

MCGRATH, MITCH^{1*}, PAUL GALEWSKI² and ANDY FUNK², (¹USDA-ARS and ²Michigan State University, 1066 Bogue Street, 494 PSSB, Michigan State University, East Lansing, MI 48824). **A reference genome assembly for sugar beet germplasm EL10.**

A high-quality reference genome sequence is required for genetic context and clarity surrounding the myriad varietal and environmental effects on beet sugar production from sugar beet, from seed to seed. To this end, the self-fertile ARS germplasm release C869 (PI 628754) was inbred for five generations by single seed descent with selection for seedling vigor and agronomic performance, and one of these lineages to be released as EL10 was subject to a range of nucleotide sequencing and assembly technologies that included short-reads from the Michigan State University genomics facility (125 bp paired end reads, 149X coverage Illumina technology), *in vitro* crosslink mate-pair (150 bp Hi-Rise, 75X; Dovetail Genomics, Santa Cruz, CA), long-reads (80X; PacBio technology done at Los Alamos National Lab, Los Alamos, NM), a physical map (279 kb average single molecule, 1.2 million mapped fragments; BioNano Genomics, San Diego, CA), and *in vivo* crosslink mate-pair (80 bp proximity library, 40X; Phase Genomics, Seattle, WA). The 'best' result was obtained using PacBio reads >40 kb assembled with the Falcon Assembler (resulting in 938 scaffolds), upon which was superimposed a physical map using the BioNano two-enzyme hybrid assembly protocol (reducing the scaffold number to 86), and finally collapsing the resulting assembly to 9 scaffolds using the Proximity Guided Assembly approach. The resulting assembly contains nine scaffolds with a mean scaffold size of 63 million bases (Mb) and a total length of 566 Mb, similar to the RefBeet genome size. Genome size estimates of EL10 were refined using fluorescently stained nuclei from 22 progeny and determined to be 716 Mb (\pm 28 Mb).