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Dairy proteins' effect on metabolism in obese non-diabetics

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Objectives

- ❑ To investigate time-dependent changes in the metabolome following ingestion of different proteins from whey
- ❑ To identify protein specific markers
- ❑ To automatically group mother compounds, adducts and fragments

Intervention study

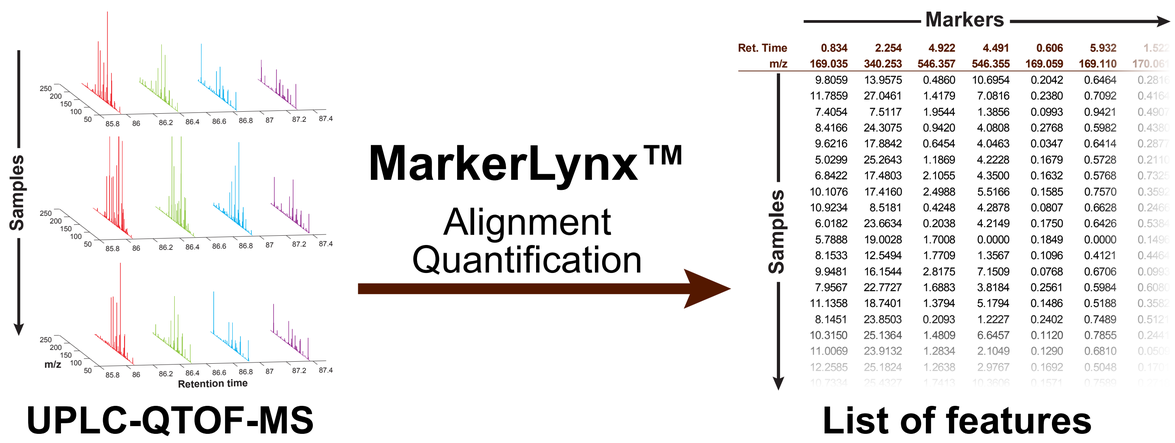
- Randomized single-blinded full crossover study
- 11 obese non-diabetic subjects
- Meals containing 80 g of fat, 45 g of carbohydrate and 45 g of protein
- The protein source was α-lactalbumin (ALPH), whey isolate (WI), whey hydrolysate (WH) or caseinoglycomacropeptide (CGMP)
- Blood samples drawn at five time points during 8-h postprandial period

Compound	T_r	$[M+H]^+$	Fragments, adducts and unknown features
	0.60		164.0
	0.60		180.0
	0.61	188.0	210.0
Proline	0.66	116.1	70.1
Methionine	0.95	150.1	133.0, 104.1, 87.0, 61.0
Tyrosine	1.11	182.1	165.1, 147.0, 136.1, 123.0, 119.1
	1.35		218.1
Isoleucine	1.36	132.1	263.2, 86.1, 69.1
	1.40		199.1
Mevalonolactone	1.42	131.1	
Phenylalanine	1.43	166.1	149. 1, 103.1, 120.1, 107.1, 93.1
	1.51		201.1
Tryptophan	1.52	205.1	409.2, 188.1, 170.1, 159.1, 146.1, 144.1, 132.1, 118.1, 100.1
γ-Glu Leu / γ-Glu Ile	1.61	261.1	244.1, 132.1
	2.37		247.1

List of features significantly different between meals

Conclusions

- ✓ Protein sources were differentiated based mainly on amino acid composition
- ✓ Strong markers of whey hydrolysate have been distinguished but remain to be identified
- ✓ Fragments, polymers and adducts were automatically grouped using a simple Matlab® algorithm



Detection of affected features using a mixed linear model

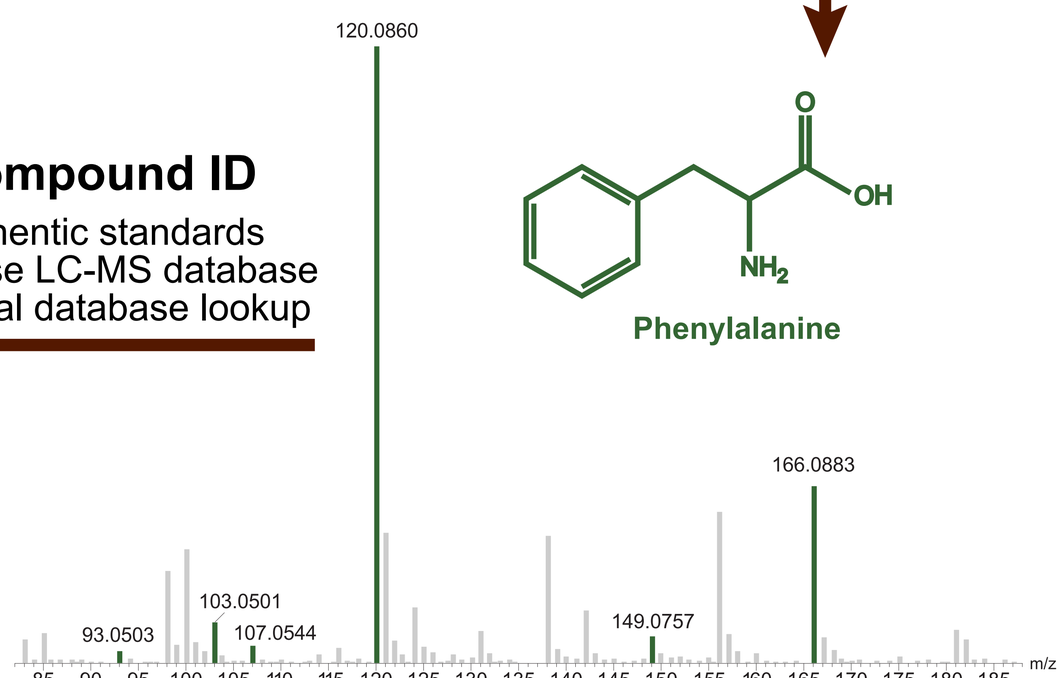
33 significantly different features reduced to 15 compounds

Automatic grouping of MS features

based on retention time and correlation across samples (in-house Matlab® function)

Compound ID

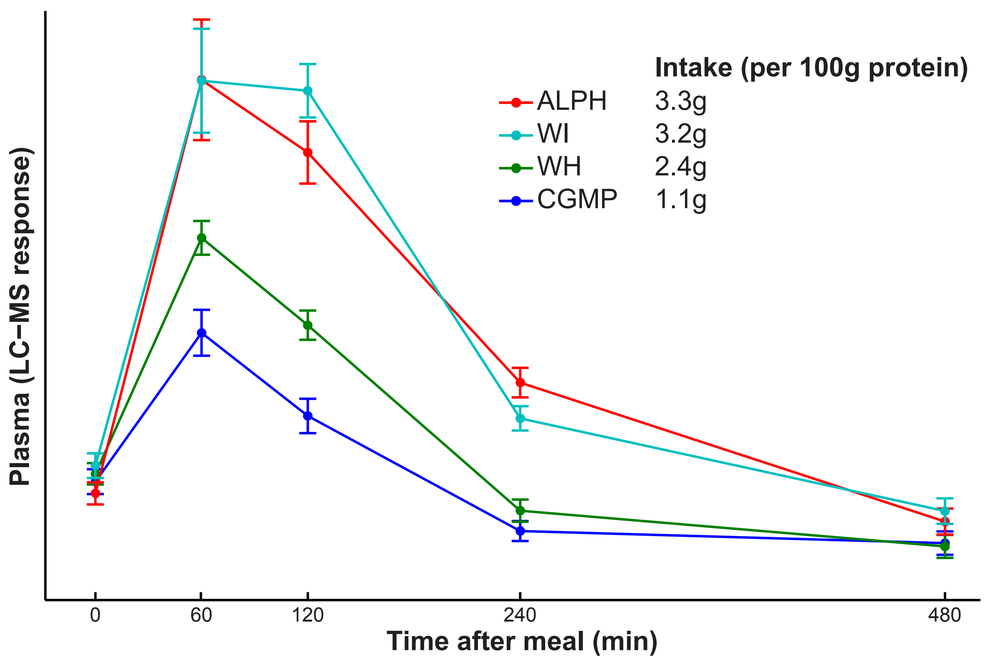
Authentic standards
In-house LC-MS database
External database lookup



Masses corresponding to phenylalanine

Results

- The features were dominated by amino acids (AAs)
- The AA composition in the protein sources was largely reflected in the blood levels of the individual AAs
- Approximately a 30 - 40 % change in intake of individual AAs could be detected with this method
- The aromatic AAs (Phe, Tyr, Trp) and mevalonolactone were found at a lower level for the CGMP group whereas the group had higher levels of Pro and Ile
- The different whey groups also showed different levels of AAs (as exemplified by phenylalanine to the right)
- Two markers with masses of 188 and 199 Da were 20 fold higher in plasma after ingestion of WH compared to the other protein sources



Kinetic profile for Phe extracted from metabolomics profiles. Error bars indicate the standard error of the mean