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To cite this version:

Laurent-Emmanuel Monfoulet, Caroline Buffière, Geoffrey Istas, Claire Dufour, Carine Le Bourvellec, et al.. Effect of apple food matrix on the distribution of plasma flavan-3-ols and on the nutrigenomic profile in the response to a nutritional challenge in minpigs. 13. European Nutrition Conference - FENS 2019, Oct 2019, Dublin, Ireland. 79 (OCE2), pp.E242-E242, 2019, 10.1017/S0029665120001901 . hal-02933429

HAL Id: hal-02933429

https://hal.inrae.fr/hal-02933429

Submitted on 8 Sep 2020

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Apple matrix modulates plasma flavan-3-ols concentration and nutrigenomic profile in a high fat challenge in minipigs

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INRA SCIENCE & IMPACT

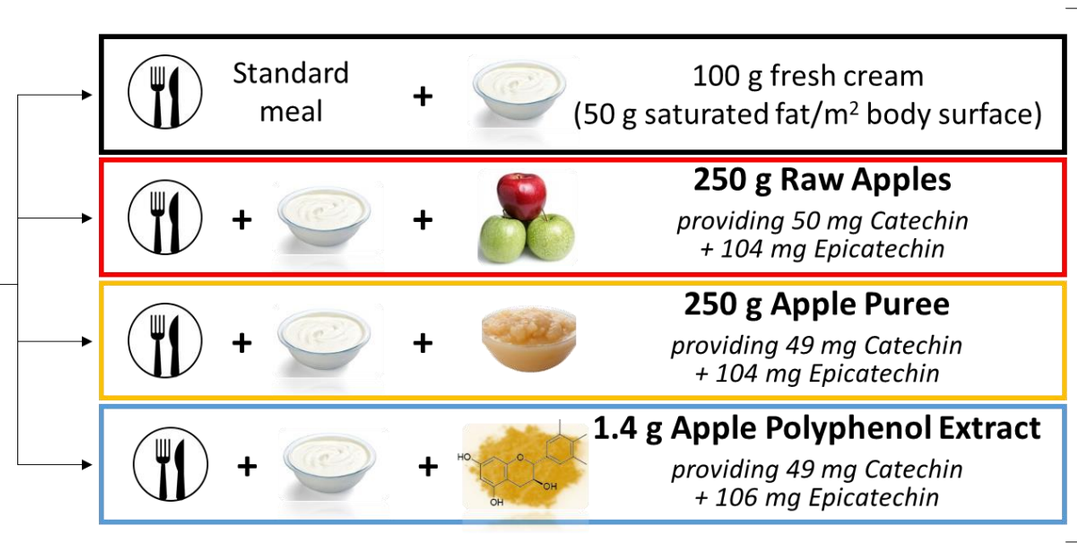
Food matrix is known to interact with some dietary constituents and microconstituents during digestion. These interactions may potentially affect the metabolism and bioavailability of some compounds such as **polyphenols**, and as a consequence modulate their biological effects. **The aim of this study was to examine the effect of the apple matrix on the bioavailability of flavan-3-ols and on the ability of these compounds to modulate the nutrigenomic response to a high fat challenge in minipigs.**

Methods

A randomized, cross-over nutritional intervention in minipigs.

- Energy supply : 1160-1290 kcal/meal.
- Wash-out period of 1 week between the intake of each 4 test meals.

Adult Male Yucatan (n=5)



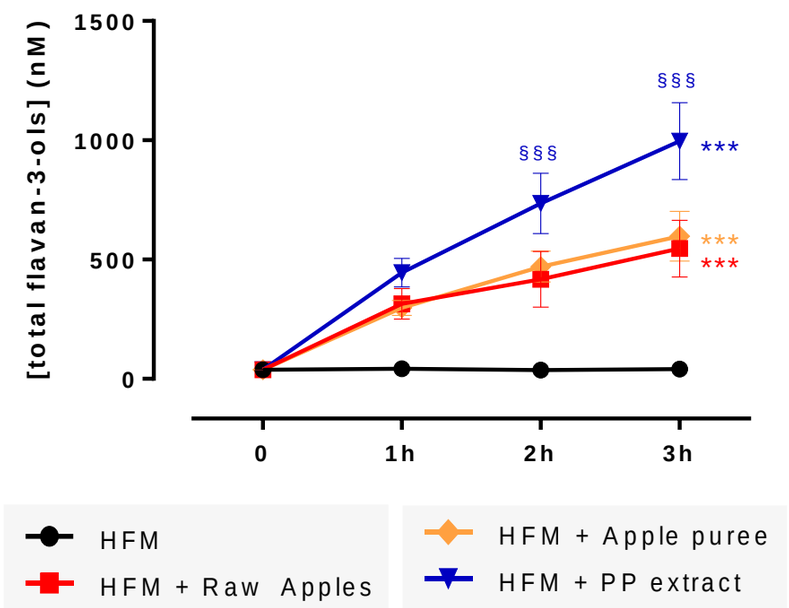
Fasting and 1h-, 2h-, 3h-Posprandial blood samples

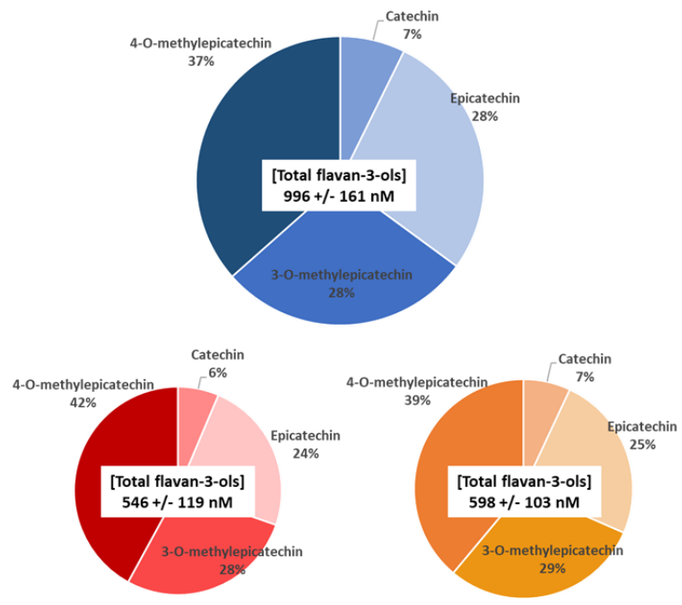
Serum
Quantification of flavan-3-ols monomers after enzymatic hydrolysis of glucuronide, sulfate conjugates (UPLC-Q-TOF MS)

Blood
Gene expression in Peripheral Blood Mononucleatic Cells (PBMCs) - (Microarray gene expression followed by bioinformatics analyses using GeneTrail2.0 and Metascape softwares)

Results

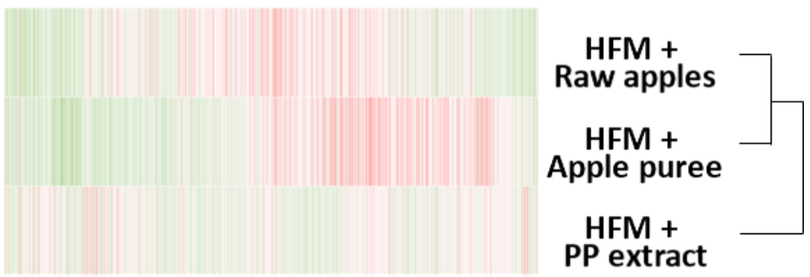
Postprandial plasma kinetic of monomeric flavan-3-ols in minipig serum





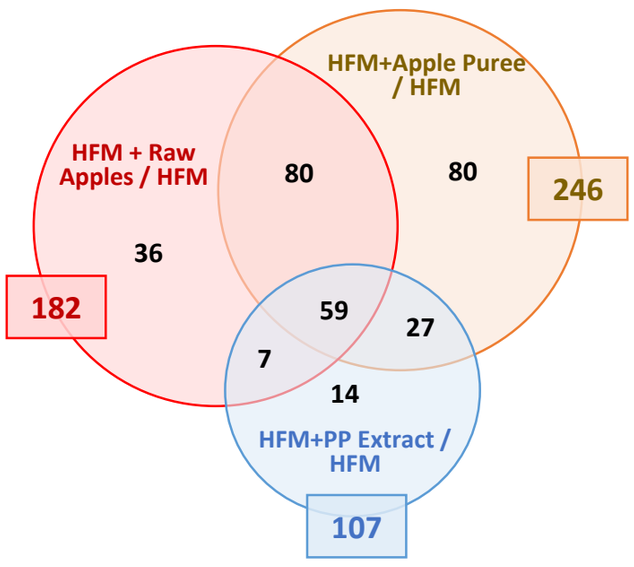
- Whatever the meal type:
  - the peak of total flavan-3-ol monomers was observed at 3h after the intake.
  - Methylated forms of Epicatechin constitutes the major circulating metabolites (65 to 70%)
- However, when compared to compounds **without matrix**, the total concentrations are **reduced by 40-50%, with raw apple and puree respectively, suggesting a reduction of intestinal absorption by food matrix**

3h-postprandial nutrigenomic response in porcine PBMCs



Hierarchical clustering dendrogram (build on significant gene expression compared to HFM).

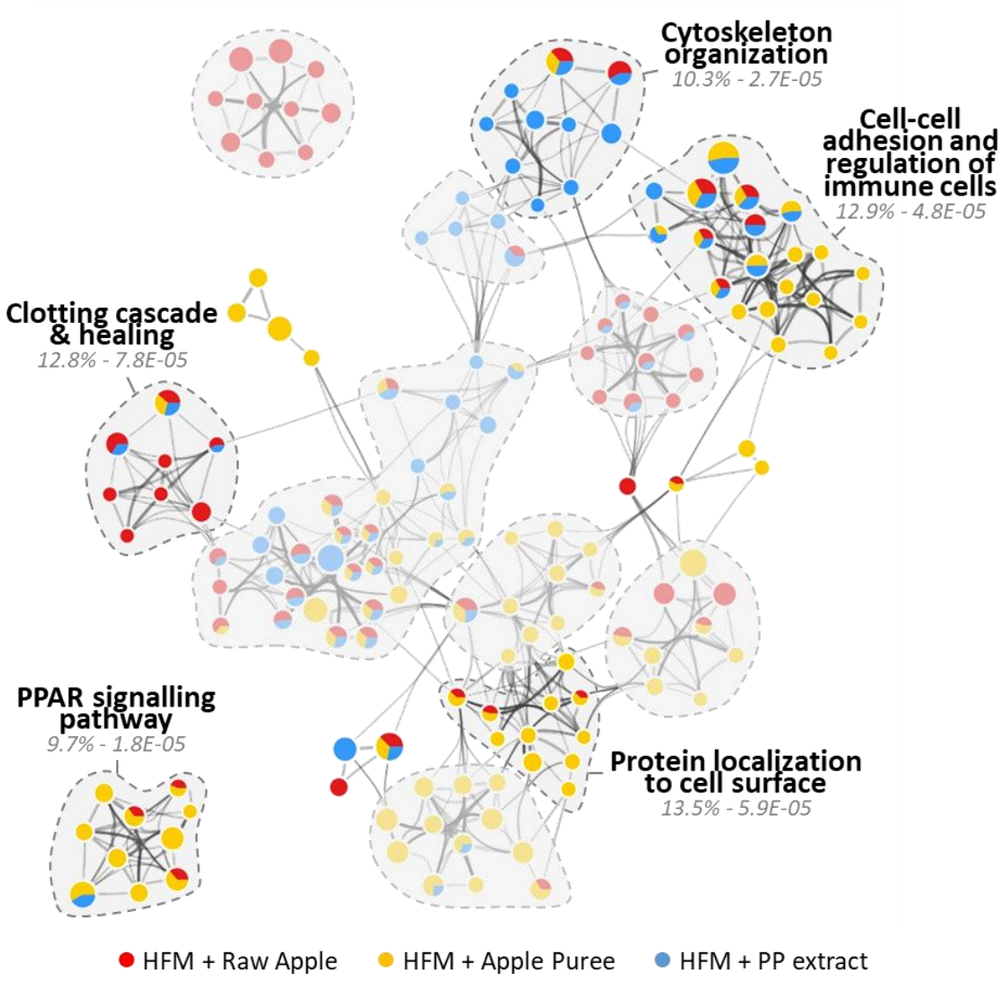
- 305 genes identified as differentially expressed in response to the supplementation with apple-derived products compared to HFM alone.
- The gene expression profile of "**HFM+PP extract**" group is **more distinct** than the profiles from the HFM+ raw apples and HFM+apple puree groups.



Number of differentially expressed genes.

- A higher number of gene changes is observed when food matrix is present, with 59 overlapping genes with PP extract.
- Among the 93 genes in common between PP extract and raw apples or apple puree, 74 genes exhibited similar changes with respect to HFM + PP extract

Biological processes revealed as affected by the differentially expressed genes after bioinformatics analysis



The Top5 biological processes affected by the apple products are involved mainly in clotting cascade, acute inflammation and leukocyte transendothelial migration.

Conclusion

The apple matrix reduced the postprandial bioavailability of flavan-3-ols without inducing any negative impact in the nutrigenomic response of PBMCs to flavan-3-ols. By contrast, additional genes were modulated in the presence of the apple matrix. Overall, the observed changes in gene expression could contribute to counteract the pro-inflammatory response induced by the intake of a high fat meal.