Genomics research in alfalfa. (C07-thro132419-Oral)

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Abstract:

Alfalfa (Medicago sativa L.) must persist for at least three years to be economically produced. Winter kill poses a major threat to persistence, but selection requires multi-year evaluations. Autumn dormancy induced by photoperiod and temperature aids winter survival, but it limits forage yield. We are working on a unified project linking physiology, biochemistry, molecular genetics, genetic mapping, and plant breeding to manipulate winter hardiness, autumn dormancy, and yield. We are isolating winter hardy related cDNA clones and evaluating their expression in diverse genotypes during autumn. These candidate genes are being mapped in diploid and tetraploid alfalfa populations segregating for winter survival. Concurrently, phenotyping of winter injury, fall forage regrowth, and root physiological and biochemical characteristics is being conducted to identify quantitative trait loci (QTL) for various components of winter hardiness. Synthesis of QTL positions for these traits with map locations and expression profiles is enabling us to develop a genetic framework for the winter hardiness genome landscape. Results have direct applicability to alfalfa breeding programs via marker-assisted selection and transformation.

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