

Alfalfa (*Medicago sativa* L.)

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Genome features

- Genome size = ca. 800-900 Mbp. There's some confusion in the literature on this number, which is often given as ca. 1500 Mbp. Cultivated alfalfa is a tetraploid, so its gamete (1C) is actually diploid. Because all alfalfa chromosome sets are the same (i.e., alfalfa is an *autotetraploid*), the true size of its genome should be one-half the size of the tetraploid gamete (or the size of a diploid alfalfa gamete). Hence, the true genome size is the lower value.
- Basic chromosome number (x) = 8
- Small chromosomes of similar size

Special biological features of interest

- *M. sativa* is one of a complex of species (or subspecies) that exist as both diploids and tetrasomic tetraploids, and a full range of hybrids are extant at both ploidies.
- Adapted to wide range of latitudes
- Close relatives include *M. truncatula*, and various other annual and perennial species, ranging in ploidy from diploid to hexaploid, and in base chromosome number ($x = 7$ and $x = 8$)
- Produces a range of secondary metabolites, with a different profile than *M. truncatula*
- Severe inbreeding depression precludes development of inbred lines
- Clonal propagation via stem cuttings is possible
- Self-incompatibility mechanisms are present but poorly defined
- Pollinated by a diversity of bees
- Many tools and resources developed in *M. truncatula* (e.g., SSR, oligo arrays) work equally well with *M. sativa*

Genetic resources

- USDA Germplasm collections (USDA-ARS, Pullman, WA)
 - ca. 4000 accessions of *M. sativa*
 - well characterized for many traits, except ploidy (unfortunately)
- Large amounts of descriptive data on germplasm in GRIN
- Genomic databases lagging behind others

BAC libraries

- None

Molecular markers

- RFLPs : 200-300
- SSRs: ~500+ (most from *M. truncatula* EST sequencing)
- SNPs/STSs: few

- AFLPs: abundant
- few isoenzymes and classical genes
- Few mapping populations (primarily F₁, F₂ and BC₁) have been characterized; several are in existence and could be clonally propagated
- QTL studies on aluminum tolerance, cold tolerance, biomass production, cell wall composition, and other agronomic traits have been or are being conducted

ESTs, experimentally defined genes, and genomic sequences

- ESTs: ~10,000 (S. Laberge, St. Foy, Quebec)
- Macroarrays (S. Laberge)
- Arrays from *M. truncatula* work well with alfalfa

Cytogenetics

- Very little work on cytogenetics
- C-banding to distinguish among germplasms

Consortium or initiatives

- National Alfalfa Alliance—generally inactive relative to genomics