

Report of the 31st General Meeting of the ASSBT
Genetics, Physiology and Biotech Forum
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In a departure from tradition, the Breeding and Genetics Forum was combined with the Physiology and Biotechnology Forum. The format was "Open", and all participants were encouraged to present ideas, questions, and concerns for general discussion. Participation was good, and topics ranging from gene discovery to mapping, to the integration of biotechnology with variety development were touched upon during discussions.

The session began with a presentation on the status and potential of Genomics for Sugarbeet Improvement. Most, if not all, participants were familiar with the basic concepts of genomics, with its foundation in genetics, physiology, and biochemistry. For instance, genes operate during growth and development and genes are inherited through transmission of chromosomes through generations. Structural genomics considers the organization of genes and other DNA sequences in chromosomes. Functional genomics considers the operation and expression of genes during development, including response to adverse conditions experienced during growth. A basic premise of genomics applied to plant breeding is that, in large part, individual or varietal performance is governed by gene expression. Differences in gene expression can be used to discover and select for better performance, similar to tagging traits with molecular markers via inheritance data, usually resulting in a linkage map. There are fundamental differences between marker inheritance and expression analyses of traits, through the goal of identifying and manipulating the genes of interest are the same. Thus, these approaches are complimentary, and represent the fundamental dichotomy between ontogeny (development of the individual) and phylogeny (conservation of the species).

One goal of genomics is to catalog each gene in an organism. This would be very helpful for sugarbeet, and it was noted that all plants derive from a common ancestor, and sugarbeet will have the majority of genes that are present in other plants, albeit with variation. Recently the entire nucleotide sequence of a plant was determined [The Arabidopsis Genome Initiative, *Nature* 408: 796-815 (2000); available at <http://www.nature.com>]. cursory inspection of the sequence shows that genes for many basal metabolic processes are conserved between all organisms, but that plants have many unique sets of genes that are not present in other multicellular lineages sequenced to date. The Arabidopsis genome sequence is a tremendous resource for sugarbeet because genes of similar sequence between the two species will likely have similar functions. Thus, a first goal of having a gene catalog for sugarbeet is roughly approximated by the gene catalog of Arabidopsis. Since the sequences between both species are not identical, it will be necessary to determine the sugarbeet sequence for those genes deemed

important by virtue of their proposed or proven involvement in sugarbeet agronomic performance.

The issue of which type of marker is "best" to use for marker assisted selection for improved agronomic performance. Many commercial outfits are using or developing SSR markers, with a plethora of marker systems such as RFLP, RAPD, AFLP, CAPS, and others in current or declining use. To date, each of these systems gives equivalent information, but all suffer from the fact that they are linked to a gene of interest but are not the gene of interest. It was asserted that the "best" marker is the gene, or genes, that control the trait. Genomics as a tool is, in essence, the ability to examine large numbers of sequences simultaneously. The challenge to sugarbeet is scale, where genomics technologies can be applied with good effect. Investment of the sugarbeet community in instrumentation and robotics, either alone or in combination with academic, industry, and government partners, is essential to meeting the economies of scale that genomics technologies can provide.

Sugarbeet breeding and germplasm enhancement continues to be high priority. Overwhelmingly, yield-limiting problems are the major concern, although each growing region has a unique set of disease complexes that require different strategies to manage. Genetic resistance is one of the most promising and environmentally friendly management options available. These problems are of immediate concern to the industry, yet progress towards genetic resistance goals is not fast enough to meet these immediate needs. Scientists should seek to improve efficiencies in the breeding process, through development and application of modern genetic tools (e.g. molecular markers, gene expression analyses, biotechnology), development and application of more efficient evaluation methods (e.g. laboratory screening of correlated responses, improved plot harvesting equipment, and field evaluation tools using image analyses). These newer activities can not supplant traditional field-based evaluation and selection activities. In summary, progress is being made on many fronts, with good cooperation among ARS and industry scientists. Future progress will continue to depend on good communication between scientists, customers, and stakeholders. Progress also depends on continued access to adequate resources to meet critical industry needs in a timely manner. The ARS appreciates the input of sugarbeet customers and stakeholders and recognizes their essential role in setting research priorities.