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The 2300-2700 Mb maize genome consists of highly repetitive sequences interspersed with single-copy, gene-rich sequences. This configuration makes standard genome sequencing strategies unproductive, and consequently, gene-targeted partial genomic sequencing using methylation filtration (MF) or High C0t selection (HC) may be of considerable use in unlocking the information contained in the sequence data. Two papers in December 19 Science show that methylation filtration alone or in combination with High C_0t can provide an efficient strategy with which to sequence maize and other highly repetitive genomes.

MF employs small-insert genomic libraries constructed in a bacterial host comprising a restriction system that prevents the propagation of clones carrying methylated inserts. In the first paper, Lance E. Palmer and colleagues at Cold Spring Harbor Laboratory compared the rice genome with MF sequences from maize. The authors observed that MF results in a more comprehensive representation of maize genes than those that result from expressed sequence tags or transposon insertion sites sequences (*Science* 2003, **302:**2115-2117).

"The elimination of more than 90% of repeats by methylation filtration reduces sequencing costs without sacrificing information, because reads within these repeats could not be assembled in any case by whole-genome shotgun analysis," conclude Palmer *et al*.

In the second paper, C.A. Whitelaw and colleagues at The Institute for Genomic Research report that methylation filtering in combination with High C_0t selection resulted in a six-fold reduction in the effective genome size and a fourfold increase in the gene identification rate in comparison with a nonenriched library (*Science* 2003, **302:**2118-2120).

"We believe the MF and HC strategies may serve as a model for sequencing this and other large, complex genomes at reduced cost relative to conventional approaches," conclude Whitelaw *et al*.

References

1. Constructing gene-enriched plant genomic libraries using methylation filtration technique

2. Studies on nucleic acid reassociation kinetics: empirical equations describing DNA reassociation

3. *Science*, [http://www.sciencemag.org]

4. Cold Spring Harbor Laboratory, [http://www.cshl.org/]

5. The Institute for Genomic Research, [http://www.tigr.org/]