

Progress on the Tetraploid Alfalfa Genome Sequence

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Alfalfa (*Medicago sativa* L.) is an out-crossing perennial forage legume crop species with an estimated haploid genome size of ~830-860 Mbp. The Alfalfa Genome Sequencing Consortium resulted from an initiative to link international efforts to sequence the alfalfa genome and generate transcriptome sequences for SNP discovery. Current efforts include sequencing and assembly of tetraploid alfalfa using both Illumina sequencing and Whole Genome Profiling. We have generated 180x genome coverage with Illumina reads from three short-insert paired-end libraries and two long-insert paired-end libraries. The long-insert paired-end library will be used to join contigs into larger super-contigs or scaffolds to generate a draft genome sequence assembly of the euchromatic regions. The whole genome shotgun contigs will be integrated with the BAC-based physical map generated via Whole Genome Profiling for *de novo* sequence assembly of this tetraploid genome. Synteny to the *M. truncatula* genome sequence will be used, when possible, to assist assembly of alfalfa scaffolds into super-scaffolds and align transcriptome sequences to identify sequence variation among genotypes. Anchoring of scaffolds to chromosomes with genetic markers will be complemented by efforts aimed at sequence annotation and development of tools to manage and visualize the available sequences. These resources will be publicly available and should enable a better understanding of legume evolution, basic and applied research, and the development of molecular breeding strategies targeting key traits for alfalfa improvement.