addition, would put strong constraints on the evolution of such proteins. Any mutation that would alter the optimal insertion ratio would be a selective disadvantage, even though it could improve the catalytic activity. The dualtopology organization of EmrE likely represents an evolutionary transitional form. The work by Rapp *et al.* tips the balance in the controversy about one protein's unusual orienta-

tion in the membrane. A broader consequence of this observation may be a plausible evolutionary path for membrane proteins with antiparallel domains.

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ECOLOGY

How the Wood Moves

Katriona Shea

t first glance, an obvious difference between animals and plants is movement: Elephants move, trees don't. This is in part why Tolkien's ents (1), Wyndham's triffids (2), and the march of Birnam Wood in Shakespeare's Macbeth (3) elicit such a strong response. But in fact plants do move, although only at certain life stages and usually with outside help. For example, dandelion seeds blow and sycamore samaras helicopter in the wind, acorns and berries are moved by mammals and birds, and pollen is spread by wind and insects. These movements spread plant genes across the landscape, generating the spatial patterns of distribution and abundance of species that we observe in nature. Recent work demonstrates just how

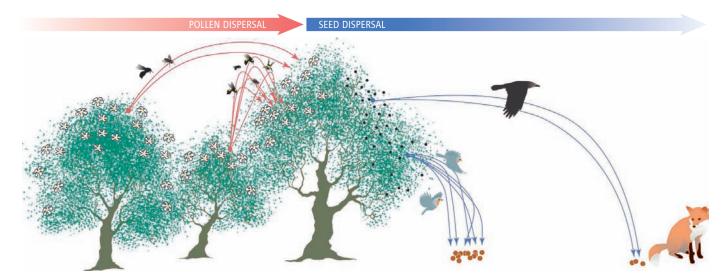
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complex the web of pollinators and fruit-eating animals that determine tree gene flow can be (see the figure).

For both plants and animals, studying movement is just as difficult as it seems. Animal ecologists have radio-collared cheetahs and lions, attached satellite-linked tracking devices to seals, and painted marks on beetles to track their movements. Plant ecologists, however, are usually faced with a problem of scale. How can we follow the movement of smaller diaspores (dispersal units), such as seeds and pollen grains? Approaches broadly fall into two categories—tracking of diaspores from a source, or relocation of diaspores at different distances from parent plants (4)—and scientists have become very creative in their quest (5). Notable approaches include observational studies of dispersers at the parent plant for animal-dispersed species; studies of the environmental conditions promoting seed release of wind-dispersed species; trapping of Recent studies show that the movement of plant genes across the landscape involves a complex web of pollinators and fruit-eating animals.

seeds at different distances from possible parents; marking of seeds on the parent plant with ink, fluorescent powder, or radioactive markers to allow later relocation and identification of seeds; genetic methods to link seeds or pollen to possible parents; and even chasing individual seeds as they blow across the landscape.

Over the past decade, Jordano and collaborators have been patiently disentangling the gene flow story for a key tree species in southeastern Spain by combining several of these methods (6). Mahaleb cherry, *Prunus mahaleb*, is a tree with delicate white flowers and black fruits. Some trees are hermaphrodites (with both male and female functions); others are functionally female. Thus, both types of trees are potential seed sources, but only the hermaphrodites can provide pollen. Jordano *et al.* have studied nine distinct populations of these trees and determined the genotypes of all reproductive individuals. Their observational studies show that mahaleb cherry fruits (each contain-



Gene flow in trees. Mahaleb cherry pollen and seeds are moved over short and long distances by strikingly different assemblages of pollinators and fruit-eating animals. This has important implications for gene flow within and between populations and for the establishment of new populations.

1231

ing a single seed) are consumed by a wide variety of animals. Most seeds are eaten by frugivorous (fruit-eating) birds such as warblers, robins, redstarts, mistle thrushes, woodpigeons, and carrion crows. However, a small proportion of fruits are also eaten by otherwise carnivorous mammals such as badgers, stone martens, and red foxes. Pollen is dispersed by a wide range of bees and flies.

A seed contains a mix of genes from both its mother and father and, as potential parents in a population may themselves be related, it can be hard to work out parentage with any degree of certainty, even with the latest molecular genetic methods. Jordano et al. exploited a key factor to get around this problem. In some species, maternal tissue is attached to the seed. For example, the samara or "propeller" of a sycamore is actually made up of maternal tissue. Similarly, mahaleb cherry seeds have a maternally derived seed coat, the endocarp, which is not digested with the rest of the fruit. Analysis of the seed coat by molecular genetic techniques allows direct identification of the mother tree.

Jordano *et al.* trapped or collected seeds from animal feces across the landscape. From this they recorded which dispersal agents excreted each seed, directly identified the mother tree, and hence determined the distance the seed was dispersed. By combining these complementary methods, this work has been able to document what moves seeds, how far they are moved, and even into what sorts of habitats they are deposited by different dis-

persers (6). Similarly, they have studied the pollinators and the pollen they deposit on the two sexes of tree (7). Eventually, they will be able to link the two components directly, by genotyping both seeds and their endocarps. This unusually thorough understanding of seed and pollen movement is a real breakthrough for the study of gene flow in trees.

As expected, birds remove most mahaleb cherry fruits, whereas mammals take relatively few. However, smaller birds move seeds only relatively short distances (usually depositing them within the boundaries of the local population); larger birds and mammals are overwhelmingly responsible for longerdistance dispersal, particularly movement between populations (6). Additionally, larger birds and mammals are more likely to disperse seeds to open habitat, where new populations may establish. Pollinators prefer female trees, and different assemblages of pollinators visit the two sexes. As a result, pollen on female trees on average comes from farther away and from more pollen donors (7). Intriguingly, there is much less long-distance pollen movement than long-distance seed dispersal.

The implications for this species are noteworthy. Although smaller birds dominate the dispersal system numerically, loss or extinction of carnivorous mammals in this system would have serious consequences for gene flow (with a large reduction in interpopulation movement) and would likely lead to increased isolation of populations (with fewer new populations being initiated). The ramifications for other ecosystems are also considerable. It is not only the obvious or putative dispersal mechanisms that are important (4), and the composite patterns arising from these multiple dispersal vectors may be very complex indeed (8). Relatively rare events may dominate certain critical processes such as establishment of new populations, range expansions, or invasions. Particularly large effects may be seen in tropical rainforests, where rapid fragmentation dramatically influences loss of large frugivores. Jordano et al. show the way forward: Only with a multipronged and synthetic approach can we hope to disentangle the multiple drivers of observed plant genetic diversity or to identify possible consequences of changes in animal communities or habitats on plant populations.

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ATMOSPHERE

Forecasting Hurricane Intensity and Impacts

Hugh E. Willoughby

In 2005, meteorologists embarked on an ambitious hurricane research project, RAINEX, to investigate how rainbands affect hurricane intensity. Flying radarequipped aircraft right into the storms—including the infamous Hurricane Katrina—before they made landfall, the scientists recorded wind speed and direction, temperature, humidity, and other data. On page 1235 of this issue, Houze *et al.* report exciting results from this project (1). The authors

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observed Hurricanes Katrina, Ophelia, and Rita and then simulated them numerically on spatial scales of less than 2 km. These highly realistic simulations represent substantial progress on the vexing problem of hurricane intensity prediction.

In the United States, 2004 and 2005 were the most devastating seasons as measured by inflation-adjusted damage, and 2005 was the deadliest since 1928. Forecasts of U.S. hurricane landfalls made as long as 60 hours before the event were excellent, but Earth's atmosphere is still fiendishly unpredictable. It was a meteorologist who instigated the modern appreciation of sensitivity

Hurricane structure and intensity can now be predicted with sufficient accuracy to support quantitative assessment of human and economic impacts.

to initial conditions in deterministic mathematical systems (2). Thus, both uncertainties in the initial state of the atmosphere and limitations of the numerical models can cause forecasts that started from nearly identical representations of today's weather to diverge after just 3 to 10 days. Hurricane prediction remains an unforgiving enterprise with constant threat of public and costly failure.

There are two crucial aspects to hurricane prediction: forecasting the path it will take (the hurricane track) and forecasting the strongest wind anywhere in the storm (the hurricane intensity). Track forecasts have