"individuals" and then replicates them depending on how well they meet some criterion of "fitness."

In Werner's model, each individual carried "genes" for heritable traits—some beneficial, some detrimental—that were tied to fitness scores. The higher an individual's fitness score, the greater its chance of reproducing. Individuals also carried "genes" for heritable mating preferences. Each female was paired with the male that most closely matched her preferences from among a random group of candidates. Standard genetic algorithm techniques allowed for random mutations.

JAN HALSKA/PHOTO RESEARCHERS

Checkout time. Computer model finds female peacocks limit time spent on choosing a mate.

After conducting numerous simulations with varying parameters, Werner found that males would accept extremely high fitness handicaps to win in sexual-selection competition. What kept runaway sexual selection from getting too far out of hand was another heritable trait—limits on females' willingness to put time and energy into looking for males with desirable traits. Werner concluded that, based on his simulation exercises, the cost to females of evaluating males "is what limits the growth of maladaptive traits."

That result is accepted wisdom among evolutionary biologists, says Andrew Pomiankowski, an evolutionary biologist at University College, London, "but I'm glad to hear he's confirming it." And Pomiankowski thinks that Werner's approach, despite its belated conclusion, can augment work based on the more traditional analytical methods used by biologists. "There's plenty of work to be done," he says.

Werner intends to refine his model to study more general population trends by adding in such factors as parental investment in offspring and mate choice. He is also collaborating with colleagues in looking at how sexual selection may facilitate speciation. In the end, he and his colleagues hope the results will speed the process by which artificial life evolves into a useful biological tool.

–Dennis Normile

DEVELOPMENTAL BIOLOGY

Corn: A Lot of Change From a Little DNA

NASHVILLE, TENNESSEE—If wolves can give rise to poodles and Pekingese, perhaps it's not so hard to believe that corn growing "as high as an elephant's eye"—as songwriters Rodgers and Hammerstein put it—is the domesticated version of a bushy and inedible weed called teosinte. Yet the two plants are incredibly different. In addition to the shape disparity, corn ears—the flowers of the domesticated plant—are covered with hundreds of soft, edible kernels, while teosinte flowers are studded with just a dozen or so, all firmly encased in armor. At the national meeting of the Society for Developmental Biology 3 weeks ago in Nashville, however, scientists heard that the plants are not only close relatives, but many of the features that make corn ears so bountiful could result from mutations in just one small stretch of teosinte DNA.

Jane Dorweiler, a graduate student at the University of Minnesota, reported that giving teosinte a single portion of corn's chromosome 4 altered the basic process of flower development, and teosinte seeds became exposed kernels just like those on corn—or maize, as it's known to botanists. The hybrid is "what teosinte may have looked like during one of the morphological steps in its evolution toward maize" some 7000 to 10,000 years ago, when archaeologists believe teosinte was domesticated in what is now Mexico, Dorweiler says.

One such archaeologist, Bruce Smith of the Smithsonian Institution's Museum of Natural History, agrees. "How you get the morphology of the corn cob out of teosinte ... has been the big puzzle remaining to be described," he says. "Having biologists move closer in on that is really of great value and interest." And plant developmental geneticist Scott Poethig of the University of Pennsylvania adds that the work supports the growing notion that minor genetic changes can result in large evolutionary leaps. Dorweiler and her colleagues think it may even point toward a way of engineering similar improvements in other cereal or grain plants.

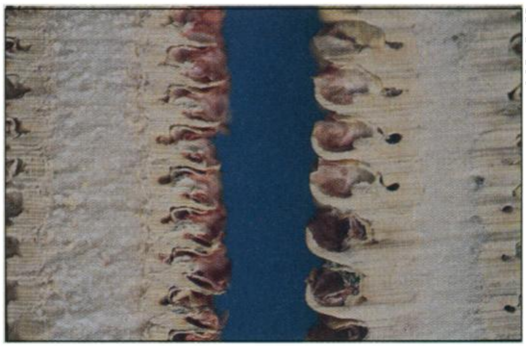
Dorweiler's investigation follows work done in 1991 by Minnesota's John Doebley and others, who used genetic markers on maize's 10 chromosomes to track several important traits that distinguish it from teosinte. They led to five "quantitative trait loci" or QTLs, the regions where the genes producing these characteristics are presumed to be (*Science*, 28 June 1991, p. 1792). Changes in one QTL, named *tga1*, seemed to account for the diminishment of the fruit case, or glume, that surrounds the seeds in teosinte, where it is "lignified" or hardened enough to crack the teeth of even the most ardent corn lover.

Dorweiler took that work a step further, watching how glume structures developed in teosinte hybrids with one copy of *tga1*. The glumes ended up shorter than in wild-type teosinte, did not completely encase the kernels, and were much softer, apparently because they contained less silica. Glumes were feebler still in teosinte carrying two copies of *tga1*—a sure sign that the locus contained a gene or genes regulating the trait.

Doebley speculates that maize may have first emerged when ancient humans cultivated a mutant teosinte strain in which the functions of genes within *tga1* were somehow attenuated, an idea that is "certainly reasonable," says Poethig. "Until you can make [corn] edible, there isn't much point in harvesting it." The researchers have yet to clone genes from the locus. But because it seems to guide several disparate aspects of glume architecture, Doebley and Dorweiler suspect that the genes may regulate very early events in ear development.

The Minnesota group's finding further strengthens the argument, made by Harvard University paleontologist Stephen Jay Gould and others, that small evolutionary changes can produce drastic—and sometimes advantageous—differences in an organism's architecture. Moreover, Doebley says, if QTLs corresponding to *tga1* can be found in other cereal crops or even noncrop plants, then knowledge about maize evolution could be used to bring other hidden fruits into the open.

–Wade Roush



J. DORWEILER

All ears. Exposed kernels make standard corn easy to harvest *(left)*. But in corn carrying a small stretch of DNA from its wild relative teosinte, kernels are protected by a hard case *(right)*.