An enhanced version of this Perspective, with live links, can be seen in *Science* Online at http://www.sciencemag.org/

shows that the IBAD process is not essential and that the textured substrate on which high-J_c YBCO can be laid down can also be prepared by common rolling methods. The prospects for the new techniques are illustrated by the magneto-optical image shown in the figure. Even in a rather well-aligned YBCO tape with a J_c of 5×10^5 A/cm^2, the current is percolating from point to point, thus indicating that we are still far from achieving the true potential of these techniques.

What will be the industrial impact of these two advances? Much depends on translating the science of small samples into conductor-relevant prototypes as explained in a recent U.S. Department of Energy–sponsored report on power applications of superconductivity (*15*). Conductors must be electrically continuous, otherwise there can be no applications. BSCCO conductors have made great strides recently as the materials science of the current-limiting mechanisms and its fabrication have become better understood (*14*). Real conductors must be strong, economical, manufacturable in long lengths, and have high overall J_c values. Here, "overall" means that all of the space required to make the conductor must be counted when the critical current is normalized by the conductor cross section. YBCO has undoubted advantages over BSCCO for use at liquid nitrogen temperatures in magnetic fields of more than about half a tesla. The exciting prospect for those working on applications of high-temperature superconductors is that excellent first-generation conductors of BSCCO are now available, and potential second-generation conductors with strongly improved prospects are in view. All in all, this is a very promising state for a field, not yet 10 years old, that 7 years ago seemed almost stillborn.

References

1. J. G. Bednorz and K. A. Müller, *Z. Phys.* **B64**, 189 (1986).
2. M. K. Wu et al., *Phys. Lett.* **58**, 908 (1987).
3. Research Briefing on High Temperature Superconductivity, J. Hulm, Ed. (National Academy of Sciences Press, Washington, DC, 1987).
4. Superconductivity: Challenge for the Future, Federal Conference on Commercial Applications of Superconductivity, Washington DC, 28–29 July, 1987.
5. K. Heine, N. Tenbrink, M. Thoener, *Appl. Phys. Lett.* **55**, 2441 (1989).
6. P. Yang and C. M. Lieber, *Science* **273**, 1836 (1996).
7. D. P. Norton *et al.*, *ibid.* **274**, 755 (1996).
8. L. Civale *et al.*, *Phys. Rev. Lett.* **67**, 648 (1991).
9. L. Krusin-Elbaum *et al.*, *Appl. Phys. Lett.* **64**, 3331 (1994).
10. J. A. Parrell *et al.*, *ibid.*, in press.
11. A. Pashitski, A. Polyanskii, A. Gurevich, J. Parrell, D. Larbalestier, *Physica C* **246**, 133 (1995).
12. Y. Iijima, N. Tanabe, O. Kohno, Y. Ikeno, *Appl. Phys. Lett.* **60**, 769 (1992).
13. X. D. Wu *et al.*, *ibid.* **67**, 2397 (1995).
14. Q. Li *et al.*, Proc. of Appl. Supercond. Conf. 1996, to appear in IEEE Trans. on Appl. Superconductivity (1997).
15. JTEC/WTEC Panel on Power Applications of Superconductivity in Japan and Germany (WTEC Office, Loyola University, MD, July 1996).

Retroelements in Genome Organization

Daniel F. Voytas

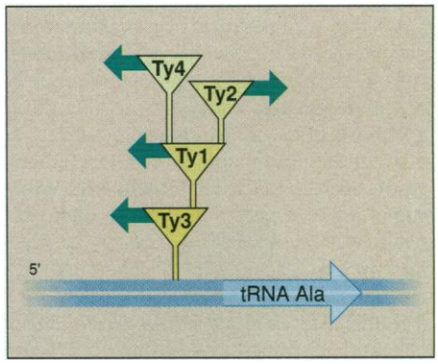
Eukaryotic genomes are riddled with genetic freeloaders—transposable pieces of DNA that require host cell functions to replicate and proliferate. Transposition poses a potential threat to the host because integration into new sites in the genome can result in deleterious mutations. Logic dictates that there should be an upper limit to the level of transposition that genomes can endure. It is therefore quite surprising to discover, as reported in this issue of *Science* (*1*), the magnitude of transposable elements in the genome of maize. Regions between maize genes are packed with transposable elements inserted within transposable elements, which together make up more than 50% of the two billion base pairs (bp) that constitute this plant's nuclear DNA.

The predominant type of transposable element in maize is the retroelement, which replicates through an RNA intermediate by reverse transcription. Particularly prevalent are two classes of retrovirus-like retrotransposons, the so-called Ty1/copia and Ty3/gypsy elements. Retrotransposons are particularly important in shaping plant genomes: Ty1/copia group retrotransposons are found in species throughout the plant kingdom (*2*), and many plant gene sequences in the DNA databases have adjacent retrotransposon insertions (*3*). In some cases, these insertions are located in the promoters of plant genes and contribute sequences important for promoter function.

By analyzing a contiguous stretch of plant genomic DNA, SanMiguel *et al.* reveal that earlier studies had uncovered only the tip of the plant retroelement iceberg. Large blocks of retroelements (greater than 50 kb) were found between single-copy gene sequences in a 280-kb region encompassing the maize *adh1* gene. These blocks are made up of at least 10 diverse retroelement families with varying numbers of copies. The five most abundant families alone make up about 25% of the maize genome. The presence of multiple low–copy number families further indicates that many hundreds, if not thousands, of distinct retroelement families exist in maize—an unprecedented wealth of retrotransposon diversity in the genome of a single organism.

The author is in the Department of Zoology and Genetics, Iowa State University, Ames, IA 50011, USA. E-mail: voytas@iastate.edu

Retrotransposons add considerable bulk to the maize genome. This principle may extend to other plants and may account for the remarkable range of sizes observed for plant genomes, from 10^8 bp for *Arabidopsis thaliana* to over 10^{11} bp for some species of lily. Although *Arabidopsis* has more than 20 characterized retroelement families, most are present at one to five copies per genome, consistent with the notable lack of interspersed repeats in this plant's nuclear DNA (*4*). The genomes of many agronomically important grasses are largely colinear yet vary extensively in size (*5*); for example, the maize genome is 3.5 times as large as that of



A retrotransposon landing pad. Retrotransposons within retrotransposons are typically found upstream of tRNA genes in *S. cerevisiae*, as shown by this region 5′ of an alanine tRNA gene on chromosome X (*6*). Present at this site are insertions from each of the four *S. cerevisiae* retrotransposon families typically associated with tRNA genes or other genes transcribed by RNA Pol III. Arrows indicate the orientation of insertions or the direction of tRNA gene transcription.

sorghum and more than 35 times as large as that of rice. Comparisons of specific intergenic regions among related grasses may reveal more directly how retroelements participate in genome expansion and contraction.

How can the maize genome function with such a large burden of retroelements? It is, of course, in the element's best interest to minimize genetic damage caused by integration, because the host's survival is necessary for persistence of the element. In the yeast *Saccharomyces cerevisiae*, in which retrotransposons have been studied extensively, it appears a bargain has been struck between element and host that allows both to survive. The five retrotransposon families of *S. cerevisiae*, designated Ty1 to Ty5, have a strong bias for sites in the genome into which they integrate. The complete *S. cerevisiae* genome sequence (6) reveals that well over 90% of the elements from the Ty1 through Ty4 families are located within 750 bp upstream of genes transcribed by RNA polymerase III (Pol III), particularly tRNA genes (see figure); the Ty5 elements are all located at the telomeres or regions that have telomeric chromatin. The association of Ty1 and Ty3 with Pol III genes and Ty5 with telomeres is due to targeted integration (7). These elements appear to recognize either specific proteins associated with Pol III transcription or particular chromatin components. Regions targeted by yeast retrotransposons are typically devoid of open reading frames, and reiterative integration can generate blocks of elements within elements (see figure). These element landing pads provide a safe haven for elements to integrate without causing deleterious mutations.

The organization of retroelements in the interspacer regions of maize is reminiscent of the retrotransposon landing pads observed in yeast. Targeted integration, as opposed to amplification by recombination, is suggested by the overall structural integrity of the retroelements and the presence of intact target-site duplications flanking most insertions. The underrepresentation of the most highly abundant retroelement families in the maize DNA sequence databases further suggests that these elements specifically avoid coding regions or that their presence near genes has been strongly selected against. Intergenic regions are hypermethylated relative to gene sequences (8), and extrapolating from the yeast model, one might predict that some such unique chromatin feature serves as a homing device for maize retroelements during integration. Hypermethylated arrays of retrotransposons within retrotransposons have also been observed in the slime mold *Physarum polycephalum* (9), suggesting that targeted integration may be a widespread strategy adopted by retroelements to proliferate within host genomes.

Much work still needs to be done to test whether retroelements are specifically targeted to intergenic regions in maize. Nonetheless, it is apparent that maize and its retroelements have coevolved a highly effective mechanism that has enabled amplification of retroelements to levels unprecedented in other eukaryotes. Although the maize elements appear to be genomic parasites, they likely contribute to genetic variability and may benefit their host over evolutionary time. It was from McClintock's work with maize that we first learned of transposable elements and their ability to reorganize genomes. The wealth of maize retroelements further speaks to the profound fluidity of genomes and their abundant capacity for change.

References

1. P. SanMiguel et al., *Science* **274**, 765 (1996).
2. D. F. Voytas, M. P. Cummings, A. Konieczny, F. M. Ausubel, S. R. Rodermel, *Proc. Natl. Acad. Sci. U.S.A.* **89**, 7124 (1992); A. Flavell *et al.*, *Nucleic Acids Res.* **20**, 3639 (1992).
3. S. E. White, L. F. Habera, S. R. Wessler, *Proc. Natl. Acad. Sci. U.S.A.* **91**, 11792 (1994).
4. A. Konieczny, D. Voytas, M. Cummings, F. Ausubel, *Genetics* **127**, 801 (1991); T. Pelissier *et al.*, *Plant Mol. Biol.* **29**, 441 (1995); D. Wright *et al.*, *Genetics* **142**, 569 (1996).
5. J. Bennetzen and M. Freeling, *Trends Genet.* **9**, 259 (1993).
6. http://genome-www.stanford.edu/Saccharomyces/
7. D. L. Chalker and S. B. Sandmeyer, *Genes Dev.* **6**, 117 (1992); S. E. Devine and J. D. Boeke, *ibid.*, p. 620; S. Zou, N. Ke, J. M. Kim, D. F. Voytas, *ibid.*, p. 634.
8. J. Bennetzen, K. Schrick, P. Springer, W. Brown, P. SanMiguel, *Genome* **37**, 565 (1994).
9. H. M. Rothnie, K. J. Mccurrach, L. A. Glover, N. Hardman, *Nucleic Acids Res.* **19**, 279 (1991).

A Chloride Channel Model?

Chris Miller

On page 761 of this issue Malashkevich *et al.* (*1*) describe a coiled-coil structure with two particularly noteworthy features. The 46-residue peptide, taken from the oligomerization domain of the cartilage oligomeric matrix protein (COMP) of the extracellular matrix, forms a pentameric coiled-coil, the first such structure observed at high resolution. The parallel bundle of α helices forms a left-handed coiled-coil 70 Å long and 30 Å wide through conventional, hydrophobic interactions at the helix-packing interfaces. Nearly all of the polar side chains project outward off the water-exposed surface, with one dramatic exception. A glutamine residue halfway down the sequence reaches brazenly inward. The resulting ring of inward-looking amide groups presents an energetic puzzle: How to match these amides with polar partners in such a greasy, leucine-dense forest?

The peptide's solution to this problem raises a second notable characteristic of the structure: possible relevance to the structures of ion channel proteins. With five strands, the bundle is wide enough to have a ~4 Å diameter hole, or channel, running along the central axis. The channel's lining is almost completely hydrophobic, except for the ring of five glutamines in the middle. The hole is filled with water. But the pore's volume is so small that not enough water can enter to slake the polar thirst of all the glutamines, so something else must fill that need. It is a Cl^- ion, a naked charge embraced in pleasing fivefold symmetry by the amide nitrogens. This fully dipolar liganding arrangement is reminiscent of the bacterial periplasmic sulfate- and phosphate-binding proteins (*2*).

The ion channel structure-and-function community, thirsty for structures of the transmembrane pore-forming proteins that underlie all cellular electrical activity, must look in unlikely places (*3*) for possible structural models of ionic coordination inside these pores. Is the COMP structure a good model for ion ligation in the pentameric, anion-selective channels opened by certain neurotransmitters (*4*) or in voltage-dependent ClC-type chloride ion channels (*5*)? Nobody knows, but to the parched tongue, a brackish pool actually at hand can taste as sweet as a distant, imagined babbling brook.

The author is at the Howard Hughes Medical Institute, Department of Biochemistry, Brandeis University, Waltham, MA 02254, USA. E-mail: cmiller@binah.cc.brandeis.edu

References

1. V. N. Malashkevich *et al.*, *Science* **274**, 761 (1996).
2. J. W. Pflugrath, and F. A. Quiocho, *J. Mol. Biol.* **200**, 163 (1988); H. Luecke and F. A. Quiocho, *Nature* **347**, 402 (1990).
3. M. D. Toney, E. Hohenester, S. W. Cowan, J. N. Jansonius, *Science* **261**, 756 (1993); H. R. Faber *et al.*, *Structure* **3**, 551 (1995); S. Rhee, K. D. Parris, A. Ahmed, E. W. Miles, D. R. Davies, *Biochemistry* **35**, 4211 (1996).
4. D. Langosch, L. Thomas, H. Betz, *Proc. Natl. Acad. Sci. U.S.A.* **85**, 7394 (1988); D. Langosch, C. M. Becker, H. Betz, *Eur. J. Biochem.* **194**, 1 (1990); N. Nayeem, T. P. Green, I. L. Martin, E. A. Barnard, *J. Neurochem.* **62**, 815 (1994).
5. R. E. Middleton, D. J. Pheasant, C. Miller, *Biochemistry* **33**, 13189 (1994); T. J. Jentsch, *Curr. Opin. Neurobiol.* **6**, 303 (1996).