the rate of 75 kilobits per second with a transmission loss of slightly more than 50%; the rate reached 1.7 megabits for lossless transmission.

One of the things that makes quantum cryptography work is that quantum information (that is, information stored in a quantum system) cannot be exactly copied. This is known as the no-cloning theorem. A consequence is that the most obvious action for an eavesdropper who has managed to intercept a message containing key bits — to make a copy of it and send the original on to the intended party — is not an option. Although it is impossible to construct perfect copies, approximate copies are allowed, but there are limits on how good the copies can be. Grosshans et al. have explicitly demonstrated that their quantum cryptographic system is secure against an attack using the best possible coherent-state eavesdropper. The use of continuous variables, rather than qubits, in quantum information and computing is an expanding area of research and shows great promise. Until recently, results in this area had been purely theoretical, but with the experimental demonstration of quantum key distribution and teleportation using continuous variables, this field of quantum information has entered the laboratory, and may soon arrive at practical applications.

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Evolutionary biology
Splitting in space
Diethard Tautz

Disjunct distributions of closely related species are not necessarily the outcome of passive fragmentation of populations. Instead, they can be the consequence of speciation within a population.

Until recently, the overriding credo for explaining how new species are formed has run as follows: first, a population of organisms splits into several subpopulations; once isolated from one another, these subpopulations become adapted to local conditions; so, over millions of years, their descendants evolve into new species. This is ‘allopatric speciation’, a concept in which spatial separation comes first and genetic divergence follows, and which has dominated biological thinking for many decades. The alternative, ‘sympatric speciation’, in which new species are created within a single population, has long been seen as a heresy — to the extent that young biologists would risk their careers if they proposed that such a mechanism could occur.

Over the past few years, however, modeling work has shown that spatial separation of populations is not a prerequisite for genetic splitting. Doebeli and Dieckmann (page 259 of this issue) now go even further. They propose that spatial separation is a secondary consequence of adaptive genetic divergence under sympatric conditions. In other words, splitting of a population in space can follow genetic splitting within it.

One of the strongest arguments against sympatric speciation, namely that there are no convincing mechanisms for genetic separation in sympatry, has already been addressed in the previous models. These models solve the problem of preventing gene flow between differently adapted genotypes, a necessity if speciation is to occur, by giving the individuals an active role in choosing their mates. This is called assortative mating or mate choice, and is a well-documented phenomenon in natural populations. One model suggests the parallel evolution of ecological adaptations and signals that enable individuals to recognize mating partners with genetic adaptations that are similar to their own. The other two show that the evolution of the signals, and specific mate choice or sexual selection alone, can in themselves lead to genetic splitting.

But although there are field studies that support these models, most biologists still see sympatric splitting only as an interesting exception. This is because there is a second argument in support of allopatry: common experience shows that closely related species are usually spatially separated. If one takes this pattern as a reflection of the process, one inevitably arrives at the conclusion that, although sympatry is possible, allopatry is the norm. But this is exactly the point at which the new work will change the prevailing view.

Doebeli and Dieckmann base their model on evolutionary branching, which has already shown its usefulness for understanding the sympatric splitting process. Evolutionary branching describes a process, known as ‘disruptive selection’, under
conditions of ‘frequency-dependent competition’. In short, this means that in any given population that becomes adapted to a particular ecological niche, there will be increasing competition among those individuals that are best adapted simply because they are the most frequent ones. The consequence is that their genotypes have a lower probability of being transmitted to the next generation than the less frequent genotypes, which use only parts of the resource spectrum of the given niche. This leads to disruptive selection for specialization and consequently to the population’s splitting into two new species with differential adaptations.

Doebeli and Dieckmann now add a spatial component to this process by considering an uneven distribution of resources caused, for example, by environmental gradients in temperature, nutrients or altitude. In this situation, local adaptation along the gradient increases the chance that interactions occur between similar individuals, and hence increases the strength of frequency-dependent selection. This leads to surprising results. First, a sharp geographical separation of populations is generated during the splitting process, although the resource distribution remains continuous. Second, the ecological and genetic conditions under which this occurs are even easier to fulfill than in the previous model without the spatial component. Most interestingly, environmental gradients with intermediate slopes work better than gradients with steep slopes, resulting in a complete contrast to predictions of classical models that are based on allopatric concepts.

Is this all only modellers’ fantasy? As yet there is no direct evidence to confirm the predictions of the model, but there are studies pointing in the right direction. For instance, Ogden and Thorpe4 have looked at the genetic differentiation of lizard populations on the Caribbean island of Martinique. By sampling the populations along carefully controlled transects, they showed that there is a sharp reduction of gene flow along a transect covering habitats at different altitudes, but not along two control transects within homogeneous habitats. Intriguingly, they also found no reduction of gene flow across an old allopatric split, indicating that habitat ecology is more important for gene flow than historical contingencies. Thorpe and Richard5 previously drew a similar conclusion in a comparable study of lizards on the island of Tenerife.

It is satisfying that the inclusion of more realistic conditions into an abstract model of sympatric speciation leads to results that explain natural patterns that have long been used as arguments against sympatric speciation. This shows that the common experience that closely related species are usually spatially separated cannot be taken as direct evidence for the prevalence of allopatric speciation. But then, science has a habit of showing that common experience is not always a reliable guide to reality.

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Developmental biology

Germ-cell attraction

Prabhat S. Kunwar and Ruth Lehmann

Cells must often travel long distances to carry out their assigned tasks in the body. New work reveals how the precursors of eggs and sperm are guided during their epic journey to the gonads.

All sexually reproducing organisms are composed of two types of cells: the ‘mortal’ somatic cells, which form the body of the organism, and the ‘immortal’ germ cells, which produce the next generation. During development, precursor germ cells (better known as primordial germ cells, PGCs) are created in one part of the embryo, often far away from their final destination. They must then migrate to the somatic part of the future gonads, where they become mature germ cells — sperm or eggs. Genetic analyses of fruitflies, zebrafish and mice have suggested that the somatic tissues that line the migratory path provide germ-cell attraction — the protein SDF-1 and its receptor CXCR4. Doetsidouet al.1,2,6 now show that SDF-1 and CXCR4 are important for PGC migration1–3. Moreover, these studies have suggested that the somatic tissues that line the migratory path provide attractive, repulsive and survival cues that direct the germ-cell precursors1,2,6. Such cues have so far proved elusive. But, writing respectively in Cell and on page 279 of this issue, Doitsidou et al.2,6 and Knaut et al.3 show that a pair of evolutionarily conserved molecules — the protein SDF-1 and its receptor CXCR4 — act to guide PGCs in zebrafish.

Cell migration is important for many biological processes, including embryonic development, immune responses, wound repair and the spread of tumour cells (metastasis). In many cases, proteins known as chemokines have been shown to trigger and guide cell migration. Initially identified as ‘defence’ proteins because of their ability to regulate immune-cell movement, chemokines have since also been found to be involved in diverse as blood and blood-vessel formation and embryo development4.

Broadly speaking, these proteins work by interacting with members of a superfamly of receptors found on the surface of motile cells. These are the G-protein-coupled receptors, so called because they interact with intracellular ‘on/off’ switches known as G proteins. The interaction between chemokine and receptor activates intracellular signal-transduction cascades, which induce cell movement, survival and gene expression in a manner that depends in part on the precise cell type and signal. For instance, during directed cell migration, the responding cells detect a small concentration gradient of the chemokine, such that the leading edge of the cell orients towards the signal’s source. The activated receptor at the front edge stimulates a specific intracellular enzyme, leading to the recruitment of proteins that contain a structural region known as the pleckstrin-homology domain, involved in protein-protein interactions. This is thought to locally amplify the response to the signal5.

One chemokine-receptor pair consists of the chemokine SDF-1 and the receptor CXCR4. The receptor was first identified as being important for HIV-1 to enter cells, and the chemokine-receptor duo has also been implicated in the metastasis of breast-cancer cells6,7. Moreover, genetic analysis of these two proteins in mice has shown that they are required for the development of blood cells (for example, in the migration of mature B cells to the bone marrow) and in the central nervous system (in the migration of granule cells within the layer of the cerebellar cortex, for instance)8–14. Doitsidou et al.2,6 and Knaut et al.3 now show that SDF-1 and CXCR4 are also involved in PGC migration in zebrafish.

The two groups used different techniques to tackle the problem of how PGCs are guided to their destination in zebrafish embryos. Doitsidou et al.1,2 started by inactivating a large group of genes, one at a time, that they thought might be important for PGC migration. To do so, they used a technique known as ‘morpholino antisense knockdown’. This led them to cxcr4b, one of two genes that encode CXCR4 proteins in zebrafish; when