DNA analysis shows true dispersal of protozoa

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In contrast to previous findings, it seems that the global distribution of macro- and microorganisms might be similar. A study in the online open access journal, *BMC Evolutionary Biology*, shows that some protozoa are globally dispersed, while others are geographically restricted - by looking at a new fast-evolving DNA marker. The study also reveals that the biodiversity of protozoa may be much higher than previously realised.

It has long been argued that the small size and huge populations of microorganisms aids their global dispersal. 'Everything is everywhere, but the environment selects' said Lourens Baas-Becking in 1934.

Today, this Ubiquitous Dispersal Hypothesis (UDH) remains controversial compared to the alternative possibility of endemicity - the tendency of organisms to be confined to specific regions - as is found for many macro-organisms. While previous morphological and molecular analyses of environmental samples from around the world have provided evidence for UDH, these markers evolve too slowly to allow a really rigorous test of the hypothesis.

David Bass and colleagues at the University of Oxford and elsewhere, have carried out an analysis of the global distribution and diversity of three narrow taxonomic groups of cercomonads (heterotrophic flagellate protozoa) based upon PCR, cloning and sequencing of ITS1 rDNA sequences from samples gathered from around the world. ITS1 is a faster-evolving marker than the more commonly used 18S rDNA and therefore allowed the study to be done at a higher phylogenetic resolution. This approach is robust, being independent of the ability to culture or see the organism being studied.

They sequenced gene libraries of soil, freshwater, and marine cercomonads constructed from 47-80 samples per group from a wide range of habitats in locations including Panama, the Pacific, the Caribbean, Peru, UK, Greece, France, Germany, India, Japan, British Columbia, Australia and New Zealand. The study is unique in screening such large numbers of globally distributed environmental DNA sequences with such narrowly targeted PCR primers.

Identical ITS sequences were found in widely separated sites from all continents for several of the genotypes studied, suggesting relatively rapid global dispersal. Some ITS types were found in both marine and non-marine environments, which usually have different protist populations. However, other ITS sequences had patchy or restricted distributions, indicating at least a moderate degree of endemicity.

Moreover, strains of cercomonads with the same 18S but different ITS1 sequences differed in phenotype with respect to characteristics such as morphology, salinity tolerance, and propensity for cyst formation. This suggests that global protist biodiversity may be richer than previously suspected.

The authors conclude that these new findings support the moderate endemicity model of microbial biogeography, with some cercomonad strains being globally dispersed while others are geographically restricted. The issue of possible under-sampling of the rich diversity of the protozoa needs to be taken into account in further studies; this way, a more accurate picture of their global distribution and importance may be obtained.

Source: BioMed Central

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