Medicago truncatula
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Genome features
- 470 - 520 Mbp per haploid genome
- 8 chromosomes per haploid complement
- Distinctly separate euchromatic gene-space and pericentromeric heterochromatin
- More than 40% of gene space sequenced as of September 2004, with entire gene-space sequence anticipated in next few years
- Gene density estimated at 1 gene per 6.4 kbp throughout gene-space
- Total gene number estimated at between 37,000 and 46,000

Special biological features of interest
- Several genes in the Rhizobium and Mycorrhizae symbiosis pathway cloned and characterized
- Symbiotic partner, Sinorhizobium genome, fully sequenced
- Same genus as alfalfa (M. sativa); close relative of clover and cool season legumes
- Highly syntenic with cool season legumes; moderately syntenic with soybean and other Phaseoleae
- Sequenced-based whole-genome comparison with other legume model, Lotus japonicus, reveals a remarkably small number of translocations and inversions.
- Target of large-scale systems biology programme, integrating transcriptome, proteome, and metabolome datasets
- Produces many of the same bioactive compounds found in food legumes, including isoflavonoids and triterpenes
- Though generally viewed as a model for legume genomics, M. truncatula is actually grown as a forage crop, especially in Australia

Genetic resources
- INRA Germplasm resource (Montpellier, FR)
- USDA Germplasm collection (USDA-ARS, Pullman, WA)
- Australian Germplasm collection (SARDI, Adelaide, AUS)
- Primary experimental genotype “Jemalong” accepted worldwide
- Multiple fast neutron mutant collections
- Agrobacterium rhizogenes / RNAi-based root gene knockouts underway
- Tnt1 transposon-based gene knockouts underway
- Large-scale gene-tilling project reduced to practice
- Multiple mapping populations, primarily RILs and F2/F3
- Multiple genome databases (eg – medicago.org/genome is a useful portal)

BAC libraries
- Jemalong – EcoRI, HindIII libraries, providing the basis for physical mapping and genome sequencing
• Approximately 155,000 BAC-end sequences

**Molecular markers**
• FPC-based physical map consisting of ~1300 contigs and covering >95% of genome
• Approximately 500 FPC contigs anchored to genetic map through BAC-based SSRs and CAPS markers
• SSRs and CAPS: ~500 AFLPs: ~300
• Numerous phenotypically defined genes, especially mutants in nodulation/nitrogen fixation pathway

**ESTs, experimentally defined genes, and genomic sequences**
• Genomic sequence: 102 Mbp non-redundant genome sequence finished or in progress (as of September 2004)
• Chloroplast genome sequence complete
• Nearly all repeat classes identified; repeat database underway
• ESTs: ~190,000, constituting ~37,000 unigenes
• 16K cDNA microarrays as well as long-oligo arrays available
• AFFYMETRIX GeneChip in progress
• Numerous genes in the *Rhizobium* and *Mycorrhiza* symbiosis pathway cloned and characterized

**Cytogenetics**
• High resolution pachytene analysis integrates all cytogenetically described chromosomes to genetic map and genome sequence
• Detailed FISH analysis locates gene-rich BAC clones to euchromatin and defines extent of pericentromeric regions

**Consortium or initiatives**
• International *Medicago truncatula* Steering Committee
• International *Medicago truncatula* Genome Sequencing Initiative