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symposium summary

The importance of being small: does size matter in biogeography?

One-day symposium at Systematics, the First BioSyst conference – Leiden, The Netherlands, 13th August 2009

Since the 18th century, scientific expeditions in remote places have discovered new species and even new orders and new classes of macro-organisms with limited distribution. In contrast, scientists have discovered that microscopic organisms found in remote places could be mostly ascribed to taxa already known in their home countries. This idea was encapsulated by Beijerinck (1913) and Baas-Becking (1934), and became known as the 'everything is everywhere' (EisE) hypothesis: micro-organisms are globally distributed due to their potential for long-range dispersal (Kellogg and Griffin 2006) and large abundances (Finlay 2002). The assumption that organisms smaller than 2 mm are cosmopolitan in their distribution is best supported when species are defined using traditional taxonomy based on morphological characters. However, the EisE hypothesis has been challenged recently as molecular evidence has revealed a high degree of cryptic diversity, restricted dispersal and phylogeographic patterns in a variety of microscopic organisms, including both prokaryotes and eukaryotes (e.g. Martiny et al. 2006, Green et al. 2008).

The recent debate on the EisE hypothesis began after the contributions by Finlay and Fenchel (e.g. Finlay and Clarke 1999, Finlay 2002, Fenchel and Finlay 2004), and different research groups are currently trying to test its reliability on different model organisms. Thus, it was considered timely to organize a full-day symposium on this topic, and that was held during the BioSyst meeting in Leiden, a joint conference of all the

European systematics associations.

The current debate on the EisE hypothesis divides scientists in two major groups (Whitfield 2005). One group follows the EisE hypothesis in its original form, assuming that species differences in samples from different areas occur because of environmental differences, and not because of restricted dispersal. Thus, 'everything is everywhere, but the environment selects' is considered the rule for micro-organisms. The other group proposes that traditional taxonomy of microscopic organisms based only on morphological characters is not able to resolve their actual diversity, and cosmopolitan ranges therefore result from misidentification and lumping of spatially isolated lineages. Thus, cosmopolitanism is considered an exception in micro-organisms, as it is in macro-organisms.

It has been suggested that the EisE hypothesis incorporating environmental selection may be difficult to falsify because of unmeasured aspects of the environment that differ consistently among regions (Foissner 2006). However, if we assume a dense sample of equivalent habitats across sampling regions, the hypothesis makes clear predictions about genotype distributions. If EisE is the rule, the degree of genetic relatedness between two individuals should be independent of the geographical distance between them. Conversely, if EisE does not hold true, spatially explicit models should work in the same way as they do for macro-organisms, and genetic diversity should be related to geographical distances by a classical

distance–decay relationship. On the other hand, it has been proposed that the EisE hypothesis should be dismissed, as it is not a testable hypothesis at all.

During the symposium we discussed results gathered from different taxa, including thermophilic bacteria, ciliates, amoeboid protists, diatoms, green algae, cacti-associated yeasts, and also macro-fungi, mosses and small aquatic animals. We had an overview of the variety of methods currently used to obtain large amounts of additional empirical evidence, especially performing Next Generation Sequencing of environmental samples. Different theoretical approaches from the biological properties in common between micro-organisms and from simulations were presented, deepening our understanding of the processes involved but with a caveat: similar patterns may mask very different processes. Things may not be so easy as expected. For example, geographic patterns with genetically more similar organisms in nearer areas may be obtained from theoretical models that both contrast and support the EisE hypothesis.

One of the main messages from the symposium is that generalizations may be dangerous and misleading, as different taxa respond in different ways to the same habitat. Biological properties other than size (e.g., dormancy) indeed influence the patterns of distribution of organisms. Thus, further work needs to be undertaken to gather more data.

Moreover, micro-organisms are becoming a highly suitable model in other fields of biology. One example is the application in conservation biology that has come from the research that the EisE hypothesis has stimulated (Brodie et al. 2009), including how different organisms respond to the same habitat. Another application is in experimental biogeography; using small organisms in mesocosm experiments to test predictions from theories in biogeography is an exciting new frontier.

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