Development of a GMO screening database with combinatory algorithms and its application in official food and feed control

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Introduction
The development and cultivation of genetically modified crops is increasing globally [1]. Food and feed imports especially from outside the EU will subsequently require more effort from the competent authorities in monitoring compliance with legal requirements for labelling.

Our aim was the development of a combinatory screening system to support an efficient and comprehensive analysis in official food, feed and seed control in Bavaria, Germany. The project is funded by the Bavarian State Ministry of the Environment and Public Health.

Different genetic elements (e.g. promoters, terminators, structural genes) are artificially introduced into plants to establish new genetic modifications (Fig. 1). The introduced elements may vary between different GMO lines, depending on the intended traits (e.g. resistance to herbicides or insects, changes in metabolite patterns, etc.).

Screening for such inserted elements with (real-time) PCR is a common first step to analyse samples for the presence of any genetical modification. From the pattern of detectable and not detectable elements found in analysed sample material, valuable conclusions about the identity of putative present GMO line(s) can be drawn (Fig. 2).

Matrix of genetic elements

Information about selected genetic elements and constructs from the literature [for example 2], applications for authorisation [for example 3] and other (web) sources [for example 4] were systematically analysed, and subsequently integrated in a matrix format.

Special care was taken to additionally record the sources of the information, thus facilitating evaluation of screening results, and tracing of possible errors in the matrix.

Up to now (03/2011), the matrix consists of 310 GMO events from 29 plant species.

Combinatory algorithms

Data from the matrix can be accessed with several implemented algorithms, for example to interpret the outcome of a screening for genetic elements/constructs, thus narrowing down the candidates for subsequent identification reactions (Fig. 3).

Further functions include a search for gaps in the matrix, convenient editing of the data, or printer-friendly presentation of results.

Matrix and algorithms are combined in a MS Access database.

References

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