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Multi-scale coral connectivity across Western Australia: integrating genetic structure and biophysical dispersal modelling

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Statements and Declarations

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Competing Interests

The authors declare no competing interests.

Data availability

All data supporting the findings of this study are available within the paper and its Supplementary Information. The data and code supporting this study are openly available on Zenodo at https://doi.org/10.5281/zenodo.20031763 (Brereton, 2026), including all input data, the complete R analysis pipeline, and manuscript figures.

CRediT authorship contribution statement

Kira Brereton: Conceptualization (lead); project administration; data curation (lead); formal analysis (lead); methodology (lead); visualisation (lead); writing – original draft (lead); writing – review and editing (equal). **Kate Quigley**: Conceptualization (supporting); supervision (equal); writing – original draft (supporting); writing – review and editing (equal). **Eric Treml**: Methodology (supporting); data curation (supporting); supervision (equal); writing – review and editing (equal). **Ryan Lowe**: Supervision (supporting); writing – review and editing (equal). **Camille Grimaldi:** Supervision (equal); data curation (supporting); writing – review and editing (equal).

Abstract

Larval connectivity underpins coral reef persistence, yet genetic and biophysical modelling approaches are rarely integrated. We synthesised coral population data sourced from either genetic or biophysical dispersal estimates across Western Australia (WA), spanning ~22° of tropical-to-temperate latitude. We found that genetic differentiation increased with geographic distance between regions, but not within them, indicating that spatial structure emerges primarily within the regional scale. Biophysical dispersal models predicted predominantly southward transport. Networks built from genetic or biophysical dispersal data identified several of the same highly connected regions, although statistical concordance was weak. 70% (16 of 23) of regional pairwise comparisons included genetic and biophysical data, with greater connectivity derived from genetic rather than biophysical dispersal. This difference could result from temporal mismatch in data collection or differences in the underlying ecological processes and temporal dynamics of each method. Overall, coral connectivity across WA appears to be highly structured by region and is largely shaped by local oceanography, coral demographic history, and species-specific reproductive biology.

Keywords

coral reef, connectivity, population genetics, larval dispersal modelling, network analysis, Indian Ocean

Introduction

Coral reef persistence in the face of increasingly frequent and severe climate-driven disturbance depends on both local population survival and connectivity among populations (Adam et al. 2021; Kannan et al. 2021). Rising ocean temperatures are a major driver of this trend, triggering more frequent and severe mass bleaching events and reshaping patterns of survival and recovery across reef systems (Munday et al. 2009; Speed et al. 2013). As recovery windows shorten, population replenishment will increasingly depend on larval dispersal followed by successful recruitment and post-settlement survival (Boschetti et al. 2020; Gleason and Hofmann 2011; Richardson and Buenafe 2025). Population connectivity — defined as the exchange of individuals among sub-populations — therefore underpins coral reef resilience, facilitating demographic rescue of isolated populations following disturbance (Gilmour et al. 2013), maintaining genetic diversity among populations (Rosser 2016), and enabling range shifts in response to changing environmental conditions (Precht and Aronson 2004; Greenstein and Pandolfi 2008; Cowen and Sponaugle 2009).

Coral reefs along the Western Australia (WA) coast span over 12,000 km and extend across a broad tropical-temperate gradient between ~11 to ~35°S (Fig. 1), encompassing substantial environmental and ecological diversity across coastal and offshore systems in this region of the south-eastern Indian Ocean (Collins 2011). Importantly, some of these coral reef systems are separated by hundreds of kilometres of deep water or non-reef habitat, suggesting that some populations may be biologically isolated and therefore particularly dependent on local recruitment for recovery following disturbance (Hatcher 1991; Rosser 2013; Gilmour et al. 2016). In contrast, the poleward-flowing Leeuwin Current can connect geographically separated locations and contributes to coral reef development at unusually high latitudes along the WA coast (Hatcher 1991; Zinke et al. 2014). Larvae entrained in this current may be transported southward over large distances (Hatcher 1991; Beckley and Muhling 2009). Existing studies have characterised genetic structure or modelled dispersal in individual parts of WA, but

their different spatial extents, taxa, and analytical approaches have not previously been synthesised into a WA-wide assessment, providing only a partial view of regional patterns.

Two main approaches dominate the study of marine population connectivity (reviewed in Bryan-Brown et al. 2017; Cowen & Sponaugle, 2009; Jahnke & Jonsson, 2022; Swearer et al. 2019). Biophysical larval-dispersal models combine hydrodynamic estimates of ocean circulation with biological parameters such as pelagic larval duration (PLD), mortality, competency, and behaviour to simulate dispersal trajectories and connection probabilities among reefs (Connolly & Baird, 2010; Jahnke & Jonsson, 2022). The resulting directional outputs can identify potential source-destination dynamics, stepping-stone pathways, and dispersal barriers (Treml et al. 2015; Choukroun et al. 2025; Dehont et al. 2026). These demographic predictions are sensitive to hydrodynamic resolution and extent, simplified assumptions about life histories and larval behaviour, and can vary substantially among models (Choukroun et al. 2025; Dehont et al. 2026). Genetic differentiation provides a complementary, longer-term multi-generational signal. Metrics such as Wright's F_{ST} (Wright 1943) G'_{ST} and Jost's D (Hedgecock et al. 2007; Meirmans and Hedrick 2011) aim to quantify population divergence, but that divergence can reflect restricted dispersal, habitat discontinuity, genetic drift, local adaptation, reproductive isolation, and demographic history as well as contemporary connectivity (Palumbi 1994; Hedgecock et al. 2007; Riginos and Liggins 2013; Riginos et al. 2016; Zhang et al. 2022). Genetic and biophysical approaches therefore represent fundamentally different processes and timescales. Their agreement can strengthen inference over multiple timescales, while disagreement can identify where directionality, temporal variability, demographic history, or model assumptions require closer examination (Riginos et al. 2016; Burt et al. 2024)

Genetic inferences can also be complicated by hidden biological structure, some of which may not be represented within existing distance-based models. For example, many coral species contain cryptic diversity, partially reproductively isolated lineages that can co-occur in sympatry or unknown diversity (Rosser 2016; Rosser et al. 2017). Cryptic lineages have been documented across at least 24 coral genera (Grupstra et al. 2024), and a recent synthesis found evidence of partially reproductively isolated groups in 68% of species within population-genomic studies (Riginos et al. 2024). Pooling such lineages can result in a Wahlund effect (Wahlund 1928), in which combining genetically distinct groups and treating them as a single population makes that population appear more differentiated than it truly is. This distorts F_{ST} values across spatial scales while deflating estimates at larger ones (Warner et al. 2015; Sheets et al. 2018). Reproductive timing may also result in signal of structure, which may be particularly relevant in WA as coral species here tend to spawn across two distinct annual events (Hatcher 1991; Rosser and Baird 2008; Collins 2011; Speed et al. 2013; Gilmour et al. 2016). This reproductive asynchrony can itself act as a temporal barrier to gene flow (Rosser 2016; Edmunds and Smith 2022), further creating structure between populations.

These biological and methodological differences motivate a synthesis that compares both, genetic and biophysical evidence, rather than treat them as interchangeable or conflicting. As such, we integrate published population genetic studies and biophysical dispersal models within a common regional framework of Western Australia. We ask three interconnected questions: (1) at what spatial scales does genetic differentiation emerge, (2) which regions of the seascape inhibit and/or facilitate connectivity creating departures from expectations of isolation-by-distance, and (3) where genetic and biophysical data overlap, how closely do their inferences agree? We also

quantify uncertainty across studies, examine biological and methodological sources of variation where the evidence base permits, and identify spatial and methodological gaps that constrain connectivity inference.

Methods

We combined a systematic literature search, quantitative data extraction, and structured evidence synthesis to characterise coral connectivity across Western Australia using two evidence streams: population genetic studies and biophysical larval dispersal models. The evidence streams differ in measurement scale and statistical structure, so they were analysed separately and compared only for matched region pairs. Pairwise genetic differentiation (F_{ST}) was synthesised using a two-stage meta-analysis design using species as a fixed factor. Biophysical connectivity was retained as ordinal evidence classes and synthesised as a regional network. This separation avoided treating non-equivalent measures as directly interchangeable while allowing for their spatial patterns to be compared.

Systematic literature review

We conducted a systematic literature review of Scopus and Web of Science to identify primary studies relevant to coral larval connectivity in Western Australia (see Supplementary Information, Fig. S1). Search strings combined biological and physical terms related to connectivity: coral AND (larv* OR propagul* OR egg* OR spawn*) AND (transport* OR retention OR dispers* OR connectivity OR dist* OR pathway*) AND ("Western Australia" OR "Eastern Indian Ocean"). After deduplication, titles and abstracts were screened for relevance to corals, larvae, and Western Australia. Full texts were assessed against five inclusion criteria: (1) the study analysed genetic or modelled dispersal data relevant to connectivity; (2) was conducted in WA waters or adjacent offshore territories; (3) focused on corals or coral larvae, or on a dispersal model explicitly used to represent reef connectivity; (4) explicitly quantified or modelled connectivity, dispersal, or exchange independently of population size or habitat extent; and (5) reported quantitative, qualitative, or spatially explicit outcomes that could inform connectivity.

Where a publication presented independent analyses for different taxa or regions, each taxon-by-study combination was retained as a distinct analytical unit when required. Screening decisions and metadata were recorded using structured templates to standardise study identifiers, regional names, biological traits, methodological domain, spatial scale, and physical drivers. These metadata were used to describe research effort and to identify spatial, taxonomic, and methodological gaps in the WA evidence base.

Genetic studies were classified by molecular marker type as allozyme, microsatellite, mitochondrial DNA (mtDNA), single-nucleotide polymorphism (SNP), or mixed marker classes (Supplementary Table S1). Marker class was used descriptively because raw F_{ST} slopes are not directly comparable across markers. It was therefore not fitted as a moderator of the pooled correlation-based isolation-by-distance (IBD) effect.

Spatial framework

To enable comparisons among studies, we used a framework that divided WA coastal waters into 17 distinct coral reef regions (Fig. 1) and included one representative region in the Timor Sea region. The Timor Sea was added as a potential genetic outgroup. Region boundaries were informed by the Integrated Marine and Coastal Regionalisation of Australia meso-scale bioregions (IMCRA v4.0; Department of the Environment and Heritage 2006), the Department of Primary Industries and Regional Development bioregions (DPIRD 2023), and existing

marine park and management zones, habitat classifications, oceanographic context, and spatial units used in other studies. Reef- and island-group names from source studies were retained as subregion labels. This framework provided a consistent spatial basis for integrating studies that used different geographic definitions. Study contributions were tallied by region, so a study spanning multiple regions contributed once to each region sampled.

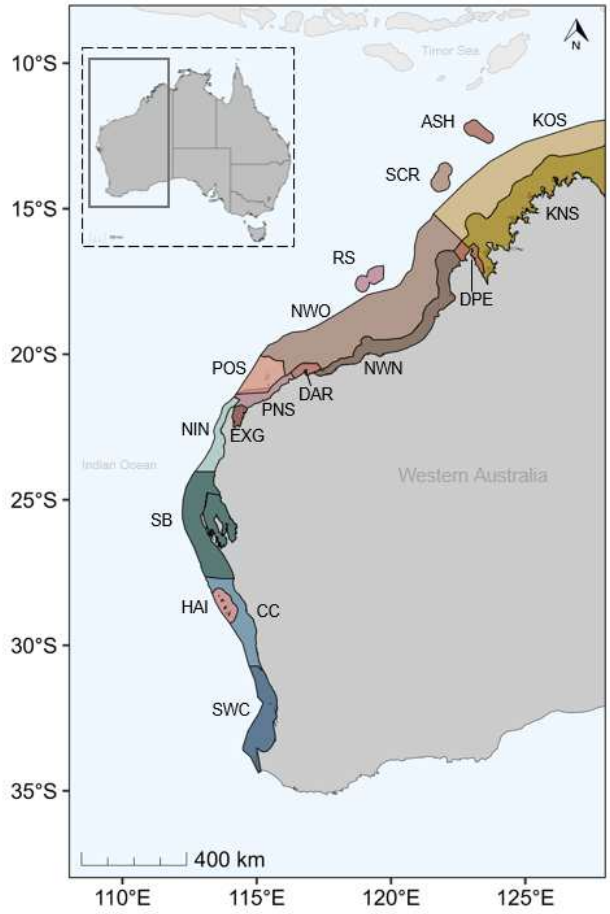


Fig. 1 Geographic extent of the study region in Western Australia and the 17 defined reef bioregions. SWC = Southwest Coast; CC = Central Coast; HAI = Houtman Abrolhos Islands (Abrolhos); SB = Shark Bay; NIN = Ningaloo; PNS = Pilbara nearshore; POS = Pilbara offshore; EXG = Exmouth Gulf; DAR = Dampier Archipelago; NWN = Northwest nearshore; NWO = Northwest offshore; DPE = Dampier Peninsula; KNS = Kimberley nearshore; KOS = Kimberley offshore; ASH = Ashmore Reef; SCR = Scott Reef; RS = Rowley Shoals.

Quantifying connectivity using genetic data

For each genetic study, we extracted author-reported pairwise F_{ST} values between sampling sites and recorded statistical significance where available. The primary analysis was restricted to ordinary F_{ST} and to the primary reporting scenario in each source to avoid mixing alternative estimators or sensitivity scenarios. Geographic distance was taken from the source study when reported or calculated from sampling-site coordinates when sufficient location information was available. Each taxon within a study was treated as a separate study-by-species unit. Units were retained for IBD analysis only when they contained at least four populations and ten pairwise comparisons, providing a minimum basis for estimating a within-unit matrix correlation while limiting very sparse units.

IBD predicts increasing genetic differentiation between populations with geographic distance, consistent with reduced gene flow across larger spatial scales (Wright 1943). Within a study, pairwise comparisons for a species are non-independent, so IBD was assessed in two stages, rather than by pooling all pairs in a single regression. First, each study-by-species unit was analysed with a Mantel test (Diniz-Filho et al. 2013) correlating the pairwise F_{ST} matrix to $\log_{10}$ transformed geographic distance. Significance was assessed using 10,000 permutations of population labels using a fixed random seed. The Mantel correlation was transformed to Fisher's z for meta-analysis (van Aert 2023), with sampling variance $1/(n-3)$, where n was the number of populations in the unit. Raw F_{ST} slopes against $\log^{10}$ distance were retained only for descriptive comparison because their magnitudes depend partly on the scale of F_{ST} generated by different marker types rather than differences in the strength of IBD.

Unit-level Fisher's z effect sizes were pooled using a random-effects meta-analysis with restricted maximum likelihood (REML) estimation (Viechtbauer 2005; Langan et al. 2019). The pooled effect was back transformed to a correlation with a 95% confidence interval, and heterogeneity was summarised using τ^2, I^2, H^2 and Cochran's Q (Choi and Kang 2025). Leave-one-unit-out analyses assessed sensitivity to individual factors. Reporting precision, species, genus, and reproductive mode were explored as moderators using mixed-effects meta-regression, but these tests were treated as descriptive because only 11 units were available. Sensitivity to the heterogeneity estimator was examined using DerSimonian-Laird, Paule-Mandel, empirical-Bayes, and Knapp-Hartung specifications, with Q-profile confidence intervals for heterogeneity where applicable (Paule and Mandel 1982; Berkey et al. 1995; Knapp and Hartung 2003; Viechtbauer 2007).

The complete two-stage analysis was repeated under pre-specified alternative decision rules for negative F_{ST} values, between region only comparisons, and leave one-out exclusion. The minimum requirement of four populations and ten comparisons was re-applied in each scenario. IBD was also estimated separately within regions and between regions because local dispersal over tens of kilometres and regional exchange over hundreds to thousands of kilometres may reflect different processes (Hellberg 2009; Riginos and Liggins 2013). All analyses were conducted in R version 4.6.1 (R Core Team 2026) using `the metafor, geosphere`, and `igraph packages` (Viechtbauer 2010; Csárdi et al. 2026; Hijmans et al. 2026).

Between region genetic comparisons were mapped onto the 18-region spatial framework for comparison with the biophysical network. For regional summaries, F_{ST} was first averaged within each species by study unit and then across units contributing to a region pair, preventing heavily sampled studies from dominating the regional estimate. Network structure was summarised using degree (the number of direct connections a region has), strength (the summed weight of those connections), and betweenness (how often a region falls on the shortest connectivity path between other region pairs), with degree normalised by network size when comparing evidence streams (Treml et al. 2008). Community structure, clusters of regions more densely connected to each other than to the rest of the network, was estimated with Louvain modularity optimisation and evaluated against 999 degree-preserving randomisations (Blondel et al. 2008). Centrality concordance between evidence streams was assessed for shared regions using permutation-based Spearman correlations (Csárdi et al. 2026).

Potential barriers and corridors were identified as region pair departures from the IBD expectation (Jenkins et al. 2010; Dalongeville et al. 2018). Linearised F_{ST}, calculated as $F_{ST}/(1-F_{ST})$ (Rousset 1997) was modelled against $\log_{10}$- transformed geographic distance with a per study by species intercept. Residuals within ±1.5 standard

deviations (SD) were considered consistent with IBD expectations. Residuals > +1.5 SD were classified as barriers and residuals below −1.5 SD as candidate corridors; departures beyond ±2 SD were classified as strong.

Quantifying connectivity using biophysical dispersal data

We extracted directional connectivity estimates from published biophysical dispersal studies when model outputs could be assigned to discrete region pairs in the spatial framework. Studies were excluded from the quantitative regional network when outputs could not be mapped to region pairs or when modelling was restricted to processes within a single reef system. Those studies were retained in the narrative synthesis when they provided relevant evidence on local retention, episodic transport, or model resolution.

The contributing models differed in hydrodynamic forcing, biological parameterisation, spatial resolution, simulation period, and output metric. Continuous values were therefore not standardised to a common dispersal probability. Instead, each region-pair connection was assigned an ordinal low, moderate, or high class using the source study's own categories where available or an explicit, documented rule based on the reported quantity. These rules translated each study's reported quantity into a strength category, for example rating a connection more strongly where the minimum PLD required for exchange between regions was shorter, where simulated propagule arrival time was earlier relative to larval competency, or where relative particle settlement contributions to a subregion were higher. A connection reported by multiple models was counted once in the unweighted network, while model disagreement was recorded separately. Transport direction was recorded only when explicitly reported and was never assumed to be symmetric.

Concordance between genetic and biophysical networks

Genetic and biophysical dispersal evidence were compared for region pairs represented by both evidence streams. Spearman rank correlations were used because the dispersal evidence was ordinal and unequal spacing among low, moderate, and high classes was not assumed. Permutation-based *p*-values were calculated from 10,000 permutations (Manly and Manly 2018). We tested associations between genetic F_{ST} and biophysical strength, genetic F_{ST} and inter-region distance, and biophysical dispersal strength and distance. Because dispersal strength was distance-dependent, the genetic-dispersal association was also evaluated after accounting for distance using a Freedman-Lane residual-permutation procedure (Freedman and Lane 1983). Genetic F_{ST} was also compared among the three biophysical classes using a Kruskal–Wallis test.

Results

The systematic literature search returned 465 records, of which 408 unique articles remained after removing duplicates. Following title and abstract screening, 128 articles were assessed at full text and 30 met the inclusion criteria (Supplementary Fig. S1). These comprised 19 primarily genetic studies and 11 biophysical dispersal modelling studies, with only two studies with both. Eighteen studies supplied extractable values for quantitative analysis, including 14 genetic and four biophysical studies. The remaining studies either lacked extractable pairwise genetic values (n = 5), did not provide region-pair dispersal outputs (n = 4), or modelled connectivity only within a single reef system (n = 3). After site-to-region matching and quality control, eight genetic studies contributed between-region F_{ST} values to the regional network and nine contributed at least one IBD analysis

(Table 1). The four biophysical studies retained for the regional network supplied 41 categorical region-pair connections across 29 unique regional pairs (Table 2). Publication dates ranged from 1984 to 2026, with most studies published after 2010 and a peak around 2016 (Fig. 2a).

Genetic studies sampled a median of 10 sites, with total sample sizes ranging from 70 to 1,156 individuals. Most genetic studies focused on branching broadcast-spawning corals, with *Acropora* spp. comprising 50% of studies that reported data to the level of genus (Fig. 2b). Other species with different reproductive strategies were represented, including two brooding corals, *Seriatopora hystrix* (15%) and *Pocillopora damicornis* (20%). Marker choice diversified over time (Fig. 2c; Table 1). The two earliest studies (1984 and 2006) used allozyme electrophoresis. Microsatellites were used alone in seven studies published between 2007 and 2020 and remained the most common single marker class overall. Five studies combined marker classes, including microsatellites with mtDNA; mtDNA with nuclear introns and microsatellites; microsatellites with SNPs; and mtDNA with SNPs. Four studies used SNP-based or other next-generation sequencing methods alone. Marker composition within the 1,270 model-ready comparisons differed from this literature wide chronology: 732 comparisons (58%) were from SNP-based studies and 538 (42%) were from microsatellite only studies (Supplementary Table S1).

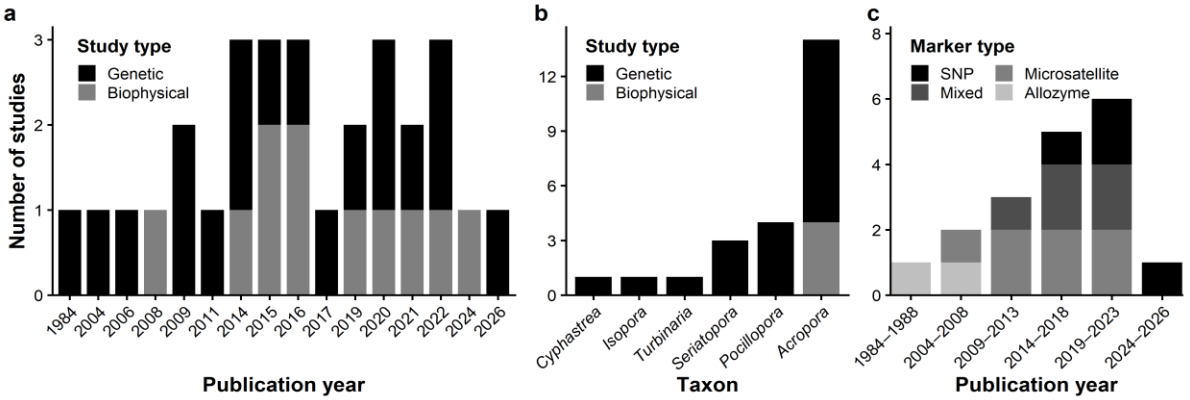


Fig. 2 Temporal, taxonomic, and molecular-resolution biases in coral-connectivity research. (a) Annual number of connectivity studies published from 1984 to 2026, classified by methodological approach; (b) taxonomic distribution of genetic-connectivity studies by genus; and (c) temporal use of molecular marker classes in genetic studies.

Research effort was geographically clustered along the mid-west and northwest coasts of Western Australia (Fig. 3), with offshore systems disproportionately represented by genetic studies. Research effort was concentrated in Ningaloo (n = 15), Dampier Archipelago (n = 13), Pilbara offshore (n = 13), Rowley Shoals (n = 10), and Scott Reef (n = 10). Sampling intensity varied substantially among regions, with offshore atolls having a disproportionate number of studies relative to nearshore reefs.

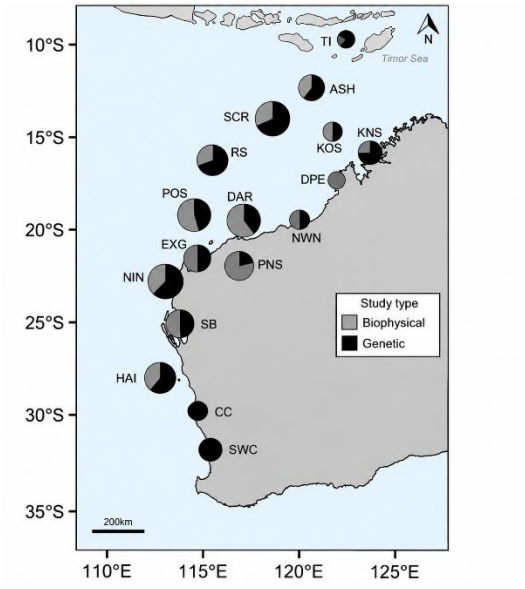


Fig. 3 Spatial distribution and methodological composition of coral-connectivity research across Western Australia. Pie sizes indicate the relative proportions of study types conducted in each region. SWC = Southwest Coast; CC = Central Coast; HAI = Houtman Abrolhos Islands (Abrolhos); SB = Shark Bay; NIN = Ningaloo; PNS = Pilbara nearshore; POS = Pilbara offshore; EXG = Exmouth Gulf; DAR = Dampier Archipelago; NWN = Northwest nearshore; DPE = Dampier Peninsula; KNS = Kimberley nearshore; KOS = Kimberley offshore; ASH = Ashmore Reef; SCR = Scott Reef; RS = Rowley Shoals; TI = Timor Sea (Indonesia).

277 **Table 1** *Summary of coral population genetic studies across Western Australia*

Location(s)	Species	Year(s) sampled	No. sites	Loci type & no. used	Sample size	Analytical approach	Global F_{ST}	Reference
NIN, ASH, RS, KNS	*Acropora digitifera*	NR	31	SNPs – RRS (1,550)	704	F-stats; clustering; GEA	0.048	Adam et al. (2022)
NIN, EXG, POS	*Acropora tenuis*	NR	14	SNPs – RRS (5,368)	158	F-stats; IBD; spatial autocorrelation	0.0047	Duffy et al. (2026)
POS, NIN, SB, DAR, KNS, EXG, PNS	*Cyphastrea microphthalma*	NR	18	Microsatellites (12)	451	F-stats; clustering; IBD	0.059	Evans et al. (2019)
NWN, DAR, POS, PNS, EXG, SB, SWC, KNS	*Turbinaria* spp.	NR	10	mtDNA; SNPs – RRS (7,117)	930	Clustering; GEA	0.148	Evans et al. (2021)
ASH, NIN, RS, DAR, POS, KNS, SCR	*Acropora tenuis*	NR	7	mtDNA (1); nuclear introns (2); microsatellites (6)	NR	F-stats; lineage analysis	0.11	Rosser (2016)
ASH, NIN, RS, DAR, POS, SCR	*Acropora tenuis*	NR	10	Microsatellites (6)	381	F-stats; clustering; IBD	0.15	Rosser et al. (2020)
KNS, HAI	*Acropora* spp.	2010, 2012	8	ITS2 amplicon (454)	70	OTU community analysis	NR	Thomas et al. (2014a)*
NIN	*Pocillopora damicornis*	2012	10	Microsatellites (9)	303	F-stats; spatial autocorrelation; lineage ID	NR	Thomas et al. (2014b)*
NIN, HAI, SWC, SB, POS	*Pocillopora damicornis*	NR	6	Microsatellites (5); SNPs – RRS (5,484)	294	F-stats; clustering; GEA	0.115	Thomas et al. (2017)
RS	*Acropora digitifera*; *Isopora brueggemanni*	NR	9	SNPs – RRS (6,231; 5,565)	242; 218	F-stats; clustering	0.004; 0.037	Thomas et al. (2020)
HAI	*Acropora spicifera*	2013, 2014	15	Microsatellites (9)	395	F-stats; IBD/IBR; biophysical modelling	0.019	Thomas et al. (2015)
RS, SCR	*Acropora tenuis*	2017–2019	5	SNPs – WGS (5,493,423); microsatellites (9)	85	Clustering; genome scans	0.25	Thomas et al. (2022)*
SCR, RS, DAR, NIN	*Acropora tenuis*	NR	26	Microsatellites (7)	1,156	F-stats	0.062	Underwood (2009)

Location(s)	Species	Year(s) sampled	No. sites	Loci type & no. used	Sample size	Analytical approach	Global F_{ST}	Reference
SCR	*Seriatopora hystrix*	2004	6	Microsatellites (8)	287	F-stats; spatial autocorrelation; assignment	NR	Underwood et al. (2007)
SCR, RS, KOS	*Acropora tenuis*; *Seriatopora hystrix*	2004–2006	16	Microsatellites (7; 8)	576; 476	F-stats; IBD; spatial autocorrelation	0.034; 0.234	Underwood et al. (2009)
DPE, ASH, KNS	*Acropora aspera-c*; *Seriatopora hystrix*	NR	15;18	SNP- RRS (3472; 2132)	534; 612	F-stats; clustering	0.101; 0.230	Underwood et al. (2020)
SCR	*Seriatopora hystrix*	2003, 2009	9	Microsatellites (10); mtDNA	336	F-stats; haplotype analysis (depth focus)	NR	Van Oppen et al. (2011)
NIN, HAI	*Pocillopora damicornis*	1991–1993	10	Allozymes (6)	644	F-stats; clustering; IBD	0.36	Whitaker (2006)
HAI, CC, SWC	*Pocillopora damicornis*	1984	25	Allozymes	NR	F-stats; clonal structure	0.391	Stoddart (1984) *
RS, ASH, KNS	*Acropora digitifera*	2017, 2018	6	SNPs – WGS (9.6 million)	75	IBD; clustering	0.02	Zhang et al. (2022)*

NR = not reported; * = study reported population differentiation, but suitable pairwise *FST* estimates were unavailable for network analysis. RRS = reduced-representation sequencing (GBS/DArTseq/RAD); WGS = whole-genome sequencing.

Location codes: SWC = Southwest Coast; CC = Central Coast; HAI = Houtman Abrolhos Islands; SB = Shark Bay; NIN = Ningaloo; PNS = Pilbara nearshore; POS = Pilbara offshore; EXG = Exmouth Gulf; DAR = Dampier Archipelago; NWN = Northwest nearshore; NWO = Northwest offshore; DPE = Dampier Peninsula; KNS = Kimberley nearshore; KOS = Kimberley offshore; ASH = Ashmore Reef; SCR = Scott Reef; RS = Rowley Shoals; TI = Timor Sea (Indonesia).

284 **Table 2** Summary of modelled biophysical dispersal connectivity studies of coral larvae across Western Australia

Location(s)	Species	Year(s)/ season modelled	No. sites	Resolution	Particles released	PLD used (days)	Mortality	Model type	Modelling approach & output	Reference
KOS, KNS, NWN, DPE, DAR, PNS, POS, NIN, EXG, SB	*Cyphastrea microphthalma*	2009–2012 (autumn)	18	8 km	1,000 per site	10; 50; 100	0.06/day	HYCOM	Lagrangian, passive, 4D biophysical; propagule dispersal probability → Nei's D	Evans et al. (2019)*
HAI	*Acropora spicifera*	2009–2012 (autumn)	15	NR	1,000 per site	3–9	Exponential	HYCOM	Lagrangian, 4D biophysical; Derived Oceanographic Resistance (DOR); recruitment probability matrix vs. genetic distance	Thomas et al. (2015)*
NIN, EXG, POS, PNS, DAR	*Acropora millepora*	2004–2009 (autumn)	3,430	1 km	900 per site	60	NR	ROMS	3D Lagrangian, passive; sensory settlement; proportion of larvae settling per zone	Feng et al. (2016)
KOS, KNS, PNS, POS, HAI, SB, NIN, EXG, DAR, SCR, RS, ASH, DPE, NWN, NWO	NR	2009–2012 (NR)	15	9 km	1 billion total	90	Exponential / 0.06	HYCOM (Conn4D)	4D Lagrangian, passive; 3D vorticity; probability of connection between CMRs (0–1 scale); colour-coded matrix	Kool & Nichol (2015)
HAI, DAR, NIN, SB, PNS, POS	NR	2010, 2011 (autumn)	5	2 km; 4 km	1,280,000 per site	up to 250	NR	WASA/OzROMS	Lagrangian, passive, 2D surface; no. particles arriving over time	Markey et al. (2016)
NIN, EXG, POS, PNS, DAR	NR	2004–2009 (autumn)	3,430	1 km	900	60	NR	ROMS	3D Lagrangian, passive; sensory settlement; proportion of larvae settling per zone	Boschetti et al. (2020)*
DAR, POS, PNS, NIN, RS, ASH, SCR	NR	1994–1999 (autumn)	7	10 km; 5 km	100,000 across all sites	7; 14; 21; 28	NR	MECO	Lagrangian, passive, 3D; cumulative particle transport probability	Condie & Andrewartha (2008)
PNS, POS, DAR	NR	1996, 2001, 2002 (Autumn)	NR	1 km	6,000	7	NR	OILMAP; GCOM3D	Lagrangian, passive, 3D; proportion of larval arrivals	Radford et al. (2014)*
DAR	*Acropora millepora*	2015–2017 (NR)	15	NR	NR	NR	NR	ROMS	2D; metric NR	Thomson et al. (2021)*

Location(s)	Species	Year(s)/ season modelled	No. sites	Resolution	Particles released	PLD used (days)	Mortality	Model type	Modelling approach & output	Reference
KOS, KNS, PNS, POS, SB, NIN, EXG, DAR, SCR, RS, ASH, DPE, NWN, NWO	*Tubastraea* sp.	2000–2018 (All seasons)	457	4 km	NR	70	0.1/day	ozROMS	Lagrangian, passive, 3D; metric NR	Sobol et al. (2024)*
RS	*Acropora spp*.	1980-2020 (spring, autumn)		30m-500m	9000	3	0.4/day	OceanParcels	2D; Lagrangian particle tracking	Grimaldi et al. (2022)*
SCR	*Acropora spp.*	2000-2020 (autumn)		120m	1,762,930	3	0.4/day	OceanParcels	Lagrangian particle tracking; 2D; local network analysis	Grimaldi et al. (2024)*

NR = not reported; * = no data available for network analysis.

Location codes: SWC = Southwest Coast; CC = Central Coast; HAI = Houtman Abrolhos Islands; SB = Shark Bay; NIN = Ningaloo; PNS = Pilbara nearshore; POS = Pilbara offshore; EXG = Exmouth Gulf; DAR = Dampier Archipelago; NWN = Northwest nearshore; NWO = Northwest offshore; DPE = Dampier Peninsula; KNS = Kimberley nearshore; KOS = Kimberley offshore; ASH = Ashmore Reef; SCR = Scott Reef; RS = Rowley Shoals; TI = Timor Sea (Indonesia).

Genetic connectivity patterns

A total of 1,270 pairwise genetic-differentiation values (F_{ST}) with assignable geographic distance were compiled from nine studies, comprising 805 between-region and 465 within-region comparisons across 14 reef regions. A broader set of 819 between-region comparisons from eight studies, spanning 15 of the 17 reef regions, was used to build the regional multi-species genetic connectivity network; this set included one study for which geographic distanced would not be reconstructed. Among 59 unique between-region pairs, 15 (25.4%) exhibited high connectivity (mean $F_{ST} < 0.05$), 25 (42.4%) moderate connectivity ($0.05 \leq F_{ST} < 0.15$), and 19 (32.2%) low connectivity ($F_{ST} \geq 0.15$; Fig. 4a).

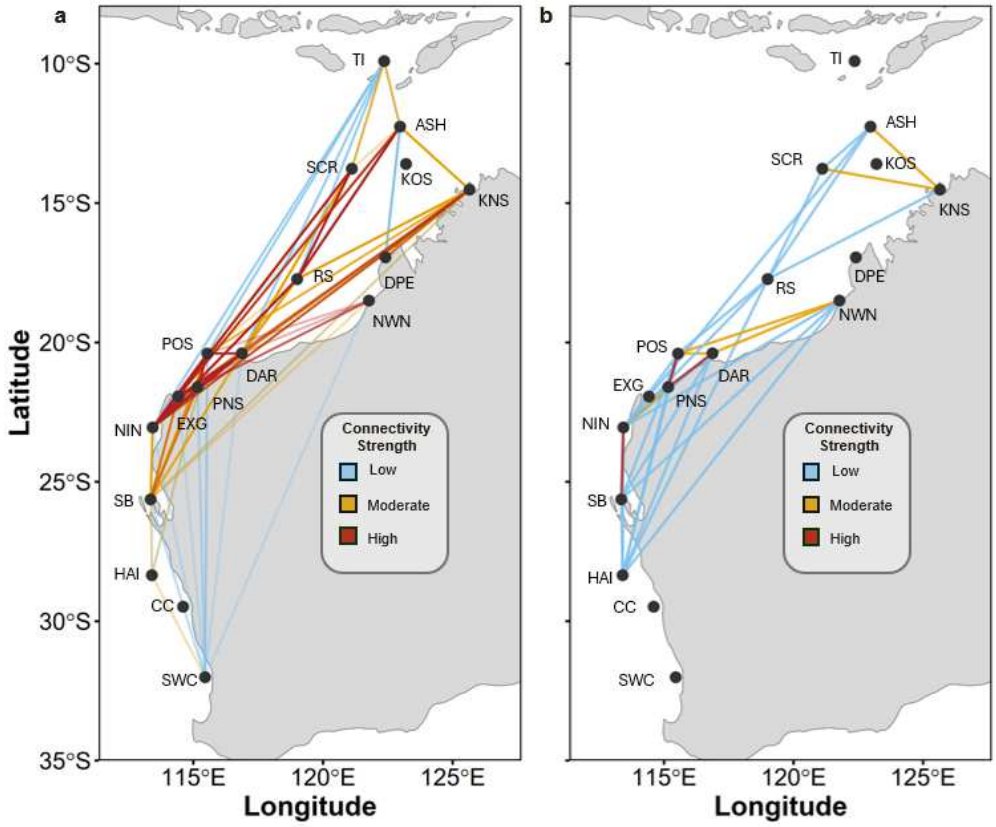


Fig. 4 Network representation of multi-species genetic (a) and biophysical modelling (b) connectivity networks across Western Australia. In **(a),** genetic connectivity classes are: high, mean $F_{ST} < 0.05$; moderate, $0.05 \leq$ mean FST < 0.15; low, mean FST ≥ 0.15; in **(b)**, biophysical connectivity classes are relative. Nodes in the network represent reef regions.

Multi-species connectivity across WA was heterogeneous and strongly structured at the regional scale. High-connectivity pairs clustered along the Pilbara and northwest nearshore regions, with mean F_{ST} as low as 0.005 between Northwest nearshore and Pilbara offshore. The offshore atolls contributed one high-connectivity pair, Rowley Shoals–Scott Reef (mean $F_{ST} = 0.032$), the strongest connection recorded outside the nearshore cluster. Moderate connectivity was more widely distributed, linking adjacent and non-adjacent regions, including connections between Ningaloo and the offshore reefs (Scott Reef and Rowley Shoals) and among the Timor Sea, Ashmore Reef, and Scott Reef (mean F_{ST} = 0.107–0.140). Low-connectivity pairs formed three geographic clusters. The Southwest Coast was weakly connected to seven of the eight regions with which it was compared

(mean F_{ST} = 0.219–0.354), with the Abrolhos as the sole moderate-connectivity exception (mean F_{ST} = 0.141). Five of these seven low-connectivity pairs were supported by a single study, and none contained more than three underlying comparisons. Ashmore Reef showed a similar pattern, with the strongest differentiation from Dampier Peninsula (mean F_{ST} = 0.420, the highest regional mean in the dataset). The Timor Sea, represented by a single study across all comparisons, showed low or moderate connectivity with every region to which it was compared (mean F_{ST} = 0.107–0.325). Concordance values for the 23 region pairs represented by both evidence streams are reported in Supplementary Table S3.

IBD was tested within each study-by-species unit (Table S5). The synthesis comprised 11 study-by-species units from nine studies, spanning geographic distances of 1–2,250 km (Table 1). Eight of the 11 units showed significant positive Mantel correlations between F_{ST} and $\log_{10}$- geographic distance (r = 0.51–0.75, $p \leq 0.004$). The remaining three units, *Seriatopora hystrix* and both taxa from a study sampled entirely within one reef system, did not show significant IBD (r = −0.35 to 0.18, $p \geq 0.187$).

Biophysical connectivity patterns

Of the 11 dispersal-modelling studies retained from the systematic review, four provided outputs that could be mapped to region-pair connections and therefore contributed to the quantitative regional network (Condie and Andrewartha 2008; Kool and Nichol 2015; Feng et al. 2016; Markey et al. 2016). These studies differed substantially in design. Hydrodynamic forcing models included HYCOM, ROMS, MECO, and WASA/OzROMS, with horizontal resolutions of 1–10 km. All four used Lagrangian particle tracking under passive-dispersal assumptions; three were three-dimensional, whereas Markey et al. (2016) used a two-dimensional surface model (Table 2). PLD ranged from 7 to 250 days, and mortality was represented by fixed daily mortality, exponential decay, or no explicit mortality function.

Larval settlement was handled differently across the four studies. Condie and Andrewartha (2008) did not model a species-specific competency window, noting that pelagic larval duration for regional corals was largely unknown, and instead reported cumulative dispersal probability at fixed intervals (7, 14, and 21 days monthly; 28, 56, and 84 days quarterly). Feng et al. (2016) modelled a minimum competency period of 3.24 days for *Acropora millepora* (Connolly and Baird 2010) within a 60-day tracked simulation, counting a particle as settled once it passed this threshold and came within 0.3 km of suitable reef habitat, the only one of the four studies to parameterise both a named coral species and its settlement behaviour. Kool and Nichol (2015) used ophiuroid (brittle star) rather than coral life history to demonstrate the underlying particle-tracking framework, tracking particles to a fixed 90-day limit with exponential mortality of 0.06 per day and no settlement threshold; this taxonomic mismatch is acknowledged as a limitation, and the resulting values are retained as a proxy for physical transport potential rather than a coral-specific prediction. Markey et al. (2016) tracked transport for up to 250 days and compared arrival times against literature-derived competency estimates of roughly 110 days rather than imposing a settlement window, finding that most modelled arrivals exceeded the known competency period for coral larvae.

Particle releases ranged from 900 to 1,280,000 per site or sub-population. Seasonal coverage also varied. Eight of the 11 biophysical studies reviewed modelled only the austral autumn mass-spawning period, two modelled all four seasons, and one modelled both austral autumn and spring spawning without covering summer or winter.

The four contributing studies reported 41 categorical region-pair connections. Two were classified as unconnected, leaving 39 connections rated as low, moderate, or high across 29 unique regional pairs (Fig. 4b). Consequently, many of the 17 reef regions were only partially characterised by biophysical modelling. Of the 39 classified connections, eight (20.5%) were high connectivity, nine (23.1%) moderate, and 22 (56.4%) low. Directional connectivity (poleward or equatorward) was reported for 18 of the 41 total connections: 15 (36.6%) were poleward (southward), one (2.4%) was equatorward (northward), and two (4.9%) were bidirectional. The remaining 23 connections (56.1%) had no explicit direction reported in the source studies.

High-connectivity corridors clustered around three geographic pairings: Pilbara offshore–Pilbara nearshore, Dampier Archipelago–Ningaloo, and Ningaloo–Shark Bay. Moderate connections linked these high-connectivity nodes to neighbouring regions and connected the offshore atolls and reefs (Ashmore Reef, Kimberley nearshore, and Scott Reef) in a separate chain. Two pairs (Abrolhos–Ningaloo and Ashmore Reef–Scott Reef) fell between low and moderate classes because contributing models disagreed. All remaining pairs were classified as low, dominated by long-distance links to the Abrolhos and connections among offshore atolls and reefs.

Comparisons of genetic and biophysical networks

Genetic and biophysical evidence overlapped for 23 regional pairs, drawn from 59 genetic region-pairs and 29 dispersal region pairs (Tables S2, S3). Across the matched pairs, genetic differentiation tended to decline as dispersal strength increased, although the permutation test did not cross the conventional 0.05 threshold ($\rho = -0.40$, permutation $p = 0.055$). Because dispersal strength could simply track geographic proximity rather than reflecting a biologically distinct transport signal, we tested whether distance alone could explain this pattern. Dispersal strength was strongly associated with inter-region distance ($\rho = -0.69$, $p < 0.001$), whereas the corresponding association between regional genetic differentiation and distance was weaker ($\rho = 0.32$, $p = 0.130$), indicating that the genetic-biophysical relationship above could be partly confounded by distance. After accounting for distance using Freedman–Lane residual permutation, the genetic–biophysical association weakened further ($\rho = -0.26$, $p = 0.245$). Consistent with this result, genetic F_{ST} did not differ significantly among low (0.069), moderate (0.035), and high (0.032) biophysical classes (Kruskal-Wallis $p = 0.267$; Supplementary Table S2).

We also compared the two networks as whole structures, extending the region-pair comparisons above to test whether genetic and biophysical evidence agree on the broader organisation of connectivity across the region, not just on individual connections. Both genetic and biophysical networks were significantly more modular than degree-preserving randomisations, indicating that each evidence stream independently supports the existence of distinct regional clusters rather than one continuously connected system. Community detection resolved four genetic communities and two biophysical communities. To test agreement more directly, we compared network centrality values (degree, strength, and betweenness) for the regions shared between the two networks, asking whether the same regions were identified as important by both evidence streams. Concordance was strongest for regional connection strength ($\rho = 0.601$, $p = 0.052$), though this association did not meet the conventional $\alpha = 0.05$ threshold; degree ($\rho = 0.299$, $p = 0.371$) and betweenness ($\rho = 0.265$, $p = 0.420$) were also not significantly associated between evidence streams (Table S2). None of the three centrality measures showed statistically robust

agreement, indicating that a region's importance in the genetic network does not reliably predict its importance in the biophysical network, or vice versa.

IBD and among-study heterogeneity

Genetic differentiation increased with geographic distance across the 11 study-by-species units. Random-effects meta-analysis of unit-level Fisher's z values gave a pooled correlation of r = 0.578 (95% CI 0.448-0.684, $p < 0.001$) with negligible residual heterogeneity under REML ($I^2 = 0.001\%$, $\tau^2 = 0$, Q (10) = 11.91, $p = 0.291$). This near-zero heterogeneity is, however, specific to the REML estimator. DerSimonian-Laird, Paule-Mandel and empirical Bayes estimators all returned τ^2 between 0.018 and 0.024, corresponding to I^2 of 16-20%, and the Q confidence interval on I^2 spanned 0-81.6%. Heterogeneity is therefore better described as weakly determined at 11 units than as absent.

The IBD signal was spatial scale dependent. Between regions, the pooled correlation was r = 0.639 (95% CI 0.326-0.825), whereas within regions it was weak and did not differ significantly from zero (r = 0.167, 95% CI -0.021 to 0.343, $p = 0.082$). The between-region estimate was also heterogeneous ($I^2 = 78.1\%$), indicating that the direction of regional distance decay was broadly consistent, but its magnitude varied substantially among studies.

The pooled point estimate was stable across alternative specifications (Table S4). Leave-one-unit-out estimates ranged from 0.535 to 0.603 across the 11 units. Alternative treatment of negative raw F_{ST} values changed the pooled estimate by < 0.01, and leave-one-study-out estimates ranged from 0.531 to 0.620. The Knapp–Hartung adjustment widened the 95% confidence interval to 0.414–0.706 without changing the point estimate. A three-level model with units nested within studies returned r = 0.566 (95% CI 0.405–0.693), and study-clustered robust standard errors returned r = 0.578 (95% CI 0.398–0.715). Restricting the synthesis to one unit per recorded sample-overlap group returned r = 0.610 (95% CI 0.468–0.721).

Under REML, the 95% prediction interval matched the confidence interval because τ^2 was estimated as zero. Exploratory Egger-type regressions did not provide clear evidence of a small-study effect ($p = 0.093$ using standard error and p = 0.096 using inverse sample size), but these diagnostics are underpowered with only 11 units and should not be interpreted as evidence that small-study bias is absent. The pipeline also reported 80% power for a correlation of r = 0.30 and 46% power for r = 0.20.

Barriers and corridors

Unit-level residuals from the linearized F_{ST} model were used to flag region pairs that depart from the general distance-decay relationship. A residual higher than expected was classified as a candidate barrier, and a residual lower than expected was classified as a candidate corridor. Of the 1,270 units assessed, 41 showed a strong barrier-consistent departure and five showed a moderate one; 18 showed a moderate corridor-consistent departure, and none showed a strong one. Because a single region pair can include several study-by-species comparisons, these unit-level departures were also summarised at the region-pair level. 14 of the 59 region pairs contained at least one comparison classified as a barrier or corridor. This region-pair label reflects only the pair's most extreme comparison, not its average, so a pair can be flagged even when most of its comparisons sit close to the fitted expectation.

Candidate barriers were concentrated around Ashmore Reef and the Southwest coast, with an additional signal between the Timor Sea and Dampier Archipelago. Candidate corridors were concentrated around Scott Reef, including comparisons with the offshore Pilbara, Ningaloo, and the Rowley Shoals. Dampier Peninsula–Kimberley nearshore was the clearest case of this within-pair heterogeneity, containing both barrier- and corridor-classified comparisons.

These classifications identify genetic differentiation that departs from the fitted IBD expectation and should be read as candidates for further investigation rather than as direct, confirmed estimates of restricted or enhanced connectivity.

Discussion

The combined evidence indicates that connectivity across WA is structured into regional groupings rather than a single, continuous system. Isolation by distance was scale dependent. Genetic differentiation increased with distance between regions, but within-region distance explained little of the observed structure. This distinction helps reconcile apparently conflicting local-scale studies, since fine-scale differentiation can be dominated by reef-scale hydrodynamics, lineage composition, reproductive timing, and demographic history even where a coast-wide regional gradient is detectable. Genetic and biophysical dispersal networks also shared several prominent regions, but their statistical concordance was weak and strongly confounded by distance. Taken together, these results suggest that genetic evidence, reflecting connectivity accumulated over long timescales, points to broader, coarser-grained regional connectivity, whereas biophysical evidence, reflecting shorter-term demographic connectivity, points to greater regional partitioning.

Genetic and biophysical studies across WA also suggest that a simple distance model is insufficient to explain the connectivity patterns detected here, for several reasons. First, deep-water gaps and current boundaries can separate coastal and offshore populations (Underwood 2009), and fine-scale hydrodynamics can produce stronger differentiation between nearby sites than between more distant ones, as seen at the Houtman Abrolhos Islands (Thomas et al. 2015). Corals at Scott Reef show depth-associated genetic structure and evidence of vertical exchange (Rosser & Gilmour 2008), a further sign that circulation structures connectivity at scales finer than simple horizontal distance. Second, environmental gradients and local adaptation add further complexity, best illustrated by the complex connectivity patterns detected in *A. digitifera* across WA (Adam et al. 2022). Third, post-glacial demographic history can leave persistent spatial signatures in offshore populations (Zhang et al. 2022; Agiadi et al. 2024). Finally, reproductive mode and timing further modify these patterns. Brooding taxa tend to show stronger local structure than broadcast spawners, and asynchronous spawning can restrict gene flow even without a physical barrier (Underwood et al. 2007, 2009; Rosser 2016; Thomas et al. 2020). Taken together, these factors show that connectivity in WA reflects local circulation, depth structuring, environmental and demographic history, and reproductive biology rather than distance alone, a pattern consistent with other reef systems such as the Great Barrier Reef (van Oppen et al. 2011).

Life-history and taxon identity can generate connectivity signals that a simple distance model would miss, and two examples from this synthesis illustrate how. In the Dampier Archipelago, brooding coral recruitment tracks coral cover within 5 m of recruitment sites, whereas spawning coral recruitment tracks coral cover at scales up to 15 km (Thomson et al. 2021), showing that demographic processes here operate at different spatial scales depending on life history. A second, independent example comes from the southern edge of the network, where

several lines of evidence point to restricted dispersal along the southwest coast. Isolation of this region in our synthesis was driven largely by *T. reniformis* (Evans et al. 2021) and is consistent with earlier evidence that local *P. damicornis* populations show highly localised, largely clonal dispersal over 0.25–1 km and small effective population sizes (Stoddart 1984). Genome-wide data for *P. damicornis* at the same high-latitude region further show pronounced differentiation and reduced diversity relative to tropical populations to the north (Thomas et al. 2017), supporting the persistence of restricted gene flow across marker generations. Because this evidence spans different taxa, it does not establish a single shared mechanism. Rather, it provides independent support for restricted connectivity along this coastline. Together, the Dampier and southwest coast examples show that the same regional network can contain genuinely different processes operating at different spatial scales, which is precisely why regional synthesis must retain biological and methodological context rather than treating connectivity as a single, uniform signal.

Genetic connectivity outpaces modelled dispersal

Patterns of genetic connectivity differed from biophysical patterns when compared regionally. Genetic data implied greater connectivity than the biophysical classification for 16 of the 23 matched region pairs. Agreement between the two methods was concentrated among well-sampled offshore and nearshore Pilbara, Ningaloo, and Dampier Archipelago pairs, all classified as high connectivity by both methods, and at Abrolhos–Pilbara offshore, classified as low connectivity by both. Disagreement was concentrated instead among long-distance and offshore-atoll comparisons, such as Rowley Shoals–Scott Reef. This pattern, genetic data implying stronger connectivity precisely where distances are largest and sampling is sparsest, is consistent with genetic structure integrating rare, cumulative dispersal events over many generations that short hydrodynamic simulations are unlikely to capture. Comparable work on Great Barrier Reef corals has shown that incorporating water current directionality is critical to relating biophysical dispersal to genetic patterns (Riginos et al. 2019). Current direction could not be incorporated here given our use of symmetric pairwise $F_{ST,}$, so future studies should do so to further resolve these differences in connectivity patterns.

In conjunction with current direction, several other non-exclusive mechanisms could plausibly contribute to the divergent patterns we detected here. First, hydrodynamic models represent finite time windows, whereas genetic structure integrates successful exchange over many generations (Bryan-Brown et al. 2017; Balbar et al. 2024). Episodic events can therefore matter disproportionately. For example, cyclone-driven modelling on the Northwest Shelf produced cross-shelf arrival probabilities of 63–91% within six days during two historical cyclones, compared with no cross-shelf connection over the same interval in a non-cyclone year (Radford et al. 2014). Second, fine-scale models show that substantial local retention can coexist with a small fraction of particles available for longer-distance export (Grimaldi et al. 2022, 2024). Repeated low-probability dispersal may therefore leave a detectable genetic signature even when it is weak in a limited set of simulations (Slatkin 1987; Radford et al. 2014). Third, the synthesis we undertook here compresses model outputs by design, including those that differ in species parameterisation, resolution, competency assumptions, and simulated years. These explanations remain hypotheses rather than demonstrated causes, but they define clear targets for paired genetic-biophysical studies that use matched species, spawning seasons, and simulation periods.

Sympatric cryptic lineages confound F_{ST}-based synthesis

The influence of unresolved lineage structure is likely present in our results, and one study in this synthesis lets us illustrate it directly. Adam et al. (2022) flagged four inshore Kimberley sites as likely harbouring cryptic species. When those sites were retained, Kimberley nearshore showed F_{ST} values of 0.45–0.50 against offshore atolls and emerged as the strongest barrier in the WA network. When they were excluded, Kimberley nearshore instead appeared moderately connected to Ashmore Reef (mean F_{ST} = 0.068) and dropped out of the strongest barrier signals entirely. Excluding four of 163 sites therefore reversed the region-scale connectivity inference for this region pair. This is not a minor sensitivity issue. It shows that a handful of unrecognised cryptic lineages can flip a region from the network's strongest apparent barrier to an unremarkable, moderately connected node, meaning that any connectivity synthesis built on F_{ST} without lineage screening risks mistaking cryptic population structure for genuine dispersal limitation.

The influence of cryptic lineages is consistent with the expected consequences of pooling partially reproductively isolated lineages. When cryptic taxa co-occur but are analysed as a single population, the resulting Wahlund effect can inflate apparent differentiation at some spatial scales and obscure broader spatial patterns (Warner et al. 2015; Sheets et al. 2018). In the *A. hyacinthus* complex, reassignment of individuals to cryptic species altered both the magnitude and spatial distribution of pairwise F_{ST} (Sheets et al. 2018). Together, these results suggest that failing to account for cryptic lineages can materially change connectivity inference, and that cryptic lineage composition should be treated as a source of biological heterogeneity in future syntheses.

In additional to cryptic lineages, reproductive asynchrony can also add an additional source of structure. Many broadcast-spawning taxa in the region have a major autumn spawning event and a smaller spring event (Rosser 2013) and in some species these cohorts correspond to genetically differentiated breeding lineages (Rosser et al. 2020). Spring- and autumn-spawning cohorts of *A. samoensis* have PaxC lineages with ΦST = 0.97 (Rosser 2015), while *A. tenuis* cohorts have been reported with ΦCT = 0.98 (Rosser 2016; Rosser et al. 2020). These values indicate very strong differentiation and suggest that reproductive timing may be influencing our results. One reef pair illustrates the potential consequence. In the pooled *A. tenuis* dataset, Rowley Shoals–Scott Reef is among the most connected pairs in the network (mean F_{ST} = 0.032). Thomas et al. (2022), however, sampled only the spring-spawning lineage of *A. tenuis* at these reefs (F_{ST} = 0.25), a value that would place the pair among the more strongly differentiated comparisons. This contrast shows that spawning-lineage identity can change the inferred status of the same reef pair from a putative corridor to a putative barrier.

Conclusions

Taken together, the evidence supports a regional-scale view of coral connectivity across Western Australia. Genetic differentiation shows a clear distance-related signal between reef regions but not within them, while local patterns are shaped by cryptic lineage composition, reproductive timing, fine-scale oceanography, and each species' demographic history. Genetic and biophysical evidence agree only partially, and where they diverge, genetic data more often imply greater connectivity, a gap this synthesis cannot yet attribute to any single cause. For management, these results support evaluating connectivity at the scale of reef regions while treating genetic and biophysical evidence as complementary rather than interchangeable. The most informative next step is purpose-designed integration, pairing matched genetic sampling and high-resolution dispersal modelling for the same taxa, spawning cohorts, and years, with directionality and lineage identity resolved explicitly.

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