***Medicago truncatula* Mutant Resources for Legume Genomics**

**Wen J**

Jiangqi.wen@okstate.edu

Institute for Agricultural Biosciences, Oklahoma State University, 3210 Sam Noble Parkway, Ardmore, Oklahoma 73401, USA

*Medicago truncatula* is widely used model legume species for genetics, genomics, and functional genomics studies. The genome sequencing of the ecotype Jemalong A17 has been completed and published in 2011. To better facilitate the characterization of gene functions in *M. truncatula* and other legume species, we spent more than 10 years and generated more than 21,700 *Tnt1* retrotransposon insertion lines, which encompass approximately 500,000 insertions in the genome of *M. truncatula*. The *Tnt1* mutant population is estimated to cover about 90% of genes in the *M. truncatula* genome. To make the maximal utilization of the mutant resources, we generated a searchable web-based database (<https://medicago-mutant.dasnr.okstate.edu/mutant>), which contains photos of all lines, phenotype description of lines exhibiting visible phenotypes during forward screening, and more than 400,000 *Tnt1*-flanking sequence tags (FSTs) from 21,000 lines. So far, we have distributed more than 17,000 *Tnt1* lines to scientists from 45 laboratories in 24 countries and more than 260 papers resulting from *Tnt1* mutants have been published. These publications cover many areas of plant biology, including plant physiology, nutrition, metabolism, growth and development, and plant-microbial and plant-environmental interactions.