

Ecography

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**Supplementary material**

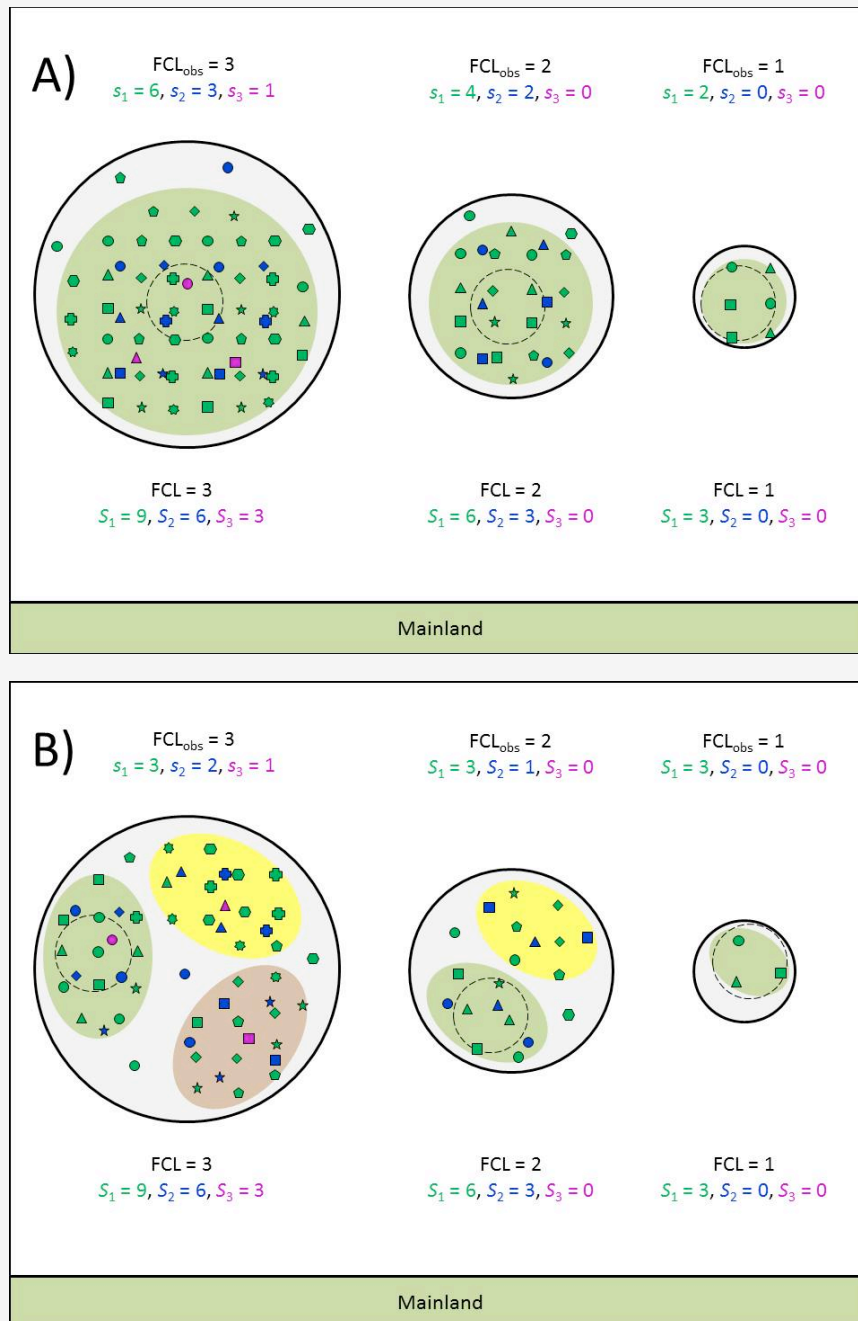
**Appendix 1. Operationalizing the predictions of Trophic Island Biogeography.** An explicit appraisal of the match between study system and model assumptions, and of how local samples reflect island-wide species richness and food chain length.

In their famous book on Island Biogeography, Robert MacArthur and Edward O. Wilson (1967) posed the question of what factors govern variation in the number of species found on islands, as a function of island area and distance from the mainland. To this basic focus on local species pools, Robert Holt (1996, 2010) was one of the first to add an explicitly trophic perspective. More explicitly, he asked how the properties of islands may affect not only the local number of species, but also the composition of local food chains and webs.

In the simplest formulation of his seminal model, Holt (2010) envisaged a set of stacked food chains, where the presence of each species at a trophic level  $i$  is conditional on the species directly underneath it. In itself, the model assumes no spatial structuring within islands, but across islands. In consequence, the incidence of all species in the chain is assumed to scale with total island size. To calculate the species richness at trophic level  $i$  as a function of island area, we may then sum the incidences of all species of rank  $i$ . If, for simplicity, we assume that all species of rank  $i$  are characterized by the same conditional incidence function, then the expected number of species of trophic rank  $i$  is simply the product of species-specific incidence and the number of chains examined,  $S_i = mp(i)$  (Holt 2010). As a species at trophic level  $i$  is always confined to the set of islands already occupied by its prey at level  $i-1$ , we may predict that the strength of the species–area slope should increase with trophic rank, and that food chain length should increase with island size (Holt 2010).

Importantly, in its basic form outlined above, the model focuses on species richness and food chain length at the island level. Yet, the full species pool of any area is notoriously hard to describe, frequently confining ecologists to operating with samples of local species pools and local food chains within islands, rather than exhaustive surveys of the entire islands. The key question is then to what extent local samples reflect the island-wide parameters of interest (i.e. total species richness and food chain length), and thereby how such data connect to the theory.

In itself, the relationship between island size and species' incidence forming the basis of both basic and trophic island biogeography may result from two fundamental factors (as summarized by Holt 2010): on the one hand, larger areas will harbor more individuals (a "pure area" effect; Fig. A1.1A), on the other, larger areas will typically contain more habitats (an "environmental diversity" effect; Fig. A1.1B). Of these, the pure area effect can reflect two processes. First, if a species' density is constant, its absolute numbers will scale with island area, and smaller populations will typically face larger dangers of extinction from demographic risk and other factors. Second, if colonization is analogous to random sampling from a continental fauna, then small islands with their few individuals offer small samples, and may thus contain fewer species by chance alone. By contrast, the environmental diversity effect derives from more habitats sustaining a larger number of specialized niches than do few habitats (Fig. A1.1B), and/or of habitat-related variation buffering populations from extinction.



**Fig. A1.1. Operationalizing the predictions of Trophic Island Biogeography.** The graph offers a schematic representation of the relationship between two parameters, Species richness ( $S$ ) and Food Chain Length (FCL), as measured at the level the whole island (large circles) and a local sample (dashed circles) under two scenarios: In A), the association between island-level species richness and area is assumed to derive from a “pure area” effect, where larger islands sustain larger populations running a lower risk of extinction. In B), larger islands also include more diverse habitats (indicated by patches of different color), thus sustaining a larger number of specialized niches and species than do small islands (an “environmental diversity” effect). In both panels, species are identified by symbol style, whereas trophic rank is distinguished by colors (with red being the highest and green the lowest trophic level). Below each symbolic island, we show the length of the whole-island food chain (i.e., the total number of trophic levels present on an island) and its species richness  $S_i$  at three individual trophic levels  $i$ . Above each island, we offer the same parameters as measured from a sample of a standardized area within the island. In both scenarios, population densities are assumed to decline with increasing trophic rank, reflecting the basic fact that any given area will sustain less individuals of a predator than of the herbivores upon which it feeds. All islands are also assumed to be equally isolated from the mainland, thus standardizing the impact of the other key ingredient of island biogeography theory, i.e. differential colonization rates with varying isolation from the mainland. Note that in the specific study system targeted by us, sampling was aimed at the most species-rich and dominant habitat within islands, i.e. forests (green patches in panel A), the area of which was shown to scale directly with overall island size. Note also that there was no indication of differential habitat diversity among islands of different size (see text for specific analyses). For this specific case, descriptors derived from a local sample will be directly reflective of island-wide parameters (see panel A) – whereas for more complex settings, associations between local and global parameters may be weak or lacking (see panel B). Note also that given a general decrease in population density with increasing trophic rank  $i$ , the higher the value of  $i$ , the smaller is the proportion of the island-level species pool  $S_i$  represented in a local sample  $s_i$ . However, this effect is independent of island size, and will therefore not distort our analysis of the effect of trophic rank on the species-area slope. (For resampling schemes aimed at correcting for multiple sampling effects, see the main paper.)

The last half-century has seen a wealth of research into “pure area” *versus* “environmental diversity” effects (see entries from MacArthur and Wilson 1967 through e.g. Williamson 1981, 1988, Brown 1988, Holt 1992 to Allouche et al. 2012). Importantly, the relative contribution of each one of these factors comes with major implications for how the theory of trophic island biogeography may be operationalized to specific study systems (Fig. A1.1): If species are randomly (or evenly) distributed within islands (as envisaged for “pure area” effects; Fig. A1.1A), it naturally follows that local samples will offer a fair reflection of variation in island-wide parameter values (cf. Fig. A1.1A). If, on the other hand, species are highly clumped within islands and/or if much of the island-level species richness derives from species turnover between habitats (as envisaged for strong “environmental diversity” effects; Fig. S1.1B), then estimates from local samples may bear no resemblance to island-wide parameter values (cf. Fig. A1.1B).

Based on these considerations, we deliberately chose a study system conforming to the first scenario as dominated by “pure area” effects (Fig. A1.1A). By focusing on a set of small, internally homogenous islands varying virtually only in size, we sought maximal agreement with the basic setting of Holt (2010), and a direct link between the data collected and the predictions tested. While our local samples will not offer *absolute* estimates of island-wide parameter values, the following considerations suggest that species richness and food chain length measured at a local level offer fair representations of island-wide characteristics (compare Fig. A1.1A):

First, all islands examined were small and habitat diversity within them (very) low. As summarized by Table 1 of the main paper, the size of the target islands ranges from 0.004 to 0.39 km<sup>2</sup>, and their highest point from 2.5 to 24.4 m.a.s.l. Among the three local habitat types, one (open cliffs) was essentially devoid of species, and a second (the heathlands) characterized by low species diversity. Thus, the vast majority of both plant and animal species occurred in the forest patches specifically targeted by our sampling. These considerations support a general lack of spatial structuring within islands (compare Fig. A1.1A vs B).

Second, the area of the main habitat type sampled (forests) scaled directly with overall island size ( $r=0.90$ ,  $n=20$ ,  $P<0.0001$ ; to determine the relative size of forest patches within islands, we applied program ArcGIS (version 9.4, Esri, Redlands, CA, USA) to aerial photographs supplied by the National Land Survey of Finland). Thus, we can assume that larger islands will offer larger habitat patches and sustain larger populations overall, consistent with the basic setting of Holt’s (1996, 2010) model.

Third, habitat diversity was equal among islands of different size, with no suggestion of higher habitat diversity on larger islands: All islands were covered by the same simple habitats, and the relative proportion of the most species-rich habitat (forest) proved constant across islands of all size (correlation between  $\ln(\text{forest area})/\ln(\text{total area})$   $r=-0.03$ ,  $n=20$ ,  $P=0.90$ ).

Fourth, estimates of sample coverage were high across islands of all sizes (see Table 1 of the main article). If habitat turnover within islands would account for a major proportion of local diversity, then we would expect to see lower coverage (due to a higher inflow of “tourist species” from other habitats) on supposedly more diverse islands (see Fig. A1.1B).

Fifth, our explicit treatment of multiple different types of potential sampling artefacts (see section *Analyses of food chain length* in the main text) add credence to the current patterns being caused by true ecological processes, not by different types of sampling biases.

Overall, the considerations outlined above support the view that habitat turnover is similar across islands of different size, and that the size of individual habitats within islands will increase in direct proportion to island size. Both patterns are consistent with “pure area” effects, and inconsistent with “environmental diversity” effects emanating from distinct spatial structuring within islands (cf. Fig. A1.1A vs B). Hence, while our current counts of species richness and food chain length from standardized sites within islands will not constitute complete censuses of all species present on the island, they will offer mutually comparable estimates of these parameters across islands of different size.

In conclusion, we believe that our system well matches basic model assumptions, and that the data collected offer a fair test of model predictions. We stress that for larger and/or oceanic islands, as characterized by stronger internal heterogeneity (Fig. A1.1B), the link to model assumptions may be tenuous, and local samples less- or unrepresentative of island-wide species richness and food chain length.

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**Appendix 2.** A detailed list of literature used in delimiting parasitoids of Lepidoptera, in assigning individual parasitoid taxa to the third *versus* fourth trophic level (i.e. to primary *versus* secondary parasitoids), and in ascribing them to an either idio- or koinobiont lifestyle. Taxa in the genus *Gelis* (Hymenoptera: Ichneumonidae; three taxa in total) were excluded from the analyses due to their wide host ranges and complex life histories, including the capability of some species to be either a primary or a secondary parasitoid. The total material thus retained encompassed 213 species of parasitic Hymenoptera, of which 87 species were considered primary and 14 species secondary parasitoids of Lepidoptera. Four taxa (encompassing a total of nine parasitoid individuals) were excluded from analyses of idio- *versus* koinobionts due to lack of sufficient information for reliable classification.

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