

## Gut microbiota composition is similar between overweight and obese pregnant women with healthy and less healthy dietary intake patterns

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Dietary intake is a major determinant of gut microbiota composition in healthy adults.<sup>(1)</sup> Associations between the composition of the gut microbiota and specific macro- and micro-nutrients have been established in pregnancy.<sup>(1, 2)</sup> However, food and nutrients are not consumed in isolation but as part of a varied diet with complex nutrient interactions and synergistic effects.<sup>(3)</sup> Dietary patterns can be used to present a comprehensive and real-world understanding of the effect of diet on health beyond a reductive focus on single nutrients or foods.<sup>(4)</sup> Short- and long-term dietary patterns have been associated with gut microbiota composition in healthy adults.<sup>(5)</sup> No literature exists examining dietary patterns and gut microbiota composition in pregnancy. This cross-sectional study aimed to investigate the associations between two diet quality scores adapted from the Australian Recommended Food Score (ARFS) and the Mediterranean Dietary score (MDS) with the composition of the gut microbiota in overweight and obese pregnant women at 28 weeks' gestation. Women from the Study of Probiotics IN Gestational diabetes (SPRING) who had completed a food frequency questionnaire ( $n = 395$ ) were classified according to three tertiles of ARFS and the MDS. Higher dietary pattern scores in both the ARFS and the MDS represented better dietary guideline adherence with these patterns. Gut microbiota composition was assessed using 16S rRNA gene amplicon sequencing and analysed using Microbiome Analyst in a subset of 196 women with faecal samples. The results showed that higher adherence to the dietary patterns defined by the ARFS and MDS was not associated with gut microbiota composition in overweight and obese pregnant women in early third trimester of pregnancy. No significant differences were found in alpha or beta diversity between the tertiles of the ARFS and the MDS. Additionally, there was little difference across tertiles; even the highest tertile for the MDS and the ARFS had insufficient fibre and dietary diversity. Out of a maximum possible score of 14 for grains in the ARFS, the mean score was 4.1 and the mean fibre intake was 19 g/day (compared with the recommended 28 g/day). These results are in line with previous results from the Australian Longitudinal Study on Women's Health and the Queensland Family Cohort. It is possible that other factors including pregnancy hormones may overshadow any dietary impact on the gut microbiota, although a lack of diet diversity and low fibre intake or other confounding factors such as high BMI may also be mitigating the effects of diet on microbiota composition.

### References

1. Garcia-Mantrana I, Selma-Royo M, Alcantara C, et al. (2018) *Front Microbiol* **9**, 890.
2. Gomez-Arango LF, Barrett HL, Wilkinson SA, et al. (2018) *Gut Microbes* **9** (3), 189–201.
3. Hoffmann K, Schulze MB, Schienkiewitz A, et al. (2004). *Am J Epidemiol* **159** (10), 935–944.
4. Hu FB (2002) *Curr Opin Lipidol* **13** (1), 3–9.
5. Zmora N, Suez J & Elinav E (2019) *Nat Rev Gastroenterol Hepatol* **16** (1), 35–56.