

A progress report, resources, and early results from the *Medicago truncatula* genome sequencing project

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The *Medicago truncatula* genome is known to be highly syntenic with alfalfa and pea, and moderately syntenic with soybean. A growing array of genomic tools includes a ~12X physical map, sequencing of ~150,000 BAC-ends, ~190,000 ESTs, and ~1,000 BACs currently sequenced. Cytogenetic evidence and the ~100 Mbp already available demonstrate that the genome is organized into separate gene-rich euchromatin and gene-poor centromeric and pericentromeric heterochromatin. A BAC-by-BAC sequencing strategy, funded by the NSF, the EU 6th Framework Programme, and the Noble Foundation will lead to the uninterrupted sequence of most of the euchromatin of *M. truncatula* by 2006. Sequencing has been distributed among four sequencing centers with Oklahoma sequencing chromosomes 1, 4, 6, and 8; TIGR sequencing chromosomes 2 and 7; Sanger/JIC sequencing chromosome 3; and Genoscope/INRA sequencing chromosome 5. Sequence data is being deposited in Genbank as BACs are sequenced.

Centralized access to the sequencing project, including views of sequencing progress, a project-wide BAC registry, map anchoring, BAC-ends, gaps and overlaps, project statistics, and links to related sites are available at <http://medicago.org/genome>. Resources at other sites include automated annotation pipelines and viewers at TIGR, the University of Oklahoma ACGT, and the University of Minnesota CCGB web sites, and integrated genetic and FPC-based physical maps are available at the UC Davis web site <http://mtgenome.ucdavis.edu>.