and secondary schools and higher education and bring all the available talent to bear on the problem of math and science teacher education." Rosen says the commission will flesh out the NRC's findings "by laying out a set of strategies and price tags that makes clear who needs to do what."

Although Lewis welcomes the heightened attention on teacher education, he says that reports won't help unless they are backed up by a national consensus that teachers count. "The schools [in Lincoln, Nebraska] start this week, but they'll close early if it gets too hot because they lack air conditioning," he says. "I'll bet that you work in an air-conditioned building. So why can't teachers? Because we aren't willing to pay what it would cost."

Can New Ph.D.s Be Persuaded to Teach?

U.S. schools will need to hire 20,000 math and science teachers a year for the next decade to handle a growing student population and high rates of retirement, according to government estimates. Where they will come from is anyone's guess, as schools are already having trouble finding qualified people. To help fill the gap, a National Research Council (NRC) committee suggests tapping a talent pool that is relatively underrepresented among teachers: newly minted Ph.D.s.

In a report[*] issued last week, the committee says many more recent science Ph.D.s would be willing to teach high school science and math if the government helped with the transition, if the certification process were compressed, and if they could retain ties to research. The committee recommends that the NRC help states with pilot projects that, if successful, could be expanded nationwide. But some educators are skeptical, noting that Ph.D.s may not be properly trained and that the research and teaching cultures are very different.

"If public schools could place an ad that read: 'Good salaries, good working conditions, summers off, and tenure after 3 years,' I think they'd get a good response from graduate students," says Ronald Morris, a professor of pharmacology at the University of Medicine and Dentistry of New Jersey in Piscataway and chair of the NRC panel, which last summer surveyed 2000 graduate students and postdocs as well as interviewing professional educators. "But most Ph.D.s don't know about the opportunities, because they are generally far removed from the world of K-12 education."

The report notes that while 36% of respondents say they had considered a K-12 teaching job at some point in their training, only 0.8% of the scientific Ph.D. workforce is actually working in the schools. "That's a significant pool of talent that we're ignoring," says Morris, who acknowledges that none of his 40 postdocs over the years has chosen to go into high school teaching.

Professional educators, however, warn that several issues must be resolved, including the teaching skills of recent Ph.D.s and how well they would fit into a high school environment. "I think it's a great idea," says Mike Lach, a high school physics teacher in Chicago who just completed a sabbatical year in Washington, D.C., working on federal legislation to improve math and science teaching (*Science*, 4 August, p. 713). "But teaching is hard, and those in higher education traditionally don't have much respect for classroom teachers." Mark Saul, a Ph.D. math teacher in Bronxville, New York, as well as an adjunct professor at City College of New York, puts it this way: "Ph.D.s are a peg with a different shape than the current hole for schoolteachers."

Morris agrees that high school teaching isn't appropriate for all Ph.D.s. But he believes that an array of incentives, including federally funded fellowships for retraining and summer research projects, might be just the ticket for those looking for a way out of a tight academic job market.

—JEFFREY MERVIS

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[*] "Attracting Science and Mathematics Ph.D.s to Secondary School Education," National Academy Press.

GENETICS

Transposons Help Sculpt a Dynamic Genome

These mobile elements cause considerable reshaping of the genome, which may contribute to evolutionary adaptability

More than 50 years ago, geneticist Barbara McClintock rocked the scientific community with her discovery that maize contains mobile genetic elements, bits of DNA that move about the genome, often causing mutations if they happen to land in functioning genes. Her findings were considered so outlandish that they were at first dismissed as anomalies unique to corn. But over the years, transposons, as the mobile elements are called, have proved to be nearly universal. They've turned up in species ranging from bacteria to mammals, where their movements have been linked to a variety of mutations, including some that cause diseases and others that add desirable diversity to genomes (*Science*, 18 August, p. 1152). Only in the past few years, however, have researchers been able to measure the rate at which transposons alter the composition of genomes, and they are finding that the restructuring they cause is more extensive than previously thought.

Researchers have known for about 20 years that transposons can expand the genome, resulting in the repetitive DNA sequences sometimes called "junk," but the new work indicates that transposons can also contribute to substantial DNA losses. What's more, these changes can be rapid—at least on an evolutionary scale. "The level of genomic dynamism is way beyond what was thought," says geneticist Susan Wessler of the University of Georgia, Athens.

The rate of transposon-mediated genomic change can vary, however, even among closely related organisms. The findings may thus help explain the so-called "C-value paradox," the fact that the size of an organism's genome is not correlated with its obvious complexity. Plants, for example, are notorious for having a 1000-fold variation in their genome sizes, ranging from the lean 125-million-base genome of *Arabidopsis* to the extravagant genome of the ornamental lily *Fritillaria*, which at 120 billion bases is about 40 times the size of the human genome. There are also hints that the environment can influence transposon activity,

The great and the small. Although it's not obvious from appearances, the genome of the lily *Fritillaria (left)* is nearly 1000 times bigger than that of *Arabidopsis (above)*.

CREDITS: (LEFT TO RIGHT) GERALD AND BUFF CORSI/VISUALS UNLIMITED; JOSHUA MYLNE

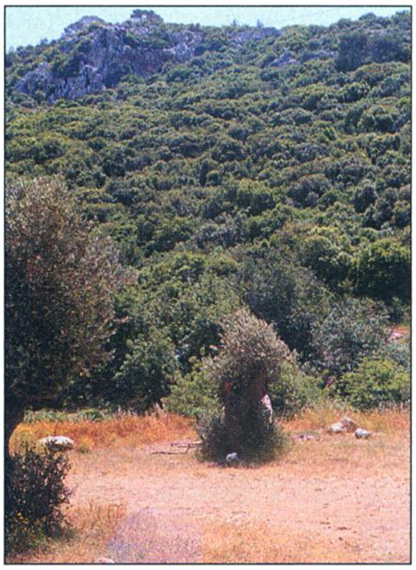
which in turn may help an organism adapt to environmental changes.

Until recently, researchers tended to focus on the stability of the genome over evolutionary time. There is ample evidence, for example, that sequences of many key genes, such as those that determine body plan, are conserved across diverse genera. The discovery, about 10 years ago, of synteny, that many genes remain grouped together in the same relative positions in the genome no matter its size, also suggested that genomes were models of stability. The potential for significant fluidity in the genome was largely ignored until a few years ago when a small number of groups began to take a different perspective, using molecular techniques to probe genomes on a large scale.

For example, work done 2 years ago by Purdue University molecular biologist Jeffery Bennetzen and Phillip SanMiguel, who is now at the University of California, Irvine, suggests that maize used amplification of retrotransposons, elements that copy themselves with the aid of RNA, to double its genome size from 1.2 billion to 2.4 billion bases 1 million to 3 million years ago—a very short period in evolutionary time. They based this conclusion on their finding that maize carries many more retrotransposons than its close relative, sorghum. The threat of "genomic obesity" was often mentioned. "It's remarkable the genome doesn't explode," says Bennetzen.

New work shows that plants have ways of counteracting transposon expansion, however. University of Helsinki retrotransposon specialist Alan Schulman and colleagues at the John Innes Centre in Norwich, U.K., report in the July issue of *Genome Research* that retrotransposons can also be eliminated from the genome. The most common retrotransposons in plants carry duplicated sequences on each end called long terminal repeats (LTRs), and these can lead to something called intrachromosomal recombination, in which the LTRs temporarily join up and the DNA between them is excised. When this happens, one of the LTRs is left behind. Schulman and his colleagues analyzed the barley genome for these molecular "scars," and they found a lot of them, indicating that many transposons had been lost. In a commentary in the same *Genome Research* issue, molecular biologist Pablo Rabinowicz of Cold Spring Harbor Laboratory in New York says these results suggest that "recombination between LTRs is an efficient way to counteract retrotransposon expansion, at least among certain grasses." He cautions, however, that it's not clear how widespread the phenomenon is.

Evolutionary biologist Dmitri Petrov, first as a graduate student in the Harvard lab of Daniel Hartl and, most recently, at Stanford University, has also found evidence of significant genome fluidity in insects. In work begun in the mid-1990s, Petrov and his colleagues used the Helena group of transposons from *Drosophila virilis* and other fruit fly species as tools for studying genomic juggling. By monitoring sequence changes in Helena transposons in eight *Drosophila* species, the researchers learned that copies of this element lose DNA at a high rate—20 times faster than in mammals.



Evolutionary hotbed. This canyon near Mount Carmel, Israel, provides a variety of environments in a small space for studying plant adaptations.

CREDIT: A. SCHULMAN

Petrov does not know what causes the shrinkage, although he suggests that it might be due to spontaneous mutations or errors in copying the DNA. But whatever the cause, he says, "I was extremely surprised by the *Drosophila* data. I thought the rate [of genome loss] would be the same as for mammals." That wasn't the only surprise, however.

Last February, Petrov, J. Spencer Johnston, an entomologist at Texas A&M University in College Station, and Harvard colleagues showed that Hawaiian crickets (*Laupala*) lose DNA more than 40 times more slowly than *Drosophila* does, even though the two insect species are closely related (*Science*, 11 February, p. 1060). In this work, the researchers used the same analytic technique with a different transposon, *Lau1*, in nine *Laupala* species. Because the *Laupala* genome is 11 times larger than that of *Drosophila*, Petrov hypothesizes that its slow loss of DNA may account for its bulk. He is now testing whether that idea holds up by measuring the rate of DNA loss in various insects, including flies, ants, butterflies, mosquitoes, damselflies, and grasshoppers.

The big question mark, however, is what does all this genomic restructuring do for the organism? A small genome may be helpful because it can replicate faster, resulting in a faster cell cycle and shorter generation time. But work reported in the 5 June issue of the *Proceedings of the National Academy of Sciences* by Schulman, along with colleagues at the Agricultural Research Centre in Jokioinen, Finland, and the University of Haifa in Israel, suggests that large genomes may have their own advantages.

The researchers collected specimens of the wild ancestor of cultivated barley from various microclimates in "Evolution Canyon," Mount Carmel, Israel. When they then looked at the plants' content of a particular type of retrotransposon, called BARE-1, they found that it is up to three times more abundant in barley plants growing at the canyon rim than in those grown near the bottom of the canyon. Their evidence suggests that this may be because plants at higher elevations lose their transposons more slowly than plants farther down. The fact that plants at the top of the canyon both gain more copies and lose fewer suggests, Schulman says, that the elements may confer some advantage.

He and his colleagues speculate that a larger genome, achieved through the ample presence of retrotransposons, may help plants deal with the more stressful high and dry areas of the canyon, for example, by influencing the physiological machinery that enables plants to seek or retain water.

Consistent with this idea, Stanford University plant scientist Virginia Walbot showed last year that shorter wavelength ultraviolet light can activate a particular Mutator transposon in maize pollen, a result that suggests that sunlight, likely more plentiful at higher elevations, may also be an environmental force involved in genomic restructuring. That remains to be demonstrated, but plant scientists say that Schulman's identification of the BARE-1 element, numerous copies of which exist in the barley genome, as an agent of genomic restructuring opens the way for a new level of experimental studies.

One possibility is to test whether plants with more elements are able to thrive in more stressful conditions. Another is to see whether transcription of the BARE-1 element changes under different environmental conditions. Georgia's Wessler says there is now "a clean molecular system to get at the important questions." The results that come from such studies of BARE-1, and other mobile genetic elements, should help to explain how and why some plants and animals have come to have genomes of extraordinary size, often much larger than that of humans.

–ANNE SIMON MOFFAT