



Integrative data analysis of genotype, microbiome and metabolomics for prediction of response to diet for improved metabolic health

Nielsen, Rikke Linnemann; Helenius, Marianne; Muktupavela, Rasa; Jensen, Cecilia Bang; Hansen, Lea Benedicte Skov; Roager, Henrik Munch; Søndertoft, Nadja B.; Vestergaard, Henrik; Hansen, Torben; Bahl, Martin Iain; Pedersen, Susanne Brix; Kristiansen, Karsten; Licht, Tine Rask; Lauritzen, Lotte; Pedersen, Oluf; Gupta, Ramneek

Publication date:
2018

Document Version
Peer reviewed version

[Link back to DTU Orbit](#)

Citation (APA):

Nielsen, R. L., Helenius, M., Muktupavela, R., Jensen, C. B., Hansen, L. B. S., Roager, H. M., ... Gupta, R. (2018). Integrative data analysis of genotype, microbiome and metabolomics for prediction of response to diet for improved metabolic health. Abstract from Manipulation of the Gut Microbiota for Metabolic Health (X3), Keystone symposia, Banff, Alberta, Canada.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

**Abstract for
2018 Keystone Symposia Conference
X3: Manipulation of the Gut Microbiota for Metabolic Health
Dates: March 4 - March 8, 2018
Location: Fairmont Banff Springs, Banff, Alberta**

Integrative data analysis of genotype, microbiome and metabolomics for prediction of response to diet for improved metabolic health

Rikke Linnemann Nielsen¹, Marianne Helenius¹, Rasa Muktopavela¹, Cecilia Bang Jensen¹, Lea Benedicte Skov Hansen¹, Henrik Munch Roager³, Nadja Buus Søndertoft⁴, Henrik Vestergaard⁴, Torben Hansen⁴, Martin Iain Bahl³, Susanne Brix⁵, Karsten Kristiansen⁶, Tine Rask Licht³, Lotte Lauritzen², Oluf Pedersen⁴, Ramneek Gupta¹.

1 Department of Bio and Health Informatics, Technical University of Denmark.

2 Department of Nutrition, Exercise and Sports, University of Copenhagen.

3 National Food Institute, Technical University of Denmark.

4 The NNF Center for Basic Metabolic Research, University of Copenhagen.

5 DTU Bioengineering, Technical University of Denmark.

6 Department of Biology, University of Copenhagen.

Diet is known as an important factor for metabolic health. This study investigated the impact of a whole grain-rich diet (75 g/d)/gluten-poor diet (< 2g/d) or refined grain diet (< 10g/d) on metabolic health in 102 healthy adult participants with a metabolic risk profile (40 male, 62 female). Intervention diets were consumed for 8 weeks followed by the opposite diet after an at least 6 weeks 'wash-out' period. Anthropometric measurements, biochemical blood samples, gut microbiome profiling, urine metabolites and host genetics were obtained in the beginning and end of each intervention. The whole grain-rich and gluten-poor diets induced statistically significant weight loss on the groups. However, response to diet is not universal across all individuals and is suggested to be influenced by a complex interplay between the host genome, gut microbiota and environment [1]. To further study personal response to diet, we integrated in this post hoc analysis data into machine learning models to predict weight loss from baseline markers (204 observations). The work is ongoing and identification of metagenomic species' interaction with host genotype and metabolite changes are expected to generate hypotheses of the personal response to diet using feature importance. Integration strategies are evolving and have involved use of top predictive features for each data type or pre-selecting features based on pathway information. The machine learning framework indicates that differences in the baseline gut microbiota partly explain the observed host physiological response. In addition to the weight loss, we are also examining immune markers as additional indicators of metabolic health outcome.

References

[1] Dabrowska et al, 2016. PMID: 27625642.