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**Original language: English**

## **INSERTION SITES OF TRANSGENES IN THE SUGAR BEET GENOME**

### **ABSTRACT**

The genetic modification of sugar beet has been relatively straightforward for several decades, although different methodologies generate plants with different numbers of insertions, expression levels, and possibly different distributions within the beet genome. The availability of a genome sequence makes an analysis of these inserts possible – an understanding may allow us to tailor our methods appropriately, and to choose the events most likely to provide the desired phenotype. We have begun the detailed characterisation of the genomic sites of insertion for transgenes derived using different technologies in sugar beet (Agrobacterium, and by direct gene transfer of different fragment types). We have used PCR primers specific to the inserted element(s) to extend into the adjacent beet genomic DNA; sequencing of these amplicons reveals the sequence of the flanking region. This flanking sequence can then be used to search the sequence of the genomic region in the SESVanderHave whole-genome assembly. A bioinformatic analysis of these “landing-sites” is capable of revealing the putative open reading frames and associated elements in the genome sequence, and the correspondence of these with known transcripts. The results will be presented for transformants which show different levels of expression for the transgene of interest, and conclusions drawn about the influence of the landing site on the desirability of the event.

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## **SITES D'INSERTION DE TRANSGENES DANS LE GENOME DE BETTERAVE SUCRIERE**

### **RÉSUMÉ**

French translation not available.

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## **INSERTIONSORTE VON TRANSGENEN IM ZUCKERRÜBENGENOM**

### **KURZFASSUNG**

German translation not available.