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WHOLE GENOME SEQUENCING OF SUGAR BEET AND SNP DEVELOPMENT

Séquençage du génome entier de la betterave sucrière et développement d'un polymorphisme nucléotidique simple (SNP) / Vollständige Genomsequenzierung von Zuckerrüben und SNP-Entwicklung

ABSTRACT

The whole genome of the sugar beet (*Beta vulgaris* subsp. *vulgaris*) doubled haploid line KDH13 has been sequenced via genome shotgun sequencing (WGS) of paired end (PE) and a mate-pair (MP) genomic libraries using Illumina HiSeq2000 platform. A total of 82.9Mb of raw sequence data was obtained of which 38.76 Mb from PE and 44.17Mb from MP with 35.56 and 33.41 quality score, respectively. The WGS achieved an estimated coverage of 63 fold of the genome. The de novo draft assembly named BvvSeq-1 was constructed from 426.7 Mb total sequence length made of 260,142 scaffolds with an N50 of 5.2Kb and a total of 269,990 contigs of 4.6Kb N50. This assembly http://www.ncbi.nlm.nih.gov/bioproject/PRJNA176558, is the first released public draft and used a public breeding line (PI663862) that was released by ARS-USDA as a genetic stock resistant to beet curly top. The first direct utilization of BvvSeq-1 was its alignment to RefBeet_0.9 to identify single nucleotides polymorphisms as the former is resistant and the later is susceptible to curly top disease. Approximately 70% of the BvvSeq-1was mapped to RefBeet_0.9. One thousand and six hundreds single nucleotide polymorphisms (SNP) were identified between KDH13 and KWS2320 which can be accessed here: http://www.ars.usda.gov/sp2UserFiles/person/40864/SNP-NWISRL-USDA-Kimberly.xlsx. Selected 384 SNP were screened in a 96X96 SNPtype™ assay chips to identify polymorphisms between parental lines among them parents that were used to produce a curly top mapping population.