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Metabolic signature of the dietary exposure of farm animals to contaminants: an example of the application of metabolomics to food science

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Les champs avec une * sont obligatoires.

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Résumé* (9200 caractères maximum : comprend tous les caractères frappés, blancs et espaces compris, aucun tableau ni aucune figure ne sont insérables dans la totalité du corps de la saisie) :

As metabolism end-products, volatile organic compound (VOC) composition of tissues and fluids may vary according to the physiological status of the animal which in turn is conditioned by the conditions of production. The aim of this work was to study in poultry the feasibility of the detection of previous animal exposure to pollutants, particularly through feeding. A target organ tissue was analysed to

identify VOCs which are generally produced by animal metabolism in response to pollutant exposure and thus constitute a potential metabolomic signature of this exposure.

To test this hypothesis, 6 groups of 10 chickens fed a similar feed either non contaminated or contaminated with one of five pollutants commonly found in poultry production chains (PCDD/Fs, PCBs, PBDEs, PAHs and coccidiostats). The liver of each animal was analysed by SPME-GC-MS for VOCs and by HRMS and LC-MS-MS for pollutants. The results show that VOC metabolic signatures could discriminate the non contaminated chickens from the chickens contaminated with PBDEs, PAHs or coccidiostats. The contaminated and not contaminated chickens could not be discriminated as efficiently for PCDD/Fs and PCBs. These results are discussed in view of the actual levels of the pollutants found in the liver by the reference analytical techniques. In the context of the regulatory control of the meat product safety, the metabolomic signatures obtained by VOC analysis could be used to screen and to select the most relevant pollutants to be quantified by reference analytical methods.

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