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Postprandial response of the blood metabolome and transcriptome of normal weight and obese men to increasing doses of a meal

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Abstract

Introduction. Validation of biomarkers reporting on the intake or bioactivity of foods requests that the dose-response behaviour of relevant nutrients be known. Establishing this relationship is, however, challenging because of the complex composition of foods. In addition, humans respond differently to caloric intake depending on their metabolic health. By allowing the measure of multi-molecular profiles, omics technologies provide better insights into these issues. We have previously measured the response of the blood cell transcriptome of normal weight (NW) and obese (OB) men to increasing caloric doses of a high-fat meal (HFM). We now describe the dose-response of the serum metabolome of these subjects and discuss the results in light of the transcriptomic response.

Material and Methods. In a randomized crossover study, we challenged 19 NW and 18 OB men with 500, 1'000, and 1'500 kcal HFM. The blood cell transcriptome was measured before and 2, 4, and 6 h after meal ingestion. The untargeted serum metabolome was assessed at the same time points. The genes and metabolites responding postprandially in a dose-dependant manner were identified.

Results. Among the 1'385 features with a postprandial response, 178 showed a significant dose-response between meals. A majority of them increased (amino acids, bile salt conjugates, metabolites in urea cycle), whereas circa one fifth, indicative of an endogenous response, decreased (e.g. carnitine esters). Overall, the postprandial metabolome showed caloric saturation, the metabolome after 1'500 kcal HFM being quantitatively only marginally different than after 1'000 kcal. Although a subset of metabolites responded differently to the caloric increase, the postprandial metabolomes of NW and OB subjects were, overall, mostly characterized by their similarity. This finding contrasted with the blood cell transcriptome, which identified a subset of OB subjects whose expression of genes of the oxidative phosphorylation pathway was, compared to the NW subjects, more increased after ingestion of 1'500 kcal HFM.

Discussion. We report, for the first time, the response of the human serum metabolome to increasing caloric doses of a meal. The saturation observed between 1'000 and 1'500 kcal reflects on the control mechanisms regulating the metabolites entering the blood circulation. Interestingly, combining the analysis of the serum metabolome with the blood cell transcriptome indicated that the elevated cellular oxidative response to 1'500 kcal HFM in a subset of OB subjects results from a dysregulation of systemic cellular mechanisms in response to food intake, rather than from changes in gastrointestinal processing.

Conflict of Interest

There is no conflict of interest