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

Rikke Linnemann Nielsen¹, Marianne Helenius¹, Rasa Muktupavela¹, 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 Licht⁵, 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