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Comparative genomics provides a powerful approach to identifying conserved non-coding sequences that regulate gene transcription. In the April 30 *Proceedings of the National Academy of Sciences* Kaplinsky *et al.* report the use of cross-species genomic DNA comparison to isolate conserved non-coding sequences in grass genomes (*Proc Natl Acad Sci USA* 2002, **99**:6147-6151). They compared the genomic sequences of rice and maize, two domesticated species in the Poaceae family of grasses. Differences in regulatory sequences between grasses are thought to account for their morphological and physiological variation. Kaplinsky *et al.* examined genomic sequences around the *liguleless1 (lg1)* gene, which is required to specify the ligule. They identified several conserved non-coding sequences by comparing genomic sequences, relative positions and lengths; and the conserved *Ig1* non-coding sequences are also conserved in other grass species, including *Staria*, *Arundo* and bamboo. Analysis of conserved non-coding sequences from other rice and maize genes suggests that such sequences are smaller and less frequent in plants than in mammalian genomes.

References

1. Conserved noncoding sequences are reliable guides to regulatory elements.
2. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
3. *liguleless1* encodes a nuclear-localized protein required for induction of ligules and auricles during maize leaf organogenesis.