Here and There or Everywhere?

Whether or not the notion that “everything is everywhere” is “taken for granted by most” (Fenchel and Finlay 2004) remains to be seen, but one cannot deny that the proposition has had stifling effects on microbial community ecology in the last century. And Tom Fenchel and Bland Finlay seem determined to perpetuate the myth of ubiquity despite all evidence to the contrary. They simply brush away serious criticisms of ubiquity (Foissner 1999, Coleman 2002, Whitaker et al. 2003) and disregard reports of endemism or vicariant distributions in microorganisms (Cho and Tiedje 2000, Curtis et al. 2002, Bohonak and Jenkins 2003, Darling et al. 2004).

The idea that small organisms are randomly spread over the planet, first formulated by Baas-Becking (Quispel 1998) and recently acclaimed by Finlay (2002), has enormous implications. According to the ubiquity dogma, microbial biogeography is a futile pursuit. Microbiologists “need not travel to exotic places,” as “most microorganisms can be found at the local seashore.” If “local extinction [of microorganisms] rarely, if ever, takes place,” then microorganisms should never play a meaningful role in conservation and a microbial species would never become globally extinct.

The first fundamental flaw in the ubiquity theorem is the acceptance of the morphological species as a meaningful concept (“the only viable operational concept”) in microbiology. This flies in the face of the recent DNA sequencing revolution in microbial systematics, which provides clear identification tools and demonstrates widespread species crypticity and genetic structuring of regional populations. It is not surprising that an identification system that fails to discern species should give rise to flat species–area curves and break every other rule of biodiversity theory. Bacteriologists and yeast systematists have been aware for quite some time that microbial classifications based on morphotypes are rather meaningless.

Fenchel and Finlay (2004) further fail the reader through their unrestrained proclivity for generalization. Let us for a moment grant that some aquatic protista may be truly “free-living,” that some can be identified correctly by simple microscopy (but see Nanney 2004), and that the global distribution of some species may be random. Extending such propositions to all small organisms, however, as Fenchel and Finlay do, is indeed a colossal leap.

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References cited


Response from Fenchel and Finlay

Curiously, we stand indicted of “perpetuating the myth of ubiquity” just when an unprecedented research effort is uncovering, for the first time, the true scale of ubiquitous microbial dispersal. Identical microbial genotypes (rRNA gene sequences) are being recorded worldwide, and outbreeding protists isolated from different continents will interbreed in the laboratory.

The neutral theory of molecular evolution predicts that organisms with huge population sizes (most microbial “species”) will display substantial genetic variation, and this is indeed the case. The fact that nominal species (phenotypically identical forms) fill out phylogenetic trees with deep roots reflects the fact that microbial phenotypes have remained identical over large stretches of geological time. They retain their identity through stabilizing selection, but the molecular clock ticks, so the rate of species turnover in microbes is very slow compared with that for mammals, for example.

We did emphasize that genetic variation occasionally generates some sort of