

Reverse ecology uses genes to predict environment

Chris Emery

A new technique dubbed “reverse ecology” expands the use of genetic data to study not only organisms themselves, but also their current environments and the ancient conditions in which they evolved, according to a recent study (*J Comput Biol* 2009; **16**: 2). The method could help scientists to predict the native environments of newly discovered bacterial species about which little is known, and to better understand how bacteria change over time in response to evolutionary forces in their surroundings. Since bacterial communities are found nearly everywhere, the technique could have broad applications in fields such as medicine, agriculture, and environmental protection.

“You can use [reverse ecology] to

study a system where the ecology itself is not known”, according to lead author Elhanan Borenstein, a postdoctoral researcher at Stanford University (Stanford, CA). “We have a lot of genomic data, but we don’t understand the environments these bacteria live and evolved in. This will tell us more about the interactions between organisms, and [those] between an organism and its environment.”

Reverse ecology uses computers to crunch genetic data emerging from modern genomics research, which focuses on mapping out an organism’s DNA. Genes control the functioning of cells by orchestrating the complex chains of chemical reactions that keep cellular machinery running. Some genes are involved in multiple chemical processes and are therefore linked with other genes in webs of relationships.

Since certain genes, and networks of genes, are better suited for

survival in certain types of environments, Borenstein uses genetic data to predict the relationship a species might have with its surroundings. To test the predictive ability of the technique, he used genomic data to match 569 bacteria species to their respective host species. In these parasite–host relationships, the host serves as the parasite’s environment, fulfilling its metabolic needs for biochemical compounds. Borenstein and his colleagues found that a bacteria species’ DNA was a good predictor of the environment – the host – that can support the species.

“We now know there is a way to learn ecology from genomic data”, says Borenstein, “and we can do this on a very large scale. This will be useful in situations where genomic data are available but ecological data are limited, and researchers can use this kind of approach to try to bridge such gaps.” ■