



Figure 1 | Comparison of a Lévy flight with a Brownian random walk. **a**, Walks of identical total length of 1,000 unit steps are shown drawn to scale. Lévy flights (or walks) have ultra-long steps, which are absent from Brownian walks. **b**, A close-up of the Brownian walk, in which the walker returns many times to previously visited locations (a phenomenon known as ‘oversampling’). By contrast, the Lévy walker occasionally takes long jumps to new territory. This reduction in oversampling is part of the theoretical basis for interest in the Lévy-flight foraging hypothesis, which predicts that Lévy flights offer higher search efficiencies in environments where prey is scarce. Humphries *et al.*² show that marine predators often move in patterns that are consistent with this hypothesis. (Plots modified from ref. 10.)

empirical scrutiny — one of the more controversial problems in theoretical movement ecology. The authors’ data set of more than 10^7 measurements, compiled from electronic tags on 55 individual fish — sharks, tuna, billfish and a sunfish — is an order of magnitude larger than the last reported data set⁷. They find strong evidence of Lévy flights, but, as predicted theoretically, these flights are not universal. Lévy flights are expected in places where prey is scarce (such as the open ocean), whereas a Brownian strategy is more likely to occur where prey is abundant (as in marine regions where the mixing of water bodies produces high densities of phytoplankton, zooplankton and organisms higher in the food chain). The observed² pattern of switching between search modes is not entirely consistent with these expectations. But it is nonetheless plausible, as seen for instance in the data on a blue shark that moved from the prey-rich waters of the western English Channel to the oceanic environment of the Bay of Biscay.

The fact that some organisms perform Lévy flights has deep implications that transcend those for marine ecosystems, and it raises many questions. Did humans disperse from Africa superdiffusively rather than diffusively? Does pollen from genetically modified crops spread superdiffusively? What are the consequences if influenza epidemics spread superdiffusively? In a reaction-diffusion context, superdiffusion leads to significantly increased overall reaction rates, because the reacting species — which may be chemical or biological — meet each other more often. What more can be learned about such interactions? These questions and many more await investigation. ■

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EVOLUTIONARY BIOLOGY

Expanding islands of speciation

Erin S. Kelleher and Daniel A. Barbash

Speciation can occur even when the incipient species coexist and can interbreed. An extensive analysis of two fruitfly strains suggests that many genomic regions contribute to speciation in such cases.

Speciation is a process of branching, whereby one species splits into two. How do the genomes of two nascent species become differentiated from each other in sympatry, the situation in which they share a geographical range and can exchange genetic information through interbreeding? In a paper published in *Proceedings of the National Academy of Sciences*, Michel *et al.*¹ address this question. They reveal that the degree of genomic differentiation in the early stages of sympatric speciation may be vastly under-appreciated.

Michel and colleagues studied two strains of the fruitfly *Rhagoletis pomonella* (Fig. 1, overleaf), which feed and breed on hawthorn and apple fruits, respectively, and demonstrate that their genomes are highly differentiated. This finding stands in contrast to ‘genomic island’ models², according to which interbreeding homogenizes the vast majority of the genome between incipient species, except for a few regions that are crucial for the reproductive isolation that is ultimately necessary for species to diverge. It is particularly unexpected because the colonization of apple fruits by hawthorn *R. pomonella* occurred only about 150 years ago, suggesting that this exceptional genomic divergence has occurred in the evolutionary blink of an eye.

Sympatric speciation has long been a contentious topic. Darwin himself was a proponent of speciation in sympatry, arguing that competition is an engine of speciation and biodiversity³. Evolutionary biologists, however, have struggled to understand how two distinct gene pools emerge from a single population of

organisms in the face of interbreeding and genetic exchange. Benjamin Walsh, an early investigator of *R. pomonella*, proposed⁴ that their specialized ecology, in which they favour a particular host plant, allows for sympatric speciation when members of the population are able to colonize a new host such as apple fruit. Adaptation to a new host requires differences in traits such as breeding time, which will isolate colonizing individuals from those that remain on the ancestral host.

Recent hypotheses about sympatric speciation have focused on the genomic architecture of divergence, such as how much genetic variation is shared between incipient species, and how this variation is distributed throughout the genome. One hypothesis^{5,6} is that chromosomal rearrangements such as inversions, in which part of a chromosome becomes reversed, can provide a ‘safe haven’ that maintains clusters of genes that influence reproductive isolation. The process of recombination between different arrangements of parental chromosomes is often suppressed or can produce inviable progeny, effectively eliminating genetic exchange and allowing divergent gene clusters to be maintained in the face of interbreeding and gene flow between incipient species.

An alternative view⁷ is that genes subject to strong divergent selection between incipient species, such as those relevant for habitat choice, can create differentiated regions in the genome even in the absence of chromosomal rearrangements. Selection on such genes will also lead to differentiation of adjacent genes owing to their physical association. If the



Figure 1 | *Rhagoletis pomonella* — genomic test case for sympatric speciation.

adjacent genes themselves acquire genetic variation that is disparately adaptive between incipient species, the differentiated region will expand in size between forms.

Genomic models of speciation with gene flow make a simple prediction — during the early stages of speciation, some genomic islands will be clearly distinguishable between incipient species, but the vast majority of the genome will remain undifferentiated because of considerable genetic exchange. Several studies have used population-genetic approaches to reveal exactly this pattern. For example, two forms of the mosquito *Anopheles gambiae* are distinguishable in only three chromosomal regions containing unique genetic variation, whereas the rest of the genome contains shared variation^{2,8,9}. In the pea aphid *Acyrtosiphon pisum pisum*, highly differentiated regions between forms that breed on red clover and alfalfa are clustered near genomic regions that affect habitat choice, linking exceptionally divergent regions with those that might influence reproductive isolation⁷.

At first glance, Michel and colleagues' study¹ seems to recapitulate previous conclusions about the genomic signatures of sympatric speciation. Their application of standard population-genetic methods reveals that genetic variation between the apple and hawthorn strains of *R. pomonella* is exceptional in only two independent regions of the genome. Both of these regions are encompassed by chromosomal rearrangements, which is consistent with the hypothesized role of reduced recombination.

However, the authors probed more deeply into the ecologically based differences between the two strains. They took into account their geographical range (according to latitude), their timing of eclosion (emergence of an adult from a pupa) and the extent of diapause (environmentally induced developmental arrest). That is, they examined how genetic variation changed across latitude, associated genetic variation with differences in eclosion time, and performed laboratory selection experiments on diapause versus direct development to observe the response of linked genetic markers. Differences in the fruiting times of apple and

hawthorn trees, the new and ancestral hosts of *R. pomonella*, make diapause and eclosion traits ecologically crucial for host adaptation and reproductive isolation.

Strikingly, Michel *et al.*¹ found that more than 50% (of 39) sampled genomic loci show evidence of adaptive differences, and many seem not to be within chromosomal rearrangements. Their results suggest that much more of the genome may be differentiated between sympatric incipient species than previously thought. Useful extensions of this work would be to obtain a better understanding of the positions and frequencies of chromosomal inversions in the apple and hawthorn strains,

and to increase the density of genetic markers to provide a more detailed picture of genomic divergence.

One implication of the results of Michel *et al.* is that studies of sympatric speciation that are confined to identifying genomic regions of exceptional differentiation between strains are potentially misleading in overlooking regions that affect reproductive isolation. This conclusion is echoed in several reports and reviews on the topic^{6,9,10}. Further investigation of candidate genomic regions involved in reproductive isolation remains a promising direction for research, both in *R. pomonella* and in other examples of incipient speciation with gene flow, such as in pea aphids, *A. gambiae* mosquitoes and cichlid fish. ■

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ORGANIC CHEMISTRY

Amide bonds made in reverse

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Amide bonds connect the amino acids in proteins and occur in many other useful molecules. An amide-forming reaction that turns the conventional approach on its head offers a practical way of making these bonds.

As the main chemical linkage found in proteins, the amide bond is incredibly important. What's more, amides are found in many synthetic polymers, biologically active naturally occurring compounds and pharmaceutically active small molecules. The usual way in which chemists make amides is by reacting a carboxylic acid group (COOH), which is electron deficient, with an amine group (NHR, where R can be a hydrogen atom or a hydrocarbon group), which is electron rich. On page 1027 of this issue, Johnston and colleagues¹ describe a fresh approach to forming amide bonds. In their process, the polarity of the reacting groups is reversed, thus overcoming some of the problems with existing methods.

At first glance, the reaction of a carboxylic acid with an amine to make an amide — known as a condensation reaction because it produces water as a side product — looks simple

(Fig. 1a). One might expect the electron-rich amine to attack and add to the electron-deficient acid when the two compounds are combined. In fact, each reactant must be chemically activated for condensation to occur, and this involves several challenges.

First, in the absence of an activating agent, the overall equilibrium of the process favours the starting materials rather than the products. Second, congestion caused by the presence of bulky groups around the amine and the acid can greatly slow the condensation. And last, but not least, the stereochemistry of the carboxylic acid — the orientation of the groups around the carbon atom to which the acid group is attached, often referred to as handedness — must be maintained.

The last issue is particularly important when constructing peptides from chiral amino acids (those that have handedness). In many cases,