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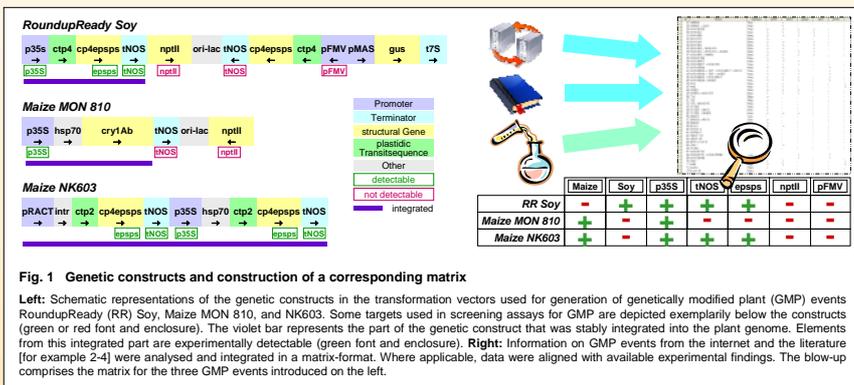## its application in official food and feed control

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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).

Fig. 1 Genetic constructs and construction of a corresponding matrix

Left: Schematic representations of the genetic constructs in the transformation vectors used for generation of genetically modified plant (GMP) events RoundupReady (RR) Soy, Maize MON 810, and NK603. Some targets used in screening assays for GMP are depicted exemplarily below the constructs (green or red font and enclosure). The violet bar represents the part of the genetic construct that was stably integrated into the plant genome. Elements from this integrated part are experimentally detectable (green font and enclosure). **Right:** Information on GMP events from the internet and the literature [for example 2-4] were analysed and integrated in a matrix-format. Where applicable, data were aligned with available experimental findings. The blow-up comprises the matrix for the three GMP events introduced on the left.
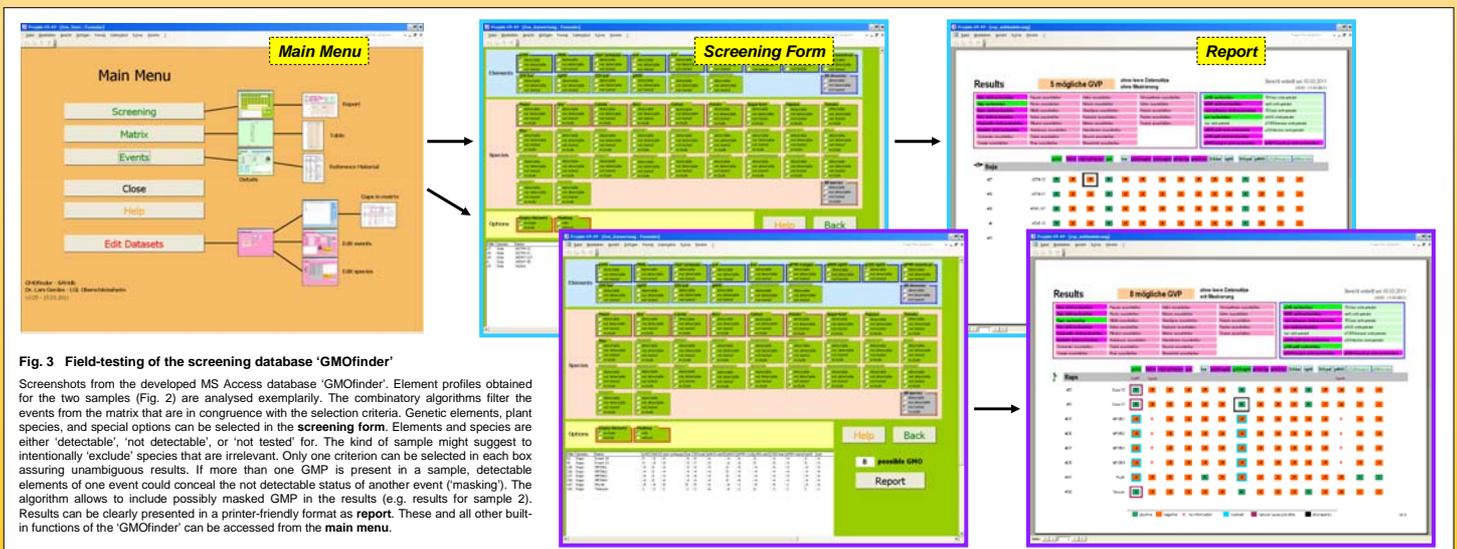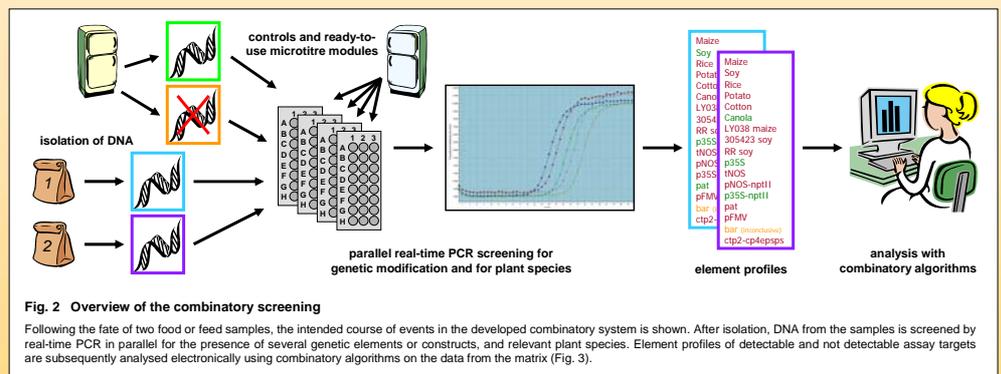
Matrix of genetic elements

- 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.

Fig. 2 Overview of the combinatory screening

Following the fate of two food or feed samples, the intended course of events in the developed combinatory system is shown. After isolation, DNA from the samples is screened by real-time PCR in parallel for the presence of several genetic elements or constructs, and relevant plant species. Element profiles of detectable and not detectable assay targets are subsequently analysed electronically using combinatory algorithms on the data from the matrix (Fig. 3).

Fig. 3 Field-testing of the screening database 'GMOfinder'

Screenshots from the developed MS Access database 'GMOfinder'. Element profiles obtained for the two samples (Fig. 2) are analysed exemplarily. The combinatory algorithms filter the events from the matrix that are in congruence with the selection criteria. Genetic elements, plant species, and special options can be selected in the **screening form**. Elements and species are either 'detectable', 'not detectable', or 'not tested' for. The kind of sample might suggest to intentionally 'exclude' species that are irrelevant. Only one criterion can be selected in each box assuring unambiguous results. If more than one GMP is present in a sample, detectable elements of one event could conceal the not detectable status of another event ('masking'). The algorithm allows to include possibly masked GMP in the results (e.g. results for sample 2). Results can be clearly presented in a printer-friendly format as **report**. These and all other built-in functions of the 'GMOfinder' can be accessed from the **main menu**.

References

[1] C. James, Global Status of Commercialized Biotech/GM Crops: 2009, *ISAAA Brief* **41** (2010).

[2] H.-U. Waiblinger, B. Boernsen und K. Pietsch, Screening-Tabelle für den Nachweis zugelassener und nicht zugelassener gentechnisch veränderter Pflanzen, *Deutsche Lebensmittel-Rundschau* **104** (6), 261-264 (2008).

[3] Japanese Ministry of the Environment. Japan Biosafety Clearing House. 2010 http://www.bch.biodic.go.jp/english/e_index.html.

[4] AGBIOS and CERA (Center for Environmental Risk Assessment). GM Crop Database. 2010 http://cera-gmc.org/index.php?action=gm_crop_database.

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