Metabolites in digestion fluids of pigs fed human diets: red versus white meat in the context of a prudent and western diet

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1. Introduction

Observational epidemiological studies have associated a high consumption of red and processed meat with a higher risk of developing chronic diseases¹, whereas no such associations are reported for the consumption of poultry. Traditionally, nutritional epidemiology focuses on single nutrient or food component intake and ignores the complexity of a human diet with many interacting components that may affect health in a multi-causal way. For example, fruits, vegetables and grains may contain protective compounds that could interfere in the causal pathways underlying the association of red meat consumption and chronic diseases². We therefore hypothesized that the dietary context may have a considerable impact on the formation of harmful compounds related to red and processed meat intake and hence the associated disease risk.

2. Approach

An untargeted mass spectrometry based metabolomics approach (UHPLC-HR-Q-Orbitrap-MS) and multivariate statistics were applied to explore the impact of chicken versus red & processed meat consumption in the context of a prudent and a western dietary pattern on the small and large intestinal metabolome of pigs used as a model for humans. Thirty-two piglets were subjected to a four week feeding experiment with four dietary treatments, all designed to mimic realistic human diets ('Prudent Chicken', 'Prudent Red', 'Western Chicken' and 'Western Red'). The piglets were euthanized and the luminal content of the small and large intestine were collected, homogenized and lyophilized before analysis.

3. Results

Data pre-processing with Compound DiscovererTM software resulted in 1851 and 1990 compounds for the small intestine and colon digests respectively. Multivariate statistical analysis using PCA-X score plots revealed good clustering for the digestion samples according to background diet. (O)PLS-DA models (Figure 1) comparing the relevant

dietary treatment groups were constructed and all differential metabolite-abundance analyses were performed using the R package *limma*. Tentative identification of the differentiating metabolites based on retention time, accurate mass and fragmentation profiles showed that mainly histidine derivatives were more abundantly present in the digestion fluids after chicken meat consumption, whereas, among others, carnosine and acylcarnitines were tentatively identified as red & processed meat associated colonic metabolites.

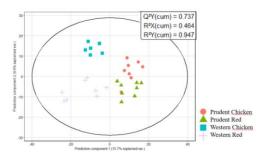


Figure 1. PLS-DA score plot of the large intestinal metabolome of pigs fed four different diets.

4. Discussion

Several of the tentatively identified metabolites have already been associated with meat intake in previous studies³, however, this study also revealed new interesting markers. The abundance of most meat associated metabolites seemed to be independent of the background diet. However, some metabolites such as long-chain acylcarnitines were highly affected by the background diet and showed the highest levels in the pigs fed the 'Western Red' diet.

References

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