RIKILT
WAGENINGEN UR

The use of a non-targeted LC-ToF-MS multi-residue method for detection of growth promotors in meat and hair

M.H. Blokland[1]*, P.W. Zoontjes[1], J.A. Zweigenbaum[2], and S.S. Sterk[1]

Introduction

Data evaluation is in general targeted towards a predefined list. In this study a more sophisticated non-targeted data evaluation technique was used. This non-targeted data evaluation of specific LC-ToF-MS data sets in combination with statistical evaluation makes it possible to mark differences between data sets. These differences, e.g. additional peaks, enhanced or reduced peaks can be used to discriminate between samples obtained from either a treated and untreated animal.

Experimental

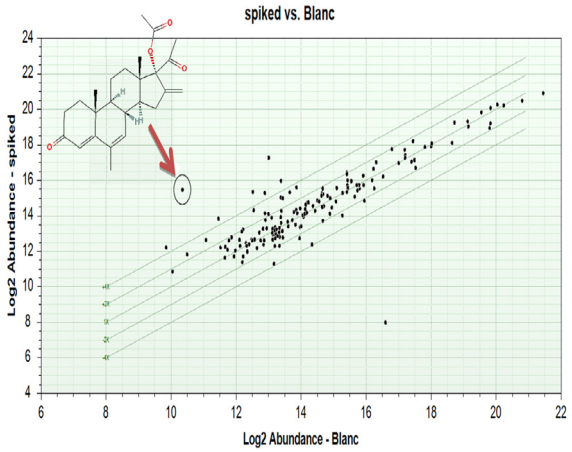

Figure 1. Melengestrol-acetate is identified in the group of spiked meat samples.

- In this study the following matrix/compound combinations were used: pro-hormones, gestagens and ß-agonists in meat, and ß-agonists in hair.
- For each matrix/compound combination 20 different samples were spiked, 2 ng g^{-1} to meat and 15 ng g^{-1} to hair, with the compounds of interest (see figure 1) and 20 blank samples.
- Clean-up methods originally developed for triple quads were used.
- Samples were analysed by a standardised LC-ToF-MS method.
- The full spectra data (200-500 amu) of each sample collected were stripped of (chemical) noise.
- The combined information of the blank and spiked samples was systematically evaluated and the differences were plotted. Figure 1 presents the abundances (log2) of the peaks detected in the blank samples versus the abundances (log2) of the peaks detected in the spiked samples. When a peak is beyond the 4-fold margin (demonstrated by the lines in the data plot) this peak is marked as nearly unique for that group. In this example the peak representing the spike melengestrol acetate to meat is outside the 4 fold margins and is specific for the group of spiked samples of meat

Results

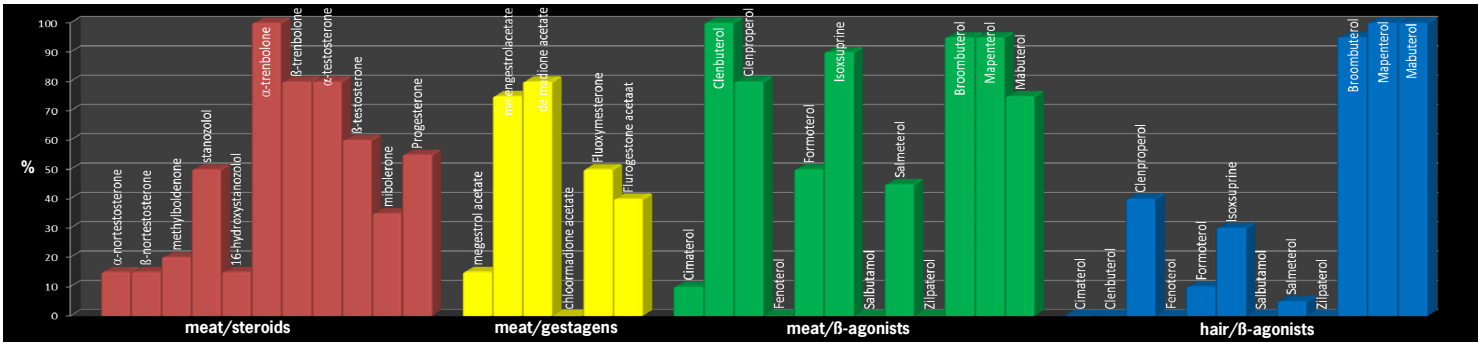

Figure 2. Percentage of spiked compounds identified in the different compound/matrix combinations using the described approach.

Conclusion

- The non-targeted approach is applicable to a broad range of compounds and matrices.
- Although the LC-ToF-MS shows adequate sensitivity for all compound classes, it is difficult to isolate all compounds resulting in a low percentage of compounds detected in the spiked groups.
- The big advantages of non-targeted software that it is possible in the near future to detect "unknowns".
- From the – statistically significant – differences, markers can be selected which can be used for monitoring purposes.
- The non-targeted (generic) approach, however, is still in its infancy, certainly at residue levels. However, using automated non-targeted data processing software, it was demonstrated that the compounds can be detected in the samples.

[1] **RIKILT – Institute of Food Safety**
P.O. Box 230, NL-6700 AE
Wageningen, The Netherlands
Phone: +31 317 48 02 56
Internet: www.rikilt.wur.nl
* Corresponding author: Marco.Blokland@wur.nl

[2] **Agilent Technologies**
Wilmington, Delaware
USA Food Safety
Internet: www.agilent.com