

Nutritional metabolomics: The search for dietary exposure variables

Akademisk avhandling

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av Millie Rådjursöga

Fakultetsopponent:

Henrik Antti, Professor
Umeå Universitet, Sverige

Avhandlingen baseras på följande delarbeten

- I. Rådjursöga, M., Karlsson, B. G., Lindqvist, H. M., Pedersen, A., Persson, C., Pinto, R. C., Ellegård, L., & Winkvist, A. *Metabolic profiles from two different breakfast meals characterized by ¹H NMR-based metabolomics*. Food Chem 2017; 231: 267-274.
- II. Rådjursöga, M., Lindqvist, H. M., Pedersen, A., Karlsson, B. G., Malmodin, D., Brunius, C., Ellegård, L., & Winkvist, A. *The ¹H NMR Serum Metabolomics Response of a Two Meal Challenge, a Cross-Over Dietary Intervention Study in Healthy Human Volunteers*. Submitted.
- III. Rådjursöga, M., Lindqvist, H. M., Pedersen, A., Karlsson, B. G., Malmodin, D., Ellegård, L., & Winkvist, A. *Nutritional metabolomics: Postprandial Response of Meals Relating to Vegan, Lacto-Ovo Vegetarian, and Omnivore Diets*. Nutrients 2018, 10(8), E1063; doi: 10.3390/nu1008106.3.
- IV. Pedersen, A., Rådjursöga, M., Malmodin, D. & Karlsson, B. G. *Improving deproteinization pre-processing throughput of NMR-based serum metabolomics*. Manuscript.

**SAHLGRENSKA AKADEMIN
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Nutritional metabolomics: The search for dietary exposure variables

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Abstract

To establish associations and causation between diet and health, objective and reliable methods are needed to measure dietary exposure. Metabolomics provide an unbiased tool for exploring the modulation of the human metabolome in response to food intake.

The aim of this doctoral thesis was to investigate the postprandial metabolic response in two cross-over meal studies using nuclear magnetic resonance (NMR) metabolomics. In addition, a methodological study with the aim to compare three pre-processing protocols for high-throughput NMR serum metabolomics for large samples series was included in the present work.

The meal studies aimed to investigate:

- (1) the postprandial metabolic response to two equicaloric breakfast meals, cereal breakfast (CB) and egg and ham breakfast (EHB) in serum and urine.
- (2) the postprandial metabolic response to breakfast meals corresponding to vegan (VE), lacto-ovo vegetarian (LOV) and omnivore (OM) diets in serum.

Metabolic profiles along with key discriminatory metabolites of biological relevance that largely reflected dietary composition were identified in both meal studies. Tyrosine and proline were found to discriminate for both the CB and LOV. Also valine was higher after the LOV compared to the VE and higher in the CB breakfast that had high dairy content. In turn, creatine, isoleucine, choline and lysine were discriminating for both the EHB and OM breakfasts in serum, that both contained comparably high content of animal protein. This implies that the metabolic response to meals high in dairy and meat can be reflected in metabolite concentrations irrespective of the total food matrix in a meal. In addition, coffee and tea consumption could be identified in urine. Comparing dilution, precipitation (methanol) and ultrafiltration as pre-processing deproteinization methods for serum, the precipitation protocol was found to be the method of choice for high-throughput NMR metabolomics for large sample series. Overall, our results demonstrate NMR metabolomics as an applicable method in the search of dietary exposure variables.

Keywords: metabolomics, nutrition, NMR, serum, urine, postprandial, dietary intake

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