Microbial Eukaryote Species

IN HIS VIEWPOINT "GLOBAL DISPERSAL OF free-living microbial eukaryote species" (Environmental Microbiology Special Issue, 10 May, p. 1061), B. J. Finlay suggests that there are a limited number of microbial eukaryote species (in the sense of recognizable morphologies) and that most of them are worldwide in distribution. The catch comes in assuming that these "species" are directly comparable to typical animal and terrestrial plant species. Finlay's assumption may be acceptable for marine protistan forms, but it is not acceptable for freshwater microbial eukaryotes, for at least two reasons.

First, some long-accepted morphospecies clearly combine entities that are products of parallel evolution, as revealed by DNA sequence comparisons (*1*, *2*). This reflects the difficulty, when treating microbial eukaryotes, of recognizing those morphological characters that are truly indicative of kinship. Thus, "species" numbers are considerably higher than indicated by morphology alone.

Second, various freshwater morphospecies of protistans have now been analyzed for the ability to interbreed and for genetic similarity by DNA sequence. Some widespread microbial eukaryote species are indeed similar to widespread animal or plant species, where some degree of potential for interbreeding persists and DNA sequence similarity is very high (*3*). However, many other protistan species are now known to include multiple subclades, totally isolated in terms of reproductive potential and displaying great DNA sequence dissimilarity. The DNA sequence disparity in some cases is equivalent to that found in the family level or higher in plants and animals (*4*). In such protistan morphospecies, there is a clear pattern of geographical localization of closely related forms (*5*). Thus, to suggest that all protistan species are randomly distributed worldwide is misleading and obscures the biologically interesting question of whether microbial eukaryotes evolve more rapidly than plants and animals (as measured by DNA sequence comparisons) or whether only a limited number of protistan morphologies can succeed in their habitats over long periods of time.

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Response

COLEMAN SUGGESTS THAT MICROBIAL eukaryotes are not directly comparable to typical animal and plant species. But whenever a "biological species concept" applies—as in protists and multicellular organisms—the two groups are surely comparable. Asexual species are also rather common in protists, as they are in invertebrates and vascular plants.

Second, she suggests that the real number of protist "species" is much greater than that of morphospecies because the latter may include genetic variants (which will include adopted neutral mutations) and also reproductively isolated gene pools known as sibling species. It is remarkable, however, as Coleman acknowledges (*1*), that we still know so little (if anything) about differences in the ecological niches occupied by different protist sibling species. Can they ever be linked to specific niches that are accessible to investigation and characterization? Or do they simply represent a range of different breeding strategies (*2*) within morphospecies that do basically the same job wherever they thrive in the natural environment?

Third, and in response to the claimed geographical localization of closely related forms, this is confounded by work on ciliates (*3*) and by Coleman's own observations (*1*) that isolates of a green algal sibling species from Nepal and California can mate with each other.

We disagree that the suggestion of large-scale random dispersal of microorganisms (including their cysts and spores) is misleading. Ubiquitous dispersal, of course, is not to be confused with the geographical distribution of habitats supporting active populations of a species.

In one important sense, microbial eukaryotes and macroscopic organisms do differ from each other. In isolation, animals and plants, although adapted to similar niches, turn out differently in different regions of the world, e.g., kangaroos and cows, euphorbias and cacti, and Galápagos finches. Nothing similar has been recorded for protists. The fact that protists such as the ciliates, which have very complex morphology, are identical to the last detail wherever they are collected illustrates a fundamental consequence of ubiquitous dispersal: Protists were never presented with the opportunity of evolutionary diversification because they were never restricted by geographical barriers.

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Letters to the Editor

Letters (~300 words) discuss material published in *Science* in the previous 6 months or issues of general interest. They can be submitted by e-mail (science_letters@aaas.org), the Web (www.letter2science.org), or regular mail (1200 New York Ave., NW, Washington, DC 20005, USA). Letters are not acknowledged upon receipt, nor are authors generally consulted before publication. Whether published in full or in part, letters are subject to editing for clarity and space.

CORRECTIONS AND CLARIFICATIONS

THE PUZZLE OF COMPLEX DISEASES: NEWS: "Lupus: mysterious disease holds its secrets tight" by E. Marshall (26 Apr., p. 689). The section on kidney disease should have cited work by immunologists Dan Eilat, Gustavo Mostoslavsky, and their colleagues at Hadassah University Hospital in Jerusalem. They showed that pathogenic anti-DNA auto-antibodies from lupus-prone mice could be distinguished from their nonpathogenic counterparts by their direct binding to the cytoskeletal protein alpha-actinin on the surface of kidney cells.

PERSPECTIVES: "Skiing toward nonstop mRNA decay" by L. E. Maquat (22 March, p. 2221). The figure should have depicted the phenylalanine codon as being UUU, not AAA.

REPORTS: "*Purkinje cell degeneration* (*pcd*) phenotypes caused by mutations in the axotomy-induced gene, *Nna1*" by A. Fernandez-Gonzalez *et al.* (8 Mar., p. 1904). The word "neither" was omitted from the sentence on p. 1905, column 3, line 10. The text should read, "This 7.8 kb insertion (GenBank accession number AF457126) appears to be neither a long-period interspersed sequence nor an intracisternal A particle (LINE and IAP, respectively), but rather contains repetitive sequences nearly identical to an ~7.8 kb segment of Mus musculus α/δ T cell receptor locus on chromosome 14 (GenBank accession number AE008685)."

PERSPECTIVES: "Scaffolding proteins–more than meets the eye" by G. Johnson (15 Feb., p. 1249). In the figure, there are two proteins labeled TAB2. The TAB2 protein adjacent to p38α is mislabeled and should have been labeled as TAB1.