

and extinction of populations of large-bodied vertebrates might bring about the decline of large-seeded trees, and concomitant community-wide changes, over much of the forests. Another possible example of the loss of seed dispersal services comes from Pacific islands, where flying foxes are also suffering dramatic population declines as a result of habitat reduction and hunting. Kim McConkey and Don Drake (Victoria University of Wellington, Wellington, New Zealand) found that in islands with reduced densities of these frugivorous bats a larger proportion of seeds fall undispersed beneath the crowns of mother plants.

The study of seed dispersal is undergoing a profound transformation⁶. The growing knowledge of the demographic consequences of seed dispersal is making

the field increasingly relevant to plant population ecology at large. Furthermore, some of the studies that I have chosen to comment on highlight the potential contribution of seed dispersal research to community ecology. The time is ripe for studying the role of seed dispersal in the assembly of plant communities in space and time, and in their potential disassembly following the loss of seed-dispersing animals and the arrival of new ones.

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Global warming and the spread of disease: the debate heats up

Many recent studies have suggested that as a consequence of global climate change there will be an increase in the incidence of vector-borne diseases, such as malaria, yellow fever, dengue fever and tick-borne encephalitis. This is based principally on the idea that, as the planet warms and parasite and vector development rates speed up, transmission will be possible at increasingly higher latitudes. However, two new papers by Sarah Randolph and David Rogers challenge this notion and suggest that due to the complex nature of most host–vector–parasite interactions it may be extremely difficult to make good generalizations about the future distributions of vector-transmitted diseases.

In a paper published in *Science*, Rogers and Randolph explore the effects of global climate change on the future incidence of cerebral malaria, a life-threatening disease caused by *Plasmodium falciparum* and transmitted by anopheline mosquitoes¹. Earlier models had predicted that cerebral malaria would spread northwards through Europe and would invade large tracts of North America. These predictions were based on models that incorporated details of the biology of the *Plasmodium*–mosquito interaction (such as temperature-dependent parasite development rates) into the forecasts produced by global circulation models (GCMs). In contrast, Rogers and Randolph used a two-step multivariate statistical approach. First, they used maximum-likelihood methods to map present day malaria distributions by determining the key climatic variables associated with the presence or absence of disease. Second, these results were used to predict the worldwide distribution of cerebral malaria in the year 2050, based on a widely accepted GCM

scenario. This predicted that changes in the distribution of *P. falciparum* will largely be restricted to the tropics and sub-tropics, with just as many people being freed of the risk of infection as being newly exposed.

In a second paper, published in *The Proceedings of the Royal Society*, Randolph and Rogers took a similar approach to predict the future distribution of tick-borne encephalitis virus (TBEv) in Europe². Again, they produced a multivariate description of the current distribution of disease risk and applied the identified predictor variables to various GCM scenarios for the future. This predicted that although TBEv would extend its distribution northwards, the overall range would decline as a result of global climate change, possibly culminating in TBEv disappearing completely from central and eastern Europe by 2080. The biological interpretation is that climate change may alter the seasonal dynamics or survival of the ticks, so disrupting virus transmission between the two immature tick life-stages co-feeding on rodents.

These two studies are interesting not only because they make predictions that run counter to conventional wisdom, but also

because they use multivariate statistical methods that incorporate predicted changes not only in temperature but also rainfall, humidity, and their interactions. In so doing, they appear to be able to capture more of the constraints on parasite transmission and development. Of course, these models are not perfect. For example, they do not allow the parasites to evolve in response to changing selection pressures. It is possible, for example, that reduced opportunities for transmission of non-systemic infections of TBEv between co-feeding ticks might lead to the evolution of alternative transmission routes or to changes in virulence. However, it is likely that models like these will be particularly useful in identifying areas where vector-borne diseases are likely to expand their distributions.

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Conflict begets diversity?

There is a long tradition in evolutionary biology that views reproductive isolation as a by-product of gradual species divergence over time. However, many studies have recently demonstrated that traits involved in reproduction, especially postmating-prezygotic characters, diverge rapidly among closely

related species. These studies have not only generated a lot of interest over the evolutionary processes underlying this rapid divergence, but they have also raised important questions about the effects of these processes on speciation, and consequently on patterns of species diversity. For example, sexual conflict