

Microbial ecology

traditionally process/ecosystem oriented

Microbial models systems in ecology Read this paper: (Jessup et al. 2004)

Advantage of simplicity, replication, ability to archive genotypes and communities.

Perceived disadvantages and counterpoints:

too simple,
too artificial
microbes are fundamentally different
too small and short in duration to be scaled up.

A few examples of how model systems have been used:**Simple assembled systems with known members**

A non-equilibrium system for maintaining diversity - rock, paper, scissors example - demonstrated the importance of spatial structure (Kerr et al. 2002).
C-R-S : colicin producing, Colicin resistant, Colicin sensitive

Interaction between predator-prey extinction and metapopulation structure. (Holyoak and Lawler 1996) - demonstrated positive affect of fragmented populations, presence of extinction-prone patches, and asynchronous population dynamics among patches.

Geographic mosaic theory (Forde et al. 2004) – background on Geographic mosaic theory ala Thompson; System: evolution of resistance and virulence in Bacteria/ Phage system B₀, B₁, B₂ vs. T_{7₀}, T_{7₁}

Interactions between diversity and productivity - problem of time in macro systems. (McGrady et al. 1997) Assemble communities with 4 trophic levels and up to 31 species, run for 80 generations - more stable CO₂ production, less susceptibility to invasion.

More complex natural systems with unknown starting components

move to organismal side require I.D. of species, and ability to count them
How do you count the uncountable? (Hughes et al. 2001) - problem (seen with species accumulation curve, fig 1). To estimate true number of species: fit to lognormal distribution, or Poisson lognormal; use non-parametric estimators that are based on ratio of singletons (Chao1 and ACE)

Species richness and productivity gradients (Horner-Devine et al. 2003); Cattle tank mesocosms with common inoculum but different P and N levels – investigate what happens to species richness (16S OTUs via Chao1 estimator). Different groups respond differently. Hump-shaped distribution for Cytophag-Favobacteria-Bacteroides, U-shaped curve for alpha-proteobacteria, no relationship for beta-proteo.

Are microbes different? e.g., are they not limited by dispersal? Everything is everywhere and the environment selects versus dispersal limitation.

"species" are different even if they look the same, and they show genetic structure over geographic distance (Whitaker et al. 2003)

Species area relationships (Horner-Devine et al. 2004)

References

Read this one: Jessup, C. M. et al. (2004). "Big questions, small worlds: microbial model systems in ecology." Trends in Ecology & Evolution **19(4)**: 189-197.

And these are in case you are especially interested:

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