das marés e a estrutura da paisagem, mas geralmente é impraticável em grandes escalas (~ centenas de quilômetros). Estudos filogeográficos e de genética populacional, por outro lado, permitem inferir a dispersão efetiva em escalas espaciais de centenas de metros (local) a milhares de quilômetros (biogeográfica) e em escalas de tempo ecológicas e evolutivas. Eles também permitem a identificação de eventos de vicariância e a detecção de diferenças genéticas decorrentes de barreiras terrestres e oceânicas que podem não mais existir. No entanto, estudos genéticos por si só não podem considerar processos oceânicos e suas características, como redemoinhos e marés (Van der Stocken et al., 2019).

A modelagem biofísica da dispersão de partículas, que considera explicitamente tais processos oceânicos, pode ser usada como uma metodologia complementar aos estudos genéticos, aumentando sua compreensão da dispersão e conectividade. Além disso, pode ser

um complemento aos estudos que correlacionam diferenciação genética à distância (isolamento por distância), com uma explicação mecanicista da variação genética usando modelos de isolamento por oceanografia (Jahnke & Jonsson, 2022). Estudos recentes têm integrado essas metodologias para diferentes organismos, como corais (Burt et al., 2024; Macleod et al., 2024; Vogt-Vincent et al., 2024), ervas marinhas (Hernawan et al., 2023) e peixes (Snead et al., 2023).

Modelos de dispersão oceanográfica biofísica consideram características abióticas, como vento e correntes oceânicas, mas não se limitam a fatores ambientais. Características funcionais específicas da espécie, como fenologia, fecundidade, flutuabilidade e tamanho de longevidade dos propágulos, também podem ser usadas para construir uma parametrização mais realista do modelo. O momento da floração e da produção de sementes determina quando os propágulos estarão disponíveis para dispersão e, portanto, se o propágulo estará sujeito a correntes favoráveis de dispersão de curta distância ou DLD. Espécies com maior fecundidade, como aquelas dos gêneros *Sonneratia* L.f. (Lythraceae), *Avicennia* e *Laguncularia* L. (Combretaceae), ou com tamanhos menores de propágulos, como *Laguncularia racemosa* (L.) C. F. Gaertn. e *Avicennia germinans* Stapf & Leechm. ex moldenke podem ter maiores chances iniciais de DLD, devido à maior disponibilidade de propágulos e propágulos menores, que teriam menor probabilidade de serem retidos no sistema radicular do manguezal (Van der Stocken et al., 2019). Complementarmente, características dos propágulos, como períodos de flutuação e viabilidade, também influenciam a dispersão e a conectividade de DLD. Propágulos de espécies como *Rhizophora mangle* L. (Rhizophoraceae), por exemplo, podem permanecer flutuantes e viáveis por mais de 300 dias, enquanto propágulos de *A. germinans*, apesar de poderem flutuar por mais de 100 dias, podem perder a viabilidade após aproximadamente 45 dias (Rabinowitz, 1978). Tais diferenças funcionais provavelmente afetam a conectividade e os padrões de dispersão específicos de espécies ou gêneros, impactando os processos em nível de comunidade. No entanto, a maioria dos estudos de dispersão concentra-se em uma ou poucas espécies.

No Hemisfério Ocidental, embora vários estudos tenham contribuído para a nossa compreensão da dispersão dos manguezais, a maioria deles se concentra em apenas um (Cisneros-de la Cruz et al., 2018; Cruz et al., 2019, 2020; Kennedy et al., 2020; Ochoa-Zavala et al., 2019) ou em algumas espécies (Cerón-Souza et al., 2015; Da Silva et al., 2021; Francisco et al., 2018; Além disso, as informações utilizadas na maioria desses estudos baseiam-se basicamente em marcadores moleculares. Uma exceção é um estudo recente que

integrou modelagem oceanográfica de correntes com dados genômicos de *R. mangle* ao longo da costa brasileira e revelou uma correspondência parcial entre simulações de partículas e padrões ancestrais de fluxo gênico (Madeira et al., 2023).

Um trabalho recente que superou parcialmente essas limitações e contribuiu significativamente para o estudo da conectividade foi um estudo que investigou a dispersão em escala global de espécies de manguezais com vários tipos de marcadores e utilizou modelagem biofísica para explicar a diferenciação entre populações. Os autores concluíram que as correntes oceânicas explicam a diferenciação genética independentemente da espécie e do marcador (Gouvêa et al., 2023). No entanto, este estudo não considera estatisticamente a direção da dispersão obtida a partir de dados genéticos, ou seja, direcionalmente, por meio da inferência do fluxo gênico (dispersão efetiva) com modelagem oceanográfica (dispersão potencial).

Dada a importância da dispersão para a resposta das espécies de manguezais às rápidas mudanças ambientais antropogênicas, **objetivamos identificar os principais fatores que moldam as trajetórias de dispersão das principais espécies de árvores de manguezais do Hemisfério Ocidental usando genética de paisagens marinhas e modelagem biofísica oceânica.**

Esta dissertação está apresentada em um capítulo único, em formato de artigo científico.

Capítulo I. Mangrove tree dispersal revealed by genetic, genomic and oceanographic simulation data: a multi-taxonomic approach in the Western Hemisphere.

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Abstract

Dispersal is a key biological process that enables connectivity between different areas, which allows, for example, population recovery and maintenance. Some organisms, such as mangroves, have a high dispersal potential with evidence supporting long-distance dispersal. However, large-scale mangrove connectivity studies often rely only on molecular markers for one species and do not consider oceanographic dynamics. This study aimed to evaluate the contribution of ocean currents to the dispersal of distinct lineages of mangrove trees in the Western Hemisphere. We used 15 microsatellite and six single nucleotide polymorphism (SNP) dataset from previous studies to infer population structure and, based on the inferred grouping, we estimated recent migration rates, performed biophysical oceanographic simulations and tested their association. Overall, we observed low recent migration rates which were not associated with oceanographic displacement nor genetic structure, an indication that long-term processes are likely to influence mangrove connectivity. We observed association between recent migration and oceanographic movement for three datasets, out of the 21, a suggestion that factors other than ocean currents, like distance by the sea, local adaptation, pollen dispersal and coastal processes, are more relevant in shaping mangrove connectivity. Our study calls for longer temporal migration inference, to complement our short-term results. The limited association between ocean currents and recent gene flow revealed that local or regional processes play a relevant role in mangrove connectivity. This finding can contribute to more effective management and conservation plans by targeting smaller scale processes that may increase the likelihood of persistence and expansion of mangrove trees.

1. Introduction and objectives

Mangroves are forests widely distributed across tropical and subtropical regions, which experience a combination of factors found in coastal environments such as sea water, coastal and ocean currents, waves and wind (Duke, 2017; Duke et al., 1998). Such broad geographic distribution is a result of the combination of past events and conditions, and climatic and geomorphological and oceanographic factors (Duke, 2017; Ellison et al., 1999; Van der Stocken et al., 2019). One key component related to mangroves broad geographic distribution regards their dispersal potential.

Dispersal enables connections between different areas, which makes it possible for organisms to repopulate lost or degraded areas, colonize new environments, and maintain populations. Although there was a decrease in the net rate of mangrove loss in Brazil, globally between 2000 and 2016, the ecosystem may have lost up to 35% of its total area since 1980 (Goldberg et al., 2020). A recent study on global mangrove loss uses historical satellite data from 1996 to 2020, showing a global net loss of 3.4% (Bunting et al., 2022). Therefore, it is essential to understand how dispersal and connectivity occur to predict the responses of organisms to ongoing environmental changes and to provide support for biodiversity conservation projects (Beger et al., 2022). This understanding involves the three stages (Bowler & Benton, 2005; Van der Stocken et al., 2019): emigration, which corresponds to the departure of water-borne mangrove propagules (dispersal units) from the parental tree; transfer, the movement of the propagule to another location; and immigration, the arrival and establishment of the propagule (Van der Stocken et al., 2019). Mangrove propagules are fruits and seeds that may float and survive for long periods in salt water (Rabinowitz, 1978; Clarke et al., 2001), allowing the dispersal and connectivity from a local to an intercontinental scale through oceanic transport (Van der Stocken et al., 2019).

Long-distance dispersal (LDD) events involved transoceanic transport are rare but no less important and have deep evolutionary and biogeographic implications (Nathan, 2006; Wu et al., 2023). For mangrove LDD to occur, factors such as predation and retention in the landscape matrix (in the roots and crowns of trees, for example) must be overcome so that propagules can reach open waters, where transport by ocean currents can take place. Although near-shore and alongshore dispersal is more likely to dominate propagule transport, large-scale eddy systems and ocean currents can allow dispersal across thousands of kilometers (Van der Stocken et al., 2019). However, detecting LDD events (Wu et al., 2023) and

identifying dispersal routes at different geographic scales remain challenging for mangroves and coastal organisms.

Release-and-recapture method considers realistic characteristics such as tidal dynamics and landscape structure but is generally impractical at large scales (~ hundreds of kilometers). Phylogeographic and population genetic studies, on the other hand, allow inferring effective dispersal on spatial scales from hundreds of meters (local) to thousands of kilometers (biogeographic) and on ecological and evolutionary time scales. They also allow the identification of vicariance events and the detection of genetic differences arising from terrestrial and oceanic barriers that may no longer exist. However, genetic studies alone cannot consider oceanic processes and their characteristics such as eddies and tides (Van der Stocken et al., 2019).

Biophysical modeling of particle dispersal, which explicitly considers such oceanic processes, can be used as a complementary methodology to genetic studies, increasing their understanding of dispersal and connectivity. Furthermore, they can be a complement to studies that correlate genetic differentiation to distance (isolation-by-distance, IBD), with a mechanistic explanation of the genetic variation using isolation-by-oceanography (IBO) models (Jahnke & Jonsson, 2022). Recent studies have been integrating these methodologies for different organisms, such as corals (Burt et al., 2024; Macleod et al., 2024; Vogt-Vincent et al., 2024), seagrasses (Hernawan et al., 2023) and fishes (Snead et al., 2023).

Biophysical oceanographic dispersal models consider abiotic characteristics such as wind and ocean currents but are not limited to environmental factors. Species-specific functional characteristics like phenology, fecundity, buoyancy and longevity size of propagules may also be used to build more realistic model parametrization. The timing of flowering and seed production determines when propagules will be available for dispersal, and therefore whether the propagule will be subject to favorable short-distance dispersal (SDD) or LDD currents. Species with higher fecundity like those from genera *Sonneratia* L.f. (Lythraceae), *Avicennia* and *Laguncularia* L. (Combretaceae), or with smaller propagule sizes *like Laguncularia racemosa* (L.) C. F. Gaertn. and *Avicennia germinans* Stapf & Leechm. ex moldenke may have greater initial chances of LD dispersal, because of the greater propagule availability and smaller propagules, which would be less likely to be retained in the mangrove root system (Van der Stocken et al., 2019). Complementarily, propagule characteristics such as fluctuation and viability periods also influence LDD dispersal and connectivity. Propagules of species such as *Rhizophora mangle* L. (Rhizophoraceae), for example, can remain floating and viable

for more than 300 days, whereas *A. germinans* propagules, despite being able to float for more than 100 days, may lose viability after approximately 45 days (Rabinowitz, 1978). Such functional differences likely affect connectivity and dispersal species- or genus-specific connectivity patterns, impacting community level processes. However, most of dispersal studies are focused on one or few species.

In the Western Hemisphere, although several studies have contributed to our understanding of mangrove dispersal, most of the focus on only one (Cisneros-de la Cruz et al., 2018; Cruz et al., 2019, 2020; Kennedy et al., 2020; Ochoa-Zavala et al., 2019) or a few species (Cerón-Souza et al., 2015; Da Silva et al., 2021; Francisco et al., 2018; Hodel et al., 2016, 2018; Mori, Zucchi, & Souza, 2015; Takayama et al., 2013). Also, the information used in most of these studies relies basically on molecular markers. One exception is a recent study that integrated oceanographic current modeling with genomic data of *R. mangle* along the Brazilian coast and unveiled a partial correspondence between particle simulations and directional ancestral gene flow patterns (Madeira et al., 2023).

One recent work that has partially overcame these limitations and contributed to the study of connectivity was a study that investigated the global-scale dispersal of mangrove species with various types of markers and used biophysical modeling to explain the differentiation between populations with previously calculated indexes of published papers. The authors concluded that ocean currents are the main factor related to genetic differentiation regardless of the species and marker (Gouvêa et al., 2023). However, this study does not statistically consider the direction of dispersal obtained from genetic data i.e., directionally through the inference of gene flow with oceanographic modeling. Therefore, it presents limitations regarding the inference of effective dispersal, which is important for predicting the establishment of organisms that can reach a location (effective dispersal) when using symmetric indices of population differentiation, such as F_{ST} (Marko & Hart, 2012; Wright, 1931). Dispersal is measured indirectly (potentially) with oceanographic modeling along with centrality measures (Graph Theory) with the assumption that there are greater gene flow and less genetic differentiation in bidirectionally connected populations compared to unidirectionally connected ones.

Given the importance of dispersal for the response of mangrove species to rapid anthropogenic environmental changes, **we aimed to identify the main factors shaping the dispersal trajectories of the main mangrove tree species of the Western Hemisphere using seascape genetics and ocean biophysical modeling.**

To achieve this goal, we inferred the genetic structure of each dataset using molecular data, estimated recent migration as a proxy for gene flow (effective dispersal) between the inferred genetic groups, and simulated oceanic propagule dispersal through biophysical modeling, that is, potential dispersal. To assess the correlation between gene flow and simulated ocean current-mediated propagule dispersal, we used Mantel tests.

We tested the null hypothesis (H_0), which assumes that all individuals sampled from different locations comprise a single panmictic population. This hypothesis predicts an absence of population genetic structure among locations, high levels of gene flow, and intense exchange of propagules among sampling locations. As an alternative hypothesis on the opposite side of the spectrum, H_1 assumes low levels of connectivity. This hypothesis predicts strong genetic structure patterns, low levels of gene flow and negligible exchange of propagules among the groups. Another hypothesis, H_2, assumes that ocean currents strongly influence gene flow among the inferred genetic groups. Under this hypothesis, the genetically inferred migration patterns would be consistent with the propagule dispersal patterns obtained in the biophysical simulations. Finally, the fourth hypothesis, H_3, assumes that gene flow patterns are influenced by multiple factors. The corollary of this hypothesis is the occurrence of discordance between direction and intensity of genetically inferred gene flow and propagule dispersal patterns. In this case, processes such as selection against migrants, a greater influence of nearshore and coastal current circulation, and a greater contribution of pollen dispersal relative to propagule-mediated dispersal could be the underlying drivers of the observed patterns.

2. Material and methods

2.1 Selection and curation of works and datasets

We selected scientific articles in the areas of Phylogeography or Population Genetics that used microsatellite or single nucleotide polymorphism markers (SNPs) as molecular markers focusing on the most studied mangrove species *sensu* Tomlinson (Tomlinson, 2016) from the Western Hemisphere. We performed the literature search on Web of Science and Google Scholar using the queries: mangrove* AND (genetic diversity OR genetic differentiation OR phylogeography). We selected articles on the species *A. germinans*, *A. schaueriana*, *L. racemosa* and *R. mangle* and retained only georeferenced genotype data (minimum of 6 loci for microsatellites) in datasets available in GenBank (https://www.ncbi.nlm.nih.gov/genbank/) or Sequence Read Archive (SRA, https://www.ncbi.nlm.nih.gov/sra), both from the US's

National Center for Biotechnology Information (NCBI) or in supplementary materials of scientific articles, open repositories such as Dryad (www.datadryad.org), Github (https://github.com/) and Zenodo (https://zenodo.org/). For unavailable datasets in any of these sources, we directly requested corresponding and first-authors of the studies. The reanalysis of raw genotype dataset was chosen to allow the use of a single comprehensive methodological framework across different genotyping methodologies, molecular markers, and biogeographic realms.

For microsatellites, we performed filtering with MICRO-CHECKER 2.2.3 program (Van Oosterhout et al., 2004) to identify missing, null, stutter bands, and loss of large alleles. We removed loci that presented any of these genotyping errors when identified in more than half of the sampling sites. We also tested for linkage disequilibrium for each pair of loci for each population of the datasets using Poppr 2.9.4 package (Kamvar et al., 2014) of the R program (CoreTeam, 2017) and performed the Bonferroni correction for multiple testing for an initial significance level of 0.05. For SNP data, datasets were available in Variant Call Format, so we chose VCFTOOLS 0.1.16 (Danecek et al., 2011) for filtering. We retained only biallelic SNPs, with a count of less frequent alleles of at least 3. To maximize the number of markers and individuals without compromising data quality, we chose to retain only loci with less than 35% of missing data and individuals with no more than 70% of missing data. We also excluded SNPs with evidence of natural selection to keep only neutral markers for downstream analyses. For this purpose, we used Lositan (Antao et al., 2008), which finds markers on the edge of the F_{ST} distribution curve (with false discovery rate < 0.1) and 95% confidence interval), pcadapt 4.3.5 R package (Luu et al., 2017), which identifies markers with significantly different F_{ST} values through a Principal Component Analysis (PCA) (q-value < 0.1) and Bayescan 2.1 (Foll & Gaggiotti, 2008), which estimates the probability that each locus is subject to selection using a Bayesian method (q-value < 0.1) and we eliminated loci that presented evidence of natural selection in all three programs.

2.2 Genetic diversity

We calculated for microsatellite markers the observed (H_O) and expected (H_E) heterozygosities with PopGenKit 1.0 package (Paquette, 2012) and the allelic richness (Ar) with diveRsity 1.9.90 package (Keenan et al., 2013), with which we also estimated inbreeding coefficient (F_{IS}).

2.3 Population genetic structure

We inferred population genetic structure using complementary methodologies. With HIERFSTAT 0.5-11 package (Goudet, 2005), we calculated pairwise Slatkin's linearized F_{ST} (D) (Slatkin, 1995), a symmetrical measure of genetic distance between groups. Also, we applied Discriminant Principal Component Analysis (DAPC) (Jombart et al., 2010) and Spatial PCA (sPCA) (Jombart et al., 2008), both implemented in the adegenet 2.1.4 package (Jombart & Ahmed, 2011) of R. DAPC allows the identification of populations independently of genetic models, using successive K-means clustering algorithm with increasing number of groups (K) and model selection using the Bayesian information criterion (Jombart et al., 2010). Additionally, we performed sPCA, which explicitly considers spatial autocorrelation of samples or individuals (Jombart et al., 2008), using neighborhood by distance network with distances for samples from each Atlantic and Pacific basin separately.

Methods based on ancestry likelihood model that assumes Hardy-Weinberg and linkage equilibria and implemented in the programs STRUCTURE 2.3.4 (Falush et al., 2003; Pritchard et al., 2000), ADMIXTURE 1.3 (Alexander et al., 2009) were used for microsatellite and SNPs data, respectively. We ran 30 independent runs for each K between 1 to 11 for datasets with up to 10 sampling locations and K equal to the number of sampling locations plus one for datasets with more than 10 sampling locations, with 10^6 Markov Chain Monte Carlo (MCMC) iterations, and 200,000 as burn-in iterations, in STRUCTURE, assuming a model with correlated allele frequencies using CIPRES platform (https://www.phylo.org/) (Miller et al., 2010), which used ParallelStructure (Besnier & Glover, 2013). To find the best K value we use the Structure Selector software (Li & Liu, 2018). For SNPs, we chose K based on the cross-validation (CV) error for different Ks in ADMIXTURE. To determine the number of K groups that best fits our data, we used *ad hoc* ΔK (Evanno et al., 2005), to detect genetic structure.

2.4 Migration rate inference

Based on the observed genetic structure pattern, we inferred recent (~ two generations) directional migration rates between groups with BayesAss 3.05 (Wilson & Rannala, 2003) and BA3-SNPS (Mussmann et al., 2019) for microsatellites and SNPs, respectively. We used genetically meaning groups to avoid migration models overparameterization and increase the number of individuals per group, which is required to adjust mixing parameters (Meirmans, 2014; Wilson & Rannala, 2003).

We performed 10^7 iterations with 10^6 burn-ins and a sampling interval of 100 with 3 independent runs for each dataset. Mixing parameters for allele frequency, inbreeding coefficient and migration rate were adjusted for an acceptance rate between 20% and 60%. Best runs were chosen based on the lowest Bayesian Deviance value, a generalization of squared residuals for likelihood models, from the *calculateDeviance* script (Faubet et al., 2007; Meirmans, 2014), with which we also evaluated MCMC convergence. When Effective Sample Size was lower than 100, we multiplied the number of iterations and burn-in by 10.

2.5 Biophysical oceanographic simulations

Oceanographic connectivity patterns were inferred with propagule passive dispersal simulations using Lagrangian, particle-tracking method (Fossette et al., 2012). We simulated mangrove propagules dispersal by drifting particles based on ocean current velocities data using the OpenDrift 1.9.0 program (Dagestad et al., 2018). We used a 1/3° grid horizontal sea surface current velocity data from Ocean Surface Current Analysis Real-time (OSCAR, https://www.esr.org/research/oscar/overview). We considered viability period (VP) as species-specific functional traits in the biophysical model by deactivating particles in the simulation (if not stranded before) according to their respective VP: 45, 90 and 365 days for *Avicennia, L. racemosa*, and *R. mangle,* respectively, following the aggregated VP information in Van der (Van der Stocken et al., 2019).

In agreement with the migration rate analyses, we also performed oceanographic connectivity inference considering genetic structure patterns. For this, we calculated the midpoint between the sampling sites of the group with *midPoint* function of R package geosphere 1.5-20 (Robert et al., 2024)and released 10^5 particles using the OpenDrift program at a distance of 50 km from the coast from the midpoint azimuth (calculated with *bearing* and *destPoint* functions of geosphere package) from the first layer of ocean current of the shapefile obtained from the OSCAR netcd4 file. However, when genetic groups were geographically discontinuous, we performed independent releases for each continuous part of the groups. For small islands (i.e. small coastline) and for nearby release sites between two groups, we released the particles at shorter distances (on average 20 km). To calculate the number of stranded particles in a latitude and longitude range, we used R calculation functions from the OpenDrift netcdf4 output files read with the R ncdf4 package version 1.24 (David, 2025), considering the continuous coastal area of each group or around a radius of 1º for isolated release sites. When there were two or more release sites in a group were considered, we performed the normalization by summing the total number of particles that

arrived in the group and dividing it by the total extension in kilometers and release sites of the arrival areas of each group. Thus, we obtained for each group the number of stranded particles per kilometer (particles/km). We released the particles for 10 years (2013-2022) and tracked particles dispersal for 11 years (until 2023).

2.6 Oceanographic Connectivity testing

We tested the role of oceanographic connectivity in explaining genetically inferred mangrove migration rates with Mantel modeling tests (Smouse et al., 1986) adapted for asymmetric matrices (Bergmann & McElroy, 2014) with 10^5 permutations. For symmetric matrices, i.e., Slatkin's linearized F_{ST} (D) (Slatkin, 1995) and shortest distance through water (Assis et al., 2013) and Euclidean distance analyses with geosphere (isolation by distance, IBD) (Robert et al., 2024) and partial Mantel (Slatkin's linearized F_{ST} (D) as a function of the shortest distance through water controlled by the Euclidean distance) we used the R vegan package (Simpson et al., 2025). The number of permutations for symmetric matrices depends on their dimension.

3. Results and discussion

3.1 Selection and curation

The literature search returned 599 studies, of which 16 met the predefined filtering criteria, totaling 19 datasets (three articles contained more than two datasets): 13 microsatellite-based datasets and six SNP-based datasets (Table 1, Figure 1). For the analyses, we had a total of 21 datasets, as two studies were separated by Atlantic and Pacific basins.

TABLE 1 Description of datasets. Species: *Avicennia germinans* (Ag), As (*Avicennia schaueriana*), Lr (*Laguncularia racemosa*) and Rm (*Rhizophora mangle*); Molecular marker (M): single nucleotide polymorphism (SNP) or microsatellite (Msat); Number of loci used (NL), Number of individuals used (NI), Number of sampling sites (N), Biogeographic realms (Realm): Tropical Atlantic (TA) and Tropical East Pacific (TEP) (Spalding et al., 2007) , main countries and/or regions sampled (PR): Bra (Brazil), Car (Caribbean), Flo (Florida, USA), Tex (Texas, USA), Mex (Mexico), Yuc (Yucatan, Mexico), Ho (Western Hemisphere), Sen (Senegal) and the Reference.

Species	M	NL	NI	N	Realm	PR	References
Ag	SNP	2260	48	6	TA	Bra	(Cruz et al., 2020)
Ag	Msat	8	150	15	TA	Flo	(Hodel et al., 2016)
Ag	Msat	12	1083	41	TA	Flo, Tex	(Kennedy et al., 2020)
Ag	Msat	22	181	7	TA	Bra	(Mori et al., 2015)
Ag	Msat	8	544	14	TA, TEP	Mex	(Ochoa-Zavala et al., 2019)
As	SNP	826	77	10	TA	Bra	(Cruz et al., 2019)
As	Msat	17	400	11	TA	Bra	(Mori et al., 2015)
Lr	SNP	1072	40	14	TA	Car, Mex, Sen	(Hodel et al., 2018)
Lr	Msat	7	102	8	TA	Bra, Car, Flo	(Sereneski-Lima et al., 2021)
Rm	Msat	8	50	5	TA	Yuc	(Cisneros-de la Cruz et al., 2018)
Rm	Msat	10	318	11	TA	Bra	(Francisco et al., 2018)
Rm	Msat	7	150	15	TA	Flo	(Hodel et al., 2016)
Rm	SNP	1953	85	12	TA	Flo	(Hodel et al., 2017)
Rm	Msat	7	96	12	TA	Flo	(Hodel et al., 2017)
Rm	SNP	10201	116	28	TA, TEP	Bra, Car, Mex	(Hodel et al., 2018)
Rm	Msat	6	237	9	TA	Car, Flo, Sen	(Kennedy et al., 2016)
Rm	Msat	7	240	8	TA	Flo	(Kennedy et al., 2017)
Rm	SNP	4376	78	11	TA	Bra	(Madeira et al., 2023)
Rm	Msat	9	625	30	TA, TEP	Ho	(Takayama et al., 2013)

The sampled points covered much of the western hemisphere mangrove distribution (Figure 1).

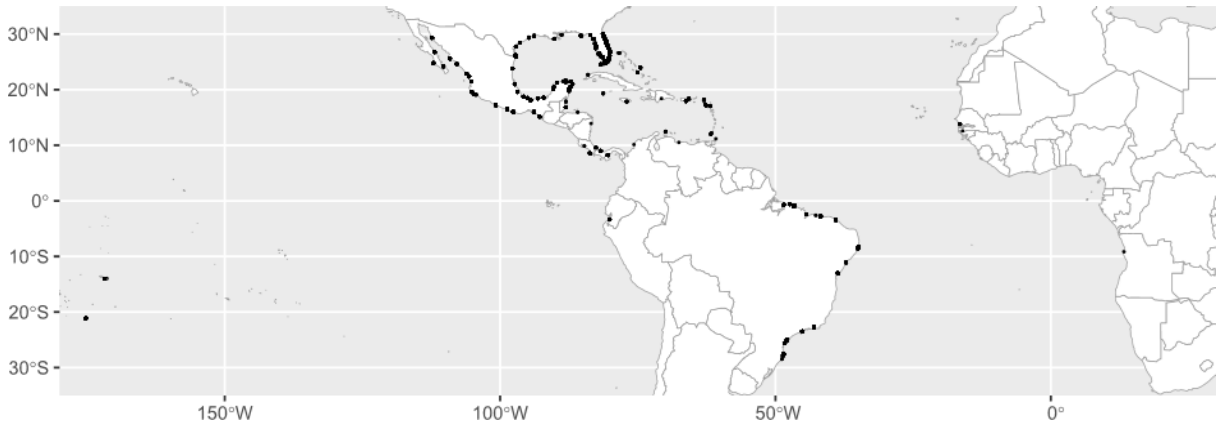


FIGURE 1 Map showing sample locations of the datasets used in this study (circles)

3.2 Genetic diversity

In our reanalysis effort, we observed extensive variation in the measures of neutral genetic diversity of microsatellite markers (Table 2). For instance, for *A. germinans* in the USA we observed the overall highest Ar value (2.260) and that of the Florida region presented the highest H_E (0.456), H_O (0.672) values. Conversely, *L. racemosa* in the Tropical Atlantic biogeographic realm presented the lowest Ar (1.551), H_O (0.106) and second lowest H_E (0.204). The lowest H_E value (0.196) was quantified for *R. mangle* in this region.

TABLE 2 Estimates of genetic diversity and total inbreeding for each dataset that used microsatellite as marker. Species: *A. germinans* (Ag), *A. schaueriana* (As), *L. racemosa* (Lr), and *R. mangle* (Rm); Allelic richness (Ar); Expected heterozygosity (H_E); Observed heterozygosity (H_O); Inbreeding coefficient (F_{IS}); and the reference for each dataset. Results are shown as mean calculated across loci of all populations of each dataset ± standard deviation.

Species	Ar	H_E	H_O	F_{IS}	References
Ag	2.543 ±0.302	0.456 ±0.071	0.672 ±0.154	-0.422 ±0.154	(Hodel et al., 2016)
Ag	2.260 ±0.390	0.325 ±0.111	0.276 ±0.127	0.181 ±0.187	(Kennedy et al., 2020)
Ag	2.624 ±0.751	0.438 ±0.171	0.432 ±0.306	0.218 ±0.244	(Mori et al., 2015)
Ag	2.551 ±0.658	0.239 ±0.108	0.224 ±0.302	0.132 ±0.158	(Ochoa-Zavala et al., 2019)

As	2.416 ±0.563	0.236 ±0.086	0.171 ±0.063	0.248 ±0.104	(Mori et al., 2015)
Lr	1.551 ±0.398	0.204 ±0.160	0.106 ±0.059	0.475 ±0.165	(Sereneski-Lima et al.,2021)
Rm	2.416 ±0.299	0,428 ±0.067	0.314 ±0.070	0.221 ±0.137	(Cisneros-de la Cruz et al., 2018)
Rm	1.798 ±0.724	0.196 ±0.156	0.190 ±0.105	-0.015 ±0.324	(Francisco et al., 2018)
Rm	2.452 ±0.247	0.425 ±0,062	0.489 ±0.105	-0.089 ±0.127	(Hodel et al., 2016)
Rm	2.350 ±0.257	0.419 ±0.071	0.493 ±0.112	-0.089 ±0.123	(Hodel et al., 2017)
Rm	2.532 ±0.500	0.350 ±0.122	0.310 ±0.106	0.093 ±0.125	(Kennedy et al., 2016)
Rm	2.407 ±0.395	0.317 ±0.096	0.265 ±0.129	0.211 ±0.222	(Kennedy et al., 2017)
Rm	1.729 ±0.237	0.370 ±0.113	0.366 ±0.129	0.026 ±0.221	(Takayama et al., 2013)

3.3 Population genetic structure

The genetic structure patterns we observed, as expected, corroborated previous studies that first presented the genetic data (Figure S1). The Americas act as a barrier to dispersal, which is evident when we analyze the data structure encompassing the regions. For this reason, the structure was analyzed separately in the Atlantic and Pacific basins (Figure S1, A to D).

Studies in the Florida region (Figure S1 M to Q), Mexican Atlantic coast (Figure S1A) and USA (Figure S1U) showed a much more complex structure than other studies such as those in the Caribbean (Figure S1 R and S) and Brazil (Figure S1 E to J).

3.4 Migration rate inference

Based on the population genetic structure patterns for each dataset, we performed migration rates inference and oceanographic simulation. Overall, recent migration rates were low for the 21 evaluated datasets. Among the studies that obtained at least 5% of migrants

toward at least one of the inferred groups among all pairs of groups are the two studies (microsatellite and SNP) in Brazil (higher from North to South in both) and the study in Yucatan in Mexico with microsatellite (higher from the Caribbean Coast to the Gulf Coast of Mexico), all three were focused on *R. mangle*. The other studies had values below this criterion.

Two studies presented values equal to or above this value toward at least one of the groups among almost half of the pairs of groups, the study with *L. racemosa* in the Caribbean (SNP) and *R. mangle* in Florida (microsatellite, data from Hodel et al., 2017).

In addition to the magnitude of migration values, we considered the direction between migration rates, even if the absolute values are relatively low. For example, in the study of *R. mangle* using microsatellite marker in Florida (data from Hodel et al., 2016), migration from the southern Gulf Coast group to the northern group was 1.54% (in the opposite direction it was 0.89%) and to the Atlantic Coast it was 1.53% (in the opposite direction it was 0.39%). Despite the relatively low values, migration from the southern Gulf Coast to the northern group was almost double in relation to the opposite direction and almost 4 times in relation to the Atlantic Coast. Without considering studies, groups, the highest values were 32% of individuals migrating in both directions between populations of the Caribbean Gulf Coast and the Atlantic Coast in the study in Florida, USA, with *A. germinans* and microsatellite marker. The second highest value of migration between pair was between the Ecuadorian group and the Panamanian group (South to North), 21%, and only 0.1% in the opposite direction in the study in the Pacific Basin with *R. mangle* (microsatellite, data from Takayama et al., 2013). And the third was from the Yucatan Peninsula to the Southwest (17% to the Southwest and 0.1% in the opposite direction) in the study on the Mexican Atlantic Coast with *A. germinans* (microsatellite, data from Ochoa-Zavala et al., 2019).

Much lower values, such as 0.37% of migrants from North to South on the Mexican Pacific coast and 0.44% to the North with the species *A. germinans*, were obtained among our results. Similar results to ours were obtained on the Mexican Pacific coast with low migrations directed from South to North (Sandoval-Castro et al., 2014). We also found cases with no migration considering 95% CI, such as in the direction from Florida to Texas/Louisiana, USA, 0.007% (+-0.007%) in the USA (*A. germinans*, microsatellite).

In migration-drift equilibrium, *Nm* (where *N* is the effective population size and *m* is the migrant rate) close to one per generation could avoid populations differentiation by genetic drift (Wright, 1931). Furthermore, in theory one and in practice up to 10 immigrants per

generation (Mills & Allendorf, 1996) would be sufficient to avoid population differentiation. For this reason, we believe that, in addition to the magnitude of migration values, it is important to consider the bidirectional proportion between migration rates, even if the absolute values are relatively low. For example, in the study of *R. mangle* using microsatellite marker in Florida (data from Hodel et al., 2016), migration from the southern Gulf Coast group to the northern group was 1.54% (in the opposite direction it was 0.89%) and to the Atlantic Coast it was 1.53% (in the opposite direction it was 0.39%). Despite the relatively low values, the flow from the southern Gulf Coast to the northern group was almost double in relation to the opposite direction and almost 4 times in relation to the Atlantic Coast. This asymmetry may indicate an important source-sink relationship. Also in this study, there was approximately 6-fold migration from the northern Gulf Coast group to the Atlantic Coast group.

3.5 Biophysical oceanographic simulations and integration with gene flow estimates

For the dispersal measured by the oceanographic model with OpenDrift, the studies that obtained at least one stranded particle per kilometer towards at least one of the inferred groups among all pairs of groups added up to 3. The two datasets with microsatellites from Florida, one with *A. germinans* and the other with *R. mangle* (data from Hodel et al., 2016) and the one with *R. mangle* in Yucatan, Mexico. The other studies had values below this criterion. Four studies showed at least one stranded particle per kilometer toward at least one of the inferred groups for most group pairs: two studies conducted with a microsatellite marker with *R. mangle* in Florida (data from Hodel et. al., 2017; data from Kennedy et al., 2017), and the two SNP datasets in the Caribbean (one with *L. racemosa* and one with *R. mangle*).

At inferred group level, the number of stranded particles per kilometer ranged from 155/km from the southern group to the northwest group in a study with *R. mangle* and microsatellite markers (data from Kennedy et al., 2017) to the complete absence of migration. Regarding proportionality, for the studies in which there was migration in both directions, the migration from South to the rest of the Gulf Coast of Mexico was approximately 311 times that recorded in the opposite direction in a study carried out with *A. germinans* and microsatellite marker in Florida. In some studies, there was practically no asymmetry between some groups, with the difference between directions being approximately 0.1 times.

Among the 21 datasets, 4 did not present migration detected by the Oceanographic model between any group (all with microsatellite marker: datasets of *L. racemosa* in the Western Atlantic, *A. germinans* in the Mexican Pacific Coast, *A. schaueriana* in Brazil; exception for

one dataset with SNP with *A. schaueriana* also in Brazil). Five datasets showed complete inconsistency between the directions with the highest migrations between the BayesAss and OpenDrift analyses (all with *R. mangle* and with microsatellite marker: in Florida, USA, data from Kennedy et al., 2017 and Hodel et al., 2017; in Yucatan, Mexico; in Brazil and exception for another dataset in Brazil with SNP). Other 5 datasets had more non-coincidences than coincidences between analyses (with microsatellite marker: with *A. germinans* in Pacific Mexican Coast, in USA and with *R. mangle* in Pacific basin with Takayama et al.,2013 dataset; with SNP marker: with *A. germinans* in Brazil and with *L. racemosa* in Caribbean).

Four datasets showed more consistencies than inconsistencies between the directions with the highest migrations between the two analyses: 3 studies in Florida, USA, with microsatellite marker (one with *A. germinans*, data from Hodel et al., 2016 and the others with *R. mangle*, data from Hodel et al., 2016 and Hodel et al., 2017) and one with SNP with the species *R. mangle* in the Caribbean. Three studies showed complete concordance between the directions with the highest migrations: all with microsatellite marker, two with *R. mangle*, one in the Caribbean, Florida and Senegal regions and the other in the Atlantic Basin (data from Takayama et al., 2013); and one with the species *A. germinans* in Brazil.

We did not observe correlation between recent migration rates and oceanographic connectivity for most of the datasets. Because pairwise migration estimates were null for four datasets, they were not considered. Out of the remaining 17 datasets, recent migrations were positively correlated with oceanography in only three cases, which were microsatellite-based data and showed strong correlation between oceanographic patterns and recent migration rates ($r > 0.9$). Two of them regarded *R. mangle* (Florida and a study of several locations in the Atlantic basin) and one *A. germinans* in Brazil (Table S1, supplementary material). Considering symmetrical distance matrices, we observed significant correlation between distance by the water ($r = 0.53$, $p = 0.04$) and Euclidian distance with D ($r = 0.59$, $p = 0.03$) for only one case, *R. mangle* from the Caribbean region evaluated with SNP markers (Table S2, supplementary material).

3.6 Drivers of mangrove dispersal

Overall, the results we obtained allowed us to challenge the major role played by oceanographic circulation patterns in shaping the intraspecific genetic structure of mangrove species presented mainly in a recent study. Based published genetic differentiation data and

oceanographic modeling, a meta-analysis study used a network-based analysis on population centrality (betweenness and closeness) and identified that in almost all tests performed (95%), oceanography is the main factor that influences genetic differentiation, explaining better than IBD (correlation in 75% of tests) in 100% of cases (Gouvêa et al., 2023). Although the authors have made efforts to explain potential dispersal by identifying possible important locations for connectivity, for example, we argue that there are important limitations regarding the prediction of effective dispersal. The use of indices that do not measure directional gene flow, such as F_{ST}, for example, is limited in predicting effective dispersal, which would be the organisms that would have migrated and established themselves (Marko & Hart, 2012; Wright, 1931). Furthermore, the use of linear regression may introduce bias into the study, since the non-directional genetic differentiation indices between pairs of populations are not independent (Legendre & Fortin, 2010; Smouse et al., 1986).

Our study complements this recent study by Gouvêa and collaborators (2023). We inferred directional gene flow, which makes inference of effective dispersal more powerful, and used Mantel tests to correlate effective dispersal with oceanographic simulation (potential) with Mantel tests, which avoids bias. For these reasons, we believe that our study brings a more realistic approach to the correlation between gene flow and oceanography. And, although some studies have shown a correlation between oceanography and genetic differentiation and/or gene flow (Gouvêa et al., 2023; Ngeve et al., 2016; Wee et al., 2014, 2020), others have shown that this correlation is partial (Madeira et al., 2023), that terrestrial dispersal by pollen may be more important than propagules-based dispersal (Hodel et al., 2018) or that propagules would not have the capacity to reach favorable locations (Cavanaugh et al., 2024; Raw et al., 2023) due to the inability to travel long distances, as demonstrated in a meta-analysis with several mangrove species in fragmented environments correlating genetic differentiation with distances (Granville & Banks-Leite, 2023).

This lack of consistency across studies highlights the complexity of underlying mechanisms related to the different dispersal stages. Regarding the emigration stage, most of the studies have little predictive power because it is assumed that propagules do reach the ocean, whereas it is most likely that most propagules are retained locally (Van der Stocken et al., 2019). This fact may inflate the number of released and stranded propagules in the particle release simulation. Below, we discuss the mechanisms related to the transfer stage—that is, potential dispersal assessed by oceanographic modeling—and the immigration stage, inferred from recent migration rates.

Overall, we identified genetic structure for all datasets, regardless of the marker and the geographic region. This result allows us to reject the hypothesis H_0, which predicts a panmictic population. Also, we could reject H_1 because we observed non-negligible arrival of virtual propagules and a diverse range of levels gene flow rates, despite signs of strong population genetic structure for some regions and species. Regarding H_2, we observed a strong correlation between gene flow and the pattern of propagule dispersal (Mantel $r > 0.95$), which suggests that ocean currents may be the main factor responsible for gene flow in some cases, and for these cases H_2 could not be rejected. However, for most of the cases in our study, we observed a mismatch between potential dispersal, assessed with biophysical oceanographic simulations, and effective dispersal, as measured by gene flow, which allows us to reject H_2 for most of the populations/species. Thus, we cannot reject hypothesis H_3, which is therefore the most consistent with our overall results. Several processes to observe these results.

One of the potential underlying processes that could lead to discordances between gene flow and propagule simulation is selection against migrants (Wright, 1931), in the case of mangroves, when the arrival of propagules is likely, but there is no significant gene flow. This scenario is observed in the study with *A. germinans* in the USA (Figure S1 U), where the arrival of particles in the East that left the West is detected, but there is no significant flow between the regions. However, this scenario was not observed for all groups in the same dataset. Another process that should explain the observed discrepancies is oceanographic characteristics at a local scale. Eddies or near-shore counter currents (Mertens et al., 2018; Van der Stocken et al., 2019), for example, may not have been sufficiently captured by the biophysical model. We believe that for some regions, particularly where gene flow detected by BayesAss was relatively low, the biophysical model detected by Opendrift may not have been able to capture such migration.

None of these inconsistent cases involved *R. mangle*, possibly because of its longer propagule viability period (Van der Stocken et al., 2019), leaving more time for a possible stranding and signs of potential dispersal detected in oceanographic simulations. We also argue, especially in cases where there was substantial inconsistency between the oceanography and gene flow, that dispersal may be occurring in some locations mainly by land via propagules at local scale or via pollen, as unveiled by chloroplast genomes coupled with nuclear SNP markers (Hodel et al., 2018). Additionally, we do not ignore the intrinsic limitation of the recent gene flow inference as it does not allow the identification of more

ancient migration processes. Thus, future efforts could concentrate on the measurement of migrations that span through a longer time scale.

4. Conclusion

Overall, low recent migration rates were observed in our analyses, indicating that short-term processes are unlike to influence the connectivity of mangrove trees. Thus, there was no clear pattern between the inferred genetic structure and recent dispersal and oceanographic. Although there was a strong association of oceanographic and migration patterns for only three out of 21 datasets used, our findings do not allow the assertion that that oceanography is the preponderant factor related to migration across regions or species. Our study indicates that other factors besides oceanography are important as dispersal factors, such as distance, local adaptation, coastal dynamics, and pollen dispersal. In addition to increasing understanding of mangrove tree dispersal, our studies can contribute to more effective management and conservation plans by considering factors other than ocean currents.

5. Perspectives

New studies covering more generations may increase the power of understanding the drivers of mangrove tree dispersal and improve the explanations presented here as in recent discoveries (Gouvêa et al., 2023). Such analyses will be performed with FASTSIMCOAL 2.6 software (Excoffier et al., 2021) and/or MIGRATE-n 5.0.4 (Beerli & Felsenstein, 2001) (Beerli & Felsenstein, 2001).

After this step, we will integrate genetic and oceanographic dispersal results by comparing taxa by calculating the similarity of non-directional and directional genetic distances using the Congruence Between Distance Matrices (CADM) (Legendre & Anderson, 2009).

6. References

Alexander, D. H., Novembre, J., & Lange, K. (2009). Fast model-based estimation of ancestry in unrelated individuals. *Genome Research*, *19*(9), 1655–1664. https://doi.org/10.1101/gr.094052.109

Antao, T., Lopes, A., Lopes, R. J., Beja-Pereira, A., & Luikart, G. (2008). LOSITAN: A workbench to detect molecular adaptation based on a Fst-outlier method. *BMC Bioinformatics*, *9*, 1–5. https://doi.org/10.1186/1471-2105-9-323

Assis, J., Castilho Coelho, N., Alberto, F., Valero, M., Raimondi, P., Reed, D., & Alvares Serrão, E. (2013). High and Distinct Range-Edge Genetic Diversity despite Local Bottlenecks. *PLoS ONE*, *8*(7), 1–11. https://doi.org/10.1371/journal.pone.0068646

Beerli, P., & Felsenstein, J. (2001). Maximum likelihood estimation of a migration matrix and effective population sizes in n subpopulations by using a coalescent approach. *Proceedings of the National Academy of Sciences of the United States of America*, *98*(8), 4563–4568. https://doi.org/10.1073/pnas.081068098

Bergmann, P. J., & McElroy, E. J. (2014). Many-to-Many Mapping of Phenotype to Performance: An Extension of the F-Matrix for Studying Functional Complexity. *Evolutionary Biology*, *41*(4), 546–560. https://doi.org/10.1007/s11692-014-9288-1

Bunting, P., Rosenqvist, A., Hilarides, L., Lucas, R. M., & Thomas, N. (2022). Global Mangrove Watch: Updated 2010 Mangrove Forest Extent (v2.5). *Remote Sensing*, *14*(4), 1–18. https://doi.org/10.3390/rs14041034

Cavanaugh, K. C., Carroll, D., Bardou, R., & Van der Stocken, T. (2024). Dispersal limits poleward expansion of mangroves on the west coast of North America. *Ecography*, *2024*(11), 1–11. https://doi.org/10.1111/ecog.07288

Cisneros-de la Cruz, D. J., Martínez-Castillo, J., Herrera-Silveira, J., Yáñez-Espinosa, L., Ortiz-García, M., Us-Santamaria, R., & Andrade, J. L. (2018). Short-distance barriers affect genetic variability of *Rhizophora mangle* L. in the Yucatan Peninsula. *Ecology and Evolution*, *8*(22), 11083–11099. https://doi.org/10.1002/ece3.4575

CoreTeam, R. (2017). *R: A Language and Environment for Statistical Computing* (Vol. 2). https://www.r-project.org/

Cruz, M. V., Mori, G. M., Oh, D. H., Dassanayake, M., Zucchi, M. I., Oliveira, R. S., & Souza, A. P. de. (2020). Molecular responses to freshwater limitation in the mangrove tree *Avicennia germinans* (Acanthaceae). *Molecular Ecology*, *29*(2), 344–362. https://doi.org/10.1111/mec.15330

Cruz, M. V., Mori, G. M., Signori-Müller, C., da Silva, C. C., Oh, D. H., Dassanayake, M., Zucchi, M. I., Oliveira, R. S., & de Souza, A. P. (2019). Local adaptation of a dominant coastal tree to freshwater availability and solar radiation suggested by genomic and ecophysiological approaches. *Scientific Reports*, *9*(1), 1–15. https://doi.org/10.1038/s41598-019-56469-w

Dagestad, K. F., Röhrs, J., Breivik, O., & Ådlandsvik, B. (2018). OpenDrift v1.0: A generic framework for trajectory modelling. *Geoscientific Model Development*, *11*(4), 1405–1420. https://doi.org/10.5194/gmd-11-1405-2018

Danecek, P., Auton, A., Abecasis, G., Albers, C. A., Banks, E., DePristo, M. A., Handsaker, R. E., Lunter, G., Marth, G. T., Sherry, S. T., McVean, G., & Durbin, R. (2011). The variant call format and VCFtools. *Bioinformatics*, *27*(15), 2156–2158. https://doi.org/10.1093/bioinformatics/btr330

David, A. (2025). *Package 'ncdf4.'*

Evanno, G., Regnaut, S., & Goudet, J. (2005). Detecting the number of clusters of individuals using the software STRUCTURE: A simulation study. *Molecular Ecology*, *14*(8), 2611–2620. https://doi.org/10.1111/j.1365-294X.2005.02553.x

Excoffier, L., Marchi, N., Marques, D. A., Matthey-Doret, R., Gouy, A., & Sousa, V. C. (2021). Fastsimcoal2: Demographic inference under complex evolutionary scenarios. *Bioinformatics*, *37*(24), 4882–4885. https://doi.org/10.1093/bioinformatics/btab468

Falush, D., Stephens, M., & Pritchard, J. K. (2003). Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics*, *164*(4), 1567–1587. https://doi.org/10.1093/genetics/164.4.1567

Faubet, P., Waples, R. S., & Gaggiotti, O. E. (2007). Evaluating the performance of a multilocus Bayesian method for the estimation of migration rates. *Molecular Ecology*, *16*(6), 1149–1166. https://doi.org/10.1111/j.1365-294X.2007.03218.x

Foll, M., & Gaggiotti, O. (2008). A genome-scan method to identify selected loci appropriate

for both dominant and codominant markers: a Bayesian perspective. *Genetics*, *180*(2), 977–993. https://doi.org/10.1534/genetics.108.092221

Fossette, S., Putman, N., Lohmann, K., Marsh, R., & Hays, G. (2012). A biologist's guide to assessing ocean currents: a review. *Marine Ecology Progress Series*, *457*, 285–301. https://doi.org/10.3354/meps09581

Francisco, P. M., Mori, G. M., Alves, F. M., Tambarussi, E. V., & de Souza, A. P. (2018). Population genetic structure, introgression, and hybridization in the genus Rhizophora along the Brazilian coast. *Ecology and Evolution*, *8*(6), 3491–3504. https://doi.org/10.1002/ece3.3900

Goldberg, L., Lagomasino, D., Thomas, N., & Fatoyinbo, T. (2020). Global declines in human-driven mangrove loss. *Global Change Biology*, *26*(10), 5844–5855. https://doi.org/10.1111/gcb.15275

Goudet, J. (2005). hierfstat, a package for r to compute and test hierarchical F-statistics. *Molecular Ecology Notes*, *5*(1), 184–186. https://doi.org/10.1111/j.1471-8286.2004.00828.x

Gouvêa, Fragkopoulou, Cavanaugh, Serrão, Araújo, Costello, Westergerling, A. (2023). Oceanographic connectivity explains the intra-specific diversity of mangrove forests at global scales. *PNAS*, *120*(14).

Granville, N. R., & Banks-Leite, C. (2023). Mangrove propagules are limited in their capacity to disperse across long distances. *Journal of Tropical Ecology*, *39*(6), 1–16. https://doi.org/10.1017/S0266467423000147

Hodel, R. G. J., Chen, S., Payton, A. C., Mcdaniel, S. F., Soltis, P., & Soltis, D. E. (2017). Adding loci improves phylogeographic resolution in red mangroves despite increased missing data : comparing microsatellites and RAD-Seq and investigating loci filtering. *Scientific Reports*, *November*, 1–14. https://doi.org/10.1038/s41598-017-16810-7

Hodel, R. G. J., De Souza Cortez, M. B., Soltis, P. S., & Soltis, D. E. (2016). Comparative phylogeography of black mangroves (*Avicennia germinans*) and red mangroves (*Rhizophora mangle*) in Florida: Testing the maritime discontinuity in coastal plants. *American Journal of Botany*, *103*(4), 730–739. https://doi.org/10.3732/ajb.1500260

Hodel, R. G. J., Knowles, L. L., McDaniel, S. F., Payton, A. C., Dunaway, J. F., Soltis, P. S.,

& Soltis, D. E. (2018). Terrestrial species adapted to sea dispersal: Differences in propagule dispersal of two Caribbean mangroves. *Molecular Ecology*, *27*(22), 4612–4626. https://doi.org/10.1111/mec.14894

Jombart, T., & Ahmed, I. (2011). adegenet 1.3-1: new tools for the analysis of genome-wide SNP data. *Bioinformatics (Oxford, England)*, *27*(21), 3070–3071. https://doi.org/10.1093/bioinformatics/btr521

Jombart, T., Devillard, S., & Balloux, F. (2010). Discriminant analysis of principal components: A new method for the analysis of genetically structured populations. *BMC Genetics*, *11*(1), 94. https://doi.org/10.1186/1471-2156-11-94

Jombart, T., Devillard, S., Dufour, A.-B., & Pontier, D. (2008). Revealing cryptic spatial patterns in genetic variability by a new multivariate method. *Heredity*, *101*(1), 92–103. https://doi.org/10.1038/hdy.2008.34

Kamvar, Z. N., Tabima, J. F., & Gŕunwald, N. J. (2014). Poppr: An R package for genetic analysis of populations with clonal, partially clonal, and/or sexual reproduction. *PeerJ*, *2014*(1), 1–14. https://doi.org/10.7717/peerj.281

Keenan, K., Mcginnity, P., Cross, T. F., Crozier, W. W., & Prodöhl, P. A. (2013). DiveRsity: An R package for the estimation and exploration of population genetics parameters and their associated errors. *Methods in Ecology and Evolution*, *4*(8), 782–788. https://doi.org/10.1111/2041-210X.12067

Kennedy, J. P., Garavelli, L., Truelove, N. K., Devlin, D. J., Box, S. J., Ch, L. M., & Feller, I. C. (2017). *Contrasting genetic effects of red mangrove (Rhizophora mangle L .) range expansion along West and East Florida*. 335–347. https://doi.org/10.1111/jbi.12813

Kennedy, J. P., Pil, M. W., Proffi, C. E., Boeger, W. A., Stanford, A. M., & Devlin, D. J. (2016). *Postglacial expansion pathways of red mangrove , Rhizophora mangle , in the Caribbean Basin and Florida 1*. *103*(2), 260–276. https://doi.org/10.3732/ajb.1500183

Kennedy, J. P., Preziosi, R. F., Rowntree, J. K., & Feller, I. C. (2020). Is the central-marginal hypothesis a general rule? Evidence from three distributions of an expanding mangrove species, *Avicennia germinans* (L.) L. *Molecular Ecology*, *29*(4), 704–719. https://doi.org/10.1111/mec.15365

Legendre, P., & Anderson, M. J. (2009). Distance-Based Redundancy Analysis : Testing

Multispecies Responses in Multifactorial Ecological Experiments Author (s): Pierre Legendre and Marti J . Anderson Source : Ecological Monographs , Vol . 69 , No . 1 (Feb ., 1999), pp . 1-24 Published by : *Ecological Monographs*, *69*(4), 512–512. https://doi.org/10.1890/0012-9615(1999)069[0001:DBRATM]2.0.CO;2

Legendre, P., & Fortin, M. J. (2010). Comparison of the Mantel test and alternative approaches for detecting complex multivariate relationships in the spatial analysis of genetic data. *Molecular Ecology Resources*, *10*(5), 831–844. https://doi.org/10.1111/j.1755-0998.2010.02866.x

Luu, K., Bazin, E., & Blum, M. G. B. (2017). pcadapt: an R package to perform genome scans for selection based on principal component analysis. *Molecular Ecology Resources*, *17*(1), 67–77. https://doi.org/10.1111/1755-0998.12592

Madeira, A. G., Tsuda, Y., Nagano, Y., Iwasaki, T., Zucchi, M. I., Kajita, T., & Mori, G. M. (2023). The role of oceanic currents in the dispersal and connectivity of the mangrove *Rhizophora mangle* on the Southwest Atlantic region. *Molecular Ecology Resources*. https://doi.org/10.1111/1755-0998.13807

Marko, P. B., & Hart, M. W. (2012). Retrospective coalescent methods and the reconstruction of metapopulation histories in the sea. *Evolutionary Ecology*, *26*(2), 291–315. https://doi.org/10.1007/s10682-011-9467-9

Meirmans, P. G. (2014). Nonconvergence in Bayesian estimation of migration rates. *Molecular Ecology Resources*, *14*(4), 726–733. https://doi.org/10.1111/1755-0998.12216

Mertens, L. E. A., Treml, E. A., & von der Heyden, S. (2018). Genetic and Biophysical Models Help Define Marine Conservation Focus Areas. *Frontiers in Marine Science*, *5*(AUG), 1–10. https://doi.org/10.3389/fmars.2018.00268

Mills, L. S., & Allendorf, F. W. (1996). The One-Migrant-per-Generation Rule in Conservation and Management. *Conservation Biology*, *10*(6), 1509–1518. https://doi.org/10.1046/j.1523-1739.1996.10061509.x

Mori, G. M., Zucchi, M. I., & Souza, A. P. (2015). Multiple-geographic-scale genetic structure of two mangrove tree species: The roles of mating system, hybridization, limited dispersal and extrinsic factors. *PLoS ONE*, *10*(2), 1–23. https://doi.org/10.1371/journal.pone.0118710

Mussmann, S. M., Douglas, M. R., Chafin, T. K., & Douglas, M. E. (2019). BA3-SNPs: Contemporary migration reconfigured in BayesAss for next-generation sequence data. *Methods in Ecology and Evolution*, *10*(10), 1808–1813. https://doi.org/10.1111/2041-210X.13252

Ngeve, M. N., Vanderstocken, T., Menemenlis, D., Koedam, N., & Triest, L. (2016). Contrasting effects of historical sea level rise and contemporary ocean currents on regional gene flow of rhizophora *racemosa* in eastern atlantic mangroves. *PLoS ONE*, *11*(3), 1–24. https://doi.org/10.1371/journal.pone.0150950

Ochoa-Zavala, M., Jaramillo-Correa, J. P., Piñero, D., Nettel-Hernanz, A., & Núñez-Farfán, J. (2019). Contrasting colonization patterns of black mangrove (*Avicennia germinans* (L.) L.) gene pools along the Mexican coasts. *Journal of Biogeography*, *46*(5), 884–898. https://doi.org/10.1111/jbi.13536

Osland, M. J., Feher, L. C., Griffith, K. T., Cavanaugh, K. C., Enwright, N. M., Day, R. H., Stagg, C. L., Krauss, K. W., Howard, R. J., Grace, J. B., & Rogers, K. (2017). Climatic controls on the global distribution, abundance, and species richness of mangrove forests. *Ecological Monographs*, *87*(2), 341–359. https://doi.org/10.1002/ecm.1248

Paquette, S. (2012). *PopGenKit: useful functions for (batch) file conversion and data resampling in microsatellite datasets. R package version 1.0*.

Primavera, J. H., Friess, D. A., Van Lavieren, H., & Lee, S. Y. (2019). The mangrove ecosystem. In *World Seas: An Environmental Evaluation Volume III: Ecological Issues and Environmental Impacts* (Second Edi, Vol. 3). Elsevier Ltd. https://doi.org/10.1016/B978-0-12-805052-1.00001-2

Pritchard, J. K., Stephens, M., & Donnelly, P. (2000). Inference of Population Structure Using Multilocus Genotype Data. *Genetics*, *155*(2), 945–959. https://doi.org/10.1093/genetics/155.2.945

Raw, J. L., Van der Stocken, T., Carroll, D., Harris, L. R., Rajkaran, A., Van Niekerk, L., & Adams, J. B. (2023). Dispersal and coastal geomorphology limit potential for mangrove range expansion under climate change. *Journal of Ecology*, *111*(1), 139–155. https://doi.org/10.1111/1365-2745.14020

Robert, A., Hijmans, J., Karney, C., Williams, E., Vennes, C., & Hijmans, M. R. J. (2024).

Package ‘ geosphere .’

Sereneski-Lima, C., Baggio, R. A., Pil, M. W., Torres Boeger, M. R., & Boeger, W. A. (2021). Historical and contemporary factors affect the genetic diversity and structure of Laguncularia *racemosa* (L.) Gaertn, along the western Atlantic coast. *Estuarine, Coastal and Shelf Science*, *249*(September 2019), 107055. https://doi.org/10.1016/j.ecss.2020.107055

Simpson, G. L., Blanchet, F. G., Solymos, P., Stevens, M. H. H., Szoecs, E., Wagner, H., Barbour, M., Bedward, M., Bolker, B., Borcard, D., Chirico, M., Durand, S., Beatriz, H., Evangelista, A., Friendly, M., Hannigan, G., Hill, M. O., Lahti, L., Martino, C., … Stier, A. (2025). *Package ‘ vegan .’*

Slatkin, M. (1995). A measure of population subdivision based on microsatellite allele frequencies. *Genetics*, *139*(1), 457–462. https://doi.org/10.1093/genetics/139.1.457

Smouse, P. E., Long, J. C., & Sokal, R. R. (1986). Multiple Regression and Correlation Extensions of the Mantel Test of Matrix Correspondence. *Systematic Zoology*, *35*(4), 627–632. https://doi.org/10.2307/2413122

Takayama, K., Tamura, M., Tateishi, Y., Webb, E. L., & Kajita, T. (2013). Strong genetic structure over the American continents and transoceanic dispersal in the mangrove genus Rhizophora (Rhizophoraceae) revealed by broad- scale nuclear and chloroplast DNA analysis. *American Journal of Botany*, *100*(6), 1191–1201. https://doi.org/10.3732/ajb.1200567

Tomlinson, P. B. (2016). *The Botany of Mangroves*. Cambridge University Press. https://doi.org/10.1017/CBO9781139946575

Van der Stocken, T., Wee, A. K. S., De Ryck, D. J. R., Vanschoenwinkel, B., Friess, D. A., Dahdouh-Guebas, F., Simard, M., Koedam, N., & Webb, E. L. (2019). A general framework for propagule dispersal in mangroves. *Biological Reviews*, *94*(4), 1547–1575. https://doi.org/10.1111/brv.12514

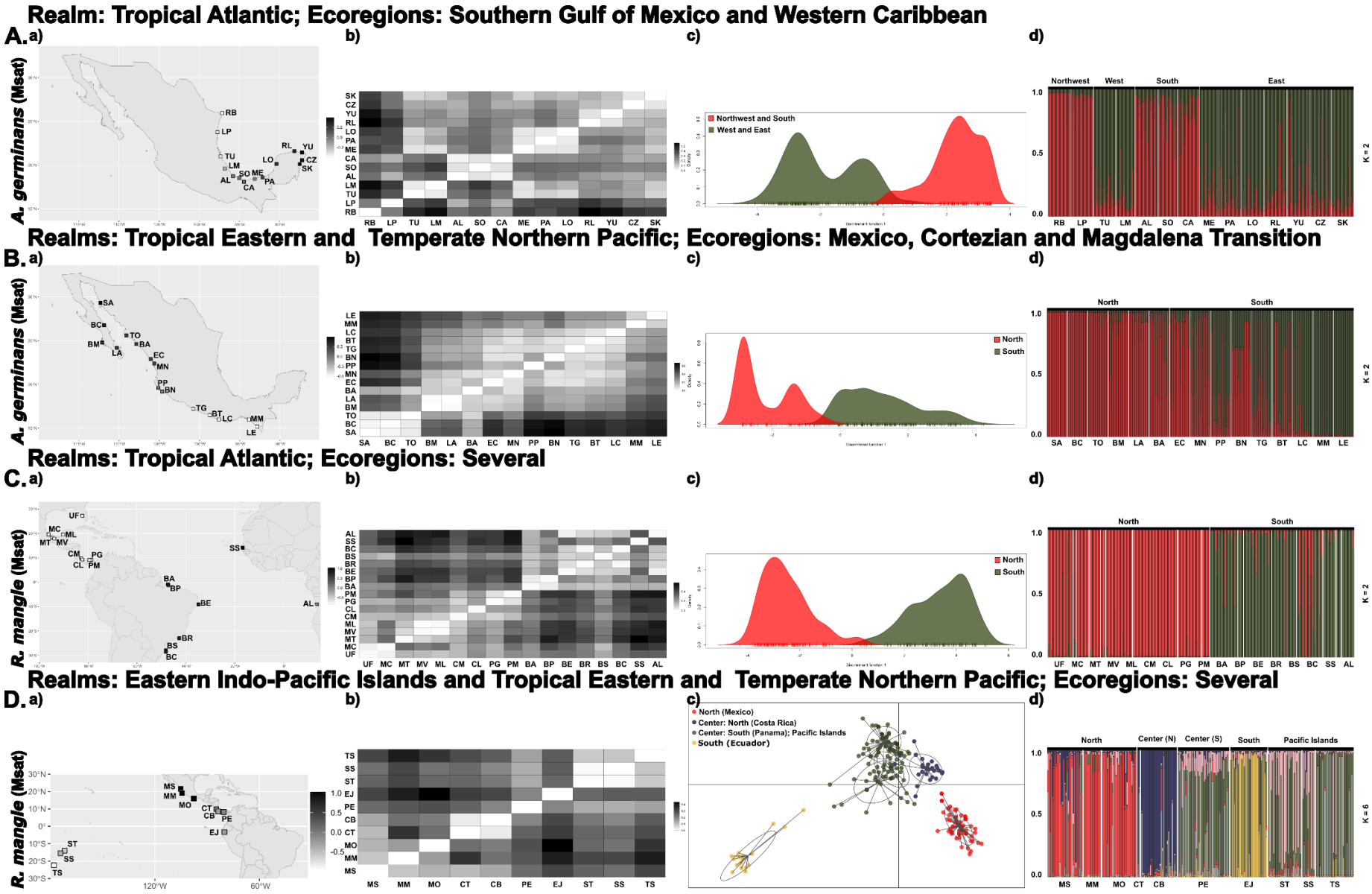
Van Oosterhout, C., Hutchinson, W. F., Wills, D. P. M., & Shipley, P. (2004). MICRO-CHECKER: Software for identifying and correcting genotyping errors in microsatellite data. *Molecular Ecology Notes*, *4*(3), 535–538. https://doi.org/10.1111/j.1471-8286.2004.00684.x

Wee, A. K. S., Noreen, A. M. E., Ono, J., Takayama, K., Kumar, P. P., Tan, H. T. W., Saleh, M. N., Kajita, T., & Webb, E. L. (2020). Genetic structures across a biogeographical barrier reflect dispersal potential of four Southeast Asian mangrove plant species. *Journal of Biogeography*, *47*(6), 1258–1271. https://doi.org/10.1111/jbi.13813

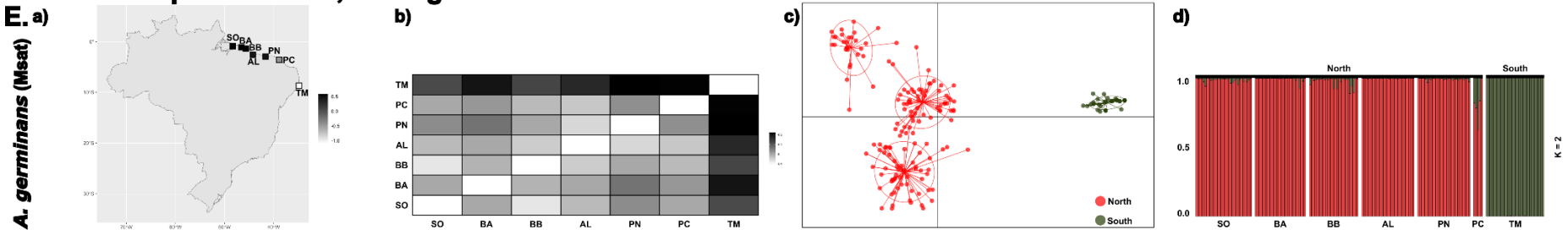
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Wilson, G. A., & Rannala, B. (2003). Bayesian Inference of Recent Migration Rates Using Multilocus Genotypes. *Genetics*, *163*(3), 1177–1191. https://doi.org/10.1093/genetics/163.3.1177

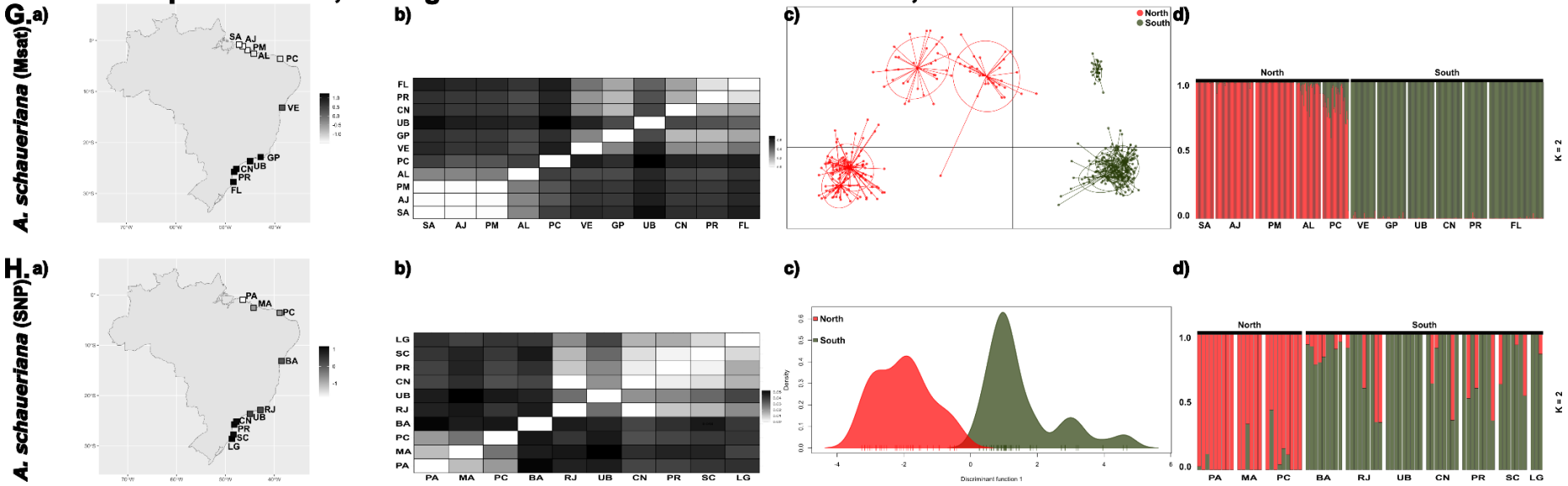
Wright, S. (1931). EVOLUTION IN MENDELIAN POPULATIONS. *Genetics*, *16*(2), 97–159. https://doi.org/10.1093/genetics/16.2.97

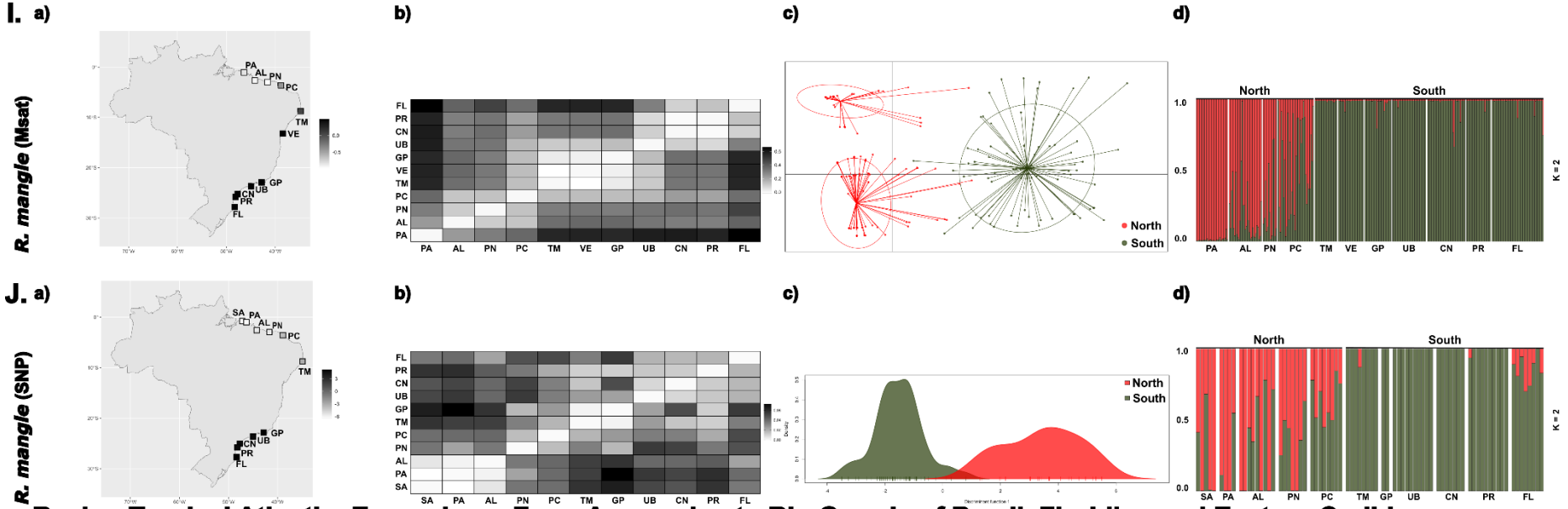

Realm: Tropical Atlantic; Ecoregions: Southern Gulf of Mexico and Western Caribbean
A.
a)
b)
c)
d)
A. germinans (Msat)
RB LP TU LM AL SO CA ME PA LO RL YU CZ SK
Northwest and South
West and East
Northwest
West
South
East
K = 2
Realms: Tropical Eastern and Temperate Northern Pacific; Ecoregions: Mexico, Cortezian and Magdalena Transition
B.
a)
b)
c)
d)
A. germinans (Msat)
SA BC TO BM LA BA EC MN PP BN TG BT LC MM LE
North
South
K = 2
Realms: Tropical Atlantic; Ecoregions: Several
C.
a)
b)
c)
d)
R. mangle (Msat)
UF MC MT MV ML CM CL PG PM BA BP BE BR BS BC SS AL
North
South
K = 2
Realms: Eastern Indo-Pacific Islands and Tropical Eastern and Temperate Northern Pacific; Ecoregions: Several
D.
a)
b)
c)
d)
R. mangle (Msat)
MS MM MO CT CB PE EJ ST SS TS
North (Mexico)
Center: North (Costa Rica)
Center: South (Panama); Pacific Islands
South (Ecuador)
North
Center (N)
Center (S)
South
Pacific Islands
K = 6

Realm: Tropical Atlantic; Ecoregions: Amazonian and Northeastern Brazil

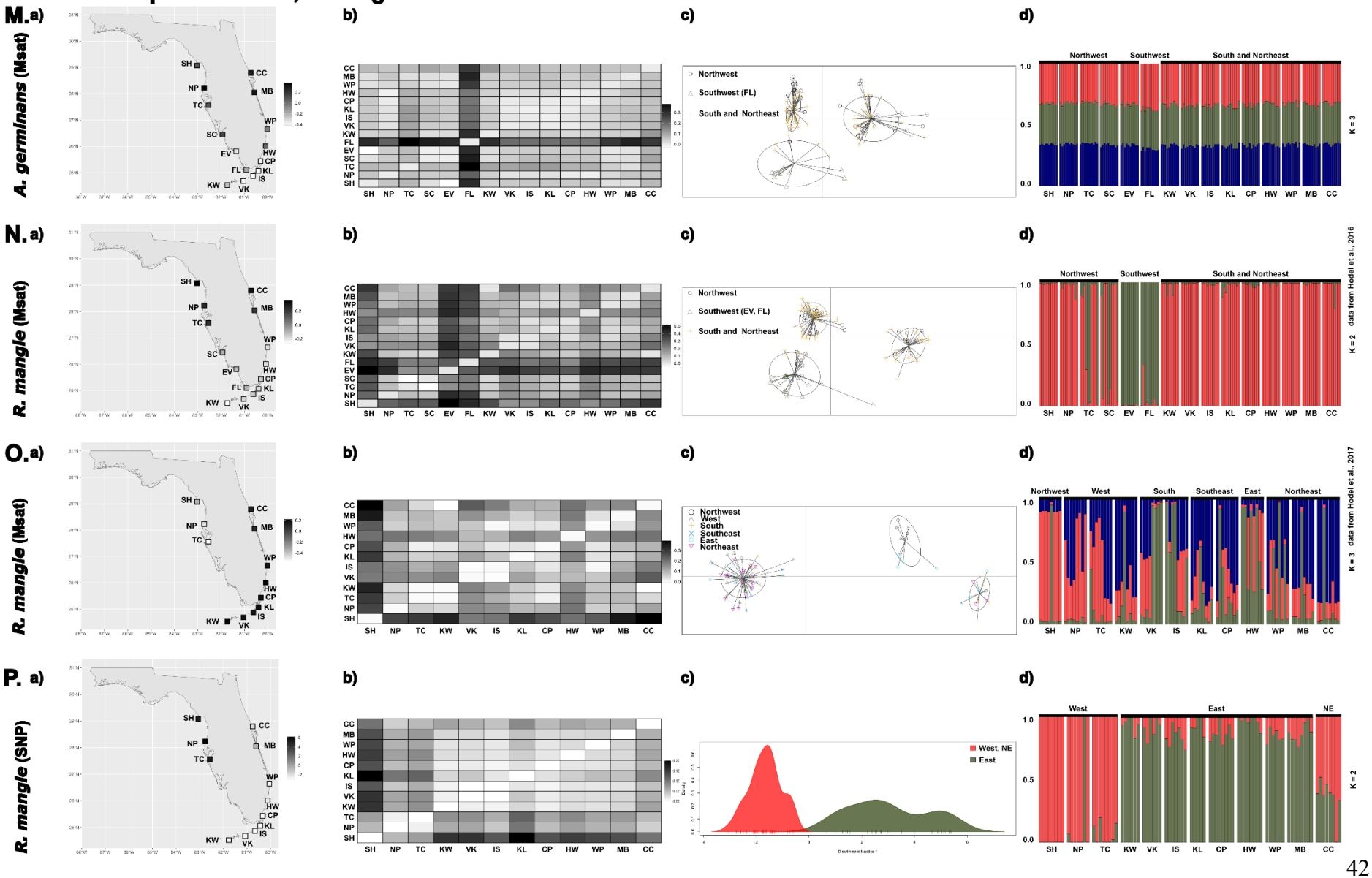


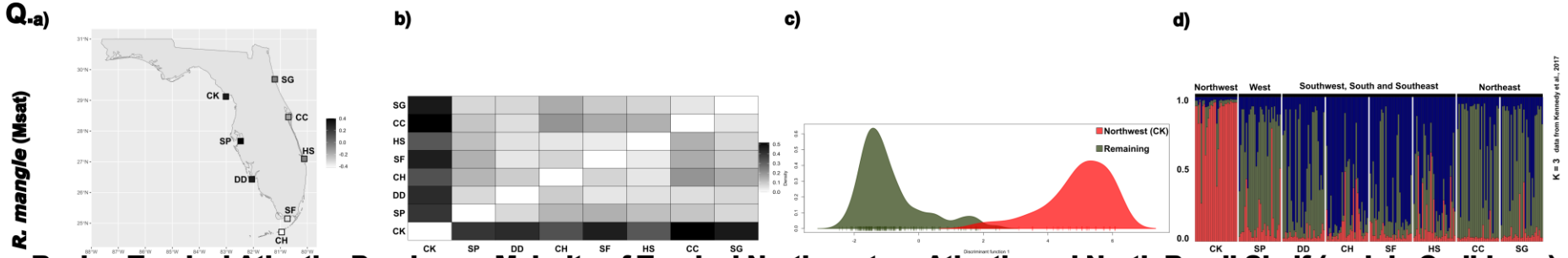
Realm: Tropical Atlantic; Ecoregions: From Amazonian to Rio Grande, Brazil



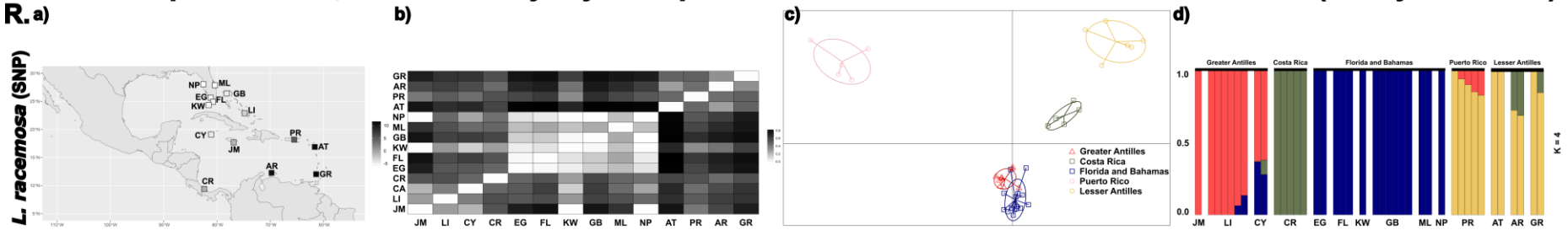

I.
a)
b)
c)
d)
R. mangle (Msat)
PA
AL
PN
PC
TM
VE
GP
UB
CN
PR
FL
North
South
K = 2
J.
R. mangle (SNP)
SA
Realm: Tropical Atlantic; Ecoregions: From Amazonian to Rio Grande of Brazil, Floridian and Eastern Caribbean
K.
L. racemosa (Msat)
LC
SK
NE
PE
SE
SC
Realm: Tropical Atlantic; Ecoregions: Floridian, Bahamian, Eastern, Southern and Southwestern Caribbean and Sahelian
L.
R. mangle (Msat)
UW
UE
BA
US
BE
Caribbean Mailand
Florida (USA)
Caribbean Island and Senegal
K = 3

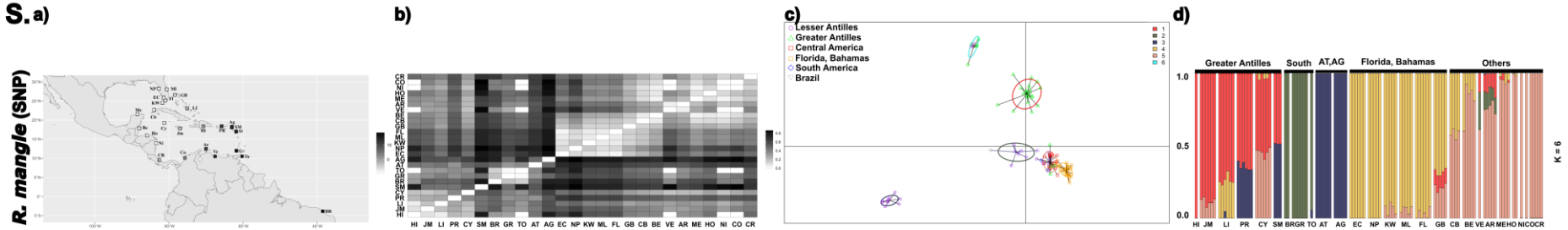
Realm: Tropical Atlantic; Ecoregion: Floridian



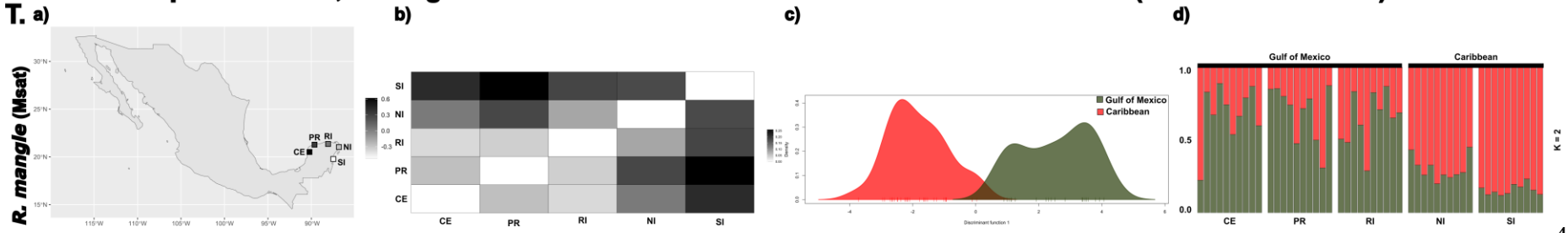


Realm: Tropical Atlantic; Provinces: Majority of Tropical Northwestern Atlantic and North Brazil Shelf (mainly Caribbean)





Realm: Tropical Atlantic; Ecoregions: Southern Gulf of Mexico and Western Caribbean (Yucatan Peninsula)



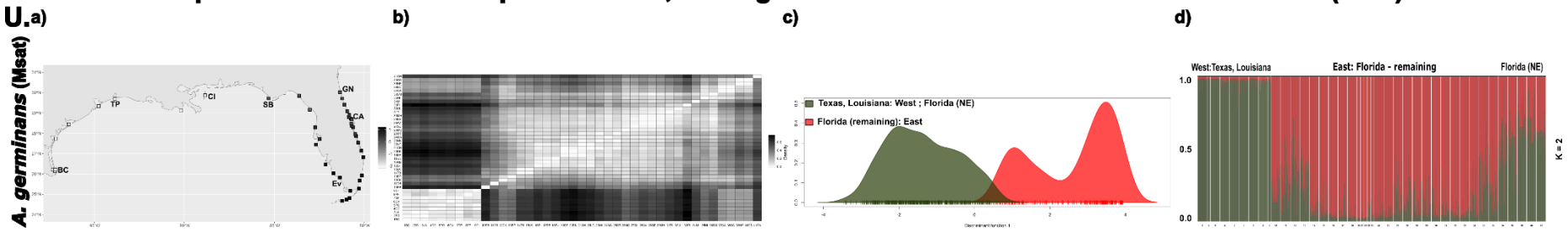


Figure S1. Population genetic structure of all (re)analyzed datasets (From A to U). For each dataset, the following are reported: Realms, Ecoregions or Provinces (according to Spalding et al., 2007), species and genetic marker (the origin of the data is informed, if the information coincide). From right to left, the following are shown - a) spatial PCA (sPCA), b) pairwise F_{ST}, c) Discriminant Analysis of Principal Components (DAPC) and d) methods based on genetic models (STRUCTURE for microsatellite data and ADMIXTURE for SNP data). Sampling site acronyms can be found in the original papers

TABLE S1 Mantel modeling tests performed with asymmetric matrices: Between Recent migration rates (RMR) and dispersal inferred by Oceanographic modeling. Pearson correlation values *(r)*. Significance values *(p)*, showed in bold for $p < 0.05$. Molecular marker: SNP or Msat (microsatellite) and Reference of data source are shown.

a) *Avicennia germinans*		
Mantel RMR		
Oceanography *r* (*p*)	Marker	Reference
-0.13 (0.84)	Msat	Hodel et al., 2016
-0.17 (0.89)	Msat	Kennedy et al., 2020
0.97 (<10^{-5})	Msat	Mori et al., 2015
-0.13 (0.85)	Msat	O.-Zavala et al., 2019[1]
0.24 (0.78)	SNP	Cruz et al., 2020
b) *Laguncularia racemosa*		
-0.17 (0.41)	SNP	Hodel et al.,2018
c) *Rhizophora mangle*		
0.14 (0.50)	Msat	de la Cruz et al., 2018
-0.30 (0.50)	Msat	Francisco et al., 2018
0.95 (0.03)	Msat	Hodel et al., 2016
-0.11 (0.56)	Msat	Hodel et al., 2017
0.23 (0.45)	Msat	Kennedy et al., 2016
-0.17 (0.73)	Msat	Kennedy et al., 2017
0.99 (<10^{-5})	Msat	Takayama et al., 2013[1]
0.42 (0.14)	Msat	Takayama et al., 2013[2]
-0.13 (0.88)	SNP	Hodel et al., 2017
0.13 (0.42)	SNP	Hodel et al., 2018
-0.25 (0.50)	SNP	Madeira et al., 2023

TABLE S2 Mantel modeling tests performed with symmetric matrices between Slatkin's linearized F_{ST} (D) and shortest distance through water and Euclidean distance and shortest distance through water controlled by Euclidean distance (Partial mantel). Pearson correlation values *(r)*. Significance values *(p)*, showed in bold for $p < 0.05$. Molecular marker: SNP or Msat (microsatellite) and Reference of data source are shown.

a) *Avicennia germinans*				
Mantel D		Partial Mantel D		
Water *r* (*p*)	Euclidean r (*p*)	Water controlled by Euclidean *r* (*p*)	Marker	Reference
-0.83 (0.83)	0.03 (0.50)	-1 (1.00)	Msat	Hodel et al., 2016
0.29 (0.50)	0.72 (0.17)	-1 (1.00)	Msat	Kennedy et al., 2020
-0.29 (0.79)	-0.27 (0.79)	-0.29 (0.71)	Msat	O.-Zavala et al., 2019
0.83 (0.17)	0.78 (0.17)	1 (0.66)	SNP	Cruz et al., 2020
b) *Laguncularia racemosa*				
0.43 (0.16)	0.46 (0.13)	-0.06 (0.43)	SNP	Hodel et al., 2018
c) *Rhizophora mangle*				
-0.99 (1.00)	-0.62 (0.84)	-1 (1.00)	Msat	Hodel et al., 2016
0.58 (0.11)	0.54 (0.16)	0.31 (0.16)	Msat	Hodel et al., 2017
-0.82 (1.00)	-0.11 (0.67)	-1(1.00)	Msat	Kennedy et al., 2016
0.28 (0.33)	-0.40 (0.75)	0.21 (0.38)	Msat	Kennedy et al., 2017
-0.18 (0.59)	-0.19 (0.60)	0.01 (0.49)	Msat	Takayama et al., 2013[2]
0.58 (0.11)	0.54 (0.16)	0.31 (0.16)	SNP	Hodel et al., 2017
0.53 (0.04)	**0.59 (0.03)**	-0.18 (0.67)	SNP	Hodel et al., 2018