

Supplementary Material

Macroecology to unite all life, large and small

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Supporting Table 1. Studies included in this work in Fig. 1.

Study (as in Fig. 1)	Micro or macro	Taxon	Method used to get the <i>in situ</i> data	Details on calculation of patterns in Fig. 1	Number of individuals	Number of taxa	Reference
Groundwater microbes (panel B left)	micro	Bacteria	Counts of OTUs based on V3-V4 region of 16S rRNA. Samples were taken from groundwater wells.	Counts of OTUs were simply ordered and plotted.	276,809	16,383	unpublished data provided by M.H. & K.K.
Fisher's moths (panel B right)	macro	Moths	Counts of moth individuals in a light trap.	Counts over 4 years were simply ordered and plotted.	15,609	240	[1]
Bacteria and archaea in human belly buttons (panel C left)	micro	Bacteria and archaea	Pyrosequencing (Roche 454) of the V4 region of the 16S rRNA gene. 1 sample from each human individual was taken using a cotton tip.	Mean number of occupied humans was plotted against mean abundance across all humans (each dot in the plot is an OTU).	109,910	3,574	Unpublished data provided by R.D. and [2]
Birds of Czech Republic (panel B right)	macro	Birds	Counts of observed birds in approx. 10 km x 10 km quadrats in Czech Republic	Mean number of occupied quadrats was plotted against mean abundance across the quadrats (each dot in the plot is a species).	42,771,392	197	[3]
Fungi in 50 ha BCI plot, Panama (panels D and E left)	micro	Soil fungi	Counts of OTUs based on ITS1 region of rRNA operon. The samples were 6.25 cm cores, 20 cm deep, each at a center of a 20 x 20 m cell.	The cores were compared using Jaccard similarity index (for the distance decay), and they were aggregated along a spatial proximity gradient to create a spatially-explicit sample-area relationship.	11,147,285	24,666	[4]
Trees in 50 ha BCI plot, Panama (panels D and C right)	macro	Trees	Counts of trees larger than 1 cm DBH, in 20 m x 20 m cells in a 50 ha forest plot.	Species composition among cells was compared using Jaccard similarity index (for the distance decay). A nested spatial increments were used to calculate the species-area relationship.	235,343	306	[5–7]

Marine microbes in English Channel (panel F left)	micro	Bacteria and archaea	Counts of OTUs based on V6 region of 16S rRNA	R package iNEXT was used to calculate the rarefaction curve for a sample taken on 8. Dec 2008.	3526	336	[8]
Marine fishes in Celtic Sea (panel F right)	macro	Fish	Counts of fish along 50 x 5 m underwater visual transects (9 sites, 16 transects).	R package iNEXT was used to calculate the rarefaction curve for a sample that is spatially closest to the microbial sample site (row above).	1669	22	[9]
Bacteria in Antarctica (panel G left)	micro	Bacteria	Counts OTUs based on 16S rRNA. Samples were taken from 10 cm x 10 cm quadrats, 5 cm deep in soil.	Numbers of OTUs in the samples were plotted against sample elevation.	Not determined	Mean = 139 (SD= 28.8)	[10]
Ants in Great Smoky Mountains, USA (panel G right)	macro	Ants	Counts of ants in 1m ² quadrats in leaf litter.	Numbers of species were plotted against sample elevation.	5310	45	[11]

Supplemental References

- 1 Fisher, R.A. *et al.* (1943) The relation between the number of species and the number of individuals in a random sample of an animal population. *J. Anim. Ecol.* 12, 42–58
- 2 Hulcr, J. *et al.* (2012) A Jungle in There: Bacteria in Belly Buttons are Highly Diverse, but Predictable. *PLoS One* 7,
- 3 Storch, D. and Šizling, A.L. (2002) Patterns of commonness and rarity in central European birds: Reliability of the core-satellite hypothesis within a large scale. *Ecography (Cop.)*. 25, 405–416
- 4 Barberán, A. *et al.* (2015) Relating belowground microbial composition to the taxonomic, phylogenetic, and functional trait distributions of trees in a tropical forest. *Ecol. Lett.* 18, 1397–1405
- 5 Hubbell, S.P. (1999) Light-Gap Disturbances, Recruitment Limitation, and Tree Diversity in a Neotropical Forest. *Science (80-.)*. 283, 554–557
- 6 Hubbell, S.P. *et al.* (2005) , Barro Colorado Forest Census Plot Data. . [Online]. Available: <http://ctfs.si.edu/webatlas/datasets/bci>
- 7 Condit, R. (1998) *Tropical Forest Census Plots*, Springer-Verlag and R.G. Landes Company.
- 8 Caporaso, J.G. *et al.* (2012) The Western English Channel contains a persistent microbial seed bank. *ISME J.* 6, 1089–1093
- 9 Edgar, G.J. and Stuart-Smith, R.D. (2014) Systematic global assessment of reef fish communities by the Reef Life Survey program. *Sci. Data* DOI: 10.1038/sdata.2014.7
- 10 Okie, J.G. *et al.* (2015) Niche and metabolic principles explain patterns of diversity and distribution: theory and a case study with soil bacterial communities. *Proc. R. Soc. B Biol. Sci.* 282, 20142630
- 11 Sanders, N.J. *et al.* (2007) Temperature, but not productivity or geometry, predicts elevational diversity gradients in ants across spatial grains. *Glob. Ecol. Biogeogr.* 16, 640–649