

THE 'C869' SUGAR BEET GENOME: A DRAFT ASSEMBLY

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Sugar beet 'C869' is a diploid, self-fertile, public germplasm release used extensively as the seed parent of recombinant inbred lines designed to genetically dissect agronomic, disease, domestication, and other traits. From the original release, three additional generations of inbreeding were done, and 68 progeny from seven F₃ families were screened with a panel of 61 SNP markers to determine heterozygosity (which ranged from 0 to 15.5%). Accession EL-A025943-17 was chosen for genomic sequencing due to no detected heterozygosity as well as its overall vigor and trueness-to-type sugar beet appearance. Sequencing was performed on the Illumina HiSeq 2000 platform with 100 bp paired-end sequences, for which five lanes of genome sequence data were collected, representing 820,126,310 pairs of reads. Reads were cleaned and quality trimmed, and the resulting ~150X coverage of the 750 Mb sugar beet genome was assembled *de novo* using ABySS 1.2.4 with a Kmer value of 61. More than 3.1 million contigs were output (N50 = 2,845 bp; max = 75,288, min = 61), with 91,343 contigs >1 kb in size (N50 = 7,778; max = 75,288, min = 1000). The latter contigs summed to >446 Mb, or ~60%, coverage of the beet genome. Since the sugar beet genome is predicted to have ~60% highly repetitive DNA elements (~450 Mb, which current algorithms do not assemble well). In addition, leaf and petiole transcriptome data from EL-A025943-17 (360,697,168 read pairs) were assembled *de novo* using Trinity to complement the genome assembly. We conclude the current genome assembly contains the majority of the genetic information encoded and organized in the 'C869' sugar beet genome.