

Unintended genetic changes and effects in NGT plants that require risk assessment

Franziska Koller

info@fachstelle-gentechnik-umwelt.de

unintended genetic changes

findings in regard to unintended genetic changes that can be caused by the application of NGTs*

*Koller, F. And Cieslak, M. (2023) A perspective from the EU: Unintended genetic changes in plants caused by NGT – their relevance for a comprehensive molecular characterisation and risk assessment. Front. Bioeng. Biotechnol. 11:1276226. doi: 10.3389/fbioe.2023.1276226

NGTs unintended genetic changes by NGTs

five categories of unintended genetic changes resulting from NGT processes based on scientific publications





- \rightarrow non-targeted integration of transgenic DNA
- \rightarrow possible effects on epigenetic and disruption of genes
- \rightarrow remains of transgenic DNA after segregation breeding



- \rightarrow unintended integration of parts of vector construct
- \rightarrow possible effects on epigenetic and disruption of genes
- \rightarrow partly difficult to detect

unintended insertion of transgenes with NGT processes





- \rightarrow off-target DNA cleavage of similar DNA sequences
- \rightarrow unintended genetic changes after DNA cleavage: large insertions, duplications
- \rightarrow partly difficult to detect
- \rightarrow occurance at genomic sites that differ compared to conventional breeding

Liu et al (2023)



- \rightarrow rearrangements after DSB
- \rightarrow loss of DNA
- \rightarrow propability of chromothripsis at specific genomic sites

Samach et al (2023)



- \rightarrow formation of new mRNA caused by (un)intended genetic change
- \rightarrow unpredictable function of new mRNA and new proteins

NGTs *unintended genetic changes by NGTs*

 \rightarrow can affect small and large sections of chromosomes and result in unintended gene products

→ the **sites of the mutations**, their **genomic context** and their **frequency (in regard to specific sites)** can differ when compared to conventionally bred plants

 \rightarrow the biological effects (phenotypes) can therefore be different and may cause specific risks for health and the environment

consequences for a comprehensive molecular characterisation and risk assessment:

 \rightarrow combination of **multiple approaches** to comprehensively identify and assess the unintended changes throughout the genome

 \rightarrow additional methods (**Omics**) to identify associated unintended biological effects



Thank you for your attention!

Liu et al (2023) Hidden prevalence of deletion-inversion bi-alleles in CRISPR-mediated deletions of tandemly arrayed genes in plants. Nat Commun 14, 6787 *Samach et al (2023)* CRISPR/Cas9-induced DNA breaks trigger crossover, chromosomal loss, and chromothripsis-like rearrangements. The Plant Cell, 35/11

Further references can be found in

Koller & Cieslak (2023) A perspective from the EU: Unintended genetic changes in plants caused by NGT – their relevance for a comprehensive molecular characterisation and risk assessment. Front. Bioeng. Biotechnol. 11:1276226.