The maize (*Zea mays*) genome is teeming with LTR retrotransposons. Transposable elements nest within one another to form repeat clusters, making identification and reconstruction of broken segments challenging. TEnest, presented in this issue by Kronmiller and Wise (pp. 45–59), is a Web-based and downloadable software package specifically designed for automated genome-wide annotation and visualization of nested plant transposable elements. Analysis of finished maize BAC contigs with TEnest shows LTR retrotransposons have experienced periods of rapid proliferation. The Opie phylogenetic tree displayed here reveals clades that also cluster based on millions of years since their insertion, indicating evolution of related LTR retrotransposons occurs within discrete time bursts.

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