McGRATH, J. MITCHELL*, USDA-ARS Sugarbeet and Bean Research, 494 PSSB, Michigan State University, East Lansing, MI 48824-1325. **Integration of genetic, physical, and expression mapping resources for gene discovery and beet improvement.**

ABSTRACT

Expressed Sequence Tags (ESTs) provide an entry into the analyses of 'gene space' at the molecular level. As expression markers, they indicate particular biochemical process that operate in various tissue and organ tissues, and can help discover developmental or response-to-environment pathways that might not have been predicted, for instance as seen in expression of seedling vigor. Most ESTs recovered may not show such an expression 'polymorphism', and these can be used to guide the development of genetic and physical maps that focus on the gene-containing regions of the yet-to-be sequenced sugarbeet genome. These gene-rich regions would be expected to harbor most genes involved in trait expression, and delimiting their genome context could provide for better markers and easier entry into map-based cloning projects. However, generally lower polymorphism levels within EST sequences expected from gene function conservation limits the utility of existing ESTs to serving as templates for re-sequencing to discover SNPs, and only a fraction of these will be expected to be segregating in a population of interest. Converting non-polymorphic markers into ones that can be mapped requires additional sequence information *cis*-linked to the EST, and BAC library pools can be deployed readily for this task. Once EST-containing BACs are identified, they become physical map markers, and the BAC clone can be searched for polymorphisms appropriate to the population of interest, through inspection of pre-existing BAC end sequences or *de novo* sequencing of the BAC clone. Using prior knowledge from model plant genomes such as Arabidopsis, genes demonstrated to operate in specific interesting biochemical pathways such as for stress tolerance can be rapidly isolated and characterized once a successful PCR primer pair has been designed.