Back-tracing an emerging environmental toxicant (hexabromocyclododecane, HBCD) in animal-derived food chain based on foodomics

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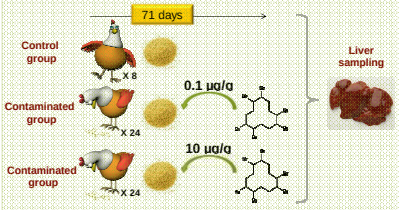
CONTEXT and OBJECTIVES

Human activity is the main cause of the emission of pollutants which may accumulate in environmental compartments, then in livestock tissues and subsequently in the food chain. These chemicals are particularly monitored in food products and include brominated flame retardants. Among brominated flame retardants, hexabromocyclododecane (HBCD) is a chemical of potential concern. HBCD is an emerging toxic micropollutant found in the environment and in animal tissues. Direct HBCD quantification is extremely difficult because it undergoes a rapid metabolism in biota. Based on a previous report showing the relevance of volatile compound metabolic signature in chicken liver for back-tracing a dietary exposure to rapidly metabolized xenobiotics[1], the present study investigates the relevance of this approach to evidence a previous HBCD contamination in laying hens.

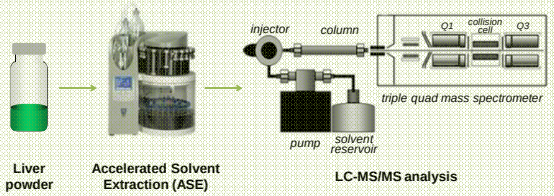
MATERIAL and METHODS

In vivo experimental approach

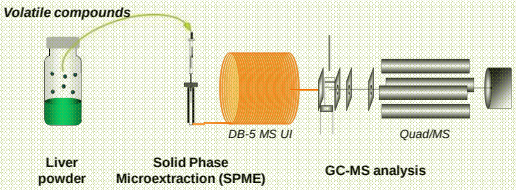


Analytical methods

❖HBCD residue quantification

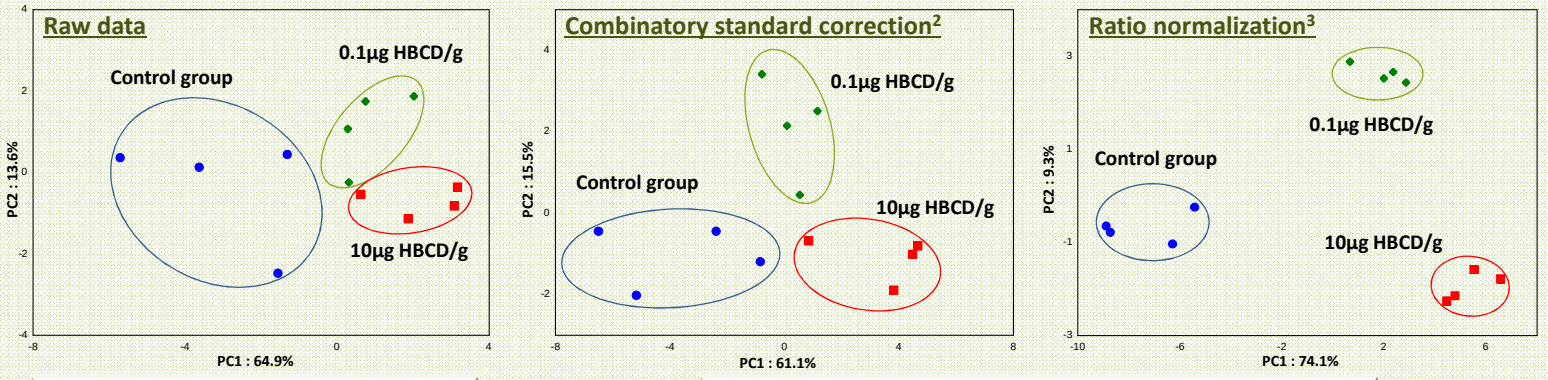


❖Volatile metabolic signature



RESULTS

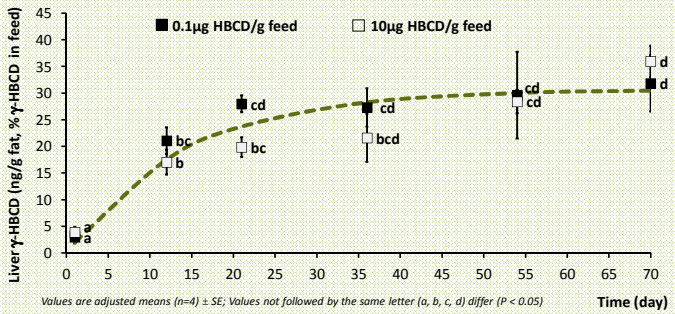
1-Relevance of volatile metabolic signature in liver for back-tracing chicken exposure to different doses of HBCD



Separation of the samples according to contamination level of animals

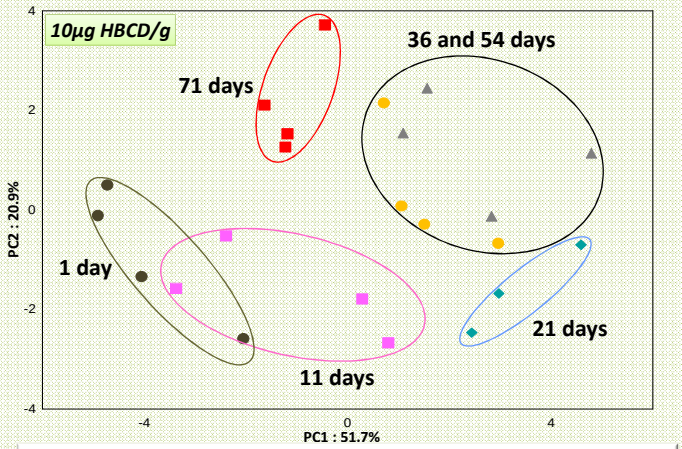
Improvement of the group separation by using normalization procedures on the signatures

2-Evolution of both HBCD concentration and volatile metabolic signature in the liver of laying hens during breeding



No change in liver HBCD concentration according to contamination level

No change in liver HBCD concentration after 21 days of contamination



Evolution of the volatile metabolic signature during breeding

CONCLUSIONS

After data normalization, volatile compound signature enabled the differentiation of samples according to HBCD contamination level of animals. For a same contamination level, a discrimination of the samples according to exposure duration was achieved. To validate the metabolomic approach and to enable its further use, new investigations are in progress in order to determine the biochemical origin of these volatile biomarkers.

REFERENCES

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