MINERAL OIL HYDROCARBONS IN UNPROCESSED MEAT: A STUDY OF SATURATED AND AROMATIC SUBCLASSES USING AN LC/GC×GC-FID/MS PLATFORM

Adv Sep Sci 2025

P. Albendea, G. Purcaro
University of Liege, Gembloux Agro-Bio Tech, Belgium.

LIÈGE université Gembloux Agro-Bio Tech

ACESSS

Background: Mineral oil hydrocarbons (MOH) are a complex mixture of liposoluble food contaminants of petrogenic origin. They are usually divided according to their molecular structure in saturated (MOSH) and aromatic (MOAH) and the analytical technique considered as routine is LC-GC-FID. However, the human ADME (Absorption, Distribution, Metabolism, and Excretion) of different compounds inside MOSH and MOAH can differ depending on their molecular structure [1]. This has increased the interest on the use of more advanced techniques, notably LC-GC×GC-FID for a deeper characterization of the type of MOSH and MOAH present in food matrices [2].

Aim: To evaluate MOH contamination in unprocessed meat, providing a detailed characterization of MOSH (i.e., open and cyclic alkanes) and MOAH subclasses, as requested by the EFSA [1]

Experimental design:

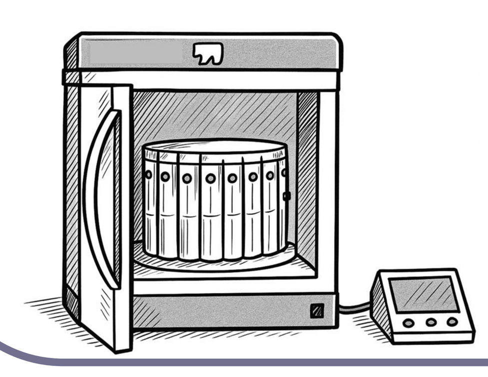
1 Optimization of sample preparation

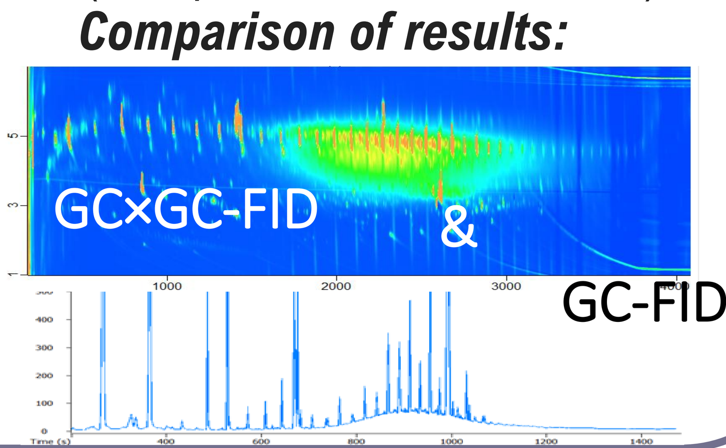
Comparison between microwave-assisted saponification and extraction (MASE) [3] & [4]

Internal standards (ISs) distribution
(n =3 per type of meat)

Recovery
(n =4 per level of MOH studied)

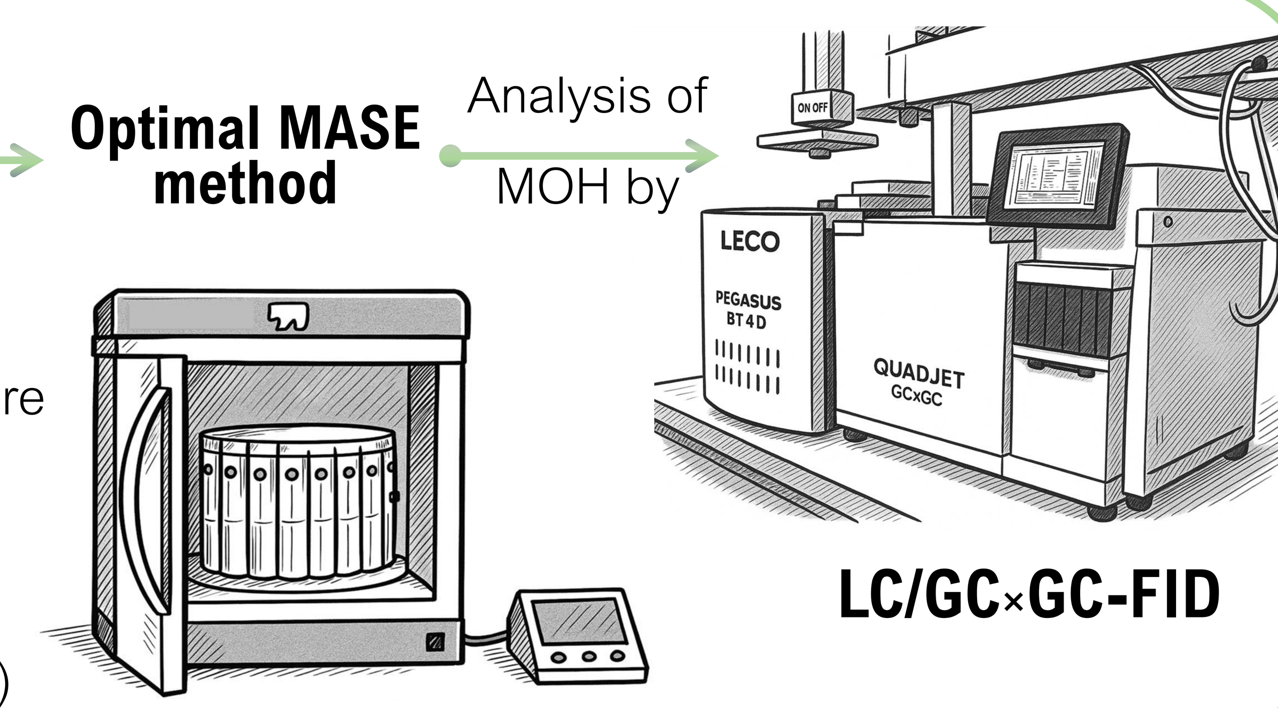
Comparison of results:





2 Analysis of MOH in meat

Subjected to → **Optimal MASE method** → Analysis of MOH by



LC/GC×GC-FID

Homogenized samples

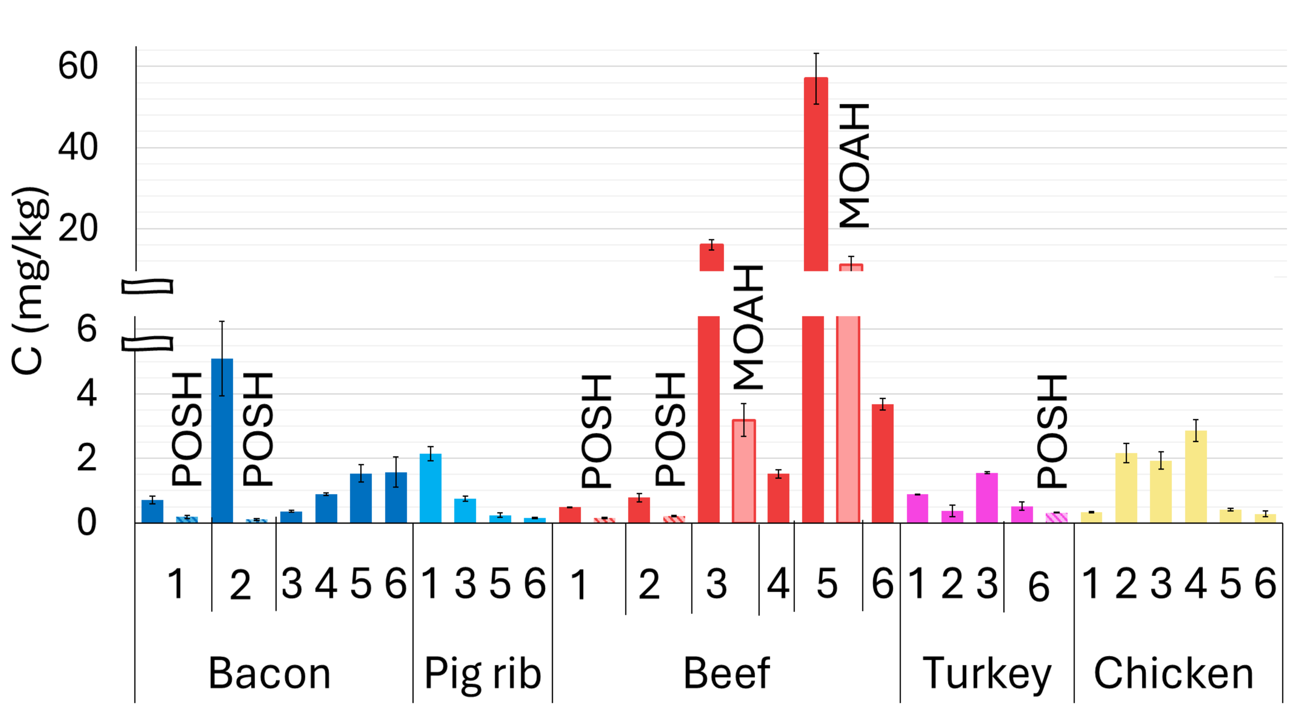
- 5 types of unprocessed meat were considered
- 30 samples (6 per each type) purchased from local supermarkets (Walonie, Belgium)

Results and discussion:

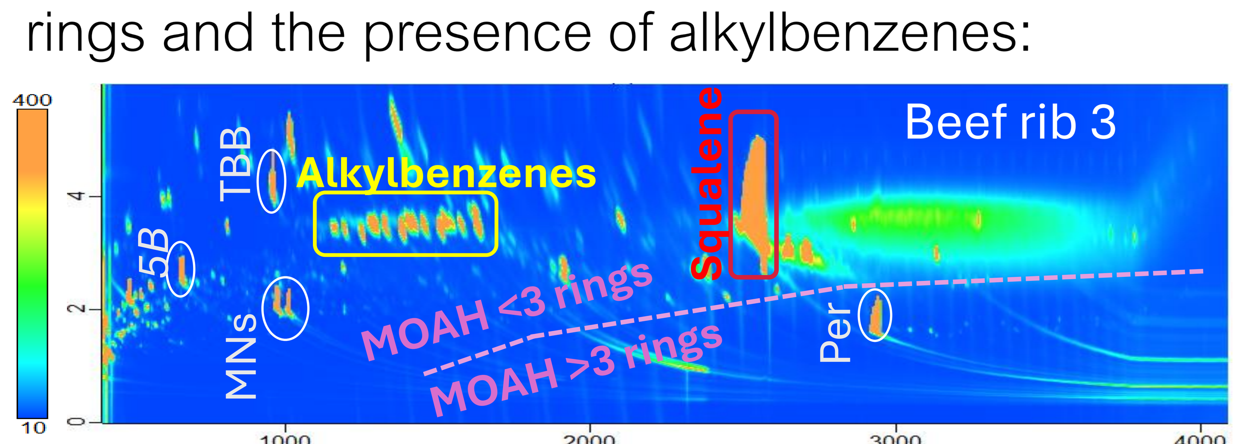
1 Optimization of sample preparation: The use of a 2M KOH in EtOH:H2O (1:1,v:v) [4] to perform the MASE showed a better performance than the method used in [3], as it led to a similar distribution of the different ISs between phases after saponification and to adequate MOSH and MOAH recoveries. Moreover, the use of GC×GC-FID and GC-FID provided similar results, which was already proven in [5].

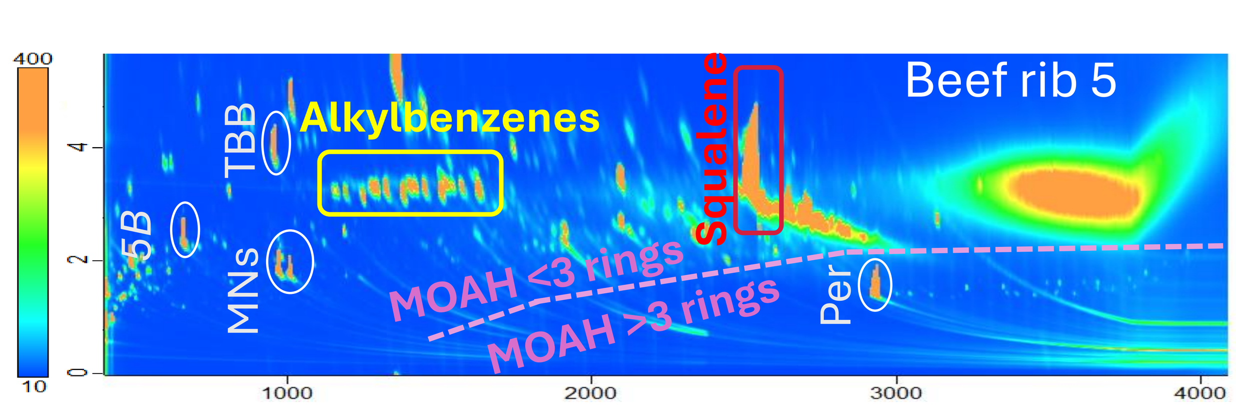
2 Analysis of MOH in meat: MOSH contamination was observed in most of the samples studied, whereas **MOAH** levels were quantifiable (>0.1 mg MOH/kg meat) only in two of them (beef 3 and 5). The GC×GC system allowed the separation of polyolefin oligomeric saturated hydrocarbons (**POSH**) from **MOSH** and, therefore, to **quantify them separately**.

Total levels of MOSH, POSH and MOAH

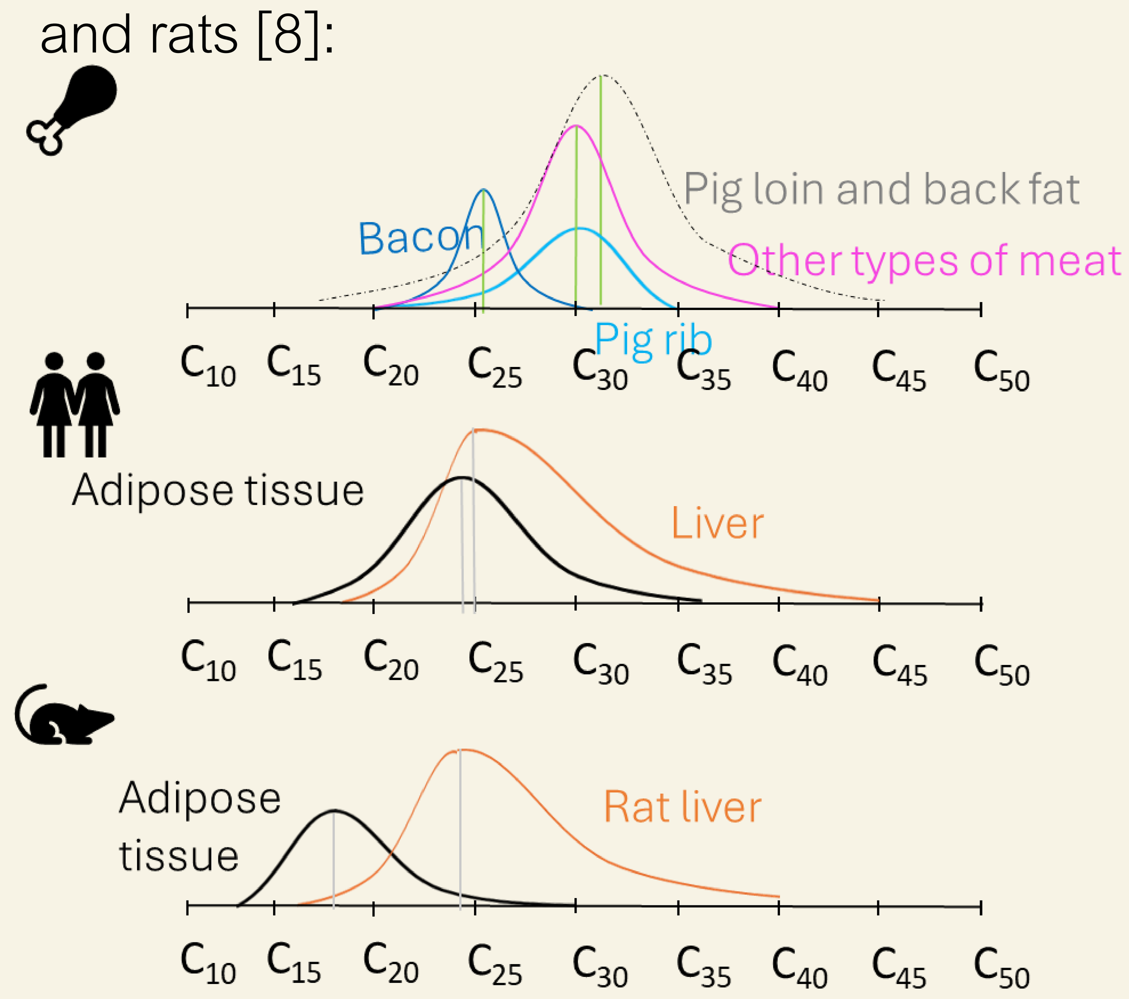


MOAH subclasses The GC×GC plots of the contaminated samples showed only MOAH with 1-2 rings and the presence of alkylbenzenes:



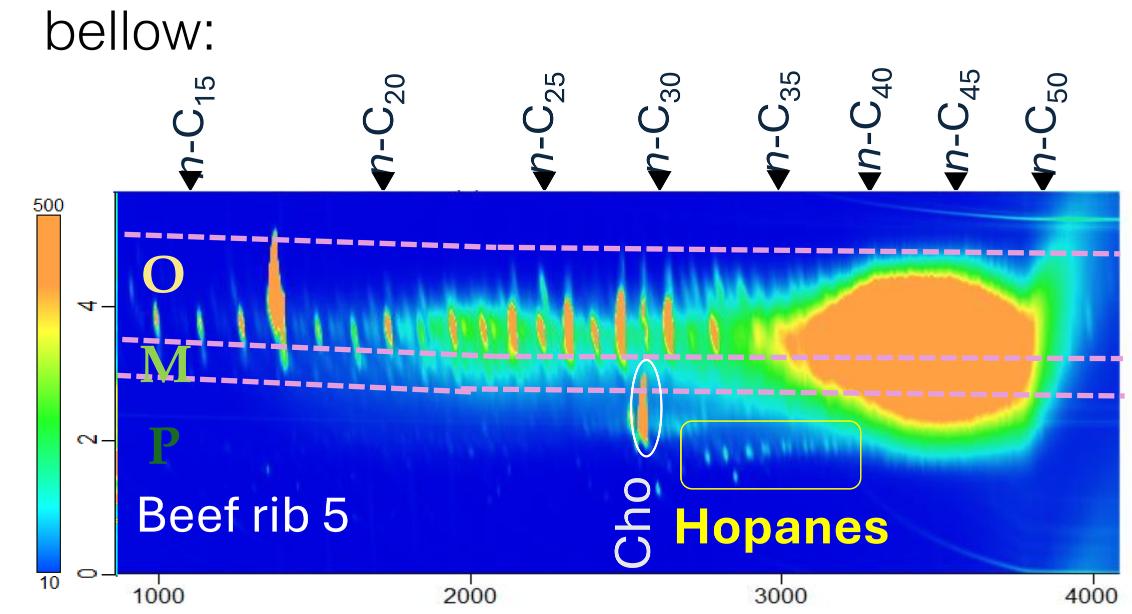


MOSH profile It was compared with the profiles retained in pig loin and back fat [6]; adipose tissues and livers from humans [7] and rats [8]:

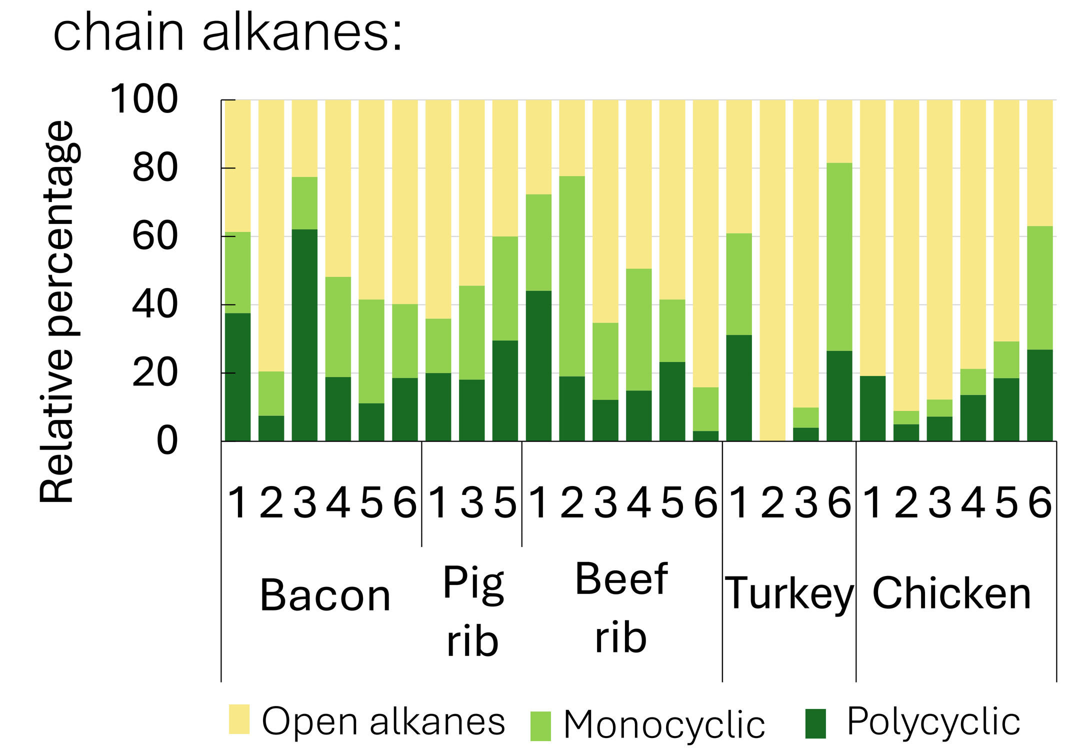


Most of the meat samples showed MOSH in a carbon chain length range that could have accumulated by the animals, showing that this could be one of the source of contamination. However, MOSH of higher carbon chain length (e.g. hopanes) were present in the samples with the highest MOSH levels (beef rib 3 and 5), suggesting a contamination post-mortem.

MOSH subclasses A classification was applied to the GC×GC chromatograms obtained for the meat samples as shown bellow:



No correlation was found between the composition of MOSH subclasses and the type of meat analysed; overall, MOSH were predominantly present as open-chain alkanes:



Conclusions: Meat samples showed varying levels of MOSH and exhibited diverse subclass profiles, with open-chain alkanes generally being the predominant type. The two samples with the highest MOSH levels (beef rib 3 and 5) also contained 1-2 rings MOAH. In both samples, the MOSH profile (characterized by long carbon chains, such as hopanes) along with the presence of MOAH and alkylbenzenes, suggested that contamination likely occurred post-slaughter, possibly during the cutting of meat into commercial portions.

References: [1] EFSA CONTAM Panel , J. EFSA 21 (2023) 1–143; [2] Bauwens, et al., ABC 415 (2023) 5067; [3] Albendea, et al., Animals 14 (2024) 1450; [4] Bauwens, Purcaro Anal. Chim. Acta 1312 (2024) 34278; [5] Bauwens, et al. Green Anal. Chem 4 (2023) 100047; [6] Albendea, et al. Animals 14 (2024) 1450; [7] Barp et al. FCT 72 (2014) 312; [8] Barp, et al, Sci. Total Environ. 575 (2017) 1263

Acknowledgments: The authors thank Milestone, LECO and Restek for their support This work is supported by ACESSS (Academic Center of Excellence for Separation Science and Sensing).