

## **Alfalfa Breeder's Toolbox (ABT): An Integrated Web Portal for Molecular Breeding**

Maria Monteros, The Samuel Roberts Noble Foundation

Chunlin He, The Samuel Roberts Noble Foundation

Jaeyoung Choi, The Samuel Roberts Noble Foundation

Patrick Zhao, The Samuel Roberts Noble Foundation

Perdeep Mehta, The Samuel Roberts Noble Foundation

Michael Trammell, The Samuel Roberts Noble Foundation

Xinbin Dai, The Samuel Roberts Noble Foundation

Junil Chang, The Samuel Roberts Noble Foundation

Nick Krom, The Samuel Roberts Noble Foundation

Christy Motes, The Samuel Roberts Noble Foundation

The Alfalfa Breeder's Toolbox (ABT) is a web-based portal for the integration of basic and applied research aimed at enhancing the cultivar development process. The Toolbox will provide breeder-friendly resource to utilize genomic and genetic tools to enhance alfalfa breeding programs focused on traits of agronomic importance. The goals of this project are to develop the Alfalfa Breeder's Toolbox as a community resource to store, manage and query datasets for practical use in a way that is compatible with other legume databases. The website is based on Drupal and the Chado database schema implemented with the Tripal web interface. The *Medicago truncatula* genome and draft genome of cultivated alfalfa at the diploid level were used as the backbone to anchor alfalfa transcriptome sequences, gene annotation models, molecular markers, genetic linkage maps and quantitative trait loci (QTLs). The current alfalfa gene models include 98% of the conservative gene orthologs in the plant kingdom based on the Maker pipeline and BUSCO analysis. Query-based approaches to search, explore and sort alfalfa data to inform research and breeding activities are being developed. Functionalities for searching data include those based on genome position, gene annotation, gene expression, sequence, molecular marker, phenotype and germplasm (clone, population or cultivar). Features implemented in JBrowse display separate tracks for the genome sequence, gene models, and SNP markers. The ABT also integrates transcriptome sequences from multiple alfalfa genotypes and tissues of plants grown under different abiotic stress conditions. A core set of SNP markers distributed across the eight alfalfa chromosomes (based on *Mt4.0*) is available for download and these are integrated in the legume primer database (LPD). Phenotypic data collection from field trials of diverse alfalfa germplasm is ongoing and will also be integrated into the ABT. Ongoing and future efforts include integrating information from additional germplasm evaluations, molecular markers, and SNP haplotypes associated with agronomic traits. The long-term goal of the Alfalfa Breeder's Toolbox is to generate a resource for the community to store, query and visualize curated alfalfa datasets to facilitate the implementation of molecular breeding approaches that accelerate the genetic improvement of alfalfa.