

1.8 million spp described
Estimated 5-20 million on earth

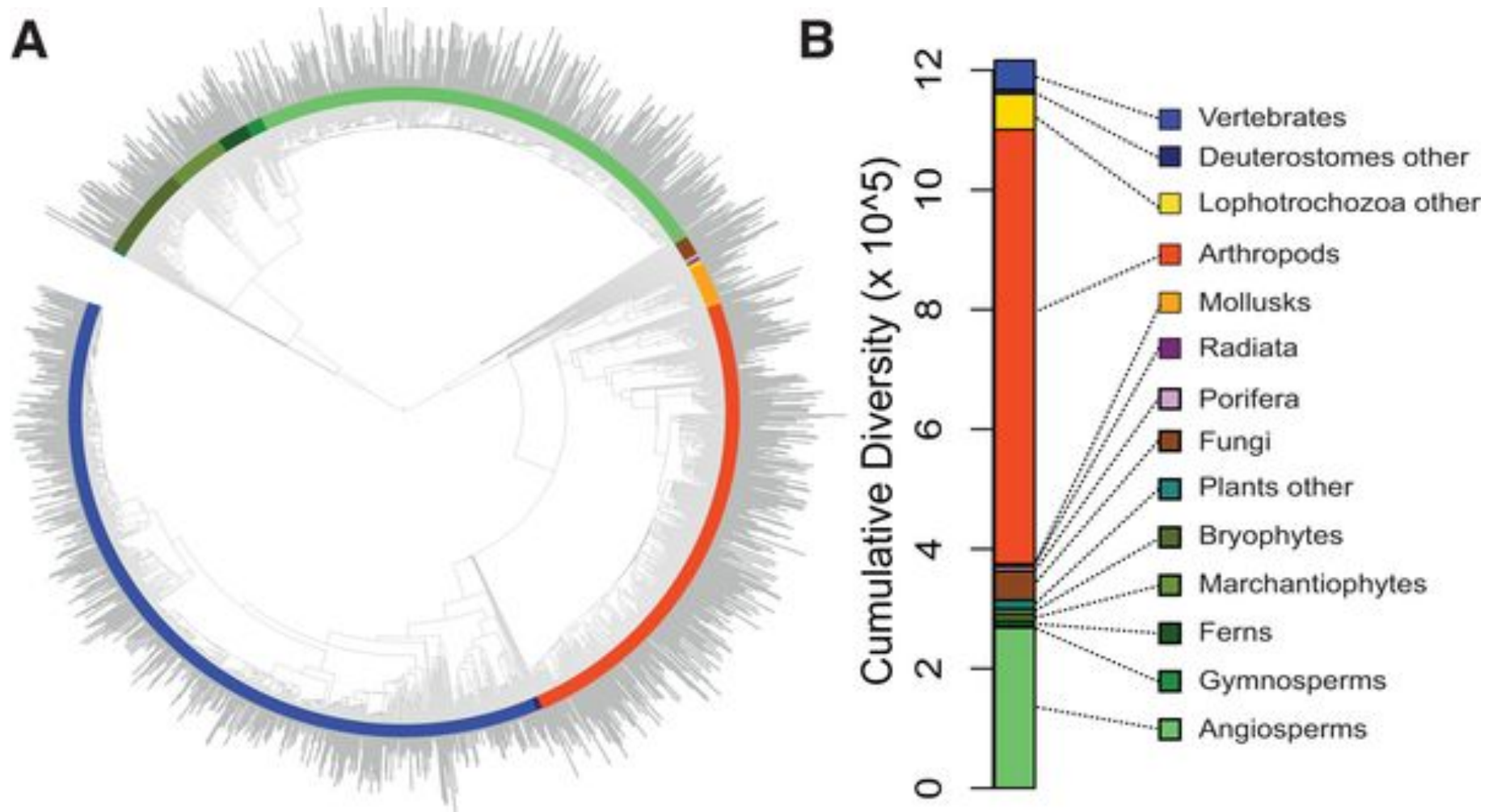
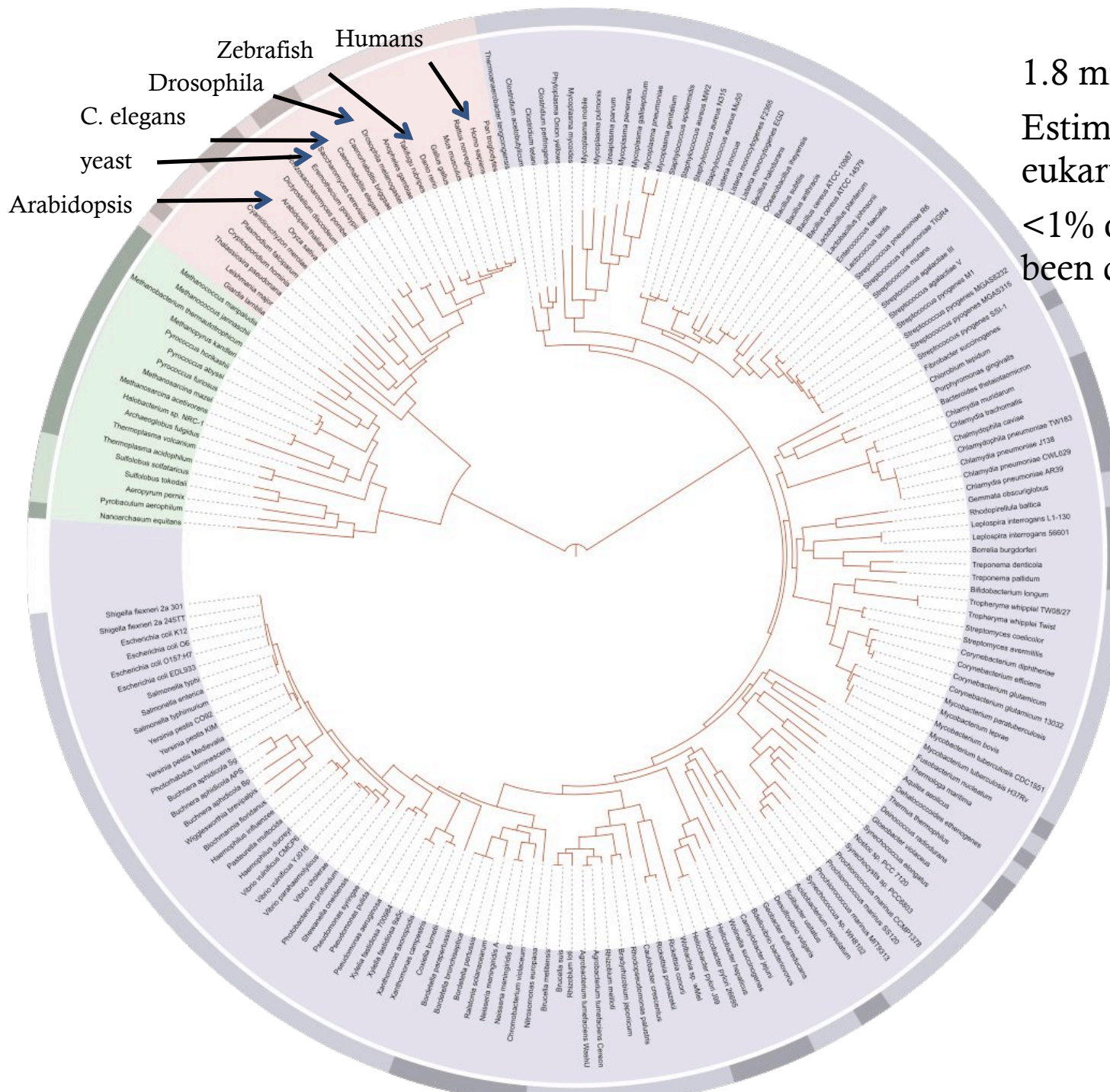


Figure 1. Phylogenetic distribution of species richness across the eukaryotic tree of life.

Rabosky DL, Slater GJ, Alfaro ME (2012) Clade Age and Species Richness Are Decoupled Across the Eukaryotic Tree of Life. *PLoS Biol* 10(8): e1001381. doi:10.1371/journal.pbio.1001381
<http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1001381>



TROPICAL FORESTS: THEIR RICHNESS IN COLEOPTERA AND OTHER ARTHROPOD SPECIES

TERRY L. ERWIN

The tropical tree *Luehea seemannii* is a medium-sized seasonal forest evergreen tree with open canopy, large and wide-spaced leaves. The trees sampled ($n = 19$) had few epiphytes or lianas generally, certainly not the epiphytic load normally thought of as being rich. These 19 trees over a three season sampling regime produced 955+ species of beetles, excluding weevils. In other samples now being processed from Brazil, there are as many weevils as leaf-beetles, usually more, so I added 206 (weevils) to the *Luehea* count and rounded to 1,200 for convenience. There can be as many as 245 species of trees in one hectare of rich forest in the tropics, often some of these in the same genus. Usually there are between 40 to 100 species and/or genera, so I used 70 as an average number of genus-group trees where host-specificity might play a role with regard to arthropods. No data are available with which to judge the proportion of host-specific arthropods per trophic group anywhere, let alone the tropics. So conservatively, I allowed 20% of the *Luehea* herbivorous beetles to be host-specific (i.e., must use this tree species in some way for successful reproduction), 5% of the predators (i.e., are tied to one or more of the host-specific herbivores), 10% of the fungivores (i.e., are tied to fungus associated only with this tree), and 5% of the scavengers (i.e., are associated in some way with only the tree or with the other three trophic groups) (Table 1).



Rolando Pérez

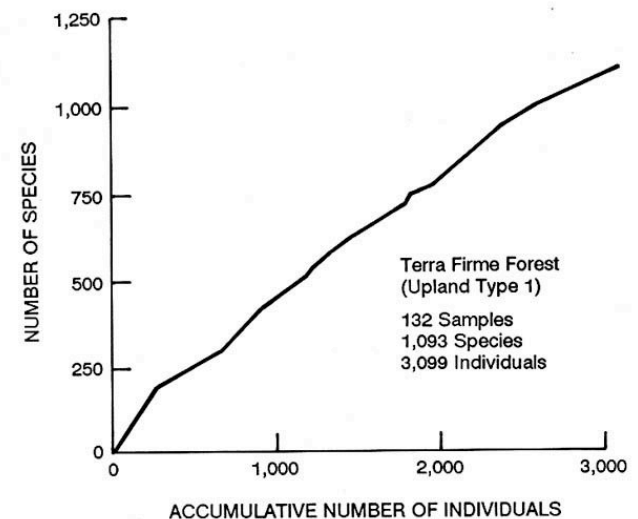
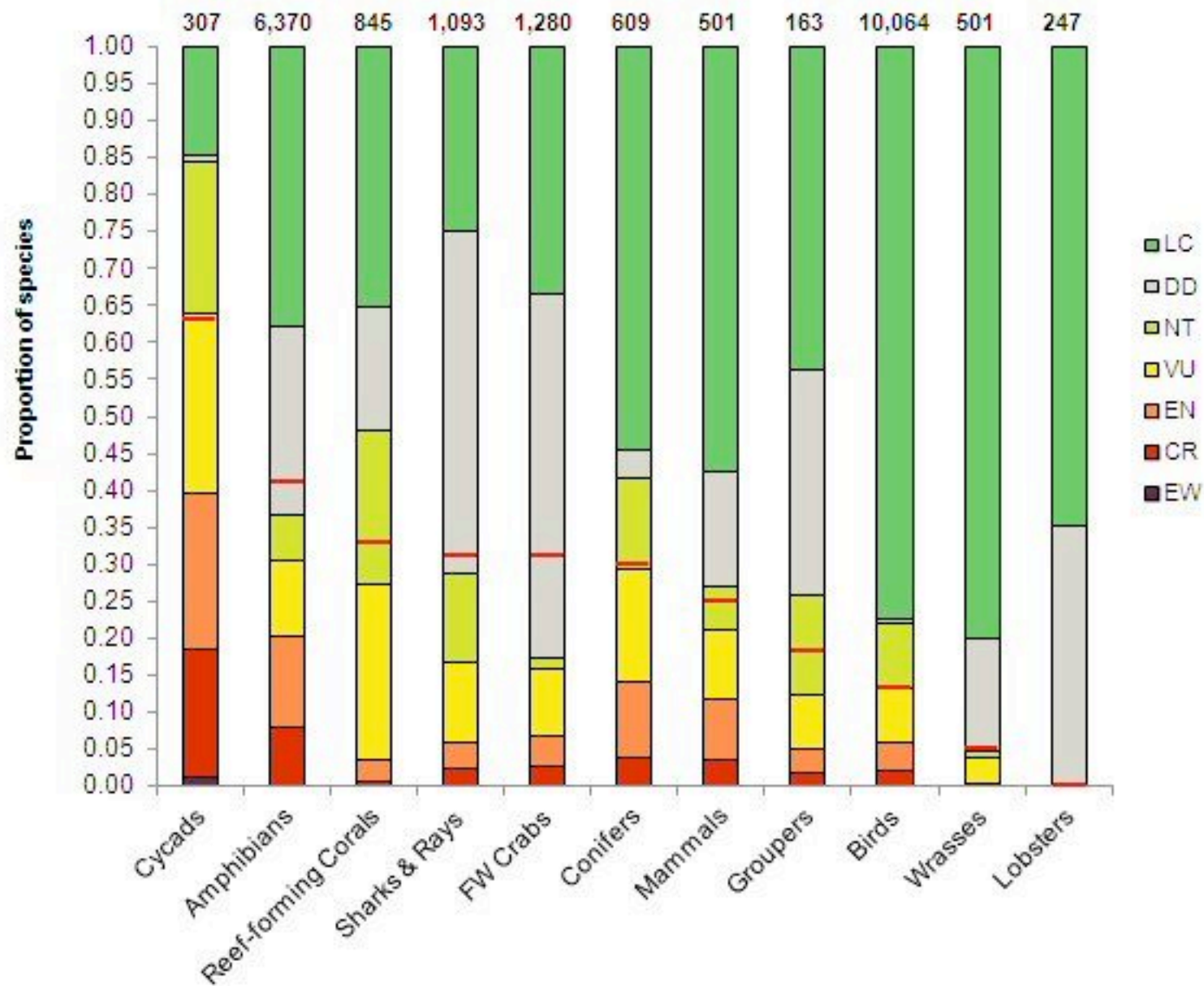


FIGURE 13-3 Numbers of species accumulated per square meter sample in 12-meter-square plot (119 square meters sampled) in Upland Forest Type I at Tambopata Reserved Zone, Peru.



IUCN <http://www.iucnredlist.org/about/summary-statistics>

Examples of extinctions in Hawaiian birds

Last seen, 1915



Bishop's O'o (*Moho bishopi*)

Last seen, 1913



Lana'i Hookbill (*Dysmorodrepanis munroi*)

Introduced species



Red Billed Leiothrix

Japanese white-eye



Malaria infected native species

photo by Jack Jeffrey



Omao

I'iwi

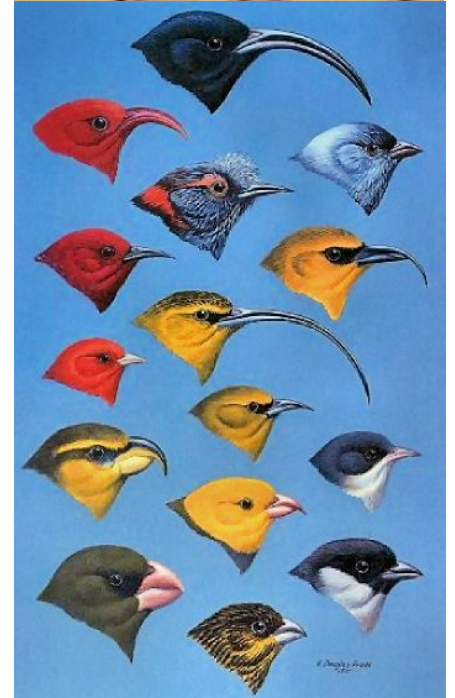
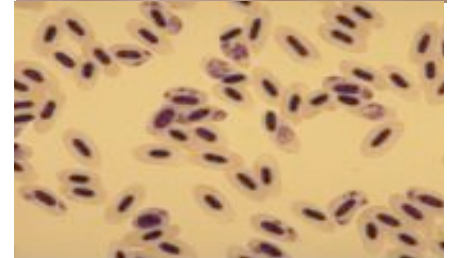


One part of the story... avian malaria



- ⌘ Until 1826 – no mosquito's
 - ⌘ *Culex quinquefasciatus* (southern house mosquito)
 - ⌘ Now 5 species of biting mosquito's
- ⌘ Early 1900's – avian malaria (*Plasmodium relictum*) introduced
- ⌘ Massive declines in Hawaii's honeycreepers
 - ⌘ Changes in geographically distributions

Largely from: van Ripper, C., III, S. G. van Ripper, M. L. Goff, and M. Laird. 1986. The epizootiology and ecological significance of malaria in Hawaiian land birds. Ecological Monographs **56**:327-344.



Distribution of natives and introduced species

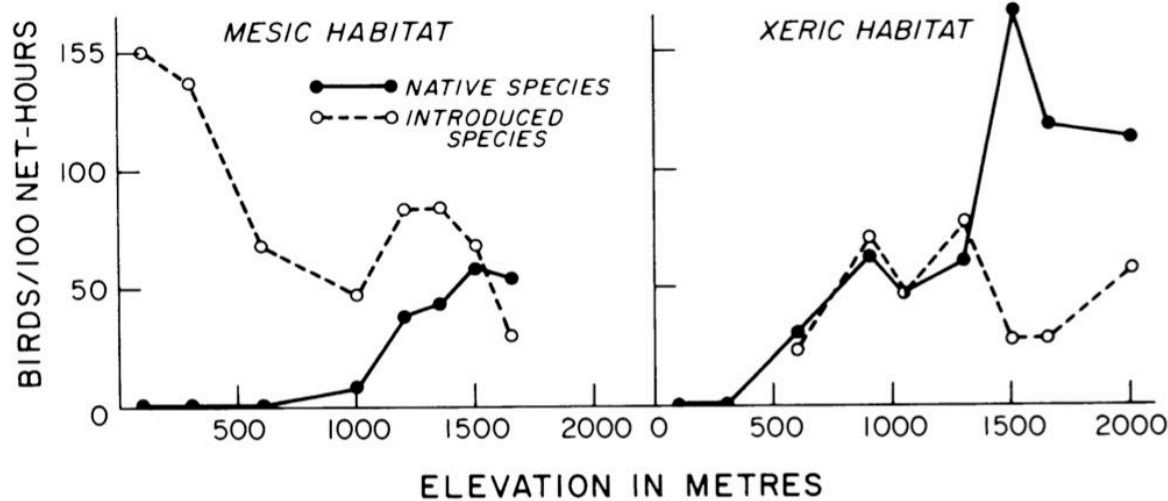


FIG. 2. Total introduced and native birds captured per 100 net-hours from 1978–1979 at 16 sampling stations on Mauna Loa, Hawaii.

...and malaria

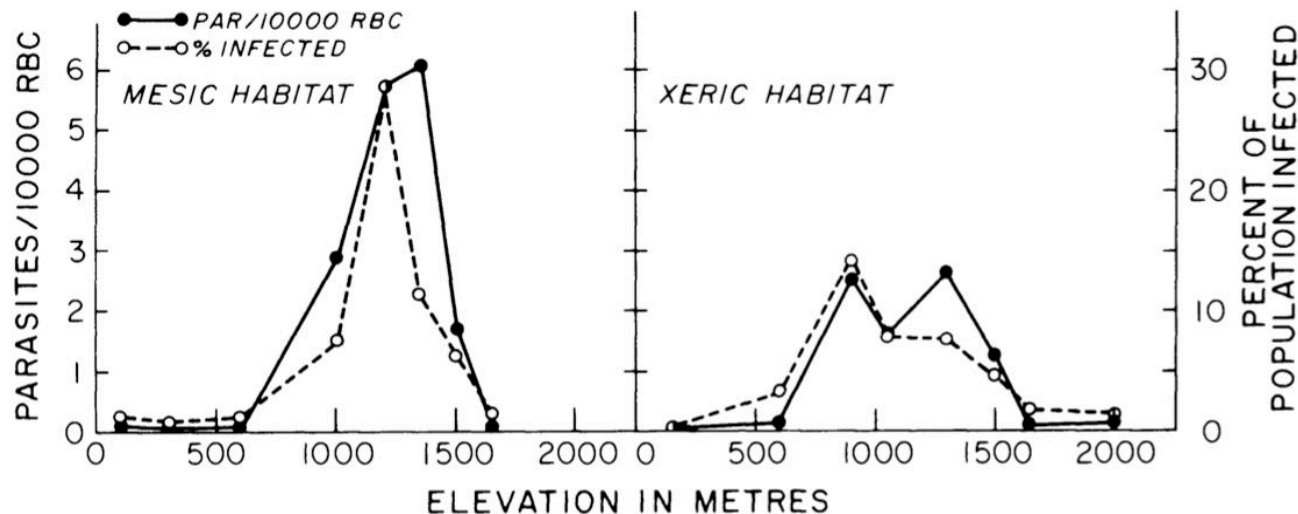


FIG. 4. Percentages of all birds captured on Mauna Loa Volcano, Hawaii, from 1978–1979 that were infected with malarial parasites, and their concomitant parasitemia levels (parasites/10 000 red blood cells), both expressed along an elevational gradient from sea level to tree line.

Percent infection by malaria in natives and introduced species

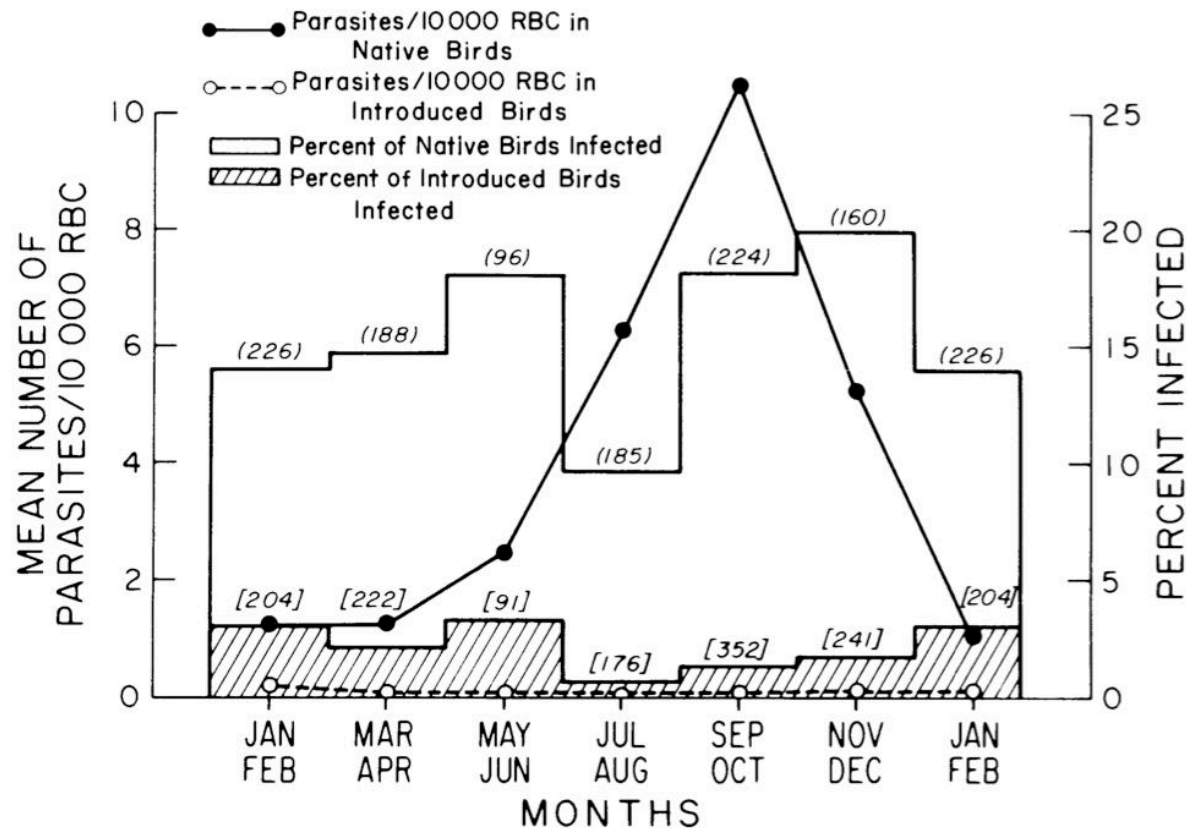


FIG. 12. A comparison of native and introduced birds' parasitemia levels and infection rates over the 1978–1979 annual cycle on Mauna Loa, Hawaii. Numbers in brackets or parentheses are sample sizes.

Experimental infection of birds with malaria

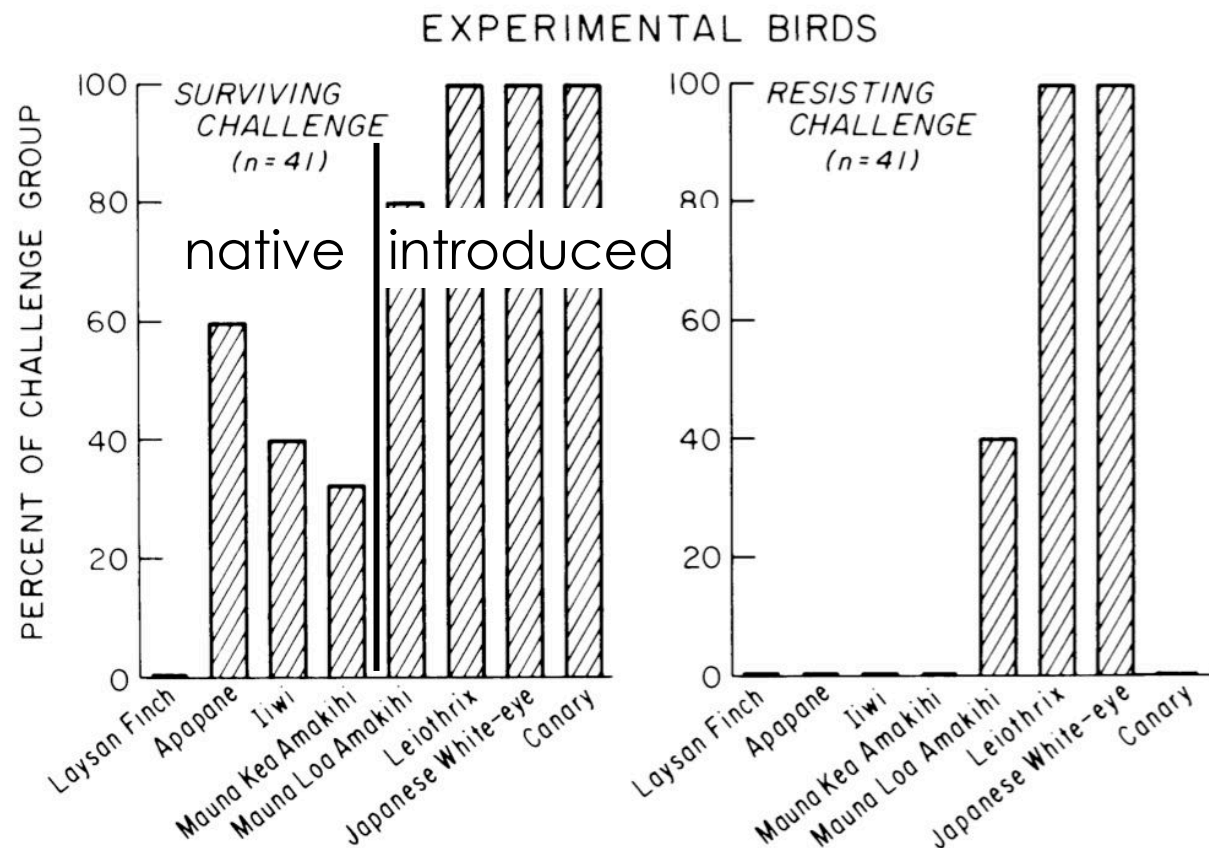


FIG. 6. Percentage of species that were resistant to and percentage that survived a challenge with avian malarial parasites (*Plasmodium relictum capistranoae*). All species had five individuals challenged except for the Mauna Kea Common Amakihi, which had six.

Model of native bird abundance

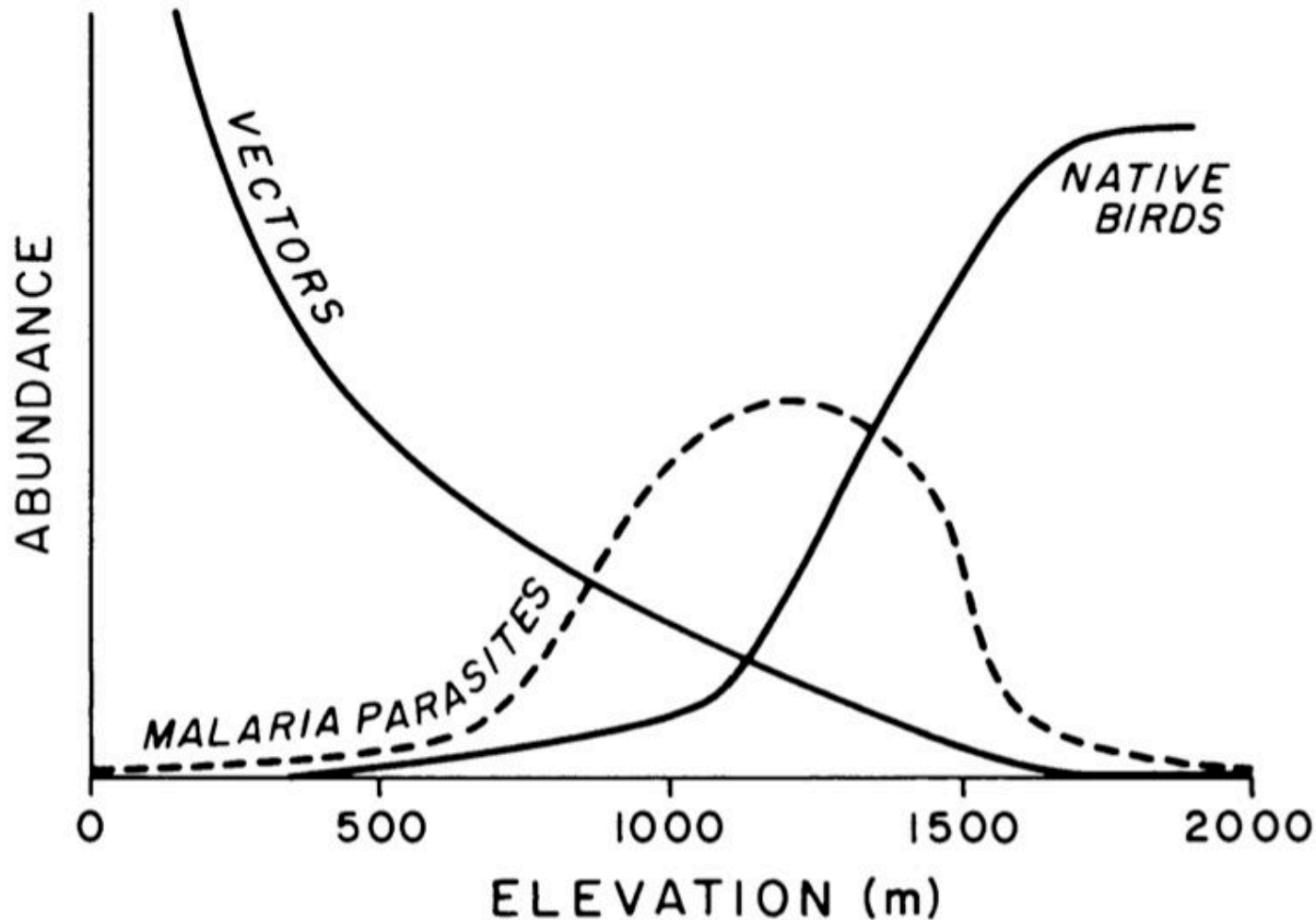


FIG. 11. A generalized model of native bird abundances, malarial parasite incidence, and mosquito vector levels along an elevation gradient on Mauna Loa, Hawaii.

Prehistoric Extinctions of Pacific Island Birds: Biodiversity Meets Zooarchaeology

David W. Steadman

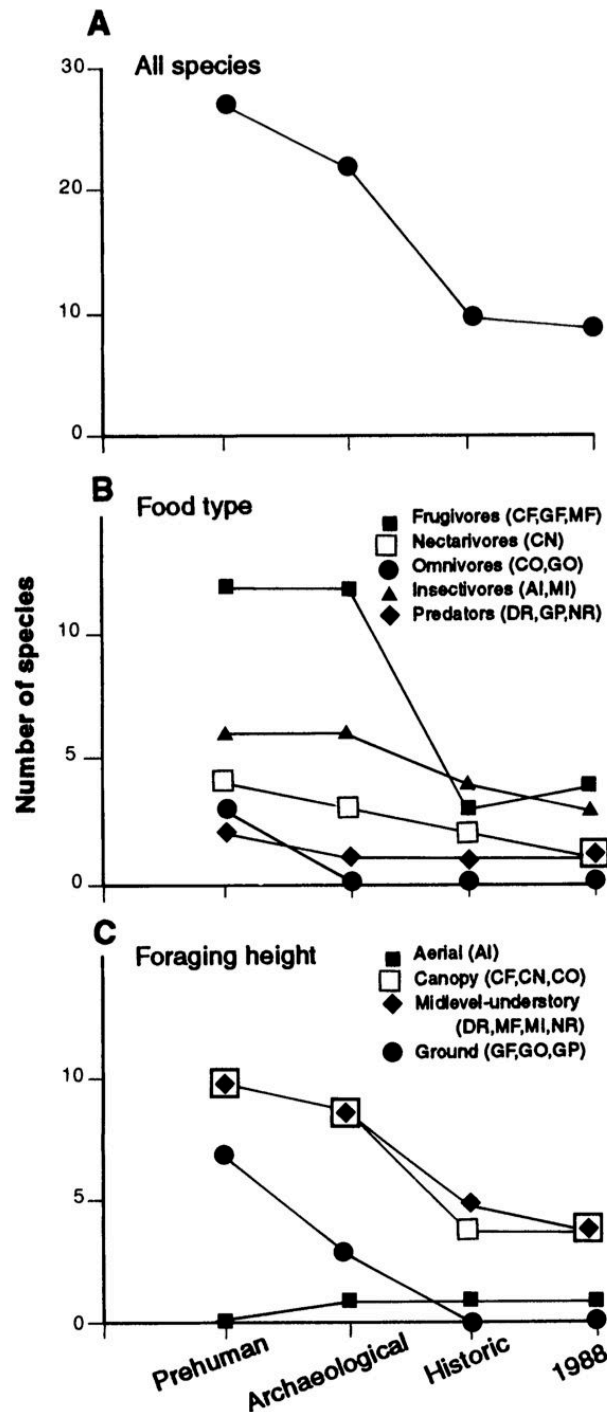
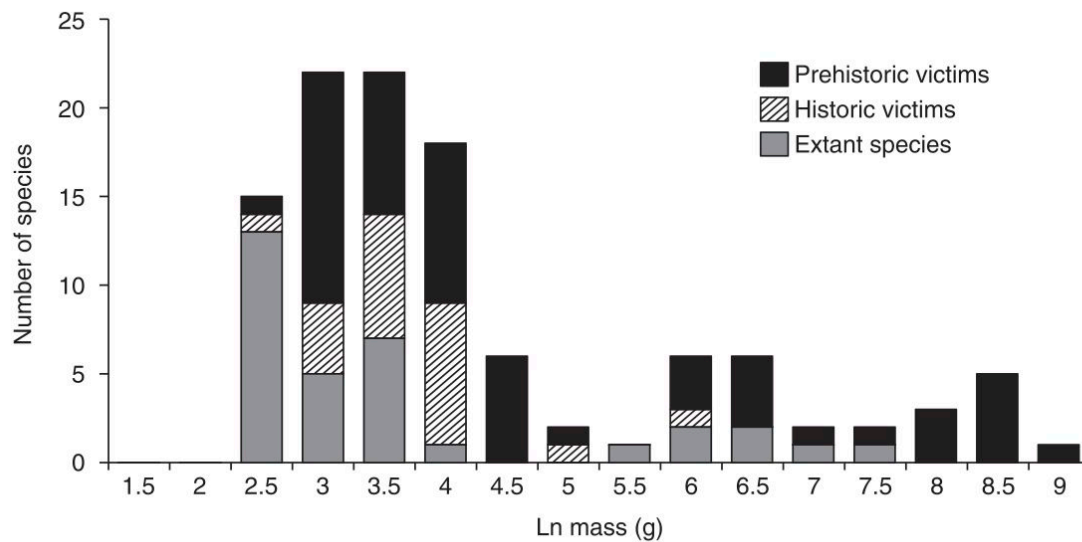
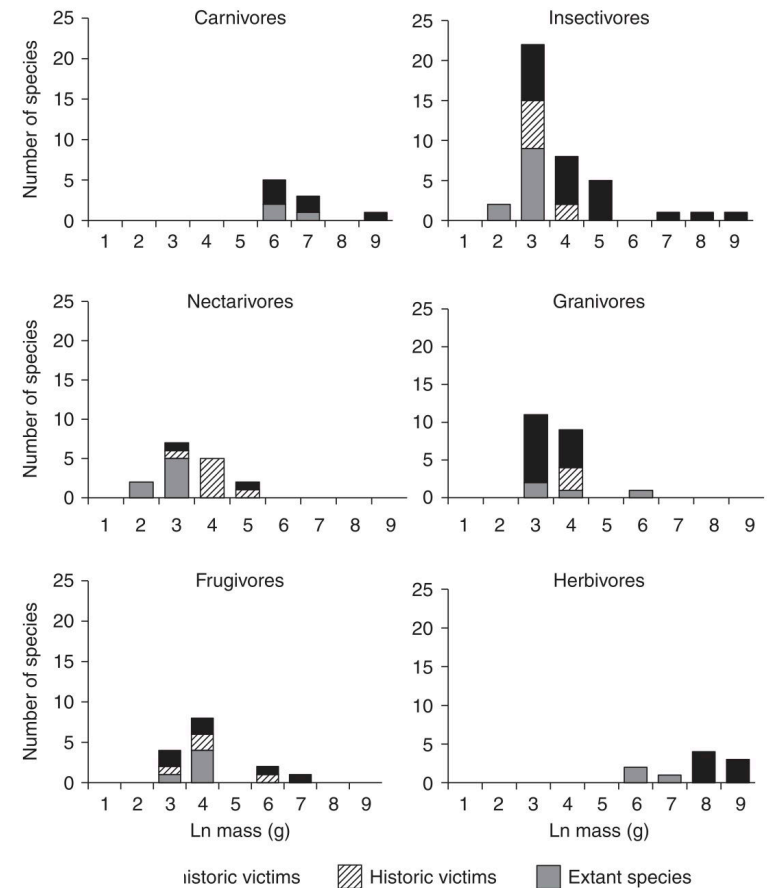


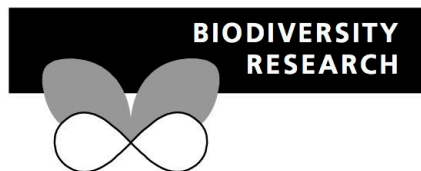
Fig. 4. Long-term changes in the species richness of forest birds on 'Eua, Kingdom of Tonga. The horizontal scale (chronology) corresponds to Table 5. **(A)** All species. **(B)** Dietary category or preference. **(C)** Foraging height. Feeding guild categories are as follows: AI, aerial insectivore; CF, canopy frugivore-granivore; CN, canopy nectarivore; CO, canopy omnivore; DR, diurnal raptor; GF, ground frugivore-granivore; GO, ground omnivore; GP, ground predator; MF, midlevel-understory frugivore-granivore; MI, midlevel-understory insectivore; NF, nonforest species; and NR, nocturnal raptor. There may be overlap between canopy and midlevel-understory habitats; some species were assigned arbitrarily to one or the other.



“One clear message from previous studies and the results presented here is that human-mediated extinction often follows predictable patterns. We must use this knowledge to help prevent further extinctions today. ” p 515



Diversity and Distributions, (Diversity Distrib.) (2008) **14**, 509–517



Extinction patterns in the avifauna of the Hawaiian islands

Alison G. Boyer

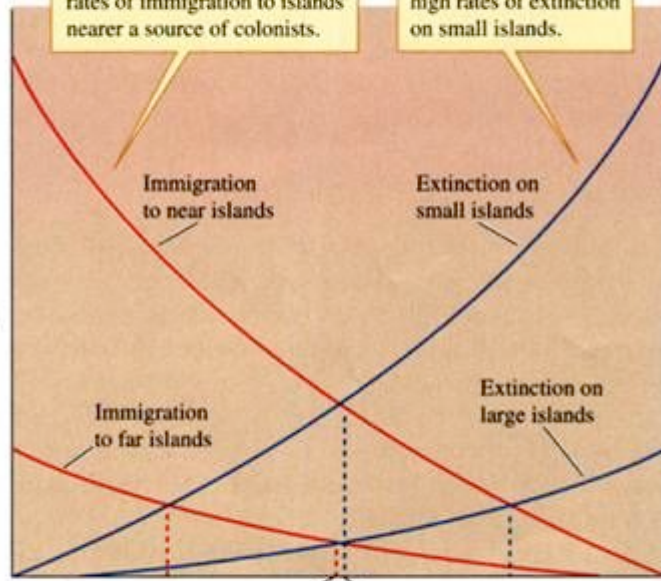
What makes a species vulnerable to extinction?

The equilibrium model of island biogeography explained variation in number of species on islands by the influences of isolation and area on rates of immigration and extinction.

The model predicted higher rates of immigration to islands nearer a source of colonists.

The model predicted high rates of extinction on small islands.

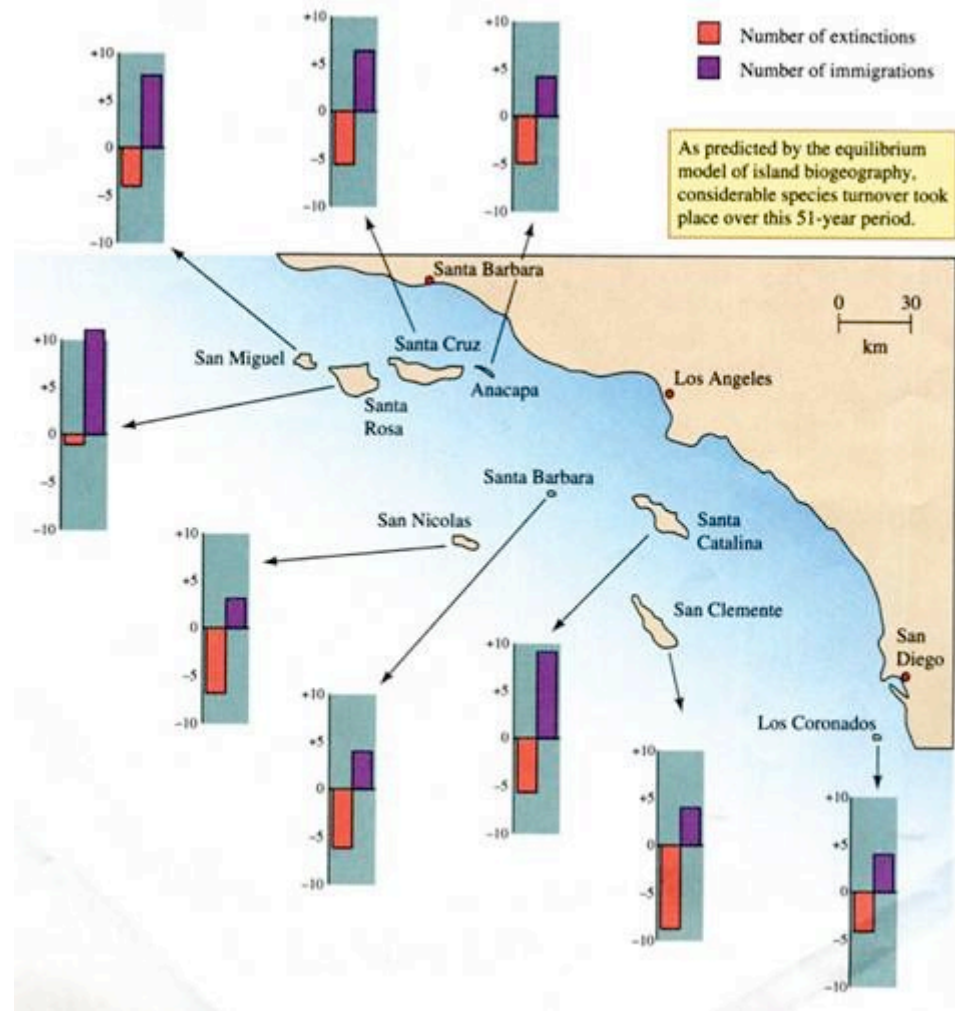
Rate of immigration or extinction



S small, far
S large, far
S small, near
S large, near
Number of species present

The model explains the low number of species on small, isolated islands.

The model also accounts for high number of species on large, near islands.





A later (1976) manipulative experiment: If you reduce the area of an island, diversity is reduced

MBERLOFF

Ecology, Vol. 57, No. 4

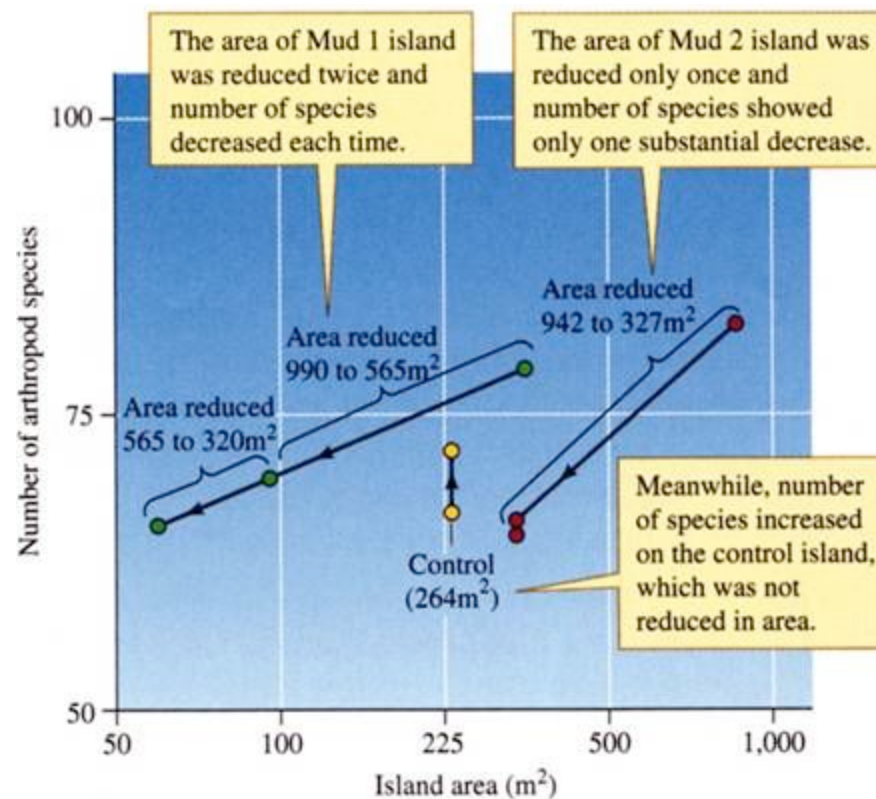
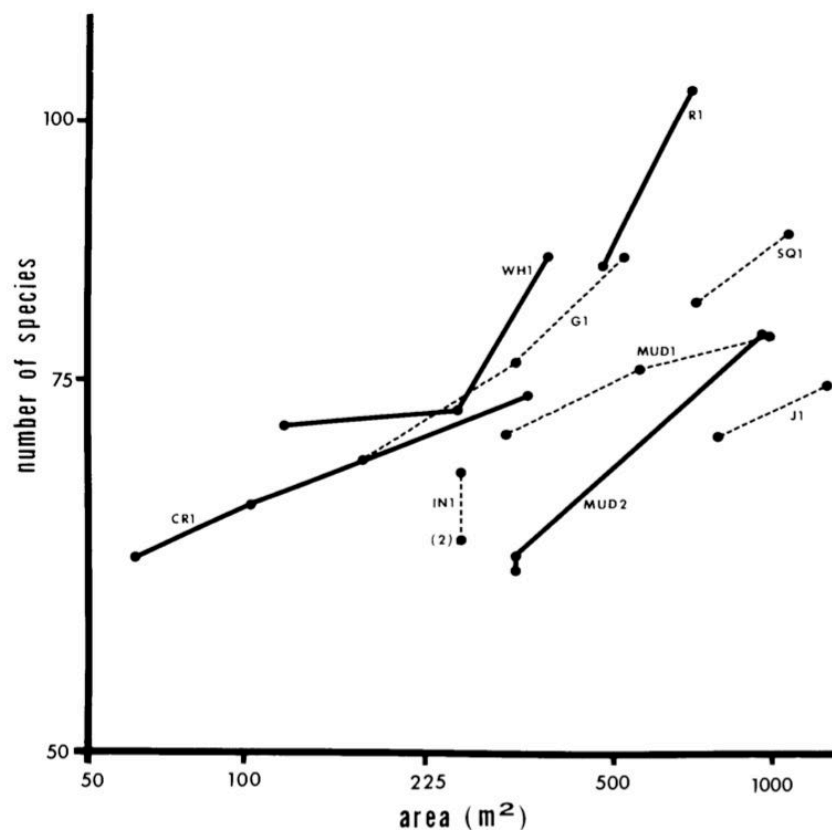


FIG. 6. Individual species number vs. area curves for the experimental islands in a log-log plot.

TABLE 2. Percentages of species that were present at both of two given censuses on four of the experimental islands

Name of experimental island	A. Censuses: just before defaunation and one year later			B. Censuses: just before defaunation and two years later			C. Censuses: one and two years after defaunation		
	No. spp. in common	Total no. in both censuses	Per cent in common	No. spp. in common	Total no. in both censuses	Per cent in common	No. spp. in common	Total no. in both censuses	Per cent in common
E1.....	2	29	6.9%	5	26	19.2%	7	18	38.9%
E2.....	10	54	18.5%	13	51	25.5%	16	34	37.2%
E3.....	8	40	20.0%	7	35	20.0%	16	31	51.6%
ST2.....	11	37	29.7%	17	31	54.8%	12	34	35.3%

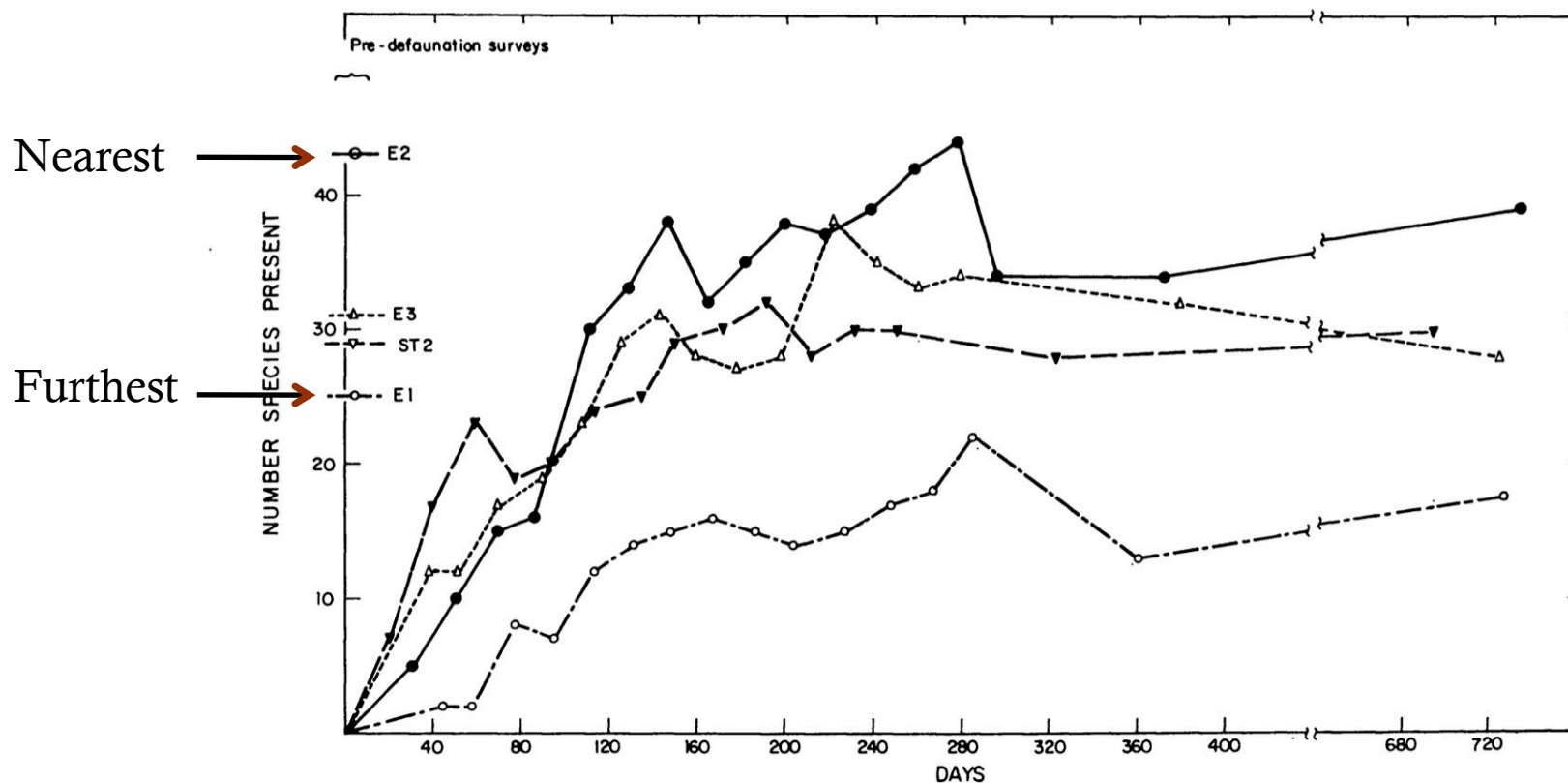


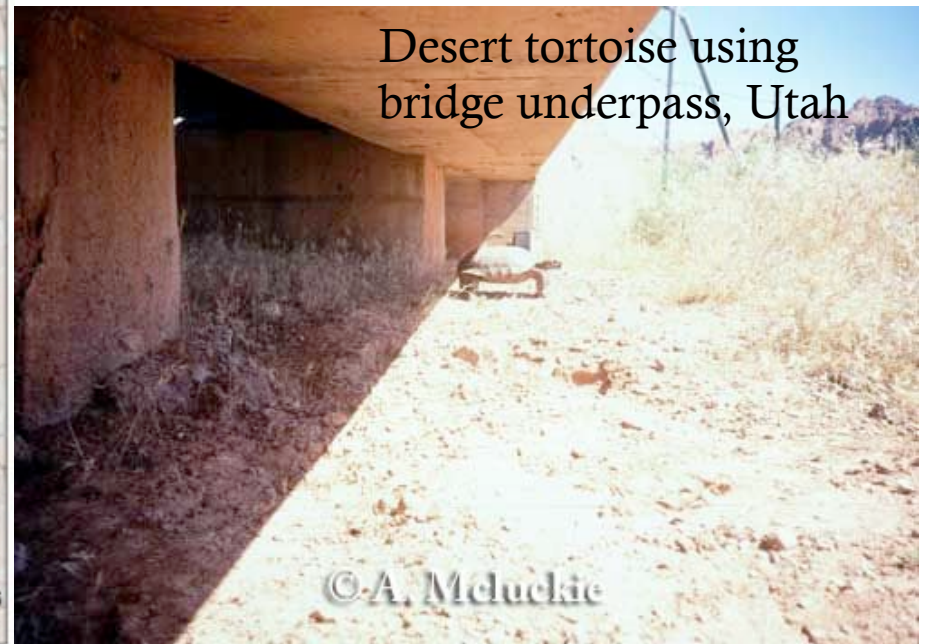
FIG. 1. The colonization curves of four small mangrove islands in the lower Florida Keys whose entire faunas, consisting almost solely of arthropods, were exterminated by methyl bromide fumigation. The figures shown are the estimated numbers of species present, which

What should a reserve look like (according to Island Biogeography)?

- ∞ Large and continuous as possible
- ∞ Incorporate redundancy
 - ∞ Replicate preserves for unique biotas, near each other
- ∞ Corridors between preserves (enhance connectedness)
- ∞ Priority to endemism and vulnerability

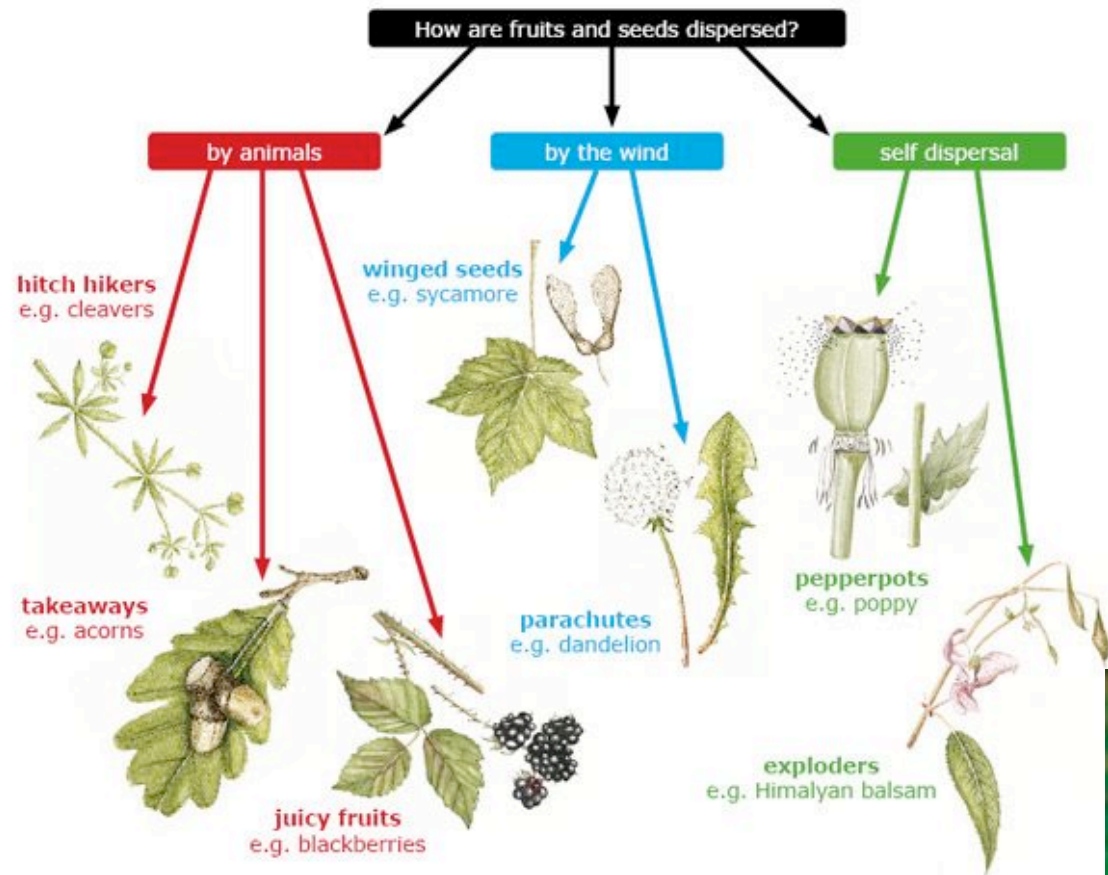


<http://www.wildlifeandroads.org/>



What does Island Biogeography assume (perhaps wrongly)?

- ∞ All species are interchangeable
 - ∞ equal colonization ability
 - ∞ equally likely to go extinct (e.g., similar population sizes)
- ∞ Area controls extinction rates (or is a surrogate for habitat diversity or allowable population sizes)
- ∞ Species do not have strong interactions (exclusion or facilitation)
- ∞ Equilibrium is reached (disturbances not too frequent)

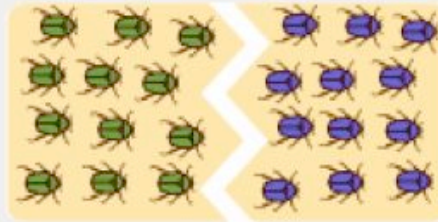


Mode of speciation

New species formed from...

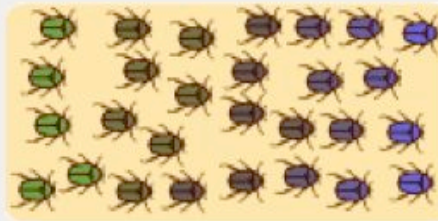
Allopatric
(allo = other,
patric = place)

geographically isolated populations



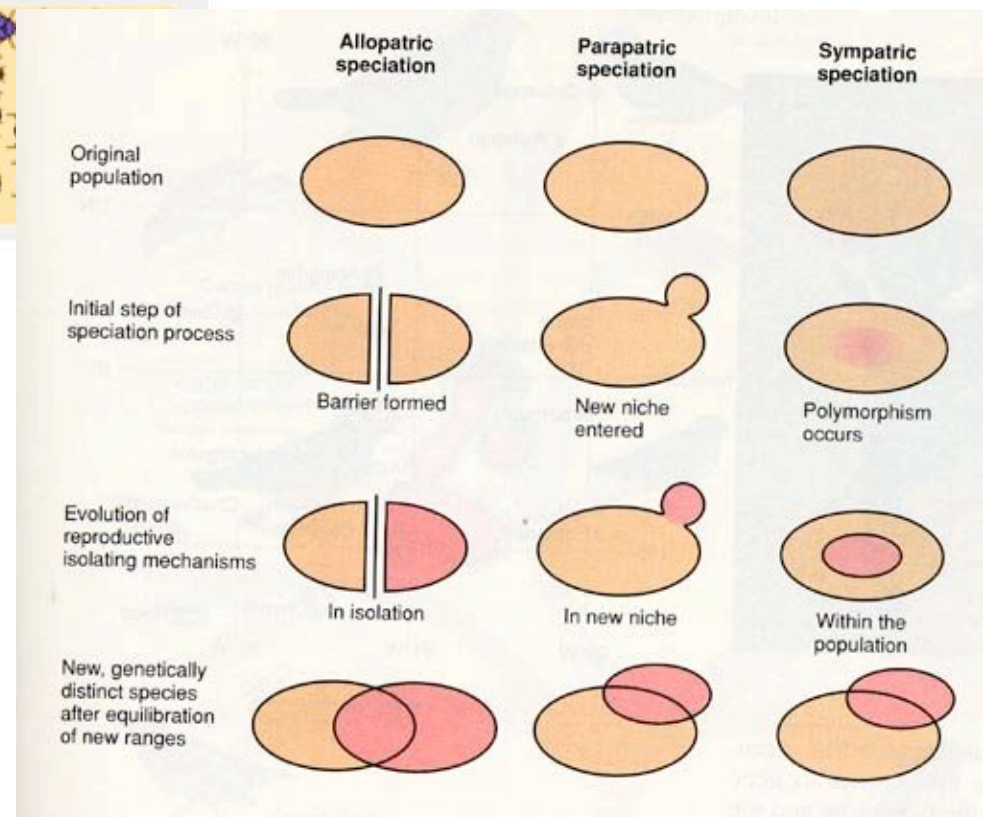
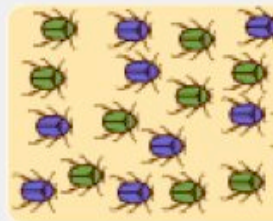
Parapatric
(para = beside,
patric = place)

a continuously distributed population

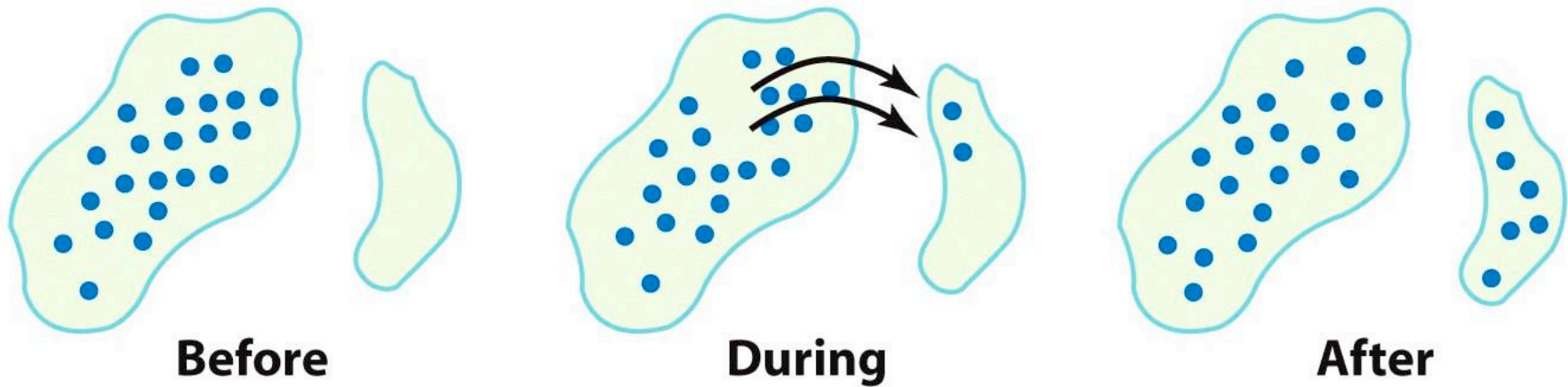


Sympatric
(sym = same,
patric = place)

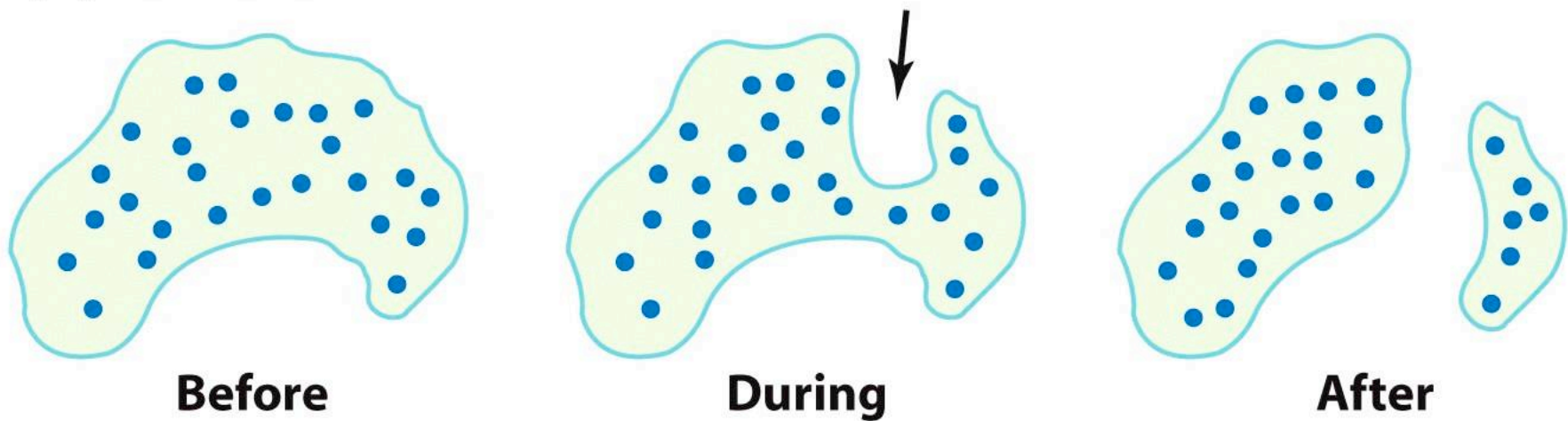
within the range of the ancestral population

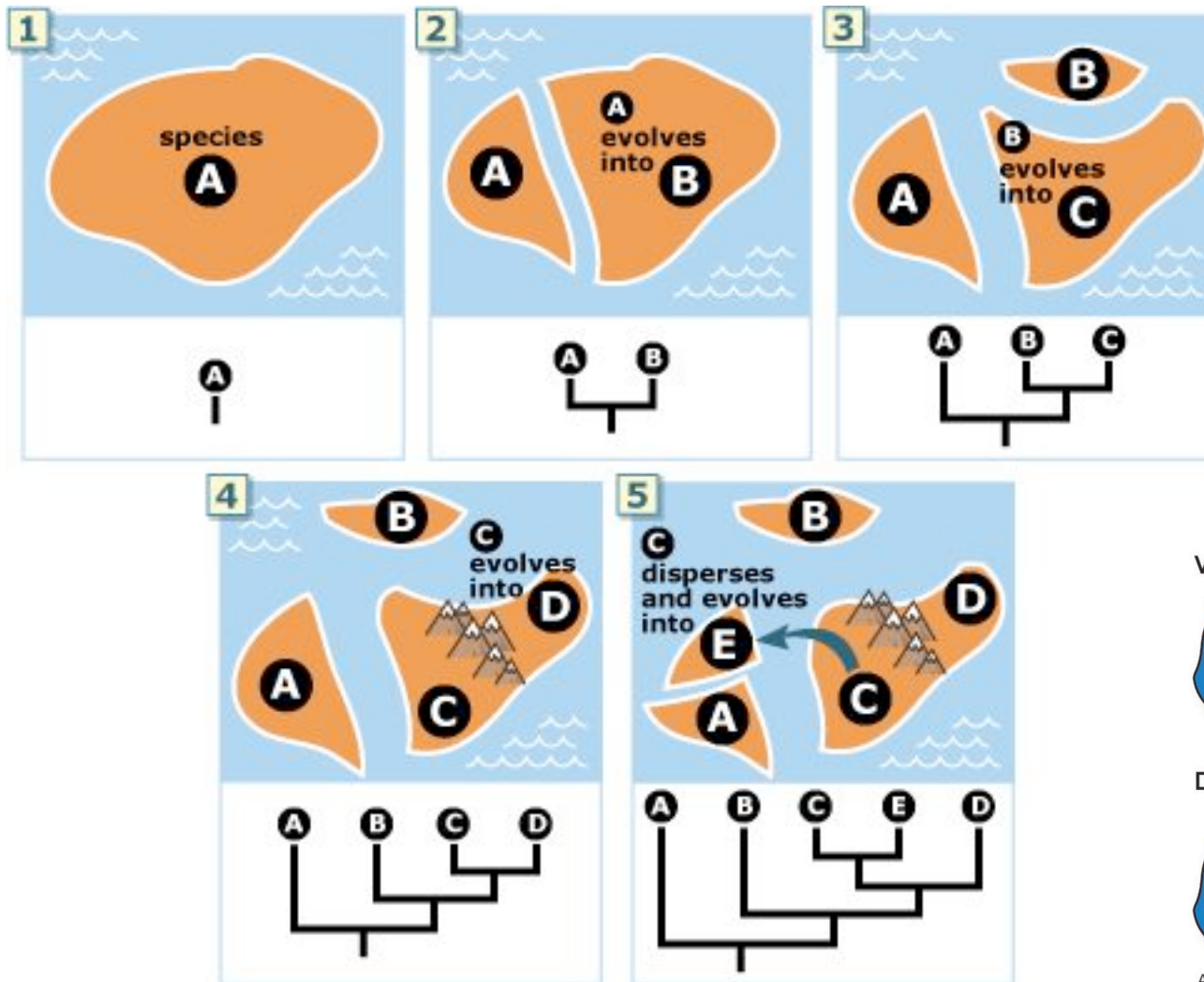


(a) Dispersal

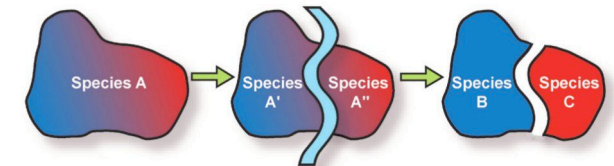


(b) Vicariance

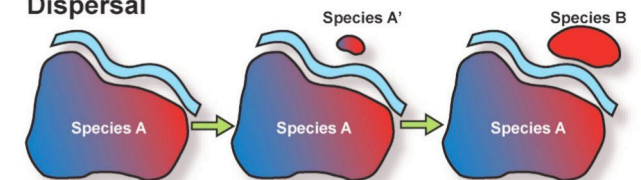




Vicariance

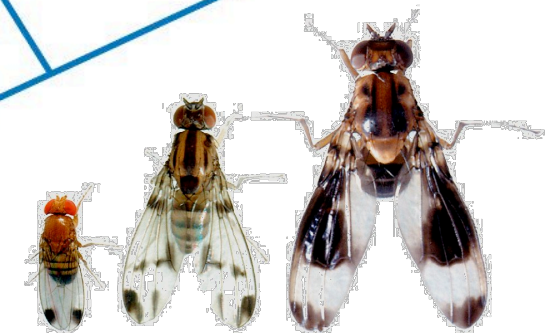
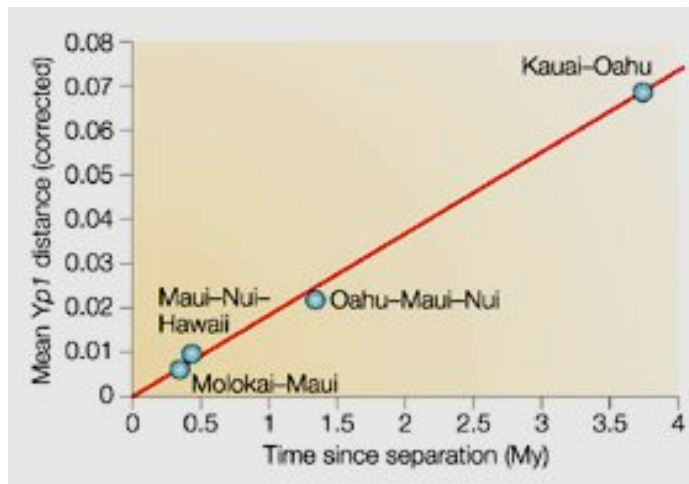
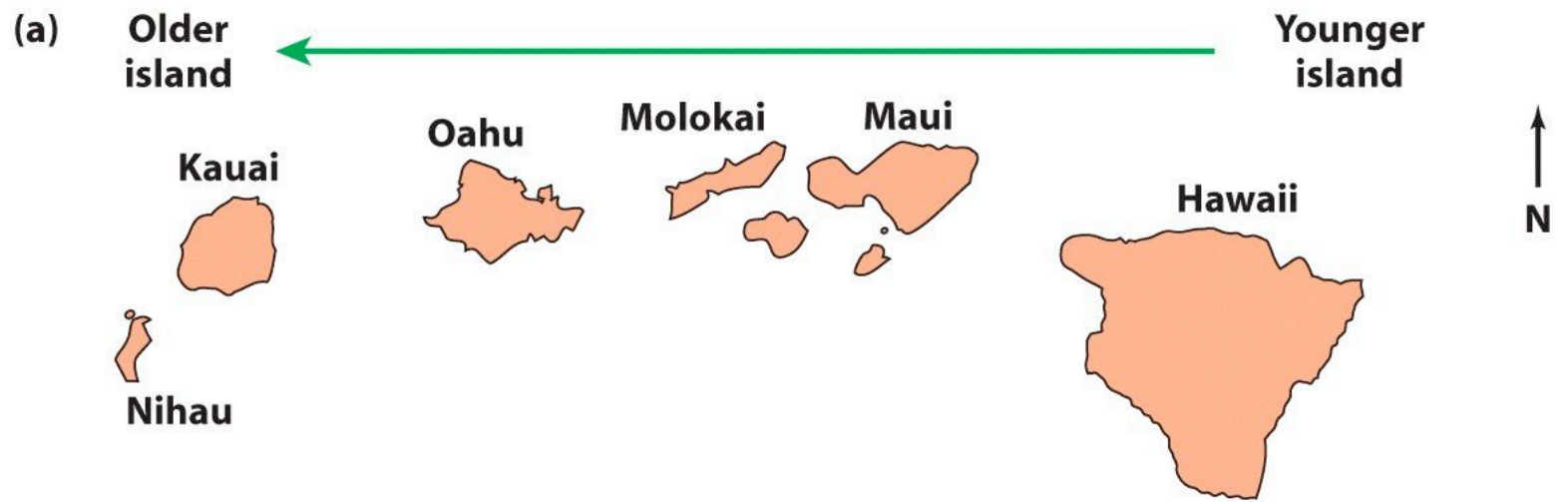


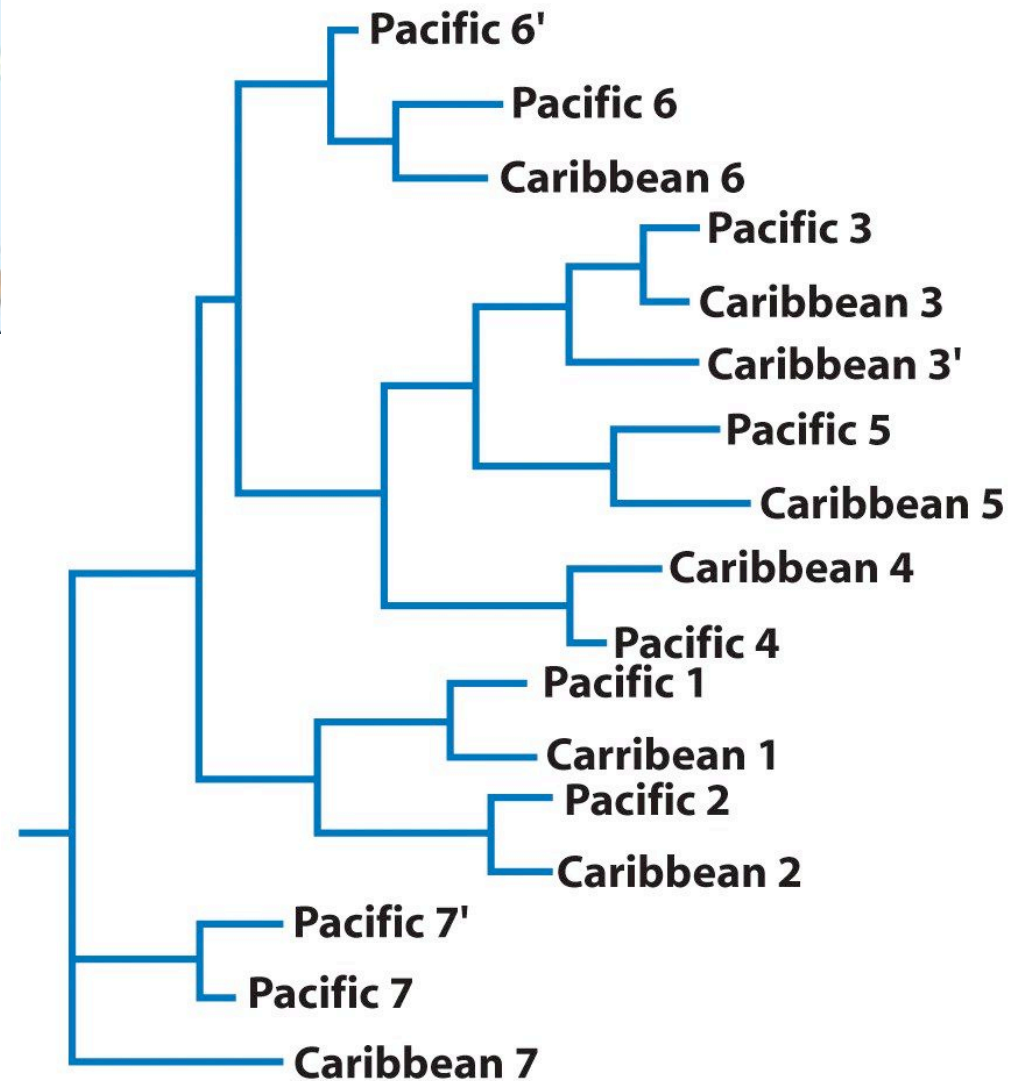
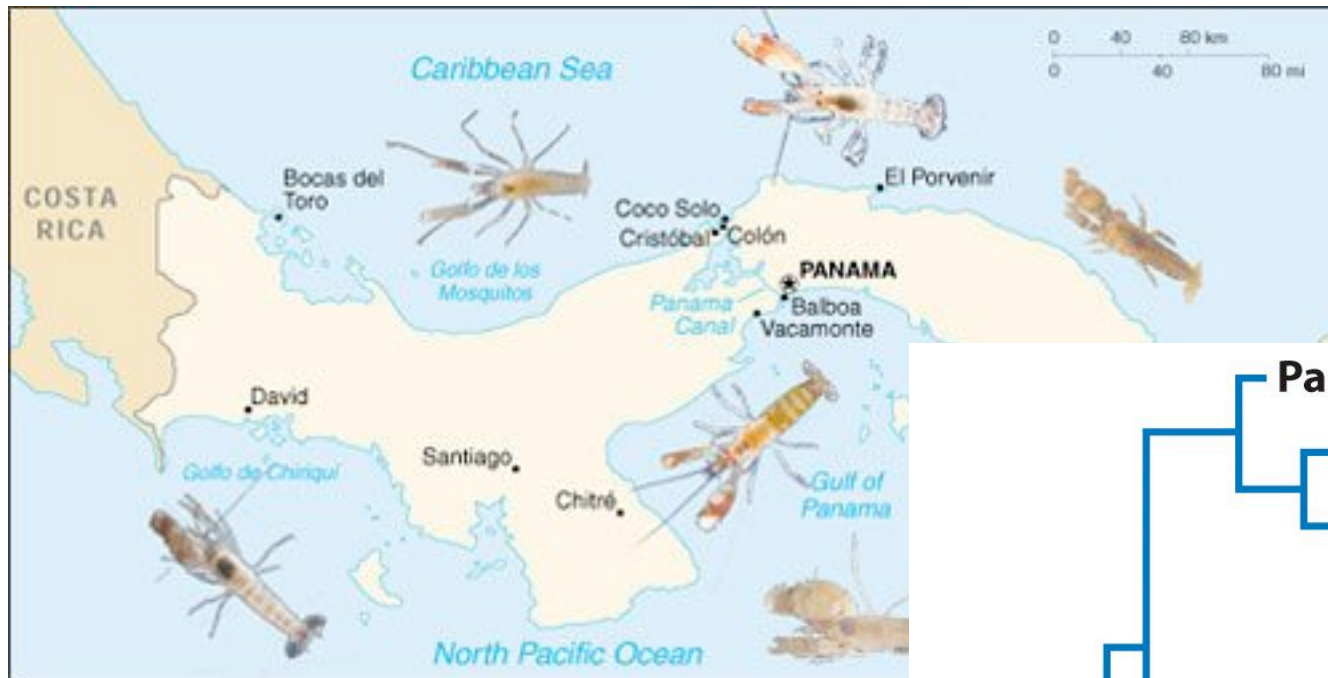
Dispersal



Ancestral population Geographic Isolation Speciation

Figure 2. Geography of allopatric speciation modes. In vicariance, the ancestral population (Species A) is passively divided by a geographic barrier. Incipient species (Species A' and A'') form during geographic isolation and later diverge to become new species (Species B and C). In dispersal, a subpopulation of the ancestral species (Species A) actively migrates across a geographic barrier to form an incipient species (Species A'), which later diverges to become a new species (Species B).



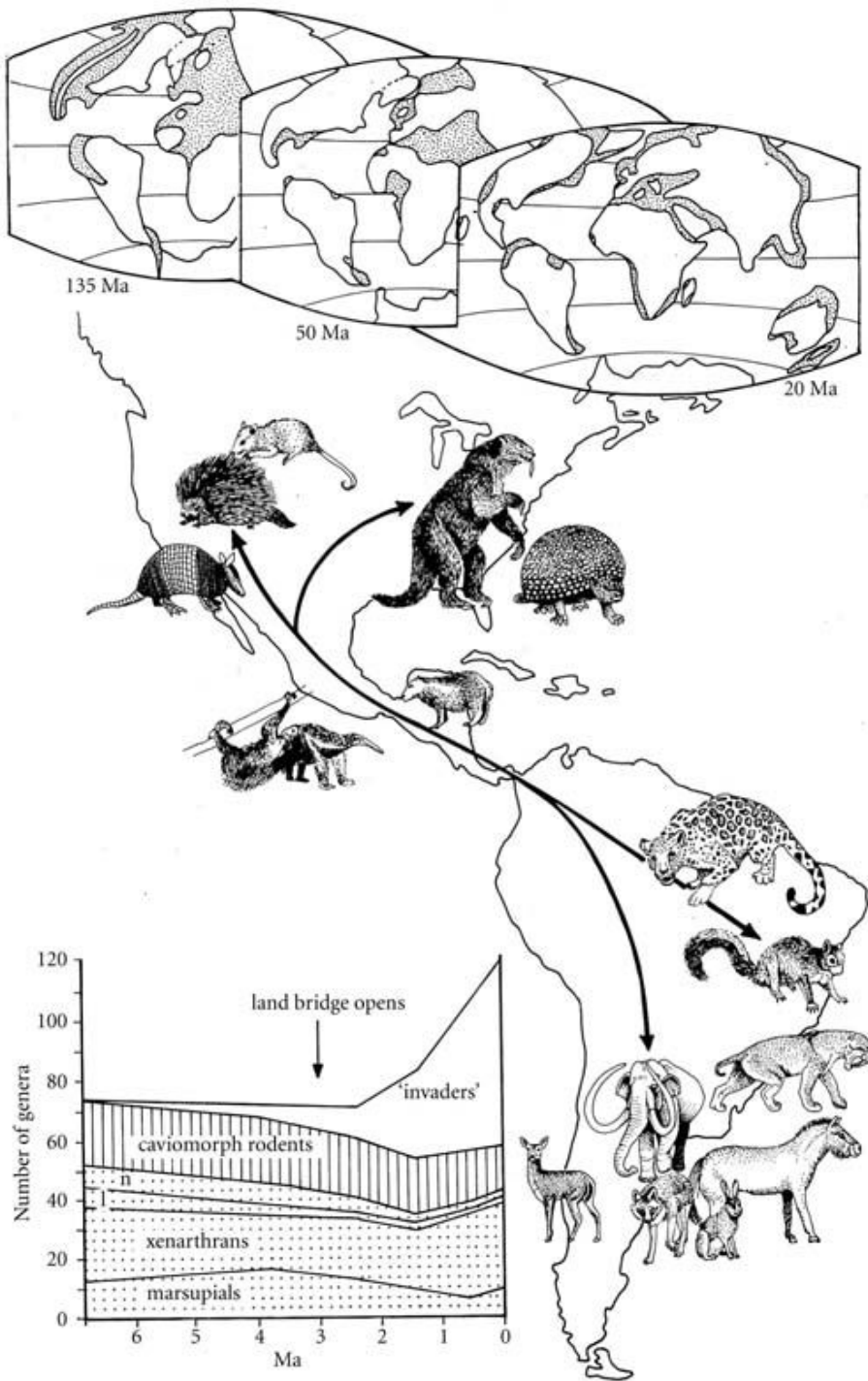


apple maggot fly (*Rhagoletis pomonella*)



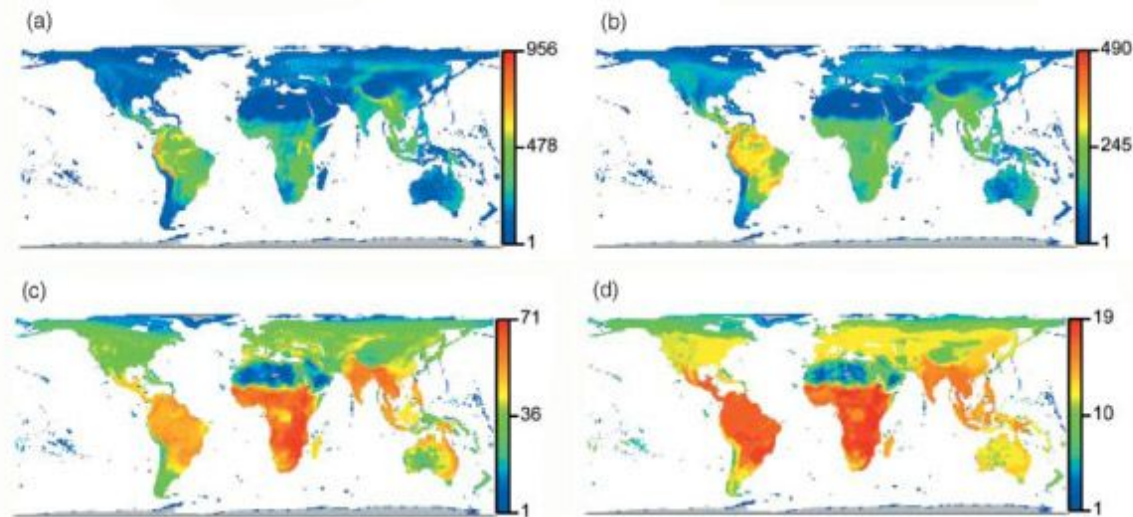
Apples

Hawthorne

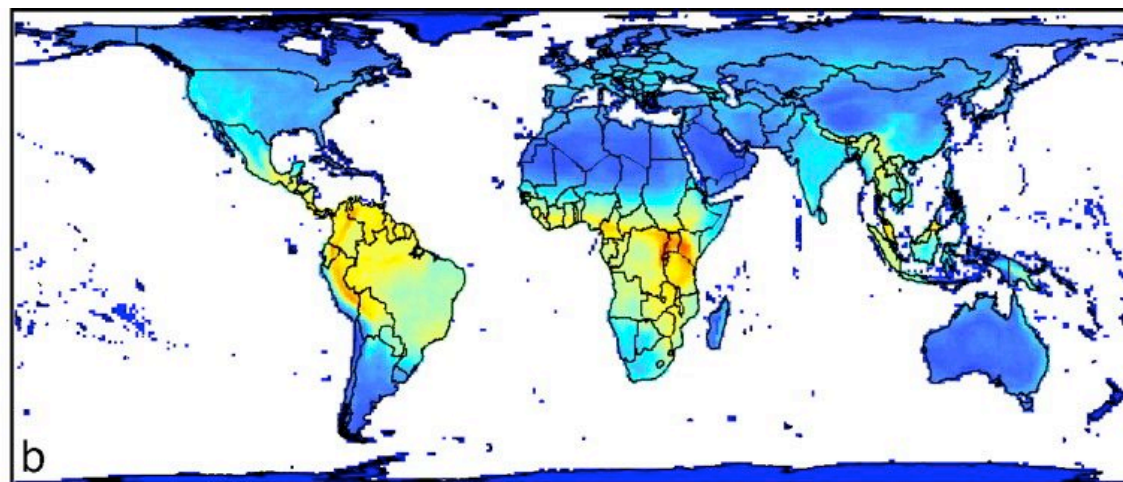
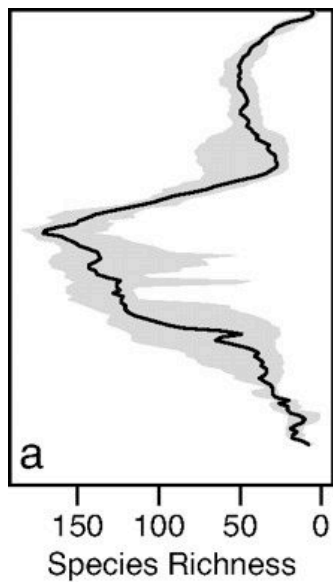


The emergence of the Isthmus of Panama promoted the great American biotic interchange (GABI) between North and South American terrestrial vertebrates together with the radiation of the shallow-water marine benthos of the Caribbean Sea. l, litopterns; n, notoungulates. (Based on Benton 2005.) From Introduction to Paleobiology and the Fossil Record, Benton and Harper.

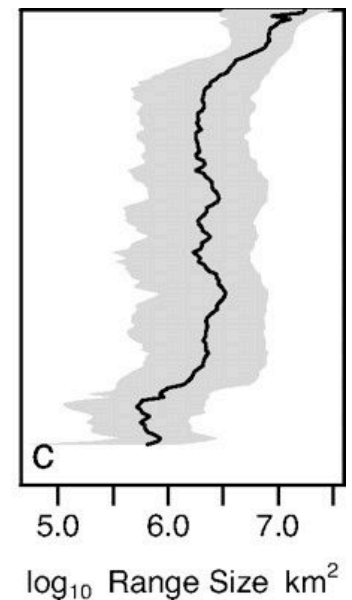
Bird Taxon Richness



A heat map depicting taxonomic richness for a) species, b) genera, c) families and d) orders. Scale bars adjacent to each map connect colors with numbers for each taxonomic level. Adapted from Thomas et al. 2008.



Geographic patterns in mammalian biodiversity.





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Latitudinal gradients in species diversity

From Wikipedia, the free encyclopedia

The increase in species richness or [biodiversity](#) that occurs from the [poles](#) to the [tropics](#), often referred to as the **latitudinal diversity gradient** (LDG), is one of the most widely recognized patterns in [ecology](#). Put another way, in the present day localities at lower [latitudes](#) generally have more [species](#) than localities at higher latitudes. The LDG has been observed to varying degrees in Earth's past.^[1]

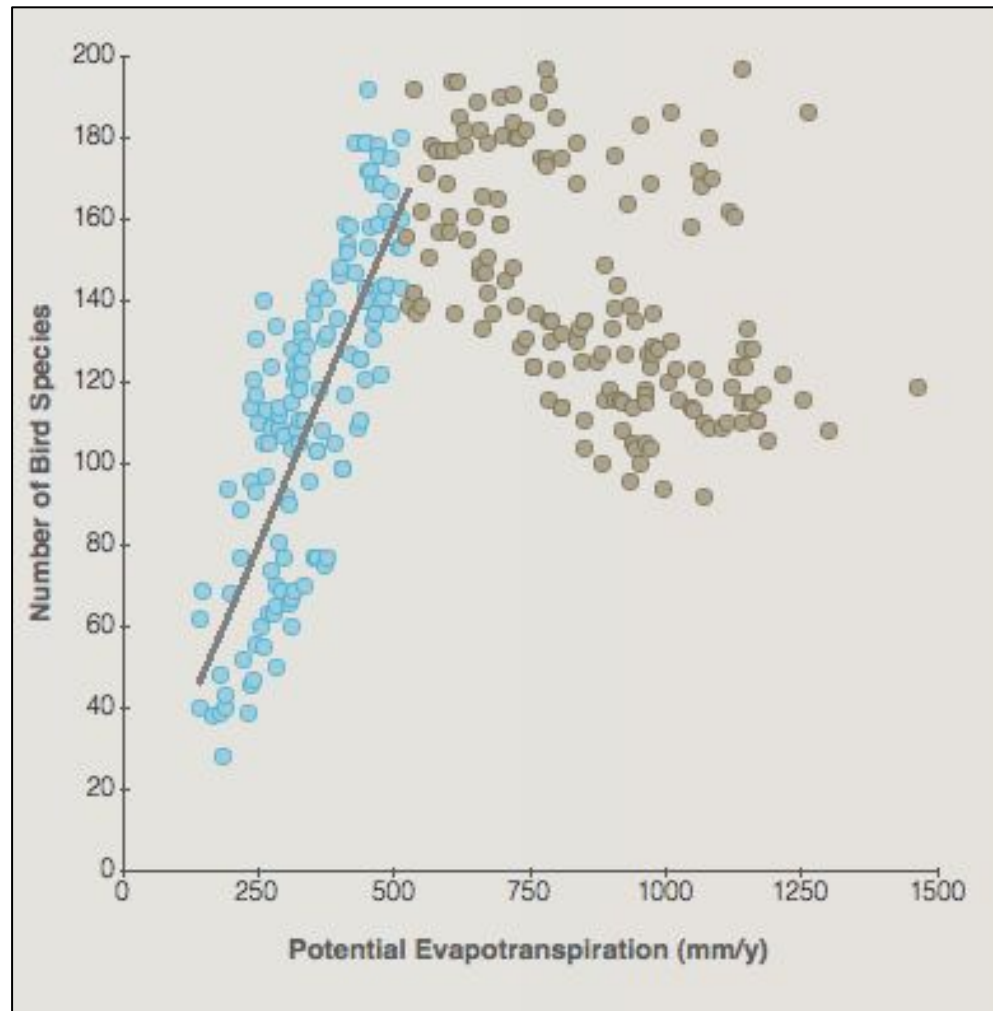
Explaining the latitudinal diversity gradient is one of the great contemporary challenges of [biogeography](#) and macroecology (Willig et al. 2003, Pimm and Brown 2004, Cardillo et al. 2005). The question "What determines patterns of species diversity?" was among the 25 key research themes for the future identified in 125th Anniversary issue of *Science* (July 2005). There is a lack of consensus among ecologists about the mechanisms underlying the pattern, and many hypotheses have been proposed and debated.

Understanding the global distribution of biodiversity is one of the most significant objectives for ecologists and biogeographers. Beyond purely scientific goals and satisfying curiosity, this understanding is essential for applied issues of major concern to humankind, such as the spread of invasive species, the control of diseases and their vectors, and the likely effects of global climate change on the maintenance of biodiversity (Gaston 2000). Tropical areas play a prominent role in the understanding of the distribution of biodiversity, as their rates of habitat degradation and biodiversity loss are exceptionally high.

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- 2 [Hypotheses for pattern](#)
 - 2.1 [Spatial/Area hypotheses](#)
 - 2.1.1 [Mid-domain effect](#)
 - 2.1.2 [Geographical area hypothesis](#)
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 - 3.1 [The generality of the latitudinal diversity gradient](#)
 - 3.2 [Conclusion](#)

Section 3, Page 21



∞ North American bird species richness versus potential evapotranspiration (PET). There is a positive relationship between richness and PET when little energy is available (blue circles; PET < 525 mm/y). However, at higher PET (brown circles) the relationship breaks down, suggesting other factors are important when energy is plentiful. This result follows that of Currie (1991).

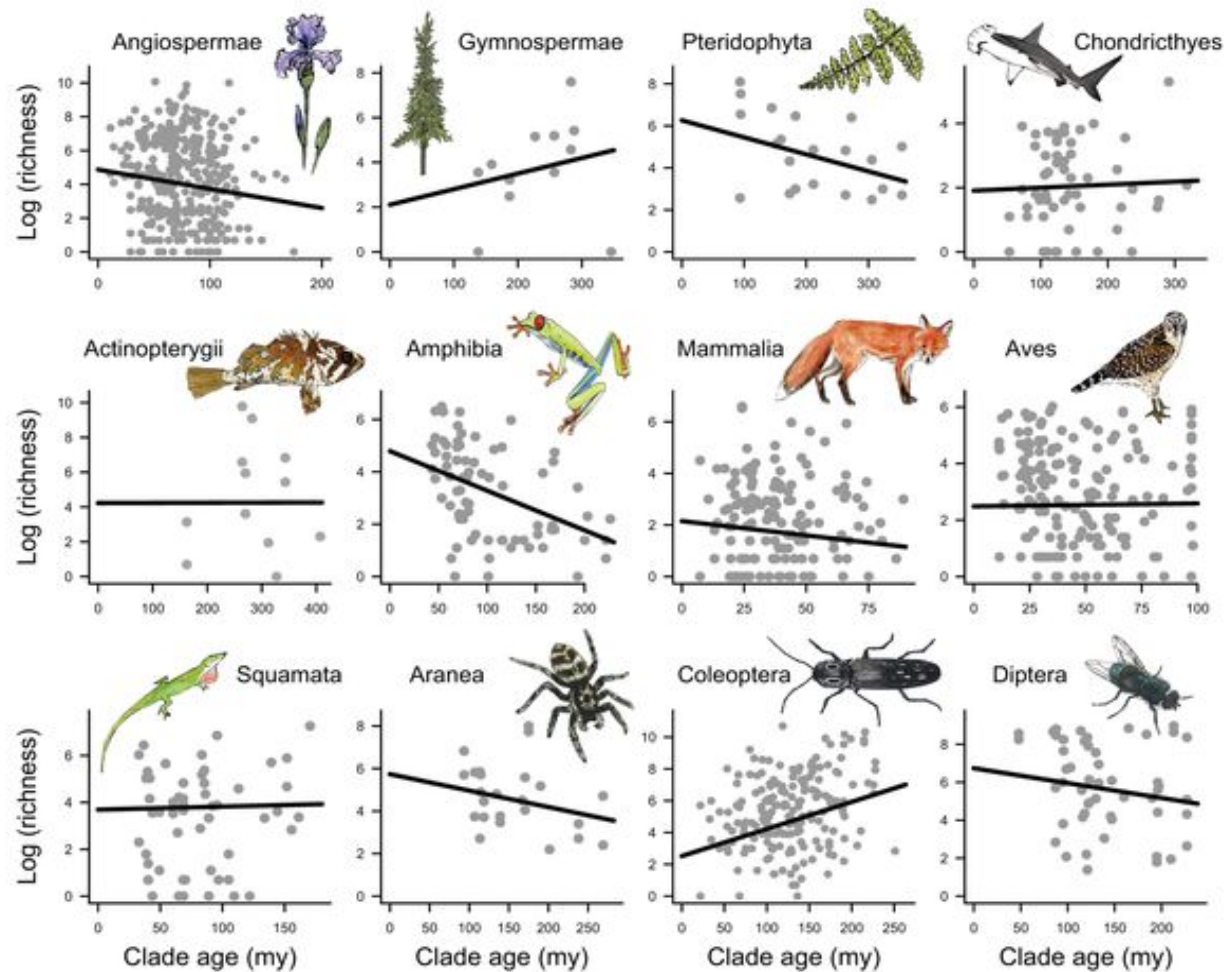
Predictions and tests of climate-based hypotheses of broad-scale variation in taxonomic richness

Abstract

Broad-scale variation in taxonomic richness is strongly correlated with climate. Many mechanisms have been hypothesized to explain these patterns; however, testable predictions that would distinguish among them have rarely been derived. Here, we examine several prominent hypotheses for climate–richness relationships, deriving and testing predictions based on their hypothesized mechanisms. The ‘energy–richness hypothesis’ (also called the ‘more individuals hypothesis’) postulates that more productive areas have more individuals and therefore more species. More productive areas do often have more species, but extant data are not consistent with the expected causal relationship from energy to numbers of individuals to numbers of species. We reject the energy–richness hypothesis in its standard form and consider some proposed modifications. The ‘physiological tolerance hypothesis’ postulates that richness varies according to the tolerances of individual species for different sets of climatic conditions. This hypothesis predicts that more combinations of physiological parameters can survive under warm and wet than cold or dry conditions. Data are qualitatively consistent with this prediction, but are inconsistent with the prediction that species should fill climatically suitable areas. Finally, the ‘speciation rate hypothesis’ postulates that speciation rates should vary with climate, due either to faster evolutionary rates or stronger biotic interactions increasing the opportunity for evolutionary diversification in some regions. The biotic interactions mechanism also has the potential to amplify shallower, underlying gradients in richness. Tests of speciation rate hypotheses are few (to date), and their results are mixed.

David J. Currie,^{1*}
Gary G. Mittelbach,²
Howard V. Cornell,³
Richard Field,⁴
Jean-Francois Guégan,⁵
Bradford A. Hawkins,⁶
Dawn M. Kaufman,⁷
Jeremy T. Kerr,¹ Thierry
Oberdorff,^{8†} Eileen O’Brien⁹
and J. R. G. Turner¹⁰

Figure 3. Relationships between age and richness within 12 major taxonomic groups for which dense subclade sampling was available as part of the timetree project [24].



Rabosky DL, Slater GJ, Alfaro ME (2012) Clade Age and Species Richness Are Decoupled Across the Eukaryotic Tree of Life. *PLoS Biol* 10(8): e1001381. doi:10.1371/journal.pbio.1001381
<http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1001381>

So what can we conclude about broad-scale patterns in diversity?



- ∞ Diversity increases with area (species-area relationships)
- ∞ Diversity on islands often a balance between
 - ∞ colonization (distance from mainland) &
 - ∞ extinction (size of island)
 - ➡ Produces a dynamic equilibrium (S^*)
 - ➡ More mixing, $S^* \rightarrow \gamma$
- ∞ Diversity decreases with distance from the equator
 - ∞ correlated with energy (NPP or PET), up to a point
- ∞ History (time, events) matters (but only up to some limits)
 - ∞ E.g., the Great Biotic Interchange
 - ∞ Maybe only (geologically) early after events