Evolutionary dynamics of the repeat landscape in sugar beet and its wild relatives

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ABSTRACT

Sugar beet (*Beta vulgaris ssp. vulgaris*) is a young crop plant that originated from wild sea beet (*Beta vulgaris ssp. maritima*), a coastal plant native to Western and Southern Europe. It has been shown that transposons have influence onto the genome structure and gene functionality of beets. Of the many different repeats contained in a genome, only a small subset is intact and fully functional. However, this small portion may have a huge impact on the genome and as consequence on the phenotype as well. By creating alternative splicing patterns, introduction of novel promoters, change of gene regulation or simply by inactivation of gene function. Thus, the genome is constantly in motion: Transposons get inserted into new positions in the genome; thereafter, selection and mutational processes act upon them. Repeats disrupting crucial functions will disappear quickly, while other elements which are neutral or even beneficial will stay on. By comparing different genomic sequence data of domesticated beets and their wild relatives, we assess the mutagenic events that took place and explore the role that transposons have played in the evolution of the beet genome. Advances in the repeat-related knowledge of the beet genome may discover new insights about recent transposon evolution and will provide a foundation for further improvements of beet as a crop plant.

OBJECTIVES

Diverse genomic sequencing data of sugar beet and its wild relatives, will be used to assess the mutagenic events that took place in the beet genome in the recent evolutionary past. One main goal is to explore the role that transposons (TEs) have played in the evolution and formation of the beet genome. One key part of this thesis is the creation of repeat libraries, which are further used for repeat annotation of the genomes (Figure A). "RepeatModeler" and "RepeatMasker" are well known programs and used for this task [1].
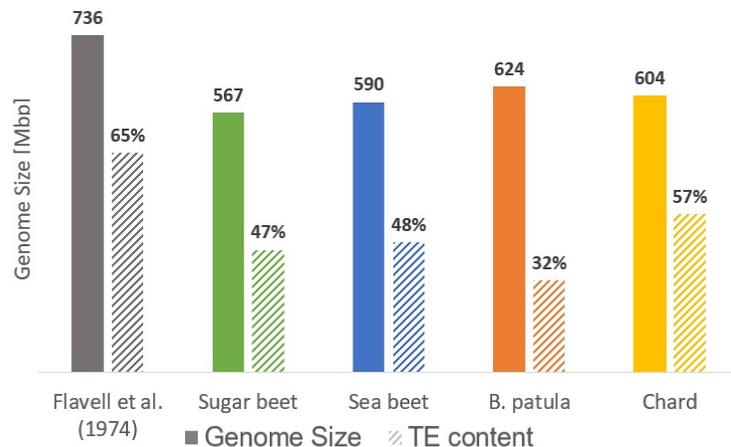
Figure A. Repeat annotation of different beet assemblies. The bold color shows the genome size of the assemblies in Mbp. The striped color shows the TE content of the assemblies. In grey is the experimentally estimated size of the sugar beet genome, as well as the estimated repetitive content after Flavell et al. (1974)[2]. Rest of the data concerning repetitive content was created using "RepeadModeler" and "RepeatMasker" [1,3,4,5].

RESEARCH TASKS

In this thesis various sequencing data from wild and cultivated beets will be used to clarify the role that TEs have played in the evolution of the beet genome by:

→ **De novo genome assembly and annotation of genes and repetitive sequences**
→ **Genome-wide identification of sugar beet genes with transposon insertions**
→ **Phylogenetic analysis**
→ **Transcriptome analysis**

Goal of this project will be to get a better understanding how TEs influence the structure of the beet genome, and how they influence the function of encoded genes. Advances in the repeat-related knowledge of the beet genome may discover new insights about recent TE evolution and will provide a foundation for further improvements of beet as a crop plant.

INTRODUCTION

This thesis is a bioinformatics project. All analysis is done on the high-performance computing cluster of the Institute of Computational Biology. Previously generated beet assemblies as well as Illumina paired-end sequencing data of ~580 domesticated beet and wild accessions are focus of this work.

Sugar beet and relatives
The sugar beet (*Beta vulgaris ssp. vulgaris*) genome was the first species of the order *Caryophyllales* ever sequenced [3]. Followed by two closely related wild beet genomes: The genome assemblies of *B. patula* and sea beet (*B. vulgaris* ssp. *maritima)* [4]. As well as the genome of chard [5], a beet that is cultivated for its leaves, rather than its root.

Transposon influence on the sugar beet genome
TEs as a class of repetitive elements can have huge influence on the genome and as consequence on the phenotype as well. By creating alternative splicing patterns, introduction of novel promoters, change of gene regulation or simply by inactivation of gene function [6]. There have been two examples described where the insertion of TEs affected the gene function in beets:

→ **Loss-of-function mutation (Figure B):** Disruption of the *Rz2* gene by TE insertion causes rhizomania susceptibility, whereas the intact gene provides rhizomania resistance [7].

→ **Gene expression modulation:** The promotor region of the flowering regulator gene *BTC*1 contains a TE insertion in domesticated beets, influencing its expression changing from an annual reproduction cycle to and biennial [8].
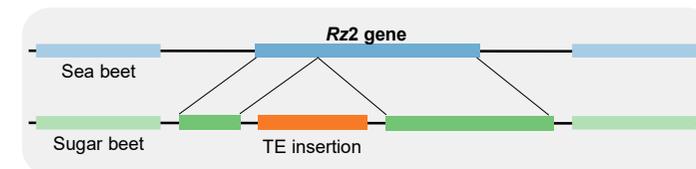
Figure B. Gene disruption (green) found in sugar beet, caused by a transposon insertion (orange), which disrupts gene functionality. Sea beet (blue) *Rz2* gene lacks these insertions, with results in a still functional gene.

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