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.

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A Chloride Channel Model?

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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.

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