

## Identification of Aluminum Tolerance in the Model Legume *Medicago truncatula*

Yanina Alarcón<sup>1</sup>, Christy M. Motes<sup>2</sup>, Kazuyo Ueda<sup>2</sup>, Wayne Parrott<sup>1</sup> and Maria J. Monteros<sup>1,2</sup>

<sup>1</sup> Institute of Plant Breeding, Genetics & Genomics, The University of Georgia, 111 Riverbend Road, Athens, GA 30602-1680

<sup>2</sup> The Samuel Roberts Noble Foundation, Forage Improvement Division, Ardmore, 2510 Sam Noble Parkway, OK 73401

[valarcon@uga.edu](mailto:valarcon@uga.edu); [mjmonteros@noble.org](mailto:mjmonteros@noble.org)

Acid soils worldwide limit agricultural productivity due to the effect of aluminum (Al) toxicity on plant growth. Al toxicity inhibits root growth and development thus reducing biomass yield and persistence of alfalfa (*Medicago sativa* L.), an important forage legume. *Medicago truncatula* is a close relative of alfalfa and the availability of an extensive genomics infrastructure can facilitate the discovery of Al tolerance mechanisms of value to other species. The objective of this research is to identify genomic regions relevant to acid and Al tolerance in *M. truncatula* using a recombinant inbred line (RIL) population. The population was generated from a cross between the *Medicago* core accessions Mt core 23 (acid and Al tolerant) and Mt core 35 (acid and Al sensitive) followed by multiple generations of single seed descent. Genotyping of the F<sub>4,5</sub> inbred lines was performed with the *Medicago* OPA that includes 1,536 single nucleotide polymorphism (SNP) and Illumina's GoldenGate Genotyping platform. Complementary approaches include genotyping of Al tolerance candidate genes using high resolution melting (HRM) analysis. Individuals from the RIL population and the parents were evaluated phenotypically using a whole plant assay with plant growth evaluated at pH 7, pH 4 and pH 4 +Al. Root growth was evaluated using WinRhizo software and data analyzed for statistical significance. Quantitative trait loci (QTLs) associated with Al tolerance were detected and the corresponding SNP markers identified. We will assess the value of multiple SNP markers identified to predict the performance of additional individuals when grown under acid and Al toxic conditions. Ultimately, understanding genes and mechanisms of aluminum tolerance in *Medicago* can be used to deploy breeding strategies in alfalfa aimed at increasing forage productivity in less than optimal growing conditions.