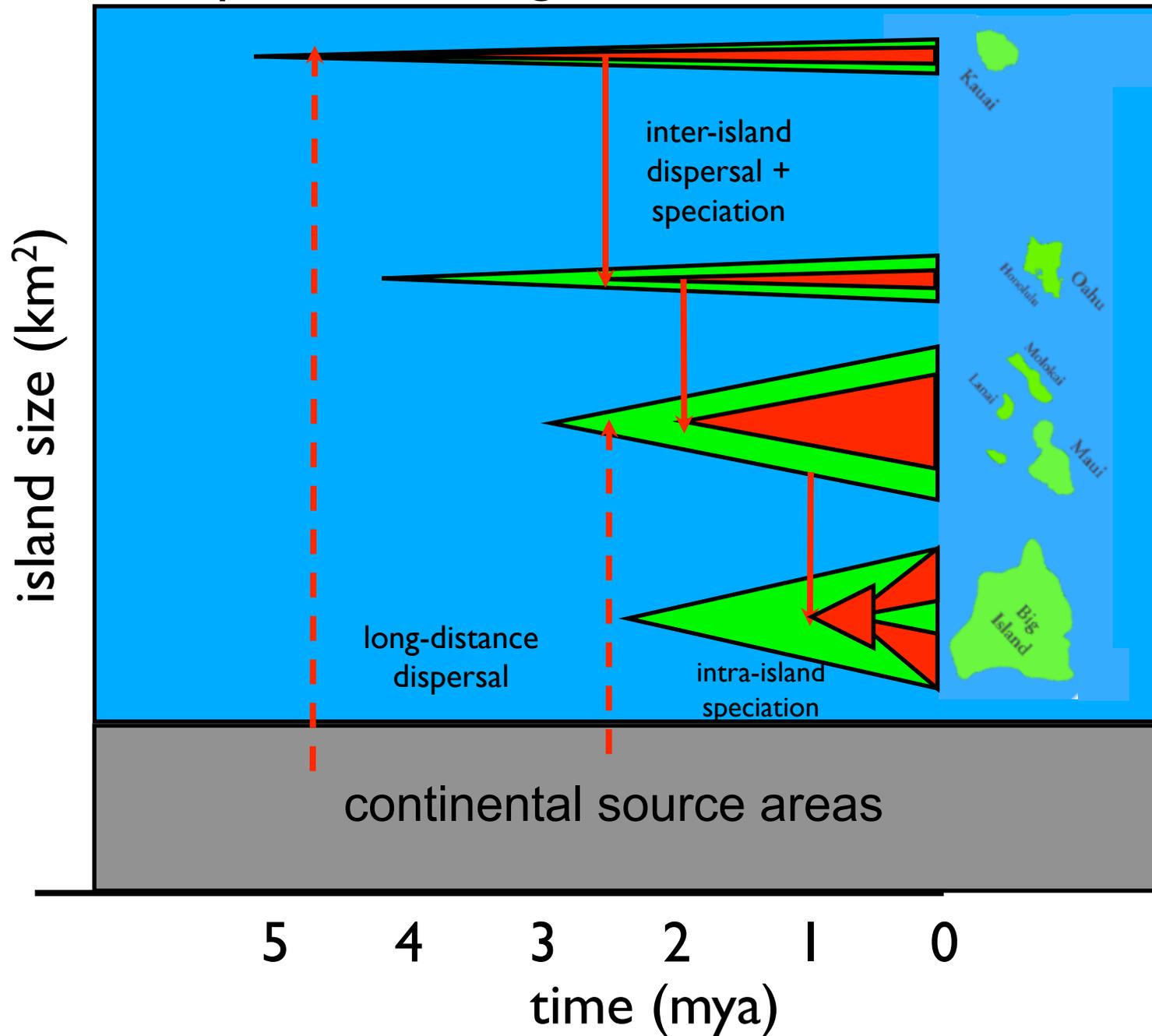


space-time diagram of Hawai'ian islands



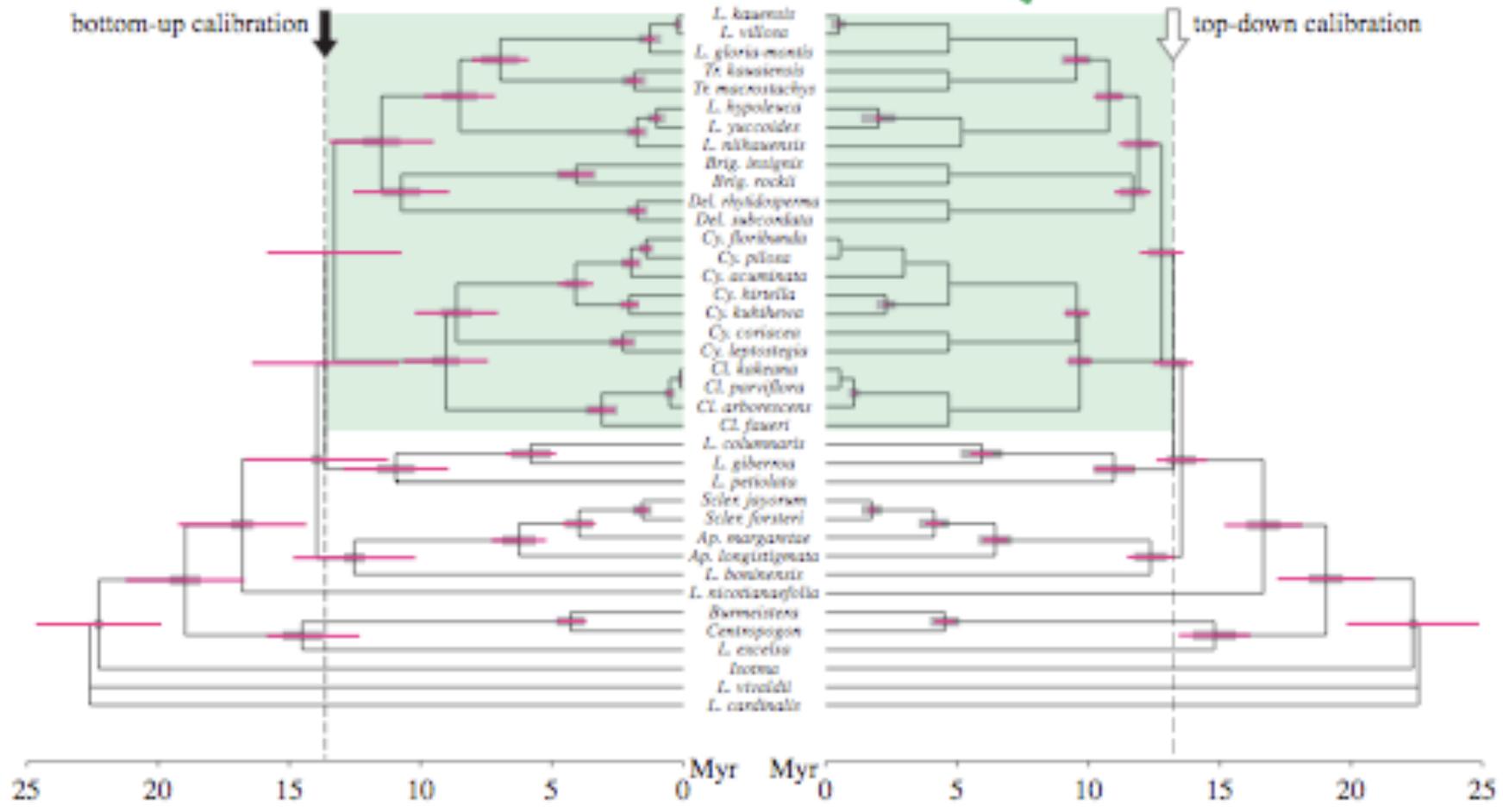
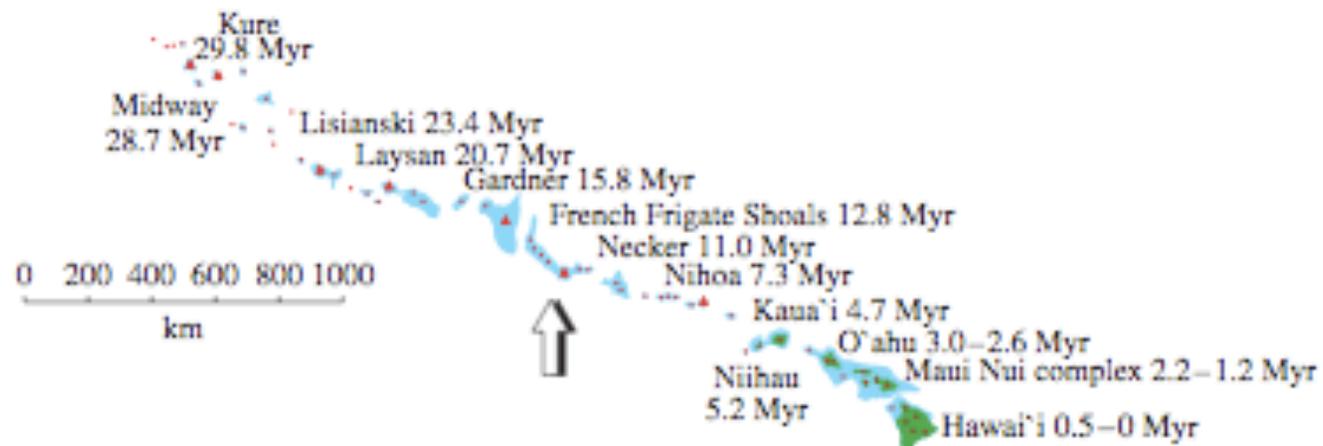
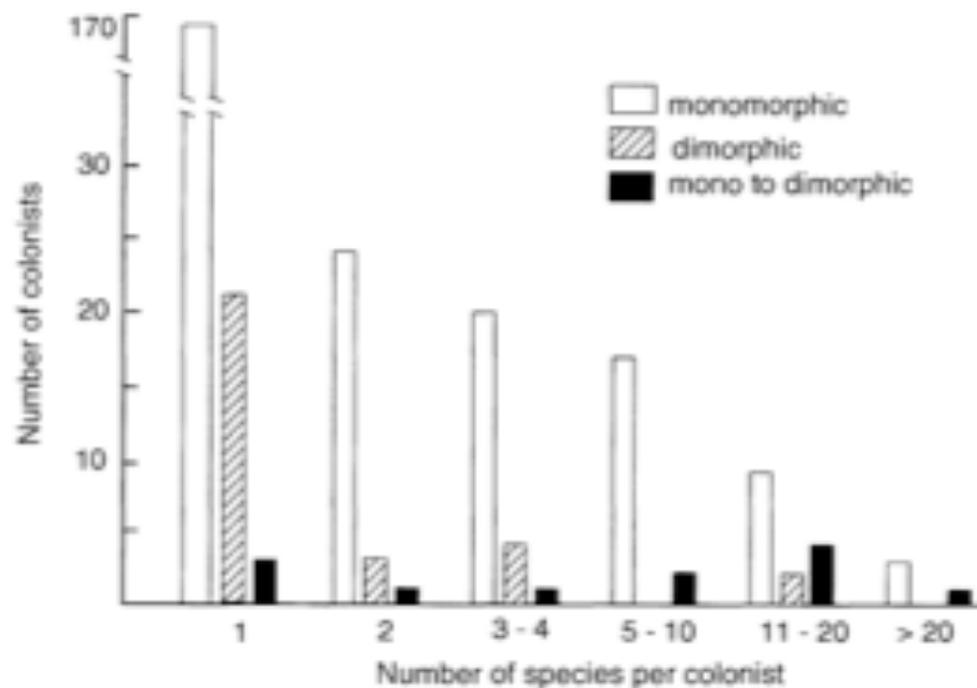


FIG. 1. Number of species per colonist. Monomorphic = monomorphic colonists giving rise to only monomorphic species. Dimorphic = dimorphic colonists giving rise to only dimorphic species. Mono to dimorphic = monomorphic colonists with autochthonous evolution of dimorphism. Seven colonists with unknown breeding systems (with 2, 3, 3, 4, 5, 10, and 20 species/colonist) are omitted from this histogram, as are two dimorphic colonists with evolution of monomorphism (with 1 and 47 species).



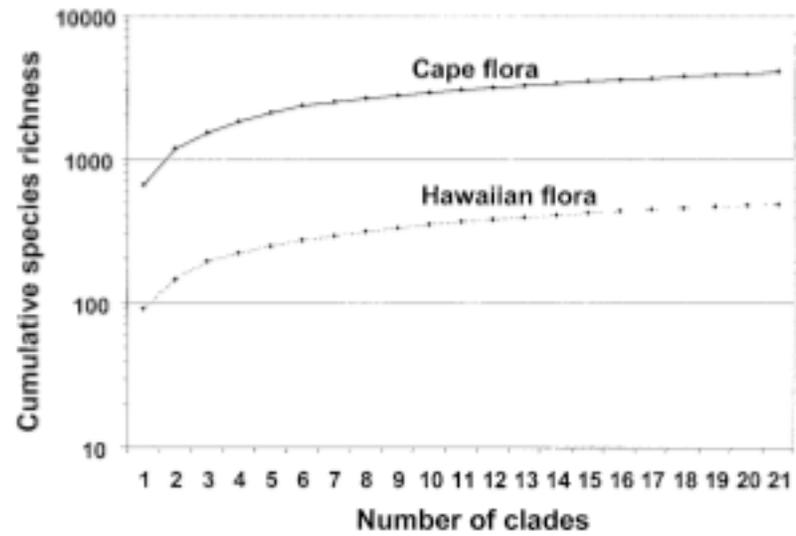
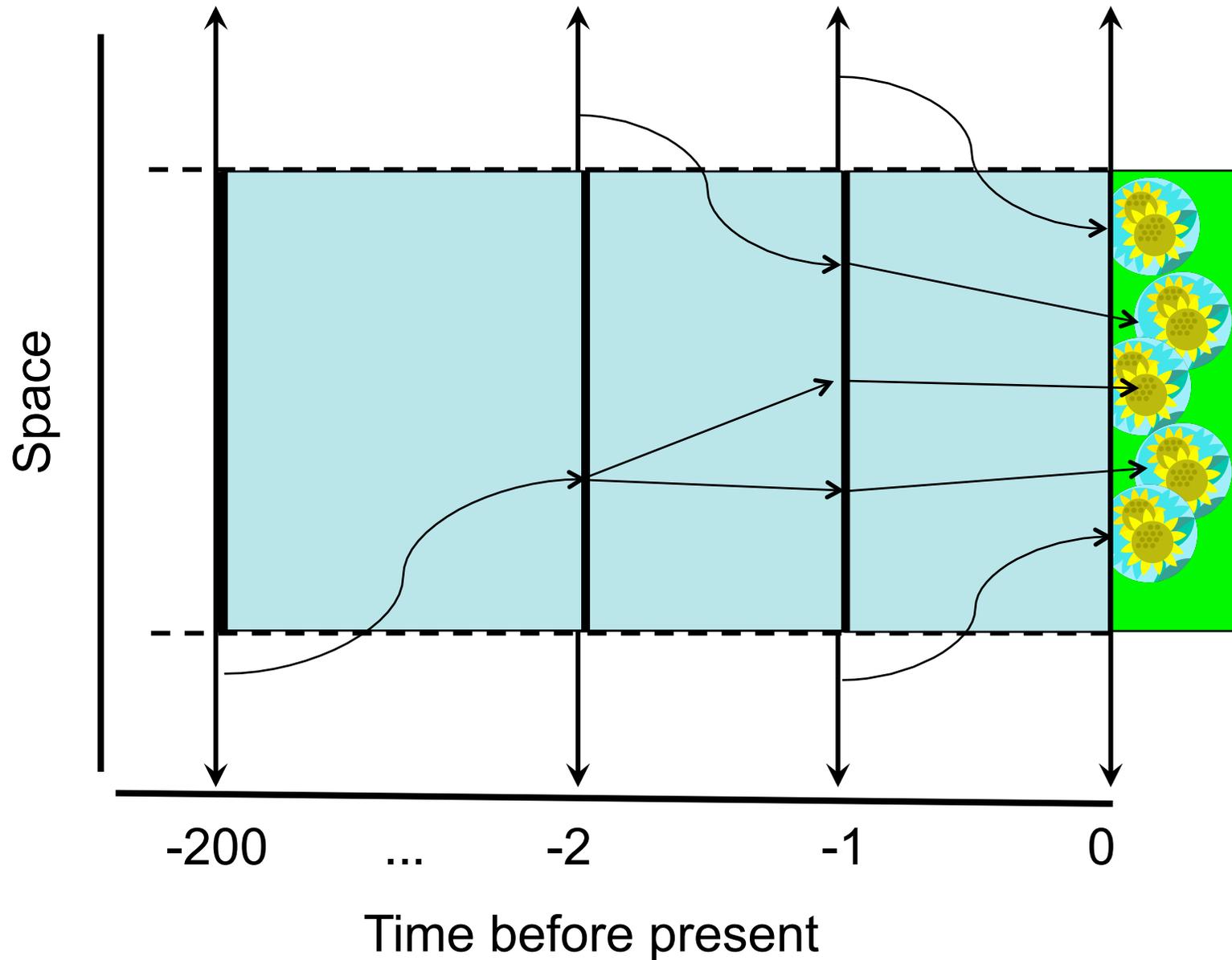
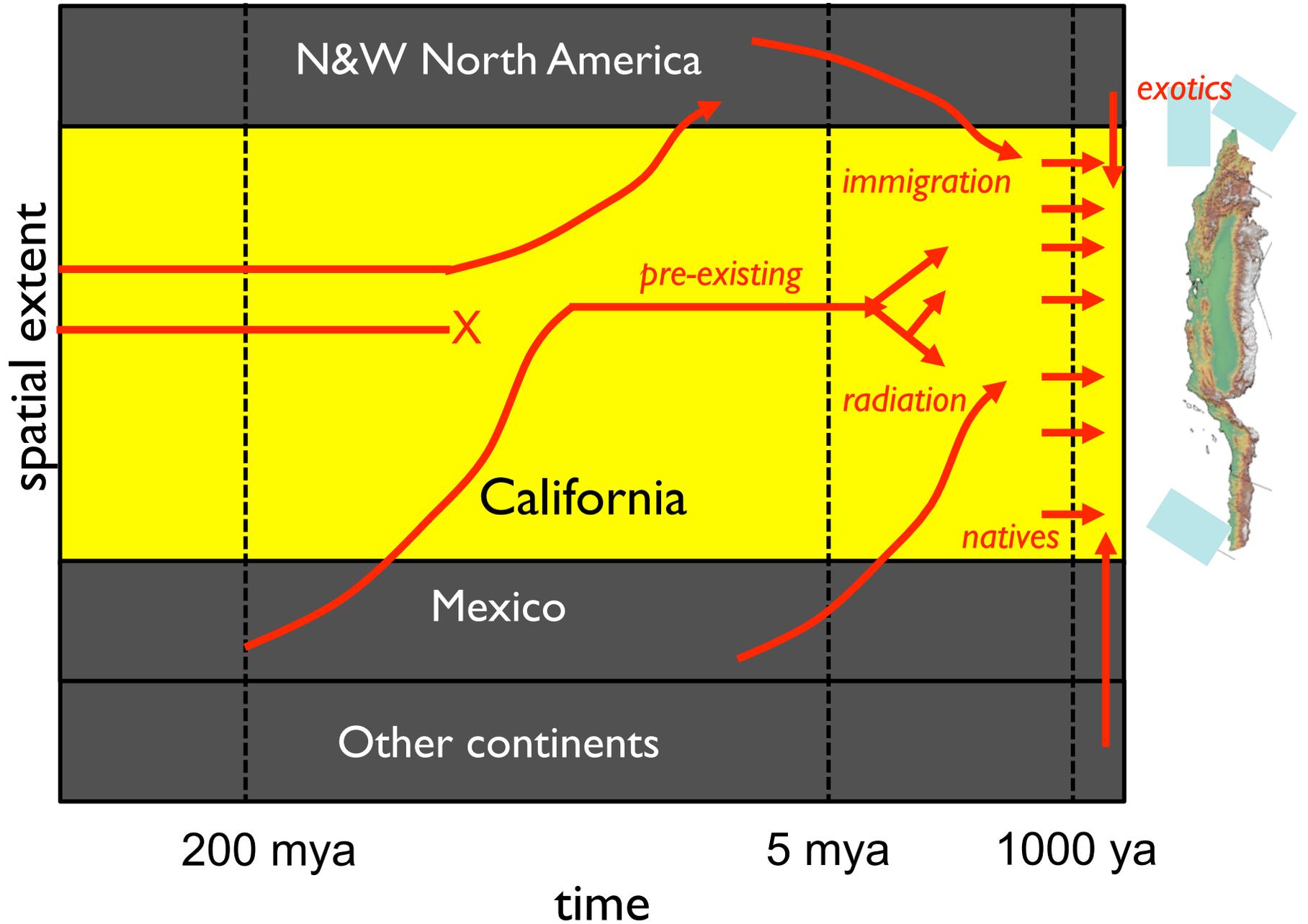


Fig. 9. Rate of accumulation of species from the Cape flora clades, compared to the Hawaiian clades. Only the 21 largest clades were used. Data for the Cape flora from Table 1, the data for Hawaii were taken from Wagner (1991). For the Hawaiian data the minimum number of colonisation events was assumed.

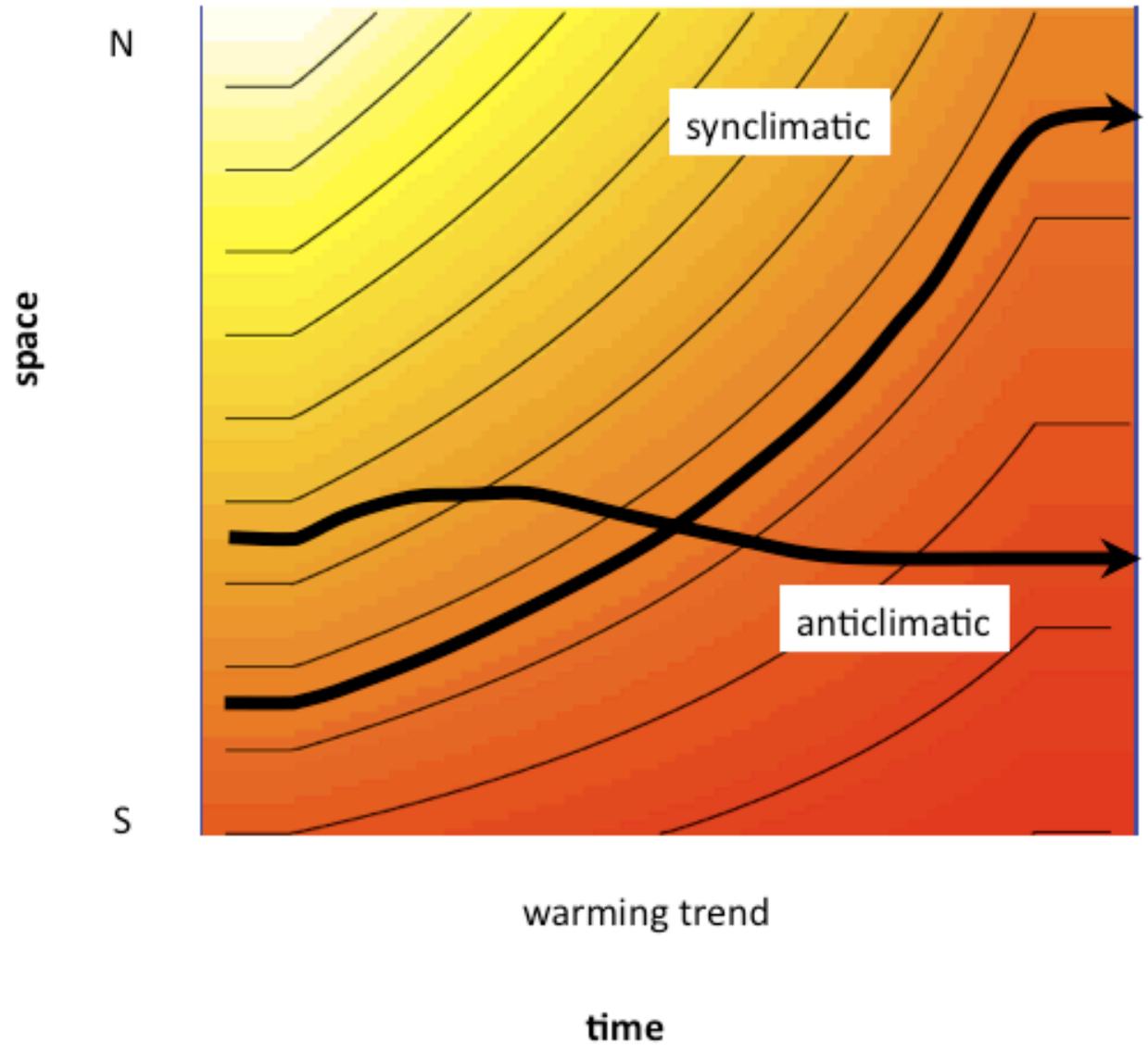
Assembly of plant communities:
migration in *space* vs. *time*



space-time diagram of California



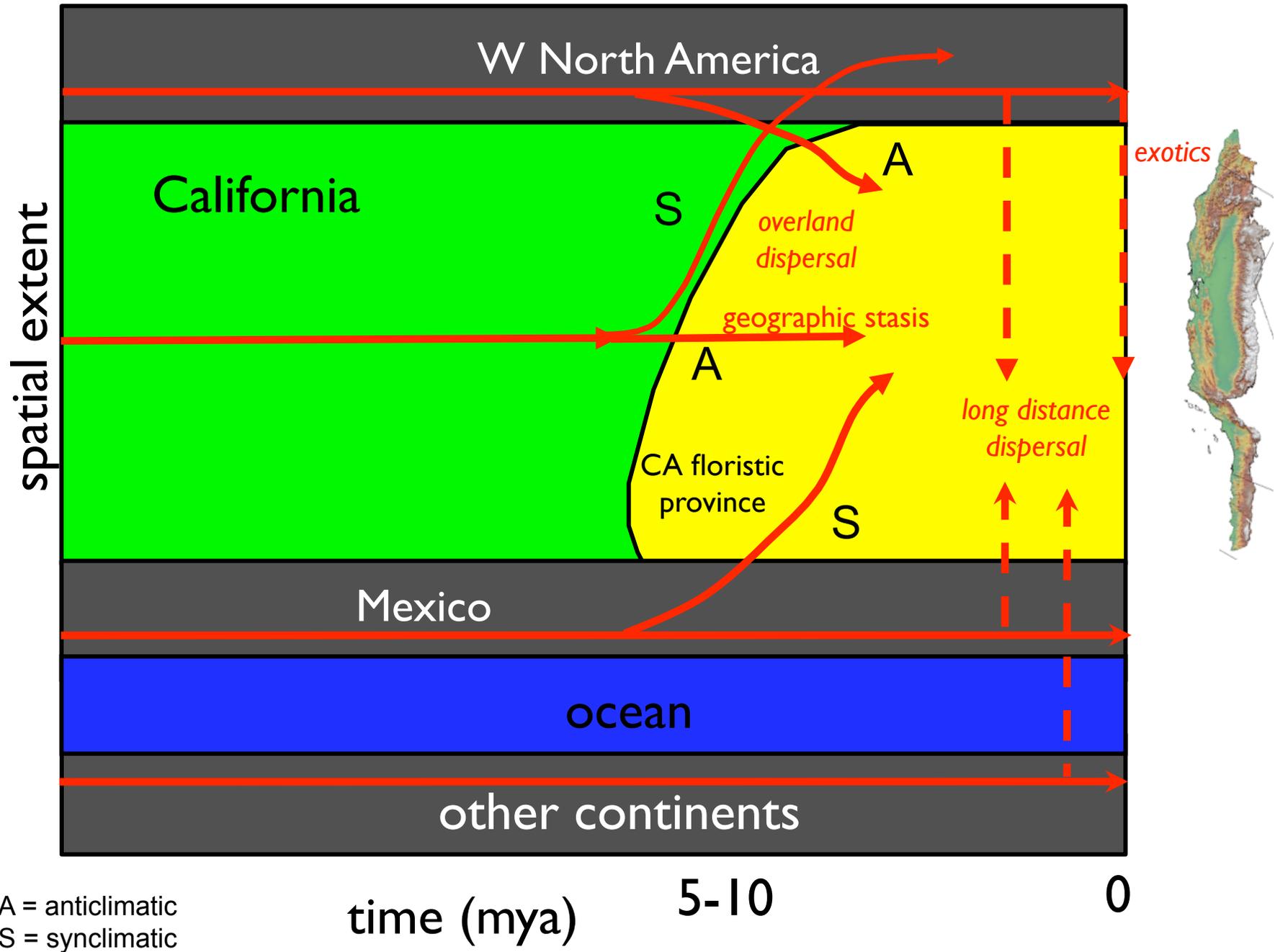
climate isotherms in space-time



warming trend

time

space-time diagram of California



Arrival modes

- Long distance dispersal (islands and continents)
- Secular migration (overland dispersal through gradual establishment of populations into new area) (regions within continents)
- Geographic stasis (climatic biomes with temporal baseline)

EXPECTATIONS

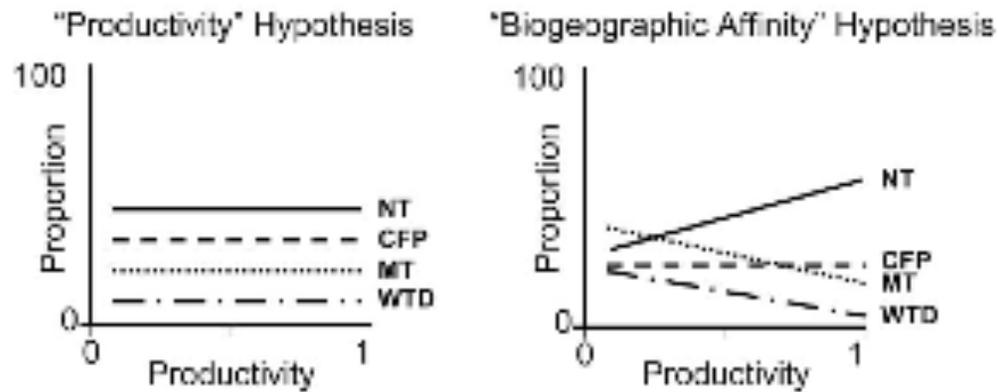
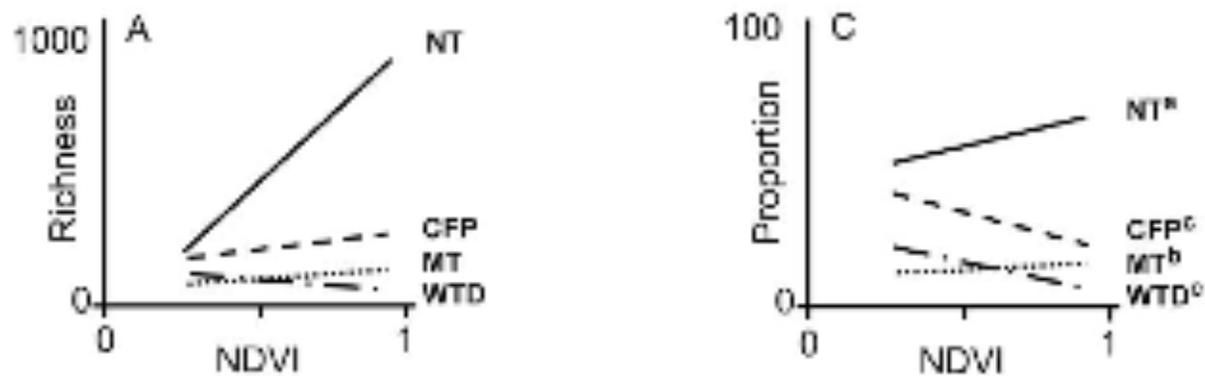


Figure 1: Expectations under the "productivity per se" and "biogeographic affinity" hypotheses. The affinity groups are north-temperate (NT), California Floristic Province (CFP), Madro-Tertiary (MT), and warm temperate desert (WTD). Under the biogeographic affinity hypothesis, we predict that the proportional contribution of these groups to total richness will vary predictably with productivity (normalized difference vegetation index) in the order $NT > MT, CFP > WTD$, while under the productivity per se hypothesis, the proportional representation of each affinity group will not vary with productivity.

RESULTS



from: Harrison and Grace 2007 Amer. Nat.

Evolutionary changes in leaf size and SLA accompanying transition to mediterranean-type climate:

<u>Clade</u>	<u>Lineage</u>	<u>Leaf size</u>	<u>SLA</u>	<u>Putative origin</u>
Anacardiaceae	<i>Malosma</i>	0	0	Subtropical
	<i>Rhus</i> (2 spp.)	0	0	Desert
Ericaceae	<i>Arbutus</i>	0	0	Subtropical
	<i>Xylococcus</i>	0	NEG	Subtropical
	<i>Comarostaphylis</i>	0	(neg)	Subtropical
	<i>Arctostaphylos</i>	(neg)	0	Subtropical
Rhamnaceae	<i>Ceanothus</i>	0	0	Subtropical?
Rosaceae	<i>Cercocarpus</i>	0	0	W North America
	<i>Lyonothamnus</i>	0	(neg)	W North America
	<i>Adenostoma</i>	NEG	(neg)	Temperate
	<i>Prunus</i>	0	NEG	Temp/subtropical
	<i>Heteromeles</i>	0	NEG	Temperate

0 = no change
 (neg) = NS reduction
 NEG = significant reduction

Taxon age and the assembly of mediterranean-type floras

(Herrera 1992)

old: 'genera having either contemporary intercontinental range disjunctions or Pliocene fossil records...'

young: 'genera lack both features'

old genera tend to be:
sclerophyllous
vertebrate-dispersed
fleshy-fruited
large-seeded.



courtesy UC Berkeley Bot Garden

Arbutus unedo

Non rank-based restatement of Herrera's conclusions:

'old' = lineages that exhibit ancestral traits that predate the mediterranean-type environment, such as: vertebrate dispersal, etc.

'young' = lineages that have undergone recent adaptive shifts to derived states, including drought-deciduous leaves, small seeds, etc.

This is a conclusion about ancestral and derived traits, not about 'taxon age'

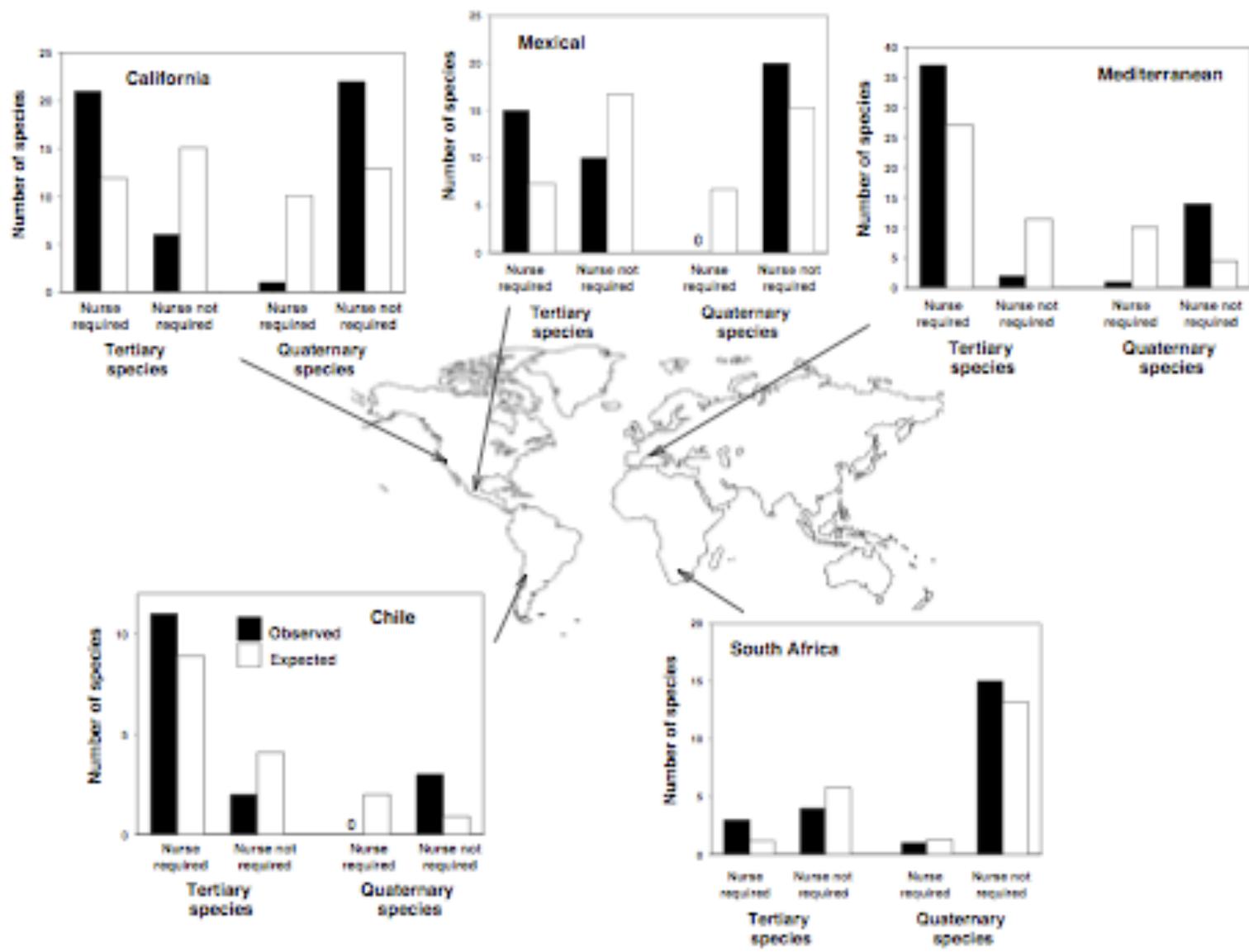


Fig. 1. Regeneration-niche requirements of Tertiary and Quaternary lineages, based on the fossil record, in the five Mediterranean areas of the world and in the Mexical shrubland of central Mexico. Filled bars show the observed numbers of species from each lineage reported in the literature that occupy particular regeneration niches, and open bars show the expected numbers of species of each lineage.

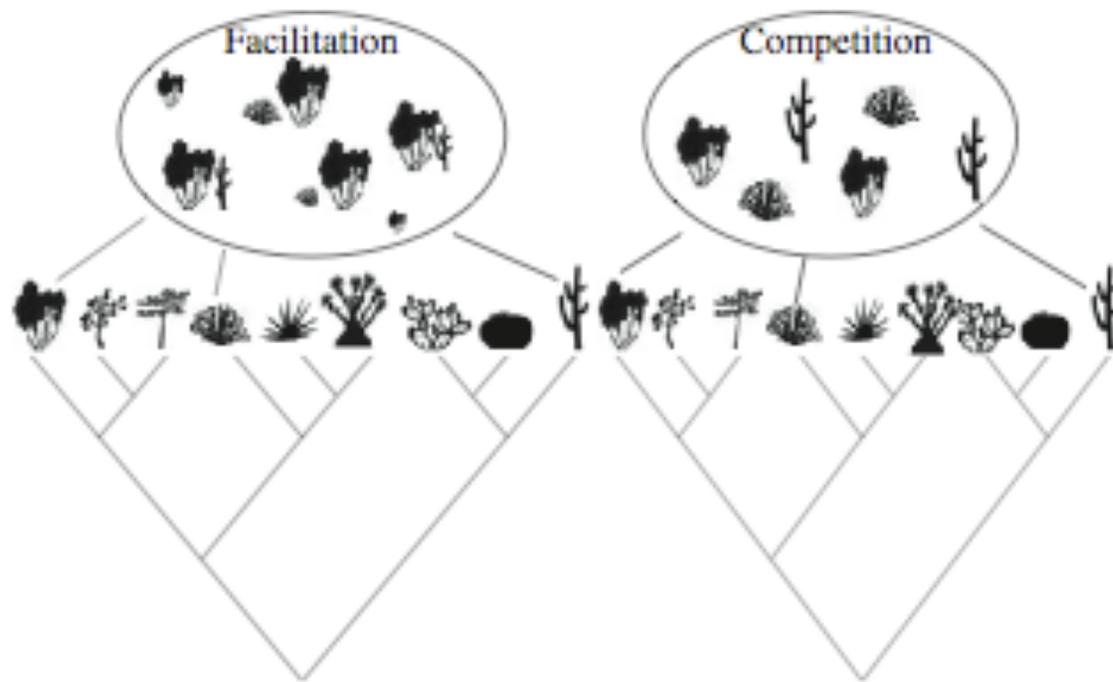


Figure 1 Two different ways how phylogenetic overdispersion in communities can be produced. In the case of competition, overdispersion is achieved by the exclusion of close-related species producing a checkerboard spatial pattern. In the case of facilitation, overdispersion is achieved because nurses add distant-related species to the community producing a clumped association pattern among species.

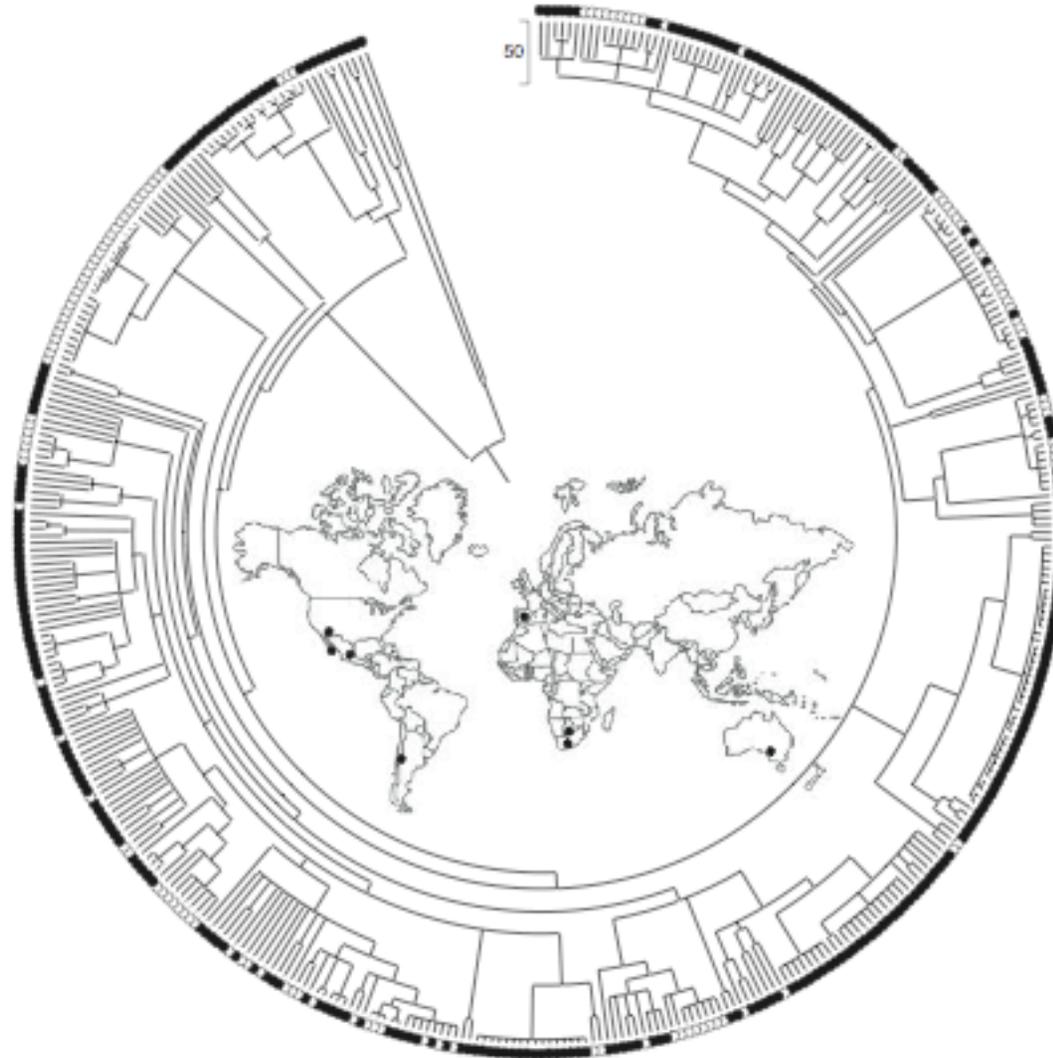


Figure 2 Phylogenetic tree showing the evolutionary relationships between the study species and the regeneration niche mapped onto the tips. Filled dots represent facilitated niche while unfilled dots represent non-facilitated niches. Species labels have been omitted for clarity. The world map shows the sites where data were obtained. (Database S4, including the phylogenetic tree, taxa labels, character scoring (facilitated vs. non-facilitated), parsimony reconstruction and null model for niche conservatism test). The file was created with the free software Mesquite (<http://mesquiteproject.org/mesquite/mesquite.html>).