W875: Sugar Beet BeetMap-3, and Steps to Improve the Genome Assembly and Genome Sequence Annotation

ABSTRACT

Saturday, January 09, 2016
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The sugar beet genome sequence was brought to publication quality within AnnoBeet and was finally published in January 2014. Since then, the AnnoBeet consortium has focused on further improvements of the genome assembly and its annotation on the one hand, and on steps towards using genomics resources for answering biological questions on the other hand.

By using a combination of existing resources for SNP calling, a set of new SNP markers was developed. The data used were Sanger EST sequences from KWS2320, representing P1 of our main mapping population, and a 454 cDNA data set from P2 of that population. For a subset of the about 1,600 loci with good SNP predictions, markers were developed and mapped. In addition, terminal chromosomal markers from Paesold et al. (2012) were integrated. Finally, the sugar beet genetic map was extended by 307 markers, resulting in BeetMap-3 comprising 1,141.4 cM.

Also, we improved the assignment of unanchored contigs to pseudochromosomes by 'genotyping by sequencing' using low coverage NGS data from F2 plants of the mapping population, and in addition offspring of an additional mapping population with two parents unrelated to P1 and P2. As a result, the assembly was improved and the number of unassigned or unanchored contigs and scaffolds was reduced. Additional measures to further increase the quality of the assembly are under way, including the evaluation of PacBio reads as well as Moleculo data for joining contigs.

Based on SMRT (PacBio) cDNA sequencing reads, deep Illumina RNA-seq data and manually annotated gene models, an improved gene set for sugar beet was created using the AUGUSTUS software. The new BeetSet-2 covers 26,923 protein coding genes that are predicted with high reliability and are supported by evidence. In addition, there are about 13,000 genes that are predicted with the improved AUGUSTUS parameters specific for sugar beet but lack experimental evidence.

Finally, we are using the genomics data to investigate specific gene families and try to validate the functional annotation of genes that has been assigned *in silico*. A total of 70 *R2R3-MYB* genes as well as genes encoding three other classes of MYB proteins containing multiple MYB repeats were identified and characterized with respect to amino acid sequence, structure and chromosomal organization. Functional classification of the gene family led to the identification of a sugar beet-specific clade with an atypical amino acid composition in the R3 domain that were predicted to encode betalain regulators. The functional classification was further verified by experimental confirmation of the prediction that the R2R3-MYB gene *Bv_iogq* encodes a flavonol regulator which was designated BvMYB12.

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