

CHANGES IN INFANT GUT MICROBIOTA ASSOCIATED WITH MATERNAL OBESITY

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Background: Maternal obesity may influence infant gut microbiota, affecting long-term health. This study examined its effects on microbial composition, metabolism, and antibiotic resistance in infants over six months.

Methods: Twenty-four mother–infant pairs were grouped by maternal BMI: obese (BMI > 36, n=35 samples) and normal-weight (n=42 samples). Infant stool samples, collected at birth, 1, 3, and 6 months, underwent shotgun metagenomic sequencing. Taxonomic profiles (MetaPhlAn 4), metabolic pathways (HUMAN 3), and antibiotic resistance genes (CARD/ABRicate) were analyzed.

Results: Infants of obese mothers showed lower alpha-diversity at 1 month ($p \leq 0.01$) and a higher

Firmicutes/Bacteroidetes ratio, peaking at 3 months ($p \leq 0.001$). Metabolic analysis indicated enhanced carbohydrate metabolism in the normal-weight group ($p \leq 0.001$) and increased lipid biosynthesis in the obese group ($p \leq 0.0001$). Strong correlations were found between Lactobacillales and fatty acid biosynthesis ($r=0.7$, $p \leq 0.0001$) and Firmicutes and lincosamide resistance ($r=0.8$, $p \leq 0.0001$).

Conclusion: Maternal obesity significantly alters infant gut microbiota, reducing early diversity and shifting metabolic and resistance profiles. These changes may impact metabolic and immune health, highlighting potential targets for interventions to mitigate long-term risks like obesity.