

NAEGELE, RACHEL P.\*<sup>1</sup>, EVAN LONG<sup>2</sup>, KEVIN DORN<sup>3</sup>, PIERGIORGIO STEVANATO<sup>4</sup> and IRWIN GOLDMAN<sup>5</sup>, <sup>1</sup>USDA-ARS, 1066 Bogue St., East Lansing, MI 48824, <sup>2</sup>USDA-ARS, 3793 North 3600 East, Kimberly, ID 83341, <sup>3</sup>USDA-ARS, 210 Centre Avenue, Ft. Collins, CO 80526, <sup>4</sup>University of Padova, Viale Universita 16 Legnaro, Italy, <sup>5</sup>University of Wisconsin, 1575 Linden Drive, Madison, WI 53706.

### **Development of a mid-density AgriSeq genotyping chip for sugar beet and its relatives.**

Cost-effective and standardized genotyping platforms are essential for the rapid improvement of crop species. For many major crop species, such as wheat, soybean, corn, potato, etc. these resources are available and have enabled community-wide testing and comparisons across germplasm. In sugar beet and related *Beta vulgaris* crops, these resources are unavailable as of yet, due to historically limited genomic resources and the high up-front costs associated with their development. Using the recently released EL10 genome, as well as whole genome data from *Beta* relatives and breeding lines, we have selected approximately 4,500 high frequency targets (SNP containing amplicons) for inclusion onto an amplicon-based SNP chip (AgriSeq chip). These targets include those associated with disease resistance to major pathogens such as *Rhizoctonia* and *Cercospora*, sugar beet quality such as sugar accumulation, as well as unassociated SNPs distributed across the genome. This resource provides a cost-effective and standardized option for genotyping large numbers of individuals and is suitable for diversity evaluation, SNP discovery, and genomic selection.