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Editorial on Food-related Metabolites Variation during Pregnancy

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Editorial

Due to the complex nature of food exposure and the reliance on self-eporting, accurate assessment of dietary intake remains a major challenge in human nutrition research. While the majority of studies use self-reported dietary intake methods such as Food Frequency Questionnaires (FFQ), 24-hour dietary recalls, and food records, they are susceptible to recall, misclassification, and measurement biases .To address this issue, metabolomics-the global analysis of low molecular weight metabolites in biological samples is increasingly being used in large-scale epidemiological studies to discover and validate food intake biomarkers. Biomarkers, which account for nutrient bioavailability and metabolism, can provide a more objective assessment of food exposures than self-reported dietary intake. An ideal biomarker [1-3] of food intake is one that can be easily measured at the population level in human biofluid (blood or urine), is highly specific for one food item or food group, has a dose- and time-dependent response, and is not extensively transformed by the microbiota and host tissue upon consumption.

However, there are complex interpretative challenges because nutrients are derived from a variety of food sources and can exhibit intercorrelation with other metabolic processes. Furthermore, the human metabolome varies due to intrinsic physiologic characteristics like age, sex, hormonal levels, and the gut microbiome, as well as extrinsic factors like habitual diet and lifestyle. Furthermore, many putative biomarkers of food intake do not come from a single food or nutrient. Trimethylamine N-oxide (TMAO), for example, is formed from a TMA-containing nutrient such as choline, which is abundant in fish, beef, and eggs, but it can also be produced from carnitine in red meat. Furthermore, many gut-microbiome-dependent metabolites and other food-specific metabolites are metabolised at different rates in the liver, depending on hepatic enzyme activity, which may contribute to the higher variability observed in the metabolite range measured in biological samples. As a result, it is critical to identify potential non-dietary sources of food-related biomarkers and assess how well these factors explain differences in metabolite concentration.

Carefully designed studies examining the relationship between non-dietary factors and biomarker concentrations are scarce, particularly in pregnant women. Observational studies, particularly birth cohort studies, are effective methods for learning about pregnancy risks and outcomes. During pregnancy, women undergo a series of metabolic changes that are likely influenced by pre-pregnancy and intrapartum factors, which may affect maternal health and disease during critical stages of foetal development. Furthermore, metabolite concentrations during pregnancy and pre-pregnancy, as well as pregnancy-related factors such as GDM differ between ethnic groups. At 24-28 weeks gestation, the maternal dietary intake was collected. Semi-quantitative [4,5] validated food-frequency questionnaires (157 items for the FAMILY and 163 items for the START) developed and validated as part of the SHARE Study were used.

Participants were asked to report on their average frequency (daily, weekly, monthly, yearly, or never) and serving size of each food or food group over the previous 12 months. The FFQ was also used to estimate fiber intake and total energy intake. Prior to inclusion in the regression analysis, data were logarithm-transformed to correct for skewness, and nutrient intakes were adjusted for energy intake using the residual approach. On targeted profiling of polar/ionic metabolites measured consistently in serum filtrate samples with stringent Quality Control (QC). A standardized method protocol was used for the identification and quantification of the maternal serum metabolome, as described in more detail elsewhere. Six metabolites, including proline betaine, 3-methylhistidine, hippuric acid, TMAO, carnitine, and tryptophan betaine, were chosen from among those consistently measured in the two cohorts for our current study because they were previously linked to self-reported dietary intake.

They also provide a mix of evidence (good, fair, or poor) for candidate biomarkers of food intake that are produced exogenously, endogenously, bio transformed by gut micro biota, and/or derived from multiple food sources. The reference intervals for these serum metabolites in various birth cohorts from across Canada, as well as their technical/biological variance and interclass correlation coefficients, have previously been reported. Continuous data were summarized using mean and standard deviation (SD) or median and interquartile range (IQR) (IQR). Random-effects hierarchical linear models (HLM) were fitted, in which each natural logarithm-transformed food-metabolite concentration was regressed on dietary and non-dietary factors after controlling for other covariates such as total energy intake (kcal), total fiber intake (g/day), and time between the day FFQ information was collected and blood was drawn (FFQ before blood, FFQ after blood, and both taken on the same day).

Conflict of Interest

None.

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