Speciation with gene flow in marine systems

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Supplementary material

TABLE 1   Potential cases of (incipient) speciation with gene flow in marine taxa. For bibliographical details of references, see the reference list in the main text.

Taxa	Reproductive isolation	Population genetic process			Gene flow during divergence	Biogeographic pattern	Other	References
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits		Overlapping distributions		
Chromista								
Gyrista: Ochrophyta								
Phaeophyceae: Fucales								
Fucaceae								
Fucus spiralis Linnaeus, 1753, *F. vesiculosus* Linnaeus, 1753, and *F. guiryi* Zardi, Nicastro, Serrão & Pearson, 2011	Extensive hybridisation and introgression occurs in sympatry between *F. guiryi* and both *F. spiralis* and *F. vesiculosus*; reproductive isolation between *F. spiralis* and *F. vesiculosus* is significant, based on microsatellite data, though introgression in mtDNA has been observed in some parts of the distribution (Coyer et al., 2011).	Vertical zonation in the intertidal zone can be seen in *Fucus* spp. morphotypes; resilience of morphotypes to emersion stress is consistent with the observed zonation; mating systems differs between *F. spiralis* and *F. guiryi* (hermaphroditic with a high degree of selfing) and *F. vesicolosus* (dioecious with obligate outcrossing); timing of gamete release differs between the species (Ladah et al., 2008).	Differences in mating system and timing gamete release may induce some assortative mating.	Differences in mating systems could act as a magic trait; evolution of different mating systems may have coincided with the initial divergence between species (Billard et al., 2010).	—	Yes	Pattern of introgression suggests that divergence between *F. guiryi* and *F. spiralis* was allopatric, followed by range expansion and secondary contact; phylogeographic patterns have been described within *Fucus* spp. (Coyer et al., 2011)	Zardi et al. (2011)
Animalia								
Porifera								
Demospongiae: Chondrillida								
Chondrillidae								
Chondrilla caribensis Rützler, Duran & Piantoni, 2007*	Possibly, mtDNA haplotypes were rarely shared between ecotypes.	Different ecotypes are associated with either mangroves or open reefs.	Possibly, by habitat-association.	Possibly, habitat-preference could act as a magic trait.	—	Yes	The two ecotypes are described as the subspecific taxa *C. caribensis* forma *manglaris* and forma *hermatypica*.	Duran & Rützler (2006); Rützler et al. (2007)
Cnidaria								
Anthozoa: Hexacorallia: Scleractinia								
Montastraeidae								
Montastraea cavernosa (Linnaeus, 1767)	Reduced vertical gene flow is likely, as a model assuming panmixia had relatively low support.	Genetically diverged populations occur at different depth ranges (see also Brazeau et al., 2013; Goodbody-Gringley et al., 2015).	Unknown, depth-segregation could induce some assortative mating; higher rates of self-recruitment at some locations could induce some assortative mating (Goodbody-Gringley et	Depth-preference could possibly act as a magic trait, but more research is necessary.	Bayesian models of gene flow showed evidence for migration from shallow to intermediate and deep populations; models incorporating gene flow where ranked higher	Yes	Strength of genetic differentiation differed among localities, possibly as a result of local hydrology; deep and shallow colonies mostly harboured the same *Symbiodinium*	Serrano et al. (2014)

Taxa	Reproductive isolation	Population genetic process				Biogeographic pattern	Other	References
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions		
			al., 2012).		than a panmictic model.		type; some geographic structure has been observed (Brazeau et al., 2013).	
Mussidae								
Favia fragum (Esper, 1793)	Reduced gene flow between morphotypes based on microsatellite data; hybridisation was observed (Carlon & Lippé, 2011).	The different ecotypes are found at different depths, correlating to different habitat types; different alleles at one locus were nearly fixed in the ecotypes, which may be the result of selection on this locus or linked loci; quantitative genetic variation between ecotypes also suggest disruptive selection.	Difference in depth preference could induce some assortative mating, especially since larvae settle very close to parent colonies (Carlon & Olson, 1993).	Depth-preference could act as a magic trait.	—	Yes	Populations showed genetic structuring over small geographic scales (1–2 km), as well as across the Caribbean (Goodbody-Gringley et al., 2010); degree of hybridisation depended on the degree of local sympatry between morphotypes (Carlon & Lippé, 2011).	Carlon & Budd (2002); Carlon et al. (2011)
Pocilloporidae								
Seriatopora hystrix Dana, 1846	Unknown, though evidence of reduced gene flow was found in microsatellite data; in some localities, recruitment of larvae from deep into shallow habitats was found (Van Oppen et al., 2011).	Genetically diverged ecotypes are associated with different, depth-segregated habitats (see also Van Oppen et al., 2011).	Unknown, though depth-segregation could induce some assortative mating.	Depth-preference could possibly act as a magic trait, but more research is necessary.	—	Yes	Some differences in gross morphology and genetic partitioning of associated *Symbiodinium* were observed across habitats as well; incipient ecological speciation is the most parsimonious explanation for this divergence; some mtDNA haplotypes matched with haplotypes from distant localities; genetic structuring has also been observed (Ayre & Dufty, 1994; Ayre * Hughes, 2000; Maier et al., 2005; Warner et al., 2015).	Bongaerts et al. (2010)
Anthozoa: Octocorallia: Alcyonacea								
Gorgoniidae								
Eunicella singularis (Esper, 1791)	Restricted gene flow between shallow- and deep-water populations.	Two morphotypes are separated by depth.	Unknown, though depth-segregation could induce some assortative mating.	Depth-segregation between morphotypes could possibly act as a magic trait, but more research is required.	—	Yes	No genetic structuring was found among shallow populations on a spatial scale of ten kilometres; depth at which genetic split occurs is similar to the	Costantini et al. (2016)

Taxa	Reproductive isolation	Population genetic process				Biogeographic pattern	Other	References
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions		
							depth of the seasonal thermocline.	
Plexauridae								
Eunicea flexuosa (Lamouroux, 1821)	Some gene flow, varying among localities, between ecotypes was observed; a narrow hybrid zone has been reported (Prada & Hellberg, 2014).	Two depth-associated ecotypes exist within *E. flexuosa* (see also Kim et al., 2004; Prada et al., 2008); transplant experiments showed a decrease in survival rate in the non-native depth range.	Based on survival rates in transplant experiments and the high age at first reproduction, hybridisation is expected to be low to very low.	Selection over a depth gradient, resulting in immigrant inviability (Pfennig, 2013), combined with a high age of first reproduction, may act as a magic trait.	Isolation–migration models support asymmetrical gene flow during or right after divergence.	Yes	Little geographic divergence was observed within the ecotypes, high connectivity among populations across large geographic distances.	Prada & Hellberg (2013)
Mollusca								
Bivalvia: Protobranchia: Nuculida								
Nuculidae								
Nucula atacellana Schenck, 1939[†]	Extremely low gene flow between depth-segregated populations.	Strong genetic divergence over depth has been observed; disruptive selection over the depth range, for example resulting from changes in pressure, could act on the populations (see also Chase et al., 1998).	Differences in depth-range could induce assortative mating.	Possibly, depth-preference could act as a magic trait	Isolation–migration models found extremely low gene flow between depth-segregated populations.	Yes	No morphological differences between depth-segregated populations; genetic divergence among populations separated by depth much greater than among geographically distant populations; low divergence within depth ranges (see also Jennings and Etter, 2014); genetic divergence over depth as a result of hydrodynamics seems unlikely (Chase et al., 1998).	Zardus et al. (2006); Jennings et al. (2013)
Gastropoda: Opisthobranchia: Nudibranchia								
Fionidae								
Phestilla spp.	No evidence for introgression in mtDNA.	Species are associated with different host species; evidence for a host shift was found within the genus (see also Ritson-Williams et al., 2003).	By host species, nudibranchs show host fidelity.	Host-preference may act as a magic trait.	—	Yes	Phylogenetic signal of host species was stronger than the signal of locality; some genetic divergence among localities; allopatric speciation played likely a smaller role within *Phestilla* spp., but cannot be precluded.	Faucci et al. (2007)
Phestilla minor Rudman, 1981	Possibly, though a low level of hybridisation may occur based on	Genetically diverged populations are associated with different	By host species, nudibranchs show host fidelity (Faucci et al.,	Host-preference may act as a magic trait.	—	Yes	Multiple cryptic clades within *P. minor* have been identified;	Fritts-Penniman (2016)

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Taxa	Reproductive isolation	Population genetic process				Biogeographic pattern	Other	References
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions		
	mtDNA haplotypes.	host species; a lysosomal membrane protein could potentially be involved in disruptive selection.	2007).				ecological speciation in sympatry is the most reasonable explanation for the observed divergence; genetic structuring of populations between either side of the Sunda Shelf was observed, but no phylogeographic structuring east of the Sunda Shelf, even across known phylogeographic barriers.	

Gastropoda: Caenogastropoda: Neogastropoda
  Muricidae

Taxa	Reproductive isolation	Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
Coralliophila violacea (Kiener, 1836)	Evidence for unidirectional gene flow and hybridisation between populations associated with different host species was found.	Populations are associated with different host species; genomic loci potentially under disruptive selection were identified; selection is possibly related to detoxification of host metabolites.	Possibly, snails are associated with different host species.	Host-preference may act as a magic trait; snails possibly show a preference for their native host.	—	Yes	Populations in the Coral Triangle were well-connected; local adaptation in peripheral populations; a genetic break was observed in populations on either side of the Sunda Shelf (see also Lin and Liu, 2008).	Simmonds (2016); Simmonds et al. (2018)

Gastropoda: Caenogastropoda: Littorinimorpha
  Littorinidae

Taxa	Reproductive isolation	Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
Littorina saxatilis (Olivi, 1792)	Partial isolation, gene flow is reduced among ecotypes (Panova et al., 2006); prezygotic isolation exists between some ecotypes (Rolán-Alvarez et al., 1999); possibly some postzygotic isolation between one pair of ecotypes (Hull et al., 1996; but see Johannesson et al., 2010).	Disruptive selection by crab predation and wave exposure directly acts on body size; ecotypes show vertical stratification or differ in microhabitat; migration between habitats decreases survival in some ecotypes; selected traits are likely polygenic (Hollander et al., 2015; Westram et al., 2016).	Size-assortative mating occurs between ecotypes, also in hybrid zones were different ecotypes coexist.	Body size may be a magic *trait (Servedio et al., 2011).*	Analyses using approximate Bayesian computation supported parallel evolution of ecotypes at different locations with gene flow during and after divergence over old divergence of ecotypes without gene flow (Butlin et al., 2014).	Yes	Evolutionary history of *L. saxatilis* is complex; different ecotypes have been found across the geographic range of *L. saxatilis* (see also Quesada et al., 2007; Butlin et al., 2014); morphology differs between ecotypes pairs; two geographically distinct mtDNA lineages were found within *L. saxatilis* (Doellman et al., 2011).	Johannesson et al. (2010) and references therein.

  Tonnoidea

Taxa	Reproductive isolation	Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
Bursina fijiensis (Watson, 1881) [‡] and *Bursa quirihorai* Beu, 1987	Likely, no evidence for hybridisation and introgression was found, even though species co-occur at some localities.	Species have different, but overlapping depth ranges.	Preference for different depth ranges could induce assortative mating.	Depth-preference could act as a magic trait.	—	Yes	Species have long-lived, planktonic larvae; no evidence exists for any biogeographic barrier at the estimated time of	Castelin et al. (2012)

Taxa	Reproductive isolation	Population genetic process				Biogeographic pattern		
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
							divergence within the present-day distribution.	
Gastropoda: Patellogastropoda								
Nacellidae								
Cellana spp.	Possibly, though evidence for rare hybridisation was found; a low level of mitochondrial introgression suggests successful back-crossing of hybrids.	Different limpet species occur in different intertidal zones.	Adaptation to a specific part could induce only limited assortative mating, as limpet species occur within centimetres of each other in some localities and limpets release gametes into high energy waves.	Unknown	—	Yes, nested geographical distribution of three limpet species in the Hawaiian Islands.	The limpet species form a monophyletic group, consistent with the nested geographical distribution, suggesting a single colonisation event; allopatric speciation cannot be precluded.	Bird et al. (2011)
Annelida								
Polychaeta: Sedentaria: Sabellida								
Siboglinidae								
Osedax spp.	Yes, prezygotic isolation may result from differences in depth range and temporal succession; incongruence between trees based on mtDNA and nuclear DNA involving the undescribed *O.* "spiral" (Vrijenhoek et al., 2009) may indicate hybridisation.	Species possibly vary in temporal succession (e.g., the undescribed sister species *O.* "yellow-collar" and *O.* "orange-collar"); depth distribution varies among species (e.g., sister species *O. rubiplumus* Rouse, Goffredi & Vrijenhoek, 2004 and *O. roseus* Rouse, Worsaae, Johnson, Jones & Vrijenhoek, 2008.	Differences in habitat associations and temporal succession could induce assortative mating.	Possibly, differences in habitat and temporal succession could act as a magic trait.	—	Yes	—	Braby et al. (2007)
Arthropoda								
Crustacea: Amphipda: Gammarida								
Anisogammaridae								
Eogammarus confervicolus (Stimpson, 1856)	Unknown; hybridisation among habitat types is possible; no evidence for postzygotic isolation was found.	Populations are associated with different habitats.	Assortative mating among habitats is likely.	Habitat-preference, as observed in laboratory experiments, could act as a magic trait.	—	Yes	High-salinity waters between optimal habitats could lead to local differentiation; evidence for a shift in habitat was found, which occurred two times independently at two locations.	Stanhope (1992, 1993)
Crustacea: Decapoda: Brachyura								
Pinnotheridae								
Nepinnotheres novaezelandiae (Filhol,	Unknown, populations are classified as a single	Populations are associated with different	Possibly by host species, as populations	Possibly, host-preference could act as a	—	Yes	Genetic differentiation was found among	Stevens (1990)

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Taxa	Reproductive isolation	Population genetic process			Biogeographic pattern	Other	References
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions		
1885) [§]	species.	host species.	are associated with different host species.	magic trait.			localities, but differentiation among host species within a locality was higher than differentiation among localities.	

Crustacea: Decapoda: Caridea
Alpheidae

Taxa	Reproductive isolation	Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
Alpheus armatus Rathbun, 1901 species complex	Yes, based on experiments by Knowlton & Keller (1985).	Species are associated with different host species and/or occupy different depth ranges.	Yes, shrimps show host fidelity.	Host-preference could be a magic trait; strong preference for the native host species has been found (Knowlton & Keller, 1985); colour pattern, which is diagnostic among the species, could also have played a role as well as depth segregation.	Isolation–migration models suggest gene flow after divergence.	Yes	Allopatric speciation followed by reinforcement after secondary contact cannot be precluded.	Hurt et al. (2013)
Synalpheus rathbunae Coutière, 1909 species complex	Possibly, based on a lack of shared alleles in most of the scored allozyme loci.	Species are associated with different host species.	Yes, species are philopatric.	Host-preference could act as a magic trait.	Unknown, but species lacks a pelagic larval stage (Dobkin, 1969).	Yes	Some genetic structure has been observed across the Caribbean.	Duffy (1996b)

Crustacea: Sessila: Balanomorpha
Pyrgomatidae

Taxa	Reproductive isolation	Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
Wanella milleporae (Darwin, 1854)	Possibly, no evidence for hybridisation in mitochondrial loci, morphological differences consistent with genetic data.	Species are associated with host species with different growth forms.	Specialisation to the host may have resulted in assortative mating.	Host-preference could act as a magic trait.	—	Yes	Some evidence was found for multiple independent host-shift events in different geographical regions (see also Mokady & Brickner, 2001); secondary contact after allopatric speciation cannot be precluded; some genetic structuring was observed around Taiwan.	Tsang et al. (2009)

Echinodermata
Asteroidea: Forcipulatida
Zoroasteridae

Taxa	Reproductive isolation	Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
Zoroaster fulgens Thomson, 1873	No evidence for hybridisation was found in mtDNA.	Morphotypes are bathymetrically separated.	Some assortative mating could take place based on depth, assortative mating may not be complete in populations close together.	Possibly, depth-preference could act as a magic trait; more research, for example on the degree of assortative mating, is required.	—	Yes	Asteroids were more closely related to geographically separated (~900 km) asteroids of the same morphotypes than to geographically close (~1	Howell et al. (2004)

| Taxa | Reproductive isolation | Population genetic process | | | | Biogeographic pattern | Other | References |
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions		
							km) asteroids of the other, bathymetrically separated morphotype; little geographic structuring was observed; allopatric speciation followed by range expansion cannot be precluded; recent climate changes in the north Atlantic may have induced range shifts.	

Chordata
Vertebrata: Actinopterygii: Gadiformes
Gadidae

Taxa	Reproductive isolation	Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
Gadus morhua Linnaeus, 1758	Partial, some hybridisation between populations still exists (see also Nielsen et al., 2005; Bradbury et al., 2014).	Populations are found in different habitats, and likely correlate with the coastal and oceanic ecotypes of *G. morhua*; multiple genomic regions showing adaptive divergence have been found (see also Berg et al., 2016; Kirubakaran et al., 2016; Sodeland et al., 2016).	Differences in habitat may induce assortative mating.	Possibly, habitat differences may act as a magic trait.	Unknown, but biophysical modelling of larval dynamics suggests high connectivity among genetically separated populations.	No, ecotypes are geographically separated (but see Neuenfeldt et al., 2013).	Large chromosomal rearrangements may have facilitated ecological adaptation (see also Berg et al., 2016; Kirubakaran et al., 2016; Sodeland et al., 2016).	Barth et al. (2017)

Vertebrata: Actinopterygii: Perciformes
Gobiidae

Taxa	Reproductive isolation	Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions	Other	References
Clevelandia ios (Jordan & Gilbert, 1882) and *Eucyclogobius newberryi* (Girard, 1856)	Possibly, no evidence for hybridisation was found in mtDNA.	Species differ in habitat preference and life history characteristics; selection may act on the tolerance for extreme estuarine conditions.	Differences in habitat may induce assortative mating.	Possibly, habitat differences may act as a magic trait.	—	Yes, distribution of *C. ios* encompasses distribution of *E. newberryi*.	Dispersal potential of *E. newberryi* is lower compared *C. ios*, based on its much deeper phylogeographic structure (see also *Dawson et al., 2001; Earl et al.,* 2010); local isolation and divergence cannot be precluded based on the complex geological history of California.	Dawson et al. (2002)
Gobiodon aoyagii Shibukawa, Suzuki & Aizawa, 2013 and *Gobiodon* sp. B¶	Possibly, no evidence for hybridisation in mtDNA.	Species are associated with different host species; evidence for a host shift was found in *Gobiodon* sp. B.	Species usually breed on their host species.	Host preference may act as a magic trait.	—	Geographic range of *Gobiodon* sp. B is restricted and completely encompassed	Low genetic diversity in *Gobiodon* sp. B; speciation following geographic isolation cannot be precluded but is less parsimonious;	Munday et al. (2004)

Taxa	Reproductive isolation	Population genetic process			Gene flow during divergence	Biogeographic pattern	Other	References
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits		Overlapping distributions		
						by the range of *G. aoyagii*.	species diverged recently (0.18–0.72 Mya).	
Grammatidae								
Gramma loreto Poey, 1868 and *G. dejongi* Victor & Randall, 2010	Unknown, potential hybridisation as no divergence was found on mtDNA.	Possibly, species show differences in colour pattern and adult size.	Unknown	Colour pattern could act as a magic trait, but more research necessary.	—	Yes, distribution of *G. loreto* encommasses distribution of *G. dejongi*.	A single individual of *G. dejongi* was found among a group of *G. loreto* at the Cayman Islands (Lohr et al., 2014).	Victor & Randall (2010)
Haemulidae								
Haemulon spp.	Yes, though evidence for two instances of (past) hybridisation between some species was found (see also Bernal et al., 2017).	Possibly, pairs of sister species differ in niche, but not in all potential cases of ecological speciation; Bernal et al. (2017) identified four genomic loci, potentially under disruptive selection and involved in the divergence between sympatric sister species *H. maculicauda* (Gill, 1862) and *H. flaviguttatum* (Desmarest, 1823), which differ in ecological niche as well.	Assortative mating could occur in species differing in ecological niche.	Habitat differences could act as a magic trait; changes in the grunt-like sounds, characteristic to the group, could potentially act as a magic trait between sympatric species not differing in habitat (such as *H. melanurum* (Linnaeus, 1758) and *H. album* Cuvier, 1830), but more research is needed.	—	Yes, overlapping distributions between some pairs of sister species.	—	Rocha et al. (2008)
Serranidae								
Hypoplectrus spp.	Hybrids between colour morphs are rare, but not absent; also, no divergence in mitochondrial markers (McCartney et al., 2003; Ramon et al., 2003; García-Machado et al., 2004).	Disruptive selection may act on colour pattern of fish; a genomic region containing *Hox* genes was identified as potentially being under disruptive selection (Puebla et al., 2014).	Assortative mating by colour morph has been observed (see also Fischer, 1980; Barreto & McCartney, 2007; Puebla et al., 2012).	Colour pattern can be considered a magic trait (Servedio et al., 2011).	—	Yes	Some genetic structuring was observed across the Caribbean (Puebla et al., 2008; Picq et al., 2016).	Puebla et al. (2007)
Tripterygiidae								
Ruanoho decemdigitatus (Clarke, 1879) and *R. whero* Hardy, 1986	Most likely, no hybrids observed in the wild; no interspecies courtship behaviour in laboratory trials.	Species show habitat partitioning by depth and exposure (see also Feary & Clements, 2006); habitat use was related to body size, which varies between species.	Based on body size, females of the smaller *R. whero* prefer smaller males, no preference observed in *R. decemdigitatus* females.	Body size could act as magic trait, though the exact role body size plays in speciation should be investigated further.	—	Yes	No phylogeographic structure was present within *R. whero* (Hickey et al., 2009); *Wellenreuther et al.* (2007) identified another pair of sister species within the family Tripterygiidae	Wellenreuther et al. (2007, 2008)

| Taxa | Reproductive isolation | Population genetic process | | | Gene flow during divergence | Biogeographic pattern | Other | References |
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits		Overlapping distributions		
							Whitley, 1931 which differ in habitat.	
Vertebrata: Actinopterygii: Scorpaeniformes **Hexagrammidae**								
Hexagrammos otakii Jordan & Starks, 1895 and *H. agrammus* (Temminck & Schlegel, 1843)	Yes, prezygotic isolation is strong, based on absence of hybrids in the wild; no evidence for postzygotic isolation between species was found, based on lab-reared hybrids.	Species have different ecological niches, with varying depth distribution of nests, nest substrates, reproductive timing, as well as variation in morphology (see also Munehara et al., 2000; Kimura & Munehara, 2010).	Mostly, as spawning season differs between species; interspecies mating behaviour has however been reported, as there is some overlap in reproductive season (Munehara et al., 2000).	Differences in habitat association and mating season may act as a magic trait.	—	Yes	The pattern of strong prezygotic and weak postzygotic isolation is reversed between the two sympatric species and the mostly allopatric *H. octogrammus* (Pallas, 1814), which is consistent with theoretical predictions of speciation with and without gene flow.	Crow et al. (2007, 2010)
Vertebrata: Acanthopterygii: Syngnathiformes **Syngnathidae**								
Hippocampus erectus Perry, 1810 and *H. zosterae* Jordan and Gilbert, 1882; *H. abdominalis* Lesson, 1827 and *H. breviceps* Peters, 1869	Most likely, no evidence was found for hybridisation, see also Teske et al. (2004).	Species differ in body size.	Size-assortative mating has been inferred based on microsatellite data on genetic parentage (see also Vincent & Sadler, 1995).	Body size can be considered a magic trait (Servedio *et al.*, 2011); simulation data suggests that size-assortative mating coupled with weak disruptive selection on body size can quicly lead to speciation.	—	Yes, two pairs of sister species occur in sympatry; *H. erectus* encompasses the distribution of *H. zosterae*; overlap between *H. abdominalis* and *H. breviceps*; see also Lourie et al. (2016).	Allopatric speciation cannot be precluded; evidence for genetic subpopulations was found in both *H. erectus* and *H. zosterae* (Boehm et al., 2015; Fedrizzi et al., 2015).	Jones et al. (2003)
Vertebrata: Elasmobranchii: Myliobatiformes **Myliobatidae**								
Mobula alfredi (Krefft, 1868) and *M. birostris* (Walbaum, 1792)**	Species are reciprocally monophyletic in a nuclear marker and no mtDNA haplotypes were shared; evidence for historic hybridisation after divergence was found based on paraphyly of a mtDNA marker; a hybrid of *M. alfredi* and *M. birostris* has been recorded from the Red Sea (Walter et al., 2014)	Species differ in habitat use, showing mosaic sympatric at some localities, though the differences in habitat between species are not as clear and consistent as originally thought (Stewart et al., 2016 and references therein)	Possibly, some assortative mating could occur based on habitat differences, but more research is required, as difference in habitat between species is not as clear as previously thought (Stewart et al., 2016)	Habitat preference could potentially act as a magic trait; behavioural isolation or sexual selection could alternatively have played a role as well (Poortvliet et al., 2015)	Based on isolation–migration models, support for isolation with migration scenario was marginally better than incomplete lineage sorting without gene flow after divergence	Yes (see also Marshall et al., 2009)	Species could not be distinguished using mtDNA marker COI, suggesting a recent divergence between species (~0.07–0.67 Mya assuming isolation with migration, even less under divergence without gene flow); relatively strong population structure was observed in *M. birostris* (Stewart et al., 2016)	Kashiwagi et al. (2011, 2012)

| Taxa | Reproductive isolation | Population genetic process | | | | Biogeographic pattern | Other | References |
		Potential for disruptive selection	Assortative mating	Link selected and assortment traits	Gene flow during divergence	Overlapping distributions		
Vertebrata: Elasmobranchii: Orectolobiformes								
Orectolobidae								
Sutorectus tentaculatus (Peters, 1864) and *Orectolobus floridus* Last & Chidlow, 2008	Possibly, no evidence was found for introgression and hybridisation between three other, closely related orectolobid species with similar degrees of mtDNA divergence (Corrigan et al., 2008).	There could be differences in habitat-associations between the species, as *S. tentaculatus* is more commonly reported in commercial catches than *O. floridus*, but this hypothesis remains speculative.	Unknown, habitat-preference could induce assortative if it indeed differs between species.	Unknown, habitat-preference could act as a magic trait, but more research is needed.	—	Yes, range of *O. floridus* completely overlaps with *S. tentaculatus* along the southwestern coast of Australia.	The species *O. floridus* has only recently been described (Last & Chidlow, 2008), biological information on this species is therefore scarce; based on a molecular clock, divergence between *S. tentaculatus* and *O. floridus* occurred in the early Pleistocene.	Corrigan & Beheregaray (2009)
Vertebrata: Reptilia: Squamata								
Elapidae								
Hydrophis cyanocinctus Daudin, 1803, *H. coggeri* (Kharin, 1984), *H. melanocephalus* Gray, 1849, and *H. parviceps* Smith, 1935	Yes, limited gene flow among four studied species, based on microsatellite data, one hybrid individual was identified.	Two ecomorphs, the macrocephalic *H. cyanocinctus*, and the microcephalic *H. coggeri*, *H. melanocephalus*, and *H. parviceps*, differing in body size, have been identified based on morphology and stomach contents; habitat differs between *H. cyanocinctus* and *H. coggeri*.	Body size is known as a mating cue in other viviparous sea snakes (Shine, 2005), assortative mating by body size is therefore likely.	Body size may act as a magic trait; habitat-preferece could also act as a magic trait in *H. cyanocinctus* and *H. coggeri*, if mating grounds overlap with feeding grounds.	Isolation–migration models provided support for gene flow among species, likelihood ratio tests rejected models without gene flow.	Yes, distributions of the four species overlap; the restricted distribution of *H. parviceps* (see also Rasmussen et al., 2012) is completely encompassed by *H. melanocephalis* and *H. cyanocinctus*.	Species diverged recently; periods of allopatry in the Pleistocene might have played a role in driving the divergence of species (see also Ukuwela et al., 2016, 2017), but ecological speciation played at least a partial role; strong phylogenetic split between eastern and western *H. cyanocinctus* populations; microcephaly likely evolved twice in the four species, and at least eight times within the whole genus *Hydrophis* Latreille, 1801 (see also *Sanders et al.,* 2013a).	Sanders et al. (2013b)

* In Duran * Rützler (2006), *Chondrilla caribensis* is referred to as *C.* cf. *nucula*.

† In Zardus et al. (2006) classified in the genus *Deminucula*, which has been synonymised with the genus *Nucula* (Bergmans, 1978)

‡ In Castelin et al. (2012) referred to as *Bursa fijiensis*, which is a synonym of *Bursina fijiensis* (Beu et al., 2012).

§ In Stevens (1990) referred to as *Pinnotheres novaezelandiae*, which was transfered to the genus *Nepinnotheres* by Ahyong & Ng (2008).

¶ In Munday et al. (2004), *Gobiodon aoyagii* is referred to as the undescribed *Gobiodon* sp. A (Shibukawa et al., 2013), *Gobiodon* sp. B remains undescribed.

** In Kashiwagi et al. (2011, 2012) classified in the genus *Manta*, moved to the genus *Mobula* by White et al. (2017).