Dataset of microsm experiment with three arthropod predators on a shared prey

authors: Florian Dirk Schneider1*, Stefan Scheu2 , and Ulrich Brose2

Description

Initial and final population and biomass densities of full factorial combinations of three arthropod predator populations on one basal springtail population.

The experiment ran in 30 x 30 x 15 cm microcosms over a period of 48 days.

Details can be found in

- Schneider, Scheu and Brose 2012 Body mass constraints on feeding rates determine the consequences of predator loss, *Ecology Letters* 15:436-443
- Schneider and Brose 2013 Beyond diversity: how nested predator effects control ecosystem functions, *Journal of Animal Ecology* 82:64-71

Invalid replicates

The replicate #43 was affected by extraordinarily high water content and was excluded from the analyses.

key to dataset fields

- **ID**: replicate ID

- **treat**: treatment binary code of scheme *.*.*.* with 0 for absence and 1 for presence of centipedes (Lithobius forficatus), spiders (Pardosa lugubris), predatory mites (Hypoaspis sp.) and springtails (Heteromurus nitidus), respectively.
- **treat_name**: treatment name one of "null" (no populations),"control" (only springtails), "full" (full community), "lith", "pard", "hypo" (monocultures of centipedes, spiders, mites), "ko_lith", "ko_pard", "ko_hypo" (knockout cultures of centipedes, spiders, mites).
- **num_pred**: number of predator species

Initial (t0) and final (t1) population densities given in individuals per microcosm (= 0.09 mˆ2)

- **N0_het**: average initial springtail density at t0 was 912 ($\pm$ 528SD, n = 5) as estimated from heat extractions of 5 replicates at t0.
- **N0_hypo**: Due to delayed availability of mites at t0 and during the first week of the experiment, only 250 mites were introduced initially. Another 100 individuals were added after one week.
- **N0_pard**: counted manually
- **N0_lith**: counted manually
- **N1_het**: counts from heat extraction applied to a quarter of the microcosm content.
- **N1_hypo**: counts from heat extraction applied to a quarter of the microcosm content.
- **N1_pard**: counted manually

- **N1_lith**: counted manually

Initial and final biomass densities given in g per microcosm (= 0.09 mˆ2)

- **B0_het**: estimated from population densities by multiplying with mean individual body mass of springtails = 0.10 mg (± 0.02SD)

- **B0_hypo**: estimated from population densities by multiplying with mean individual body mass of mites = 0.16 mg (± 0.02SD)

- **B0_pard**: weighed individually

- **B0_lith**: weighed individually

- **B1_het**: estimated from population densities by multiplying with mean individual body mass of springtails = 0.10 mg (± 0.02SD)

- **B1_hypo**: estimated from population densities by multiplying with mean individual body mass of mites = 0.16 mg (± 0.02SD)

- **B1_pard**: weighed individually

- **B1_lith**: weighed individually

- **B1_miclitt**: final microbial biomass on the litter layer was estimated from a fresh sample (2.8 g) taken at the end of the experiment by measuring substrate induced O2 consumption in an electrolytic microrespirometer (see Schneider & Brose 2013 Journal of Animal Ecology 82:64-71).

License

---

1 Institut des Sciences de l'Evolution, CNRS, Université Montpellier 2 - CC065, Montpellier Cedex 05, 34095, France

2 Georg August University Göttingen, J.F. Blumenbach Institute of Zoology and Anthropology, Berliner Str. 28, 37073 Göttingen, Germany

* Correspondence E-mail: florian.schneider@univ-montp2.fr