should attempt to explain at least three phenomena," say Beehler and Foster: "(1) production of an initial mating skew among males in nonclustered court systems, (2) males' shift from solitary dispersion to display clusters, and (3) behavioral adjustments that give the lek its social structure."

The first of these is probably the trickiest to explain, but, say Beehler and Foster, it could derive in part simply from conservative mating habits of females. "Field evidence indicates that females are more conservative than they are choosy," they note. In other words, once a preference is established, for whatever reason, it can build upon itself: "an initially successful male acquires more and more mates with each passing year."

In the question of male clustering, less successful males may increase both their chance of copulation by associating with a more successful individual and their chance of survival through protection offered by a group. The hotshot may tolerate companions, again for reasons of survival but also perhaps because females will be more attracted to a group than to a single individual. How large a lek may be and how they might be dispersed across female territories remains more difficult to resolve.

Lastly, the structure of the lek itself will be influenced greatly by the amount of competition between males, both in establishing hierarchies and in attempts to disrupt matings: in some cases males will coexist closely, and in others will be widely spread out. Once this is established, say Beehler and Foster, "females may largely abdicate their active role in selecting a mate and follow a passive *default strategy* of mate selection, in which the males sort out dominance among themselves and the visiting female simply selects an arena and mates with the dominant male."

The impact of the hotshot model seems likely to be a shift of emphasis—in terms of accommodating male influence in leks—rather than a complete replacement of established models. It is not so much that all of the field data that Beehler and Foster adduce in their hotshot model are new, but what the Smithsonian researchers have done is bring them together in a coherent construct. "I'm glad to see the idea formalized," Bradbury told *Science*, "but I should also like to see their verbal model put on a more quantitative basis." ■ **ROGER LEWIN**

ADDITIONAL READING

B. M. Beehler and M. S. Foster, "Hotshots, hotspots, and female preference in the organization of lek mating systems," *Am. Nat.* **131**, 203 (1988).

J. Bradbury *et al.*, Hotspots and the evolution of leks," *Anim. Behav.* **34**, 1694 (1986).

Mapping by X-Ray Zapping

Tracking down genes can be a frustrating business, as David Cox and Richard Myers well know. Even after a gene has been assigned to a chromosome, it can still take years to find the gene itself with conventional genetic linkage mapping. The gene for Huntington's disease is a case in point. It was mapped to chromosome 4 in 1983 but still remains elusive.

Now Cox and Myers, both at the University of California at San Francisco, think they have circumvented at least part of the problem with a new mapping technique, which they announced at a recent meeting at Cold Spring Harbor Laboratory. They call it a new type of genetic mapping, but others, like Charles Cantor at Columbia University, say it is more akin to physical mapping. Whatever it is called, this hybrid genetic-physical mapping strategy promises to expedite work on both fronts.

Where conventional linkage mapping falls short, says Cox, is in determining the order of closely spaced DNA markers, the landmarks in a genetic map. Genetic maps are used to intuit the actual physical order of genes and markers on chromosomes. In linkage mapping, a gene's location is calculated by how often it is inherited along with a known marker on the chromosome. The closer the gene and the marker, the less frequently they will be separated during meiosis, when genetic recombination occurs. Once the rough location of a gene has been determined this way, the usual strategy to narrow the search is to find more markers in the vicinity, determine their order along the chromosome, and then try to locate the gene between two of them. The catch is that the closer the markers are to each other, the trickier it is to determine their relative positions.

What Cox and Myers have devised is essentially a new unit of measurement: instead of looking at how often two markers are separated during meiosis, they look at how often they are broken apart if the chromosome is zapped with x-rays. The crux of this idea was laid out some 10 years ago by Henry Harris and Steve Goss, says Cox, but "no one believed it would work." It does.

They start with a somatic cell hybrid—a hamster cell that contains a single human chromosome, say chromosome 21, in just one copy. They then zap it with enough x-rays to shatter the chromosome into pieces. Before doing anything else they must "resurrect" the cell, which has been so heavily irradiated that it is essentially dead. They do so by fusing it with another hamster cell. They end up with about 100 hybrid clones, each containing different pieces of chromosome 21. Then they look at these cells to see how often various sets of markers have broken apart. For any two markers, say markers A and B, some cells will contain just A, some just B, some both, and some neither. (That a cell contains both or neither is not illuminating in itself, since the two could have been retained or lost together or separately.)

To compute the genetic distance, Cox and Myers have devised a mathematical algorithm that can reconstruct how often A and B were broken apart according to how many cells contain A only, B only, both, or neither. This process is then repeated for all pairs of markers to determine their order and thus construct a genetic map.

Cox and Myers have now tried the technique on two chromosomes: on 21, where they are looking for the putative Alzheimer's gene; and on 4, where they are looking for the Huntington's gene. Using pulsed field gel electrophoresis, they have confirmed that the order predicted by this genetic map is indeed the order in which the markers appear in the physical world.

What's more, says Cox, if a high dose of radiation is used, this approach can offer 20-fold greater resolution than conventional linkage mapping. Resolution simply depends on the number of breakpoints in the chromosome. By zapping a chromosome with 7000 rads, breaks occur roughly every 50 kilobases, as compared with the 1-million-base resolution offered by linkage mapping. With a genetic map of this resolution, say Cox and others, it should be relatively easy to construct a physical map, which in turn makes it possible to clone the DNA between flanking markers and pull out the desired gene.

Cox cautions, however, that the genetic distance in this map will not necessarily mirror physical distance. Just as there are "hotspots" of recombination on chromosomes where the genetic distance far exceeds the physical distance, there will likely be certain regions that are more susceptible than others to breakage by x-rays.

■ **LESLIE ROBERTS**