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Diet quality, fibre intake and the gut microbiota of mothers and babies in the 'BABY1000' prospective birth cohort study

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Pregnancy prompts a cascade of anatomical, metabolic, hormonal, and immunological adaptations important for foetal development, labour and birth[1]. These multi–system adaptations interact with the maternal gut microbiome and may affect pregnancy and infancy outcomes[2]. However, the nature and extent of changes to gut microbiome composition and diversity during pregnancy and the influence of dietary intake remains contentious. The 'BABY1000' pilot prospective birth cohort study based in Sydney, Australia[3] sought to explore associations between maternal diet, the maternal gut microbiome before and across pregnancy, and the infant gut microbiome. Primary aims were to (1) explore the composition and diversity of the gut microbiome of women at preconception, at 12-, 28- and 36-weeks' gestation, and in infants at six weeks of age; and (2) determine how maternal and infant gut microbiomes are influenced by diet quality and fibre intake during pregnancy. Mothers (n = 146) and infants (n = 105), encompassing 86 mother–infant dyads were involved. RStudio (v 4.2.3) was used to perform microbiome composition and diversity analyses using 350 maternal and 102 infant stool samples. Maternal dietary quality was assessed at recruitment (preconception or 12 weeks' gestation) and at 36 weeks' gestation using the Australian Eating Survey (AES)[4]. At the group level, maternal dietary quality was suboptimal and did not change significantly across pregnancy (mean scores of 37.5 ± 7.3 and 38.3 ± 6.7 out of 73 points at recruitment and late pregnancy, respectively; $p > 0.05$). Although differences in gut microbiome alpha (within–person) diversity between mothers and infants was highly significant ($p < 0.0001$), no differences in gut microbiome composition or diversity related to pregnancy status or gestational stage were observed. Maternal diet quality in pregnancy was also not significantly correlated with microbial beta (between–people) diversity in samples taken in late pregnancy (PERMANOVA: $R^2 = 0.039$, $p > 0.05$). When fibre intake was separated into quartiles, there was a significant ($p < 0.01$) difference in alpha diversity between the lowest and highest quartiles of intake, though differences in beta diversity were not significant (PERMANOVA: $R^2 = 0.06$, $p > 0.05$). Microbiota composition and diversity in infant samples was also not significantly affected by maternal dietary quality or fibre intake, but rather by birth mode and feeding type. Significantly different clustering of infant samples was clear between vaginal and caesarean births (PERMANOVA: $R^2 = 0.029$, $p = 0.005$). Gut bacterial alpha diversity was significantly lower ($p < 0.01$) between infants receiving breastmilk compared to formula. As this area of research is still in its 'infancy', appropriately powered longitudinal studies are required to understand the processes that shape diet and microbiome interactions during the critical first 1,000 days of life and beyond.

References

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