Ahmed, F.E. (ed.): **Testing of Genetically Modified Organisms in Food.** - The Haworth Press, New York 2004. 324 pp. Paperback USD 49.95. ISBN 1-56022-273-3.

This compendium describing different aspects of detection of genetically modified organisms in agricultural products food is not is not a product of scientific meeting, but it was written by different authors to give comprehensive view on the topic. All the authors but one are from Europe where the attitude to GMO is much more sensitive than elsewhere in the world. General public in Europe has objections to the use of raw materials for the production of food and feed, although it has no rational background. Nevertheless, sophisticated very sensitive qualitative and quantitative methods based on DNA and proteins have been developed. The basis tool are DNA-based methods (quantitative PCR, microarrays, microchips) but also other methods are used (ELISA, near-infrared spectroscopy, metabolic profilling, proteomocs). The generally used, irreplacible gtroup of methods is based on quantitative PCR. Assessment of risks and safety issues is also given.

The book consists of 10 chapters describing different aspects of problematics and all of them are treated with maximum professional skill. The real probability of individual risks connected with GMO is considered with great outlook. Great care is given to the sampling of material for quantitative analysis, which might be the source of errors. It gives the rules of sampling and sample size, which come out from statistical calculations to reach the appropriate limits of quantitative detection (which differ, in different countries, from 5 to 1 %). The principles and limits of the methods of quantitative PCR are considered in detail. They could be of interest not only for laboratory staff of laboratories detecting GMO, but to broad range of readers who are more deeply interested in the problematics. As comes from the statistics, to get sufficient probability of detection 0.1 % admixture of transgenic material, it is necessary to sample almost 1 kg of maize seeds in simplified supposition that the transgenic seeds are distributed uniformely in the lot. Actually the lots are stratified and it further complicates the sampling and sample size. As still more and more types of transgenic crops will be released in near future, their determination will be more and more complicated and expensive.

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